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

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Abstract:	Although seed represents an important means of plant pathogen dispersion, the seed-pathogen dialogue remains largely unexplored. A multi-omic approach (*i.e.* dual RNAseq, plant small RNAs and methylome) was performed at different seed developmental stages of common bean (*Phaseolus vulgaris* L.) during asymptomatic colonization by *Xanthomonas citri* pv. *fuscans* (*Xcf*). In this condition, *Xcf* did not produce disease symptoms, neither affect seed development. Although, an intense molecular dialogue, via important transcriptional changes, was observed at the early seed developmental stages with down-regulation of plant defense signal transduction, via action of plant miR, and upregulation of the bacterial Type 3 Secretion System. At later seed maturation stages, molecular dialogue between host and pathogen was reduced to few transcriptome changes, but marked by changes in DNA methylation of plant defense and germination genes, in response to *Xcf* colonization, potentially acting as defense priming to prepare the host for the post-germination battle . This distinct response of infected seeds during maturation, with a more active role at early stages refutes the widely diffused assumption considering seeds as passive carriers of microbes. Finally, our data support a novel plant-pathogen interaction model, specific to the seed tissues, which differs from others by the existence of distinct phases during seed-pathogen interaction with seeds first actively interacting with colonizing pathogens, then both belligerents switch to more passive mode at later stages. We contextualized this

	observed scenario in a novel hypothetical model that we called "ceasefire", where both the pathogen and the host benefit from temporarily laying down their weapons until the moment of germination.

Supplementary Data S1.xlsx
Supplementary Data S3.xlsx

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

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Summary

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

maturation, with a more active role at early stages refutes the widely diffused assumption considering seeds as passive carriers of microbes.

- Finally, our data support a novel plant-pathogen interaction model, specific to the seed tissues, which differs from others by the existence of distinct phases during seed-pathogen interaction with seeds first actively interacting with colonizing pathogens, then both belligerents switch to more passive mode at later stages. We contextualized this observed scenario in a novel hypothetical model that we called "ceasefire", where both the pathogen and the host benefit from temporarily laying down their weapons until the moment of germination.

Key words: Seed, *Xanthomonas*, transmission, dialogue, epigenome, *Phaseolus vulgaris*, dual transcriptomics.

Introduction

Legumes provide a sustainable source of proteins for human and livestock diet, moreover their symbiotic nitrogen fixation capacity contributes to soil preservation and reduces the need for chemical fertilizers (Stagnari et al., 2017; Ferreira et al., 2021). An important factor limiting legume utilization is their relatively high yield variability, greatly due to their susceptibility to environmental factors such as biotic and abiotic stresses (Cernay et al., 2015; Martins et al., 2020). While legumes are expected to better perform under changing climatic conditions in relation to other crops thanks to higher biomass accumulation under increased atmospheric CO_2 levels and higher photosynthetic efficiency under increased irradiation levels, other traits are predicted to be negatively affected, such as seed quality and resistance to pathogens (Myers et al., 2014).

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

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

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

Materials and Methods

Bacterial strain and inoculum preparation

The *Xcf* bacterial strain 7767R (Rif^R, Darrasse et al., 2018) was grown for 24h at 28°C in Tryptic Soy Agar at 10% (1.7 g.L^{-1} tryptone, 0.3 g.L^{-1} soybean peptone, 0.25 g.L^{-1} glucose, 0.5 g.L^{-1} NaCl, 0.5 g.L^{-1} K_2HPO_4 and 15 g.L^{-1} agar) supplemented with 50 mg.L^{-1} rifamycin.

Bacterial cells were suspended in sterile distilled water, calibrated at 10^8 CFU.mL^{-1} (OD_{600} = 0.1) and adjusted to 10^6 CFU.mL^{-1} for spray-inoculation.

Plant materials and production of contaminated seeds

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

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

Monitoring of bacterial population sizes

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

Seed physiological analyses

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

Plant and bacterial RNA extraction and RNA sequencing

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

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

Using the same seed lots as for plant RNAs, bacterial macerates were collected after soaking contaminated seeds (2 mL per gram of seed) overnight in KPO_4 buffer, (50 mM, pH 6.8), supplemented with 20% of blocking agent (RNAlater, Thermofisher scientific, Carlsbad, CA, United States). After centrifugation (15 min at 15,000 *g*) and removal of the supernatant, total RNAs were extracted as previously described (Darsonval et al., 2009). Concentration and integrity of RNAs were assessed with Qubit (Invitrogen, Carlsbad, CA, USA) and a 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA), respectively. As total RNA extracted from bacterial macerates corresponded mainly to plant transcripts (not shown), we designed a procedure of bacterial transcript enrichment. Bacterial mRNAs were captured using the SureSelectXT RNA Direct technology (Agilent, Santa Clara, CA, USA). A total of 54,548 probes of 120-nts length were designed based on the predicted mRNAs of *Xcf*7767R genome sequence (GCA_900234465; Chen et al., 2018). Quality and quantity of sequencing libraries were evaluated and quantified using Bioanalyzer and KAPA Library Quantification assay (Roche, Basel Switzerland). Paired-end sequencing (2 × 75 bp) was performed with a NextSeq 550 System High OutPut kit (Illumina, San Diego, CA, USA). Raw reads are available at GSE227386.

After quality control, high-quality reads were mapped either on *Xcf* 7767R transcriptome (Briand et al., 2021) (https://bbric-pipelines.toulouse.inra.fr/myGenomeBrowser?browse=1&portalname=Xcf7767Rpb&owner=armelle.darrasse@inrae.fr&key=TwzQ08DA) or on *P. vulgaris* transcriptome version 2.1 (https://phytozome-next.jgi.doe.gov/info/Pvulgaris_v2_1) using quasi-mapping alignment and quantification methods of Salmon algorithm v.1.2 (Patro et al., 2017). RNA-Seq data were normalized as transcripts per million (TPM). Differentially expressed genes (DEGs) were determined using DESeq2 v1.22.2 (Love et al., 2014), using an adjusted p-value <5%. *Xcf* DEGs were analyzed between sampling dates. *P. vulgaris* DEGs were obtained by comparing *Xcf*- versus H_2O-inoculated seeds at each developmental stage. Gene annotations were provided with the *P. vulgaris* version 2.1 genome and Mapman functional categories v.4 were determined using Mercator tool from the predicted protein sequences (Schwacke et al., 2019). Bacterial Type III effectors were predicted using the automated machine-learning based web server Effectidor (Wagner et al., 2022). Over representation analyses of MapMan or COG terms were performed, respectively for plant and bacteria DEGs, using Clusterprofiler (Yu et al., 2012) package in R by applying an adjusted *p*-value cut-off <0.05 obtained after the Bonferroni-Hochberg procedure.

Differentially expressed genes during seed germination were identified using the data generated by Narsai et al. (2017) available in the SRA database (accession GSE94457). Raw reads were downloaded and mapped against the Arabidopsis transcriptome using Salmon algorithm and DEGs during germination kinetic were determined using ImpulseDE2 algorithm (Fischer et al., 2018) following an adjusted *p*-value <1%.

To determine genes involved in post-germination defense, we inoculated healthy seeds with 10^7 of *Xcf* CFU.mL^{-1} or H_2O during 25 min followed by 3 min of vacuum infiltration before seed drying at room temperature. Inoculated dried seeds displaying between 10^4 and 10^5 CFU.seed^{-1} of *Xcf* were used for germination assay on Whatman paper in 16h-light growth chamber at 25°C. *Xcf*- and H_2O-inoculated seeds were collected at 3 and 7 Days After Imbibition (DAI) and dissected as separated cotyledons and radicles for real-time qRT-PCR experiments. RNA were extracted at different germination timepoints and in different tissues using the NucleoSpin® RNA Plant and Fungi Kit (Macherey-Nagel, Düren, Germany) as described above but including a DNAse treatment (Macherey-Nagel, rDNAse set, Düren, Germany). RNA were quantified using a using a NanoDrop ND-1000 (NanoDrop Technologies, Wilmington, DE, USA) and cDNA was synthesized from 1 µg of total RNA using the Reverse Transcription system (iScriptTM cDNA synthesis kit, Bio-Rad). Quantitative Real time PCR was performed using Sybr Green Master Mix (SYBR Green master mix, Bio-Rad) on a CFX96 real-time detection system (Bio-Rad Laboratories). *EF1* and *UBI* genes were used as housekeeping genes as described in Darrasse et al. (2010). Primers used for Real-time PCR are listed in Supplementary Table S4.

small RNA extraction and analysis (sRNA-seq)

Using the same frozen powders obtained from *Xcf*- and H_2O-inoculated seeds from 24 DAP and 42 DAP, we extracted small RNA using the NucleoSpin® miRNA Kit (Macherey-Nagel, Düren, Germany), according to the manufacturer's instructions. Small RNA enrichment was validated using Bioanalyzer small RNA analysis. Small RNAs were sequenced using DNBseq sequencing technology (SE50 40M, BGI) and Unique Sequence identifiers (UMI) to correctly quantify unique reads. Reads of 20 to 24 nucleotides were extracted and mapped on the reference mature miRNA database available in miRBase version 22 (Kozomara et al., 2019) using bowtie (Langmead et al., 2009) and quantified using SAMtools (Li et al., 2009). Differentially expressed small RNA between *Xcf*-inoculated versus

H_2O-inoculated seeds at 24 and 42 DAP were determined using DESeq2 following a *p*-value threshold < 5% from the SARTools R package (Varet et al., 2016). Known and putative novel small RNAs were mapped to the *P. vulgaris* genome sequence using ShortStack4 algorithm (Johnson et al., 2016) and displayed in the dedicated Jbrowse https://iris.angers.inrae.fr/pvulgaris_v2 in the 'small RNA tracks' section. Transcripts potentially targeted by miRNAs were predicted via analyzing complementary matching between sRNA and target and evaluating target site accessibility using psRNATarget tool (Dai and Zhao, 2011; Dai et al., 2018) and a threshold of expectation below 5 was set to consider transcripts as putative miRNA targets. Raw reads are publicly available at GSE226920.

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

From the same frozen seed powders used for RNA extractions, we performed DNA extraction, on the three biological replicates of *Xcf*- and H_2O-inoculated seeds at 42 DAP, using the NucleoSpin® DNA Food Kit (Macherey-Nagel, Düren, Germany), according to the manufacturer's instructions. DNA samples were sent to the BGI Genomics (Hong Kong) for bisulfite treatment using a ZYMO EZ DNA Methylation-Gold kit, library construction and paired-end sequencing using BGISEQ-500 sequencing technology (PE100 45M). FastQC was used to check sequencing quality and clean reads were mapped to the *P. vulgaris* genome version 2.1 using Bismark software (Krueger and Andrews, 2011). After mapping, deduplication of sequences and quantification of cytosine methylation were performed using Bismark_deduplicate and Bismark_methylation_extractor. Each context of methylation was considered independently: CG, CHG, or CHH and corresponding bigwig files were generated using bismark_to_bigwig python script and displayed in the dedicated Jbrowse: https://iris.angers.inrae.fr/pvulgaris_v2. Putative differentially methylated regions (DMRs) were identified in each independent methylation context using DMRCaller algorithm available in R (Catoni et al., 2018). Raw reads are publicly available at https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226919.

Results

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

Seed transmission of *Xcf* 7767R was investigated following spray-inoculation of *P. vulgaris* L. cv Flavert. Three stages of seed development were targeted: (i) 24 DAP (seed filling), (ii) 35 DAP (seed maturation) and 42 DAP (seed maturity). Seed water content (Fig. 1A) and dry seed weight (Fig. 1B) were not significantly impacted by *Xcf*-inoculation. As described in Darsonval et al. (2008), we used 10^6 CFU.mL^{-1} for *Xcf* spray-inoculation at flowering time to allow seed bacterial transmission without apparition of symptoms during seed development. Otherwise, higher concentration could generate symptomatic seed bacterial transmission leading to defect in germination of infected seeds. Following this mild treatment, about 80% of seeds were contaminated with *Xcf* with an average population size of 10^5 CFU.g^{-1} of seeds at 24 DAP (Fig. 1C). Over the course of seed development, the frequency of detection of *Xcf* decreased from 80% to 50%. This was accompanied by a significant decrease in *Xcf* population size from 35 to 42 DAP, down to an average of 10^3 CFU.g^{-1} of seeds at maturity (Fig. 1C).

Changes in the Xcf bacterial transcriptome during seed development

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

A focus on the COG related to secretion processes revealed that all T3SS encoding genes and several *xps* genes involved in the T2SS were up-regulated at the seed filling stage, but not later during seed maturation (Supplementary Table S1). This was consistent with the observed up-regulation of the master regulator *hrpG* that is known to control many genes involved in the interaction with the host plant (Teper et al., 2021) such as the T3SS transcriptional activator *hrpX* and cognate effectors (T3Es) but also the *xps* genes involved in the secretion of cell wall degrading enzymes (Szczesny et al., 2010). In line with this result, 26/40 (65%) of T3E-encoding genes and several genes encoding pectin lyase (1), pectate lyases (2), glycoside hydrolases (34) and proteases (40) were only up-regulated at early stage (Supplementary Table S1). As demonstrated in Darsonval et al. (2008), T3SS encoding genes, including hrpG and hrpX are essential genes for efficient bacterial seed transmission. Together, these results suggested that bacteria were actively interacting with the host plant only at early seed maturation stages, but not later.

Transcriptomic analysis of bean seeds in response to pathogen colonization

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

Small RNAs associated with Xcf seed colonization

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

To reveal the potential response mediated by these miRNAs, we identified putative transcript targets using (i) psRNATarget predictive tool (Dai *et al.* 2018) combined with (ii) our generated transcriptomic data at these two stages (Supplementary Table S2). To clarify, a transcript was considered as putative miRNA target if (i) its expectation (E) score from PsRNATarget was below 5 and if (ii) its expression was down-regulated when miRNA was up-regulated or inversely. Following these criteria, we identified between one to 11 putative miRNA target transcripts depending on miRNA families (Table 1). Among miRNAs up-regulated at 24 DAP in *Xcf*-inoculated, there were target transcripts related to defense such as miR8175 that could down-regulate key defense genes such as *PAD4-LIKE* involved in the defense pathway mediated by salicylic acid or more generic ones potentially involved in defense signaling such as a calcium-dependent-lipid-binding domain gene (CalB) or phospholipase A1 (Table 1). At the opposite, in the *Xcf*-inoculated seeds, we observed down-regulation of miRNA families such as let7, miR21, miR2111 and miR482 that potentially enhanced expression of developmental/growth genes such as TOR-LIKE, MED15, MED13, NOC1/SWA2. At 42 DAP, only three miR families, miR31, miR451 and miR164, showed significant expression changes between *Xcf*-infected and healthy seeds. An unique putative transcript target was identified associated with miR451, which encodes a UBP26-LIKE protein potentially involved in the heterochromatin silencing at the end of the seed maturation (Luo et al., 2008). In conclusion, these results suggested that miRNA did mediate seed growth by silencing defense response at 24 DAP during early seed development. On the other hand at maturity, even if miR164 up-regulation was already shown to be involved in plant defense against fungi in cotton (*Gossypium hirsutum*) and *Populus tomentosa* (Hu et al., 2020; Chen et al., 2021b), in our susceptible host this miR was down-regulated at 42 DAP, which did not support the hypothesis that specific miRNA were accumulated in *Xcf*-inoculated seeds to prepare plant defense during germination. Interestingly, at 24 and 42 DAP, we observed that plant miRNA could support seed defense silencing probably due to the bacteria infection arsenal such as its T3Es activated early during seed development.

Seed methylome dynamics associated with Xanthomonas seed colonization

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

We identified a total of 102 DMRs located within either coding (n=66) or promoter regions (n=36) of annotated genes, affecting 99 unique genes. Among coding sequences, 33 genes resulted in hypomethylation and 33 hypermethylation, while among promoter regions 27 genes were hypomethylated and 9 hypermethylated (Fig. 3B). To understand the role of genes differentially methylated in promoter and coding sequences at seed maturity, we compared with their changes in expression and did not observe any overlap with the DEGs between *Xcf*-colonized and non-colonized mature seeds, suggesting that differentially methylated regions did not regulate gene expression during seed development. To understand the potential role of these DMRs in the host-pathogen interaction, we looked at genes involved both in the germination and defense processes. First, from the dataset generated from Narsai et al. (2017) during ten early stages of *A. thaliana* seed germination, we identified 21,015 genes showing a differential expression (adjusted *p*value <1% using ImpulseDE2) during germination process, therefore potentially involved in germination. By mapping *P. vulgaris* transcripts on Arabidopsis transcripts, we identified potential homologous transcripts in these two species and revealed a statistically significant enrichment (Fig. 3B, Fisher's Exact test p-value< 2.2e-16) of *P. vulgaris* genes displaying DMRs following pathogen colonization with those differentially expressed during germination. Indeed, out of the 90 homologous genes identified in *A. thaliana* and displaying DMR, 78 were genes differentially expressed during germination (Fig. 3C). Second, by analyzing the list of 99 unique genes displaying changes in methylation levels following bacterial colonization, we compiled a list of genes with putative roles in defense. We identified 17 genes, 10 hypomethylated and 7 hypermethylated following bacterial infection (Table 2). As example, we observed five LRR-related protein kinases, two PR proteins, and some genes identified as involved in immune response such as *PUB13-LIKE*, *CES11-LIKE* or *WRKY72* (complete list in Supplementary Table S3). As it is known that changes in the methylation state of transposable regions can also spread to adjacent regions and regulate nearby gene expression (Ahmed et al., 2011), we extended our search to coding sequences that are 5kb nearby DMRs located in transposable regions. This analysis detected additional 280 genes potentially associated with DMRs located in transposable regions (61.4% with hypomethylated regions and 38.6% with hypermethylated regions). Among these genes, we observed a subgroup coding for disease resistance proteins, with 5 additional putative TIR-NB-LRR proteins (*Phvul.004G105600, Phvul.004G100300, Phvul.010G026400, Phvul.010G027900, Phvul.010G028000*), 3 putative NB-ARC proteins (*Phvul.002G130300, Phvul.002G130400, Phvul.004G076100*) and 4 putative LRR kinases (*Phvul.008G164500, Phvul.008G164600, Phvul.005G162100, Phvul.005G162000*) (Table 2, Supplementary Table S3 and in the dedicated Jbrowse). In total, we listed 17 DMRs nearby genes associated with defense processes (Table 2). A comparison between these two lists revealed that 5 genes encoding three *LRR related proteins (Phvul.008G164600, Phvul.005G162000 and Phvul.005G163000), one TIR NBS LRR protein (Phvul.010G026400) and WRKY72 TF (Phvul.003G068700),* displayed DMRs both within their gene sequences and in transposable elements located in proximal genomic regions. To define if these DMRs present in defense genes could be associated to a mechanism of defense priming induced by the presence of the pathogen during seed development, we selected the most differentially methylated, the *WRKY72* gene, and validated its implication in *Xcf* response during germination. By qRT-PCR, we analyzed the expression profile of *WRKY72* during germination in healthy seeds that germinated in presence of water versus *Xcf*. We clearly observed an over-expression of *WRKY72* at 7 days after imbibition in radicle of germinated seeds in presence of *Xcf*, showing the role of this gene in the defense response to *Xcf* infection during germination (Fig. 3D).

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

Discussion

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

To look into molecular dialogue, transcriptomic changes were assessed using dual RNAseq, which implies that we profiled both bacterial and plant transcripts during seed development generating the first dual transcriptomic analysis of a seed-pathogen interaction ever made. Profiling of bacterial transcripts represented the main challenge we faced due to the low concentration of bacterial cells within seeds. In this study, we successfully achieved this technological breakthrough by an enrichment step of bacterial transcripts using an RNA capture technology provided by Agilent. Our study revealed that *Xcf* and common bean seeds establish an intense molecular dialogue at the early stages of seed development that appears to become less intense as seed maturity approaches (Fig. 2).

On the pathogen side, the up-regulation of the T3SS genes and cognate effectors observed in the early stages in comparison with 42 DAP suggests they could play a role in the host defense silencing during the early step of seed colonization (Buttner, 2016). Indeed, xanthomonads T3SS and T3Es are known to play two crucial roles in allowing efficient bacterial seed transmission (Darsonval et al., 2008) and in suppressing plant innate immunity and modulate plant pathways for the benefits of the bacteria (Büttner, 2016). Interestingly, down-regulated categories at early stages include basic biological processes such as translation, protein turnover and DNA replication. This might suggest that *Xcf* multiplication is hampered, consistently with the observation that number of *Xcf* cells in seeds does not increase significantly throughout seed developmental stages (Fig. 1C). Fewer functional categories were enriched at 35 DAP (Fig. 2D). The up-regulated ones (4 out of 5) included peptidases, glycosylases and methyl transferases. Such functions can be associated with both suppression of defense (peptidases, Figaj et al., 2019) and cell wall remodeling, which could help bacterial colonization of seed tissues, with no detectable impact on the seed physiology and morphology, although more subtle microscopical effects cannot be excluded (Fig. 1).

On the host side, we also observed intense gene expression changes at early seed developmental stage (24 DAP) in comparison to later ones, concomitantly with the intense bacterial secretion activity. We observed an enrichment of up-regulated Leucine Rich Repeat (LRR) protein kinases (2 categories out of 6, LRR class VIII and class Xb), which are known to have prominent roles in microbe perception and defense activation in non-seed tissues (Chakraborty et al., 2019), suggesting that the host may be able to recognize the pathogen. On the other hand, RNA-Seq data highlighted a down-regulation of gene categories with well characterized roles in the transduction of defense signaling pathways, including Mitogen-Activated Protein Kinases (MAPKs such as MAPKKK3, MAPK3 or MAPK4) and transcription factors of the bZIP (basic leucine ZIPper), TIFY, and AP2/ERF (APETALA 2/ Ethylene Responsive Factor) families (Bethke et al., 2009; Bai et al., 2011; Tintor et al., 2013; Noman et al., 2017). In line with this, we observed down-regulation of transcription factor families known to have wider functions in plant stress signaling, such as the TUB or TLP (TUBBY-Like Proteins) and the HSF (Heat Shock Transcription factor), as well as genes encoding PR proteins, including *JAZ* and *JAR* genes involved in the jasmonic acid pathway, and *PAD4* involved in the salicylic acid pathway. Such data suggest that even the transduction components of the defense pathway are inhibited, potentially due to the bacterial T3E, ultimately avoiding a defense response.

Similar to transcriptomic data, changes in expression of small RNA at 24 DAP and 42 DAP were consistent with silencing of downstream defense gene response. Indeed, analysis of the differentially expressed miRNA at 24 DAP and their putative target genes suggest a growth/defense trade-off mechanism in favor of growth in *Xcf*-inoculated seeds, with down-regulation of defense-associated transcripts (e.g. putative ortholog of PAD4 (*Phvul002G274500*, Phyto Alexin Deficient 4, involved in salicylic acid signaling in *A. thaliana* (Pruitt et al., 2021)), a pepsin-type protease (*Phvul001G229200*)) and up-regulation of development-associated transcripts (*e.g.* TOR-LIKE (*Phvul011G050300*) and MED15 (*Phvul010G157900*, MEDIATOR 15, required for correct embryogenesis in *A. thaliana* (Kim et al., 2016)). Interestingly, a heat shock protein (HSP70, *Phvul003G154800*) was detected as down-regulated genes at 24 DAP in *Xcf*-inoculated seeds and potential target of miR396, which complete the observed downregulation of HSF and smallHSP from our infected host transcriptome data (Fig. 2D). Recently it was showed that heat shock proteins are the most represented family among the down-regulated DEGs in leaf in a resistant common bean genotype towards common bacterial blight (caused by *Xcf* and *Xanthomonas phaseoli* pv. *phaseoli*) in comparison to a susceptible one (Foucher et al., 2020). On the other hand, data obtained at 42 DAP revealed only down-regulation of one miRNA family miR451, potentially regulating the up-regulation of its predicted target gene (*Phvul009G100000*) (Table 1). Its *A. thaliana* homolog (AT3G49600.1) deubiquitinates the histone H2B and is required for heterochromatin silencing during seed development (Luo et al., 2008). It is worth noting that chromatin reorganization processes due to histone modifications are among the categories enriched at 42 DAP (Fig. 2D), therefore suggesting that epigenetic regulation is a relevant component of the seed-pathogen molecular dialogue at this stage, potentially acting as priming for post-germination phase. Globally, the transcriptomic response of the susceptible host plant suggests that developing seeds are able to perceive the pathogen, and that defense responses might be largely inhibited by the bacterial T3SS arsenal. Consistent with suppression of the plant defense, up-regulation of photosynthesis and down-regulation of cell wall organization enzymes (Fig.2D) were also previously observed in leaves of susceptible common bean plants upon infection (Foucher et al., 2020). On the other hand, down-regulation of HSP and HSF, and AP2/ERF transcription factors (Fig.2D) were the hallmark of resistant plants. This suggests that a balance between susceptibility and resistance exist in *Xcf*-infected seeds, which could explain why, despite active bacterial colonization, the seeds were asymptomatic and presented no obvious physiological impact.

In this study, we also revealed that DNA methylation changes in *Xcf*-inoculated seed may also act as defense priming for post-germination phase. Indeed, the seed host methylome analysis at 42 DAP revealed significant changes in methylation status in 826 different genomic regions, affecting a total of 99 different genes, which did not display any change in gene expression during seed maturation. Of these, 17 can be associated to defense processes in a relatively straightforward manner (Table 2). As hypomethylation of defense genes has been widely associated with increased resistance to biotic stress (Dowen et al., 2012; Annacondia et al., 2021), the hypomethylated genes of this list (10 out of 17) can be considered as candidates for epigenetic-dependent defense priming. The concept of defense priming postulates that plants conserve the memory of previous encounters with pathogens by preparing their defense networks to respond more rapidly and strongly to a future aggression (Martinez-Medina et al., 2016). Enhanced chromatin access to defense genes through hypomethylation is one of the best characterized mechanisms in this sense (Hannan Parker et al., 2022). Furthermore, epigenetic defense priming can be transmitted to the next generations (Slaughter et al., 2012). This would be consistent with a scenario where *Xcf* colonization does not directly induce defense gene activation in common bean seeds, but rather triggers a primed state that prepare defense networks for the moment when the pathogen will again become virulent (after germination). Hypomethylation of transposable elements is another well-characterized mechanism of epigenetic regulation of plant defenses, as it can lead to the euchromatisation of wide genomic regions, both proximal and distal (López Sánchez et al., 2016; Halter et al., 2021). The five defense genes present in Table 2 are thus likely to be good candidates for relevant roles in bean resistance against *Xcf*. They include three genes affected by hypomethylation (*Phvul.008G164600*, *Phvul.005G163000*, *Phvul.010G026400*), namely two putative LRR kinase receptors and one effector receptor, all uncharacterized. The other two genes affected by hypermethylation are another uncharacterized LRR kinase receptor (*Phvul.005G162000*) and the putative bean homolog of WRKY72 (*Phvul.003G068700*). This transcription factor has the highest methylation gain among all the genes detected (fold change of +4,3), suggesting that its methylation status might be important in response to *Xcf* infection. Indeed, the role of WRKY72 orthologs is contradictory in different species. A positive role on defense responses was showed in *A. thaliana* and tomato (*Solanum lycopersicum*) against oomycetes and bacteria, respectively (Bhattarai et al., 2010), but regarding the interaction between rice (*Oryza sativa*) and *Xanthomonas oryzae* pv. *Oryzae, it was* showed to negatively regulate rice defense responses by repressing jasmonate biosynthetic genes (Hou et al., 2019). In our study, we validated its role as *Xcf*-response genes during germination by highlighting its over-expression at 7 DAI in radicles of germinated seeds in presence of *Xcf*. Another consideration regarding our methylome data is the high overlap between DMRs-containing genes and germination-DEGs (Fig. 3B). This suggests that the DMR-containing genes following bacterial infection detected in this study may serve during the germination process through a defense priming mechanism. More investigation will be required to define if these methylation changes will have positive or negative impacts on defense- and/or germination-related gene expressions and will require extensive transcriptomic analyses.

All together, these results indicate that the molecular mechanisms involved in the pathogen-seed dialogue change radically across the developmental stages for both the host and the pathogen side, potentially suggesting the existence of distinct phases in the considered seed-pathogen interaction. It would be interesting to explore whether such pattern takes place in other seed-pathogen interactions. By summing our physiological and molecular observations, with the previous findings of Terrasson et al. (2015), we can propose a model where the recognition of a host-specific pathogen at the early stages of seed development fails to trigger seed defense activation, as if the presence of the pathogen was “accepted” by the host. Even if we cannot define whether this suppression is caused by the pathogen or by the host, two Xanthomonas studies would support the role of bacterial T3SS in host defense silencing. Darsonval et al. (2008) showed the essential role of T3E for an efficient seed colonization in the *X. citri* pv. *fuscans*-bean seed interaction and Terrasson et al. (2015) showed that *X. euvesicatoria* pv. *Alfalfae* was able to silence some defense genes in a compatible interaction, but not in an incompatible one. In any case, the result is a situation where the seed develops normally without any obvious fitness costs associated to an eventual defense activation, while the host-specific pathogen displays a non-aggressive behavior throughout all the seed development and limits its proliferation (Fig. 4). Such “ceasefire” scenario might be advantageous for both parts: the seed is able to reach maturity, which would potentially be beneficial for the pathogen as well by allowing it to infect the future germinated seedling, therefore giving it access to nourishment and facilitating its dispersal. On the other hand, data at 42 DAP suggest a relevant role for epigenetic modifications in the host. It is tempting to speculate that such modifications contribute to prepare the host to face a novel pathogen assault after germination (Fig. 4). Detailed analysis of the transcriptome and epigenome of the bean-*Xcf* interaction during the germination process would be a promising future research direction in this sense. Recent data from the compatible interaction *Alternaria brassicicola*-*A. thaliana*, used as seed transmission model, showed that host defense pathways are subjected to drastic changes during the germination process (Ortega-Cuadros et al., 2022). It would be interesting to explore whether such rearrangements take place in other compatible interactions such as *Xcf*-bean and if a link with epigenetic modifications exists.

To summarize, the present study adds novel elements to the current knowledge gap of seed-pathogen interactions. The dual transcriptomic analysis allowed for the first time to describe the molecular dialogue from both host and pathogen sides, while methylome and sRNAs profiling added further indications on the potential regulatory mechanisms and the genes involved. A dedicated Jbrowse containing all these generated data will serve as baseline tool for the scientific communities and will be enriched by future related studies. An important general conclusion that we can draw is that seeds have primarily an active role in this interaction at early seed maturation stage, contrary to the widely diffused assumption considering seeds as passive carriers of microbes (Dutta et al., 2014). As the role of seedborne pathogens in causing yield losses receives relatively little attention, we hope that the present study can stimulate novel research efforts in this sense to shed light on the many obscure points still shrouding seed-pathogen interactions.

Supplemental data

Supplementary Data S1: Result tables of RNA-seq data

Supplementary Data S2: Result tables of sRNA-seq data

Supplementary Data S3: Result tables of BS-seq data

Supplementary Data S4: Primers used for qPCR experiments.

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Author contributions

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

Data availability

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

RNAseq, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226918), GSE226919 (plant methylome, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226919) and GSE226920 (sRNA-Seq, https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE226920).

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Legends

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

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

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

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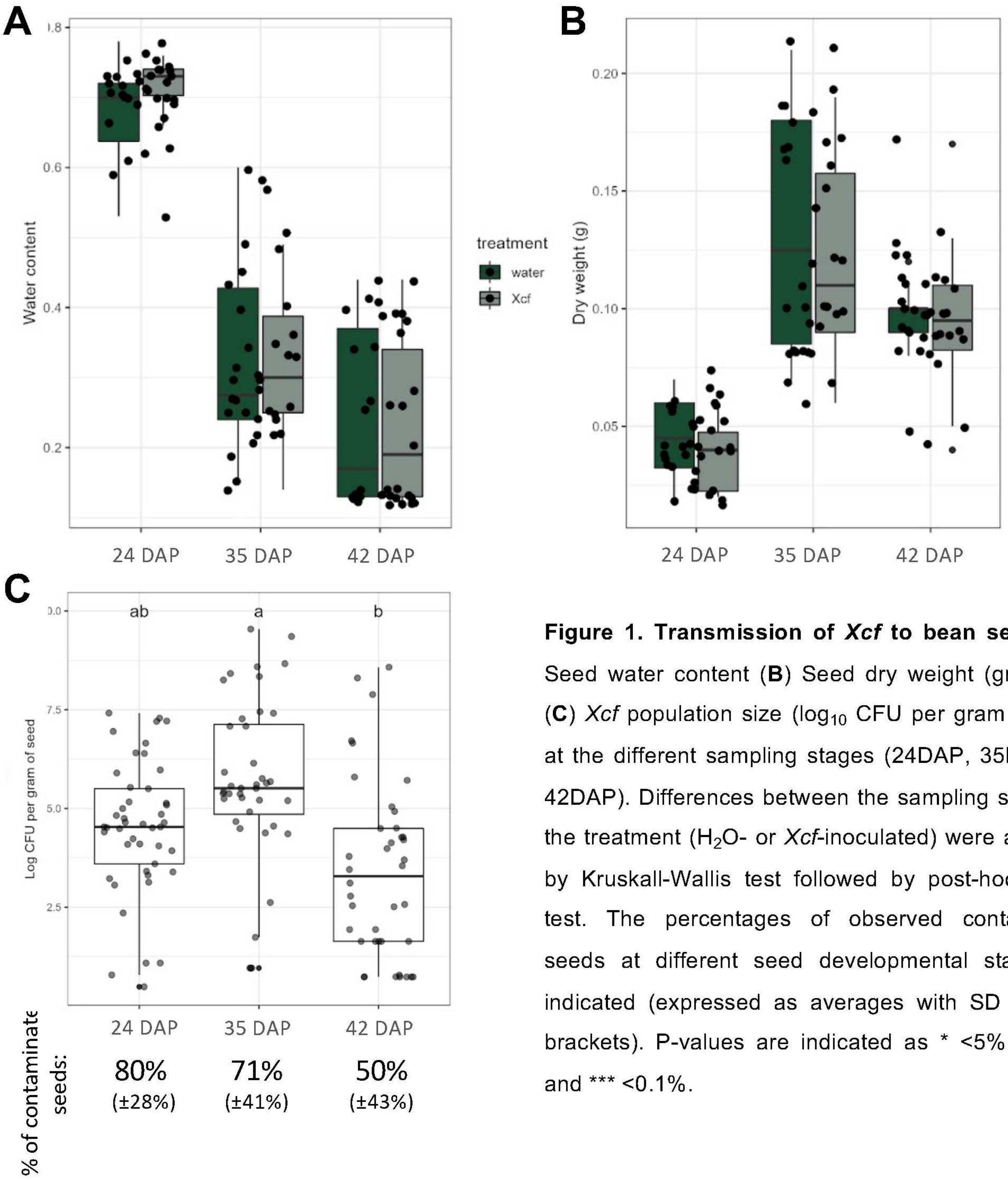
Tables

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

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

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

***P. vulgaris* locus ID**	**Location**	***P. vulgaris* annotation**	***A. thaliana* putative ortholog**	***A. thaliana* symbol**	***A. thaliana* annotation**	**Methylation FC (Xcf vs H2O)**	**Gain or loss of methylation in *Xcf*-treated seeds**
Phvul.001G233000	gene	protein kinase (SD-1)	AT3G16030	CES101	lectin protein kinase family protein	0.52	loss
Phvul.002G125500	within 5kb	not annotated	AT5G08315		Defensin-like (DEFL) family protein		loss
Phvul.002G130300	within 5kb	not annotated	AT3G14470		NB-ARC domain-containing disease resistance protein		gain
Phvul.002G130400	within 5kb	not annotated	AT3G14470		NB-ARC domain-containing disease resistance protein		gain
Phvul.003G021700	1kbProm	transferase transferring phosphorus-containing group	AT1G70740		Protein kinase superfamily protein	0.51	loss
Phvul.003G040300	1kbProm	6-deoxocastasterone 6-oxidase	AT3G30180	BR6OX2	brassinosteroid-6-oxidase 2	2.98	gain
Phvul.003G056900	within 5kb	systemic acquired resistance (SAR) regulator protein (SNI1)	AT4G18470	SNI1	negative regulator of systemic acquired resistance (SNI1)		loss
Phvul.003G068700	gene	transcription factor (WRKY)	AT5G15130	WRKY72	WRKY DNA-binding protein 72	4.30	gain
Phvul.003G068700	within 5kb	transcription factor (WRKY)	AT5G15130	WRKY72	WRKY DNA-binding protein 72		gain
Phvul.003G175700	gene	DRB4-DRB7.1 regulator complex.component DRB7	AT5G20320	DCL4	dicer-like 4	0.37	loss
Phvul.004G076100	within 5kb	not annotated	AT3G14470		NB-ARC domain-containing disease resistance protein		loss
Phvul.004G105600	within 5kb	not annotated	AT2G34930		disease resistance family protein / LRR family protein		loss
Phvul.005G162000	1kbProm	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein	2.36	gain
Phvul.005G162000	within 5kb	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein		gain
Phvul.005G162100	within 5kb	transferase transferring phosphorus-containing group	AT1G51800		Leucine-rich repeat protein kinase family protein		gain
Phvul.005G163000	gene	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein	0.38	loss
Phvul.005G163000	within 5kb	transferase transferring phosphorus-containing group	AT4G29990		Leucine-rich repeat transmembrane protein kinase protein		loss
Phvul.006G006800	gene	TKL protein kinase superfamily.protein kinase (DUF26)	AT4G05200	CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	0.18	loss
Phvul.006G033200	gene	not annotated	AT5G38280	PR5K	PR5-like receptor kinase	0.52	loss
Phvul.007G187700	1kbProm	not annotated	AT3G04720	PR4	pathogenesis-related 4	0.37	loss
Phvul.007G241200	gene	transcription factor (MYB-related)	AT5G47390		myb-like transcription factor family protein	3.25	gain
Phvul.007G241200	within 5kb	transcription factor (MYB-related)	AT5G47390		myb-like transcription factor family protein		gain
Phvul.007G241300	within 5kb	Ser/Thr protein kinase	AT1G50240	FU	Protein kinase family protein with ARM repeat domain		gain
Phvul.008G164500	within 5kb	transferase transferring phosphorus-containing group	AT3G21340		Leucine-rich repeat protein kinase family protein		loss
Phvul.008G164600	gene	not annotated	AT1G05700		Leucine-rich repeat transmembrane protein kinase protein	0.45	loss
Phvul.008G164600	within 5kb	not annotated	AT1G05700		Leucine-rich repeat transmembrane protein kinase protein		loss
Phvul.008G228714	gene	S8-class protease (subtilisin) families.protease (SBT4)	AT3G46850		Subtilase family protein	4.29	gain
Phvul.008G229400	gene	S8-class protease (subtilisin) families.protease (SBT4)	AT5G59100		Subtilisin-like serine endopeptidase family protein	0.48	loss
Phvul.010G026400	1kbProm	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family	0.35	loss
Phvul.010G026400	within 5kb	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family		loss
Phvul.010G027900	within 5kb	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family		loss
Phvul.010G028000	within 5kb	effector receptor (NLR)	AT5G36930		Disease resistance protein (TIR-NBS-LRR class) family		loss
Phvul.010G062500	within 5kb	WRKY33-dependent plant immunity transcription factor	AT2G38470	WRKY33	WRKY DNA-binding protein 33		loss
Phvul.011G064700	gene	U-Box E3 ligase activities.E3 ubiquitin ligase (PUB)	AT3G46510	PUB13	plant U-box 13	4.06	gain
Phvul.011G108300	gene	transferase transferring phosphorus-containing group	AT1G29730		Leucine-rich repeat transmembrane protein kinase	2.32	gain
Phvul.011G176100	gene	transferase transferring one-carbon group	AT3G11480	BSMT1	S-adenosyl-L-methionine-dependent methyltransferases family protein	2.56	gain



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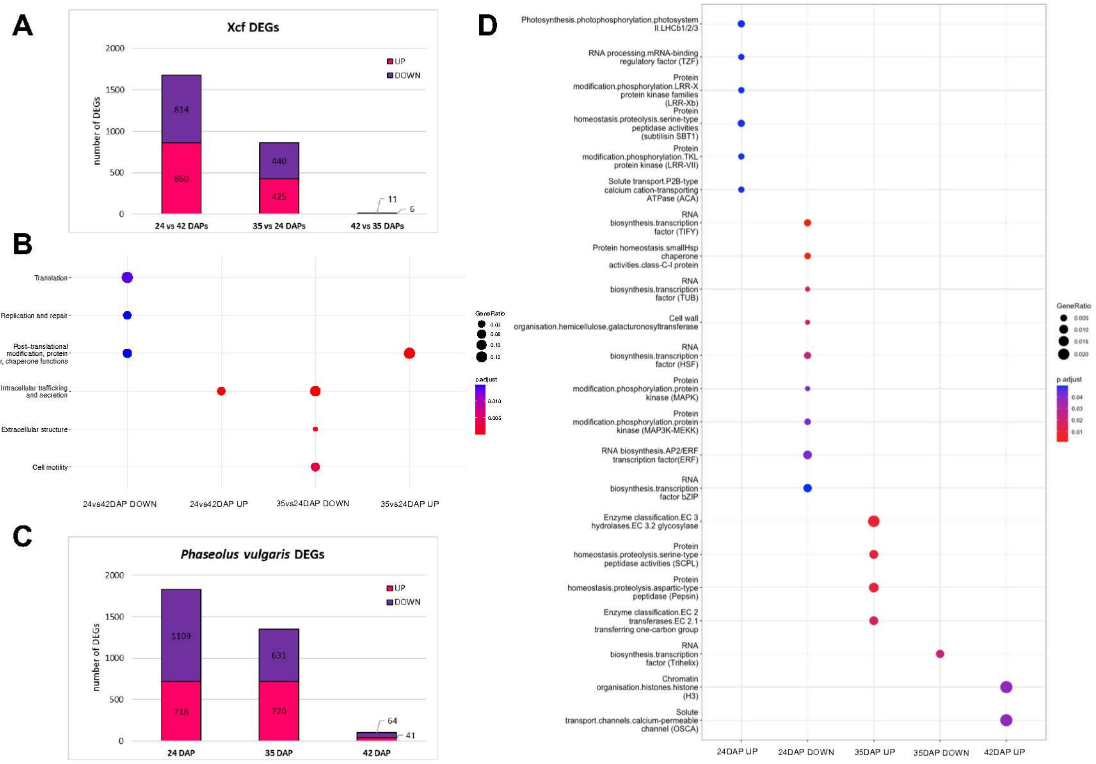

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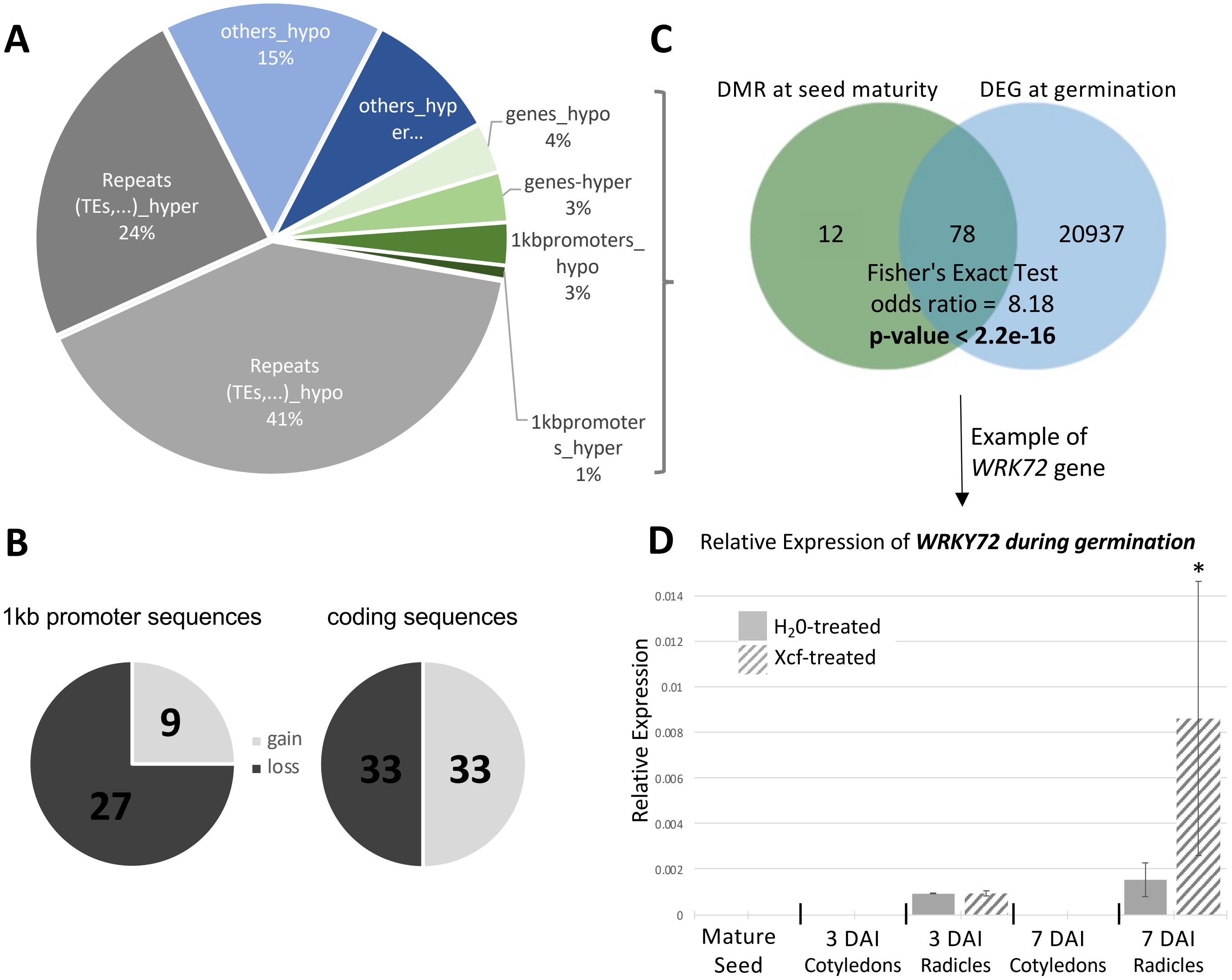

Figure 3. Summary of methylome analysis data generated by comparing *Xcf*-colonized and uncolonized seeds at 42 DAP. (**A**) Pie chart illustrating the repartition of differentially methylated regions (DMRs) following *Xcf* colonization on *P. vulgaris* genome at 42 DAP. (**B**) Pie charts illustrating the number of hypo-(loss) and hyper-(gain) methylated DMRs located in annotated genes (1kb promoter or coding sequences). (**C**) Venn diagram illustrating the overlap between gene sequences containing DMRs at 42 DAP and differentially expressed genes (DEGs) during germination (see details in text). (**D**) Relative expression of *WRKY72* during germination (at 3 and 7 Days after imbibition, DAI) in H_2O- and *Xcf*-treated seeds.

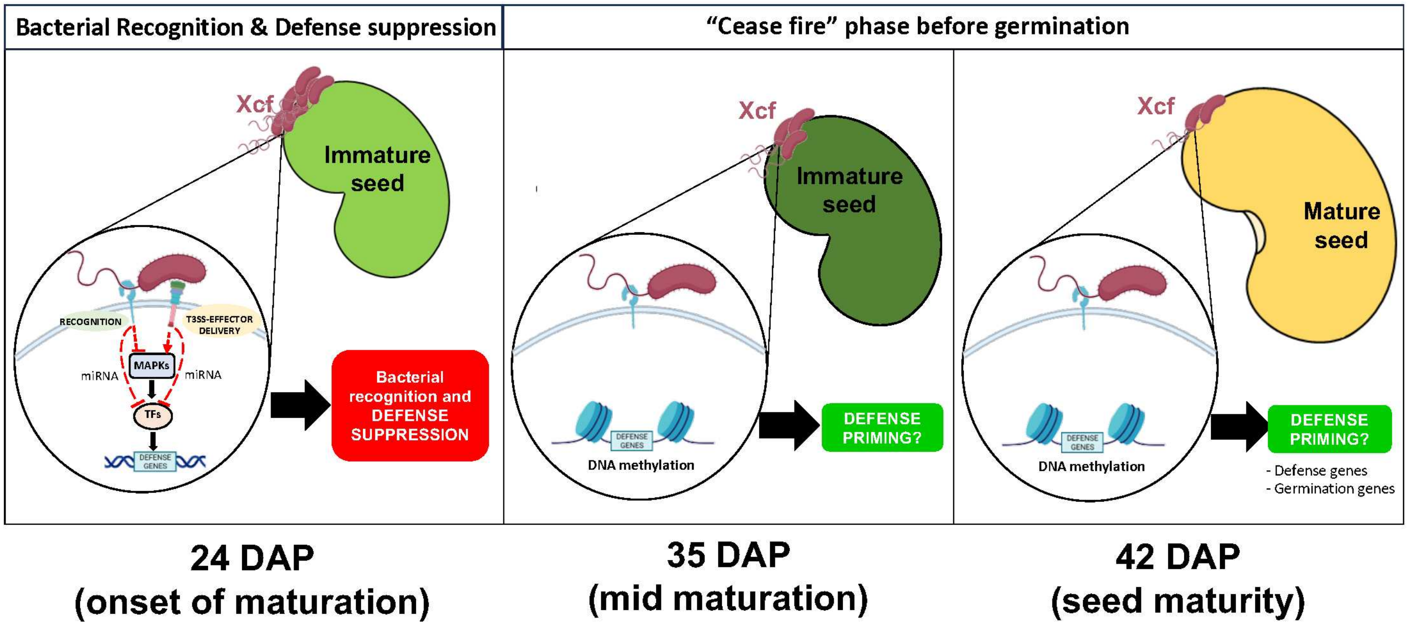

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Table 2. List of differentially methylated regions located in defense-associated genes in of P. vulg

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

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

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

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

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

n was filled according to the P. vulgaris genome (v2.1). The location indicates whether the region is l ocalized in a coding region (gene) or in the promoter (1kbprom) or in TE within 5kb of genic regions (

within 5kb). The putative ortholog was assigned as best hit based on sequence similarity in the A. tha aliana genome (v.11). The “gain or loss” column shows whether the differentially methylated region a associated with the corresponding P. vulgaris gene is hypo- (loss) or hypermethylated (gain) in respor nse to Xcf colonization at 42 DAP. FC, fold change of methylation between Xcf- versus H2O-treated se eeds. FC ratios are not indicated for DMRs within 5kb of genic regions because they correspond to mu ultiple DMR

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

psRNAtarget combined with corresponding significant expression changes from RNAseq data
putative targets using psRNAtarget (= miRNA potential target genes)
Phvul.007G067800 (HSF), Phvul.008G055500 (TGD3), Phvul.006G176000 (trihelix DNA-binding), Phvul.008G114700 (Rab-GDF)
Phvul.009G014600 (cardiolipin deacylase), Phvul.001G212400 (RING-domain E3 ligase), Phvul.005G068800 (Probable E3 ubiquitin-protein ligase), Phvul.003G053000 (glycosyltransferase)
Phvul.009G246000 (SNF4-like), Phvul.001G229200 (pepsin-type protease), Phvul.002G026300 integrin-like protein), Phvul.003G154800 (HSP70)
Phvul.011G149100 Transducin/WD40 repeat-like), Phvul.008G055500 (ATPase component TGD3 of TGD), Phvul.003G295800 (ATG2-like), Phvul.011G082700 (P-loop NTPase), Phvul.010G141400 (DOF1-like TF), Phvul.002G261500 (RNA polymerase regulatory protein)
Phvul.003G155500 (component SR-alpha of SRP)
Phvul.002G059000 (Phospholipase A1), Phvul.002G274500 (PAD4-like), Phvul.010G082300 (UDP-D-glucuronic acid 4-epimerase), Phvul.005G035400 (mRNA-splicing factor 18), Phvul.001G240600 (CalB domain)
Phvul.001G022700 (REMORIN-LIKE), Phvul.003G119100 (calcium-dependent lipid-binding), Phvul.011G061600 (PTAC16 -like), Phvul.003G035400 (XYL1-like), Phvul.004G121666 (subunit of CF1 of ATP synthase), Phvul.008G163350 (cohesin cofactor (PDS5)), Phvul.011G050300 (protein kinase (PIKK) TOR-like), Phvul.003G050600 (catalytic protein (CER2)), Phvul.007G069900, Phvul.011G001200 (SAC1-like), Phvul.002G185150 (sodium:proton antiporter (SOS1))
Phvul.010G157900 (MED15-like), Phvul.007G191600 (CHR8-like)
Phvul.001G269300 (MED13-like), Phvul.001G179300 (PGP1-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G168500 (Solute transport channels)
Phvul.004G170000 (STT3-like), Phvul.010G125200 (NOC1/SWA2-like), Phvul.007G244066, Phvul.002G189700 (UPL1-like)
-
Phvul.009G100000 (UBP26-like)
-

Id	H24_1	H24_2	H24_3	X24_1	X24_2
csi-miR482e-3p	492	0	0	1	0
ata-miR5168-3p	314	1	0	2	1
bdi-miR166h-3p	314	1	0	2	1
osa-miR166k-3p	314	1	0	2	1
osa-miR166l-3p	314	1	0	2	1
sbi-miR166e	314	1	0	2	1
sbi-miR166g	314	1	0	2	1
zma-miR166j-3p	314	1	0	2	1
zma-miR166k-3p	314	1	0	2	1
zma-miR166n-3p	314	1	0	2	1
ami-let-7f-5p	53	36	153	10	39
ggo-let-7f	53	36	153	10	39
oar-let-7f	53	36	153	10	39
efu-let-7c	106	111	486	62	89
abu-let-7c	96	107	463	60	82
aca-let-7c-5p	96	107	463	60	82
ami-let-7c-5p	96	107	463	60	82
bta-let-7c	96	107	463	60	82
cfa-let-7c	96	107	463	60	82
chi-let-7c-5p	96	107	463	60	82
cja-let-7c	96	107	463	60	82
cli-let-7c-5p	96	107	463	60	82
cpi-let-7c-5p	96	107	463	60	82
cpo-let-7c-5p	96	107	463	60	82
dma-let-7c	96	107	463	60	82
dno-let-7c-5p	96	107	463	60	82
dre-let-7c-5p	96	107	463	60	82
eca-let-7c	96	107	463	60	82
gga-let-7c-5p	96	107	463	60	82
gmo-let-7c-5p	96	107	463	60	82
hhi-let-7c	96	107	463	60	82
hsa-let-7c-5p	96	107	463	60	82
ipu-let-7c	96	107	463	60	82
mml-let-7c-5p	96	107	463	60	82
mmr-let-7c	96	107	463	60	82
mmu-let-7c-5p	96	107	463	60	82
mze-let-7c	96	107	463	60	82
nbr-let-7c	96	107	463	60	82
nle-let-7c	96	107	463	60	82
oan-let-7c-5p	96	107	463	60	82
oar-let-7c	96	107	463	60	82
ocu-let-7c-5p	96	107	463	60	82

oga-let-7c	96	107	463	60	82
oha-let-7c-5p	96	107	463	60	82
oni-let-7c	96	107	463	60	82
pal-let-7c-5p	96	107	463	60	82
pbv-let-7c-5p	96	107	463	60	82
pha-let-7c	96	107	463	60	82
pny-let-7c	96	107	463	60	82
pol-let-7a-5p	96	107	463	60	82
ppa-let-7c	96	107	463	60	82
ppy-let-7c	96	107	463	60	82
ptr-let-7c	96	107	463	60	82
rno-let-7c-5p	96	107	463	60	82
ssa-let-7c-5p	96	107	463	60	82
ssc-let-7c	96	107	463	60	82
tcf-let-7-5p	96	107	463	60	82
tgu-let-7c-5p	96	107	463	60	82
xla-let-7c-5p	96	107	463	60	82
xtr-let-7c	96	107	463	60	82
efu-let-7f	174	117	380	52	105
aca-let-7f-5p	172	115	379	52	105
bta-let-7f	172	115	379	52	105
cfa-let-7f	172	115	379	52	105
cgr-let-7f	172	115	379	52	105
chi-let-7f-5p	172	115	379	52	105
cja-let-7f	172	115	379	52	105
cli-let-7f-5p	172	115	379	52	105
cpi-let-7f-5p	172	115	379	52	105
cpo-let-7f-5p	172	115	379	52	105
dma-let-7f	172	115	379	52	105
dno-let-7f-5p	172	115	379	52	105
dre-let-7f	172	115	379	52	105
eca-let-7f	172	115	379	52	105
gga-let-7f-5p	172	115	379	52	105
gmo-let-7f-5p	172	115	379	52	105
hsa-let-7f-5p	172	115	379	52	105
ipu-let-7f	172	115	379	52	105
mdo-let-7f-5p	172	115	379	52	105
mml-let-7f-5p	172	115	379	52	105
mmr-let-7f	172	115	379	52	105
mmu-let-7f-5p	172	115	379	52	105
nle-let-7f	172	115	379	52	105
oan-let-7f-5p	172	115	379	52	105
ocu-let-7f-5p	172	115	379	52	105

oga-let-7f	172	115	379	52	105
oha-let-7f-5p	172	115	379	52	105
oni-let-7f	172	115	379	52	105
pal-let-7f-5p	172	115	379	52	105
pbv-let-7f-5p	172	115	379	52	105
pha-let-7f	172	115	379	52	105
ppa-let-7f	172	115	379	52	105
ppy-let-7f	172	115	379	52	105
ptr-let-7f	172	115	379	52	105
rno-let-7f-5p	172	115	379	52	105
sbo-let-7f	172	115	379	52	105
ssc-let-7f-5p	172	115	379	52	105
tch-let-7f-5p	172	115	379	52	105
tgu-let-7f-5p	172	115	379	52	105
xla-let-7f-5p	172	115	379	52	105
xtr-let-7f	172	115	379	52	105
aly-miR2111a-5p	555	707	456	105	264
aly-miR2111b-5p	555	707	456	105	264
aly-miR2111c-5p	555	707	456	105	264
ath-miR2111a-5p	555	707	456	105	264
ath-miR2111b-5p	555	707	456	105	264
bna-miR2111a-5p	555	707	456	105	264
bna-miR2111b-5p	555	707	456	105	264
bna-miR2111d	555	707	456	105	264
bra-miR2111a-5p	555	707	456	105	264
bra-miR2111b-5p	555	707	456	105	264
cme-miR2111a	555	707	456	105	264
cme-miR2111b	555	707	456	105	264
gma-miR2111b	555	707	456	105	264
gma-miR2111c	555	707	456	105	264
gma-miR2111e	555	707	456	105	264
gma-miR2111f	555	707	456	105	264
lja-miR2111-5p	555	707	456	105	264
mdm-miR2111a	555	707	456	105	264
mdm-miR2111b	555	707	456	105	264
mes-miR2111a	555	707	456	105	264
mes-miR2111b	555	707	456	105	264
mtr-miR2111a-5p	555	707	456	105	264
mtr-miR2111b	555	707	456	105	264
mtr-miR2111c	555	707	456	105	264
mtr-miR2111d-5p	555	707	456	105	264
mtr-miR2111e-5p	555	707	456	105	264
mtr-miR2111f	555	707	456	105	264

mtr-miR2111g-5p	555	707	456	105	264
mtr-miR2111h	555	707	456	105	264
mtr-miR2111i	555	707	456	105	264
mtr-miR2111j	555	707	456	105	264
mtr-miR2111k	555	707	456	105	264
mtr-miR2111m-5p	555	707	456	105	264
mtr-miR2111n	555	707	456	105	264
mtr-miR2111o	555	707	456	105	264
ppe-miR2111a	555	707	456	105	264
ppe-miR2111b	555	707	456	105	264
ppe-miR2111c	555	707	456	105	264
ppe-miR2111d	555	707	456	105	264
tcc-miR2111	555	707	456	105	264
csi-miR2111-5p	509	626	412	92	239
ptc-miR2111a	509	626	412	92	239
ptc-miR2111b	509	626	412	92	239
fve-miR2111a	509	626	411	92	239
fve-miR2111b-5p	509	626	411	92	239
fve-miR2111c	509	626	411	92	239
efu-let-7d	73	45	170	27	42
bta-let-7d	65	44	166	25	42
cgr-let-7d-5p	65	44	166	25	42
chi-let-7d-5p	65	44	166	25	42
cja-let-7d	65	44	166	25	42
cli-let-7d-5p	65	44	166	25	42
cpi-let-7d-5p	65	44	166	25	42
cpo-let-7d-5p	65	44	166	25	42
dno-let-7d-5p	65	44	166	25	42
eca-let-7d	65	44	166	25	42
hsa-let-7d-5p	65	44	166	25	42
mml-let-7d	65	44	166	25	42
mmu-let-7d-5p	65	44	166	25	42
oan-let-7d-5p	65	44	166	25	42
ocu-let-7d-5p	65	44	166	25	42
oha-let-7d-5p	65	44	166	25	42
pbv-let-7d-5p	65	44	166	25	42
ppy-let-7d	65	44	166	25	42
ptr-let-7d	65	44	166	25	42
rno-let-7d-5p	65	44	166	25	42
ssc-let-7d-5p	65	44	166	25	42
tgu-let-7d-5p	65	44	166	25	42
pvu-miR482-5p	395	278	197	141	106
bta-miR-21-5p	5527	1944	4924	1486	1872

cpo-miR-21-5p	5527	1944	4924	1486	1872
dno-miR-21-5p	5527	1944	4924	1486	1872
ocu-miR-21-5p	5527	1944	4924	1486	1872
sha-miR-21	5527	1944	4924	1486	1872
ami-miR-21-5p	5489	1934	4893	1478	1859
chi-miR-21-5p	5489	1934	4893	1478	1859
dma-miR-21	5489	1934	4893	1478	1859
mmr-miR-21	5489	1934	4893	1478	1859
nle-miR-21	5489	1934	4893	1478	1859
oar-miR-21	5489	1934	4893	1478	1859
oga-miR-21	5489	1934	4893	1478	1859
pbv-miR-21-5p	5489	1934	4893	1478	1859
pha-miR-21	5489	1934	4893	1478	1859
sbo-miR-21	5489	1934	4893	1478	1859
aca-miR-21-5p	1292	407	432	239	354
age-miR-21	1292	407	432	239	354
cfa-miR-21	1292	407	432	239	354
cgr-miR-21-5p	1292	407	432	239	354
cja-miR-21	1292	407	432	239	354
cli-miR-21-5p	1292	407	432	239	354
cpi-miR-21-5p	1292	407	432	239	354
eca-miR-21	1292	407	432	239	354
gga-miR-21-5p	1292	407	432	239	354
ggo-miR-21	1292	407	432	239	354
hsa-miR-21-5p	1292	407	432	239	354
mdo-miR-21-5p	1292	407	432	239	354
mml-miR-21-5p	1292	407	432	239	354
mmu-miR-21a-5p	1292	407	432	239	354
mne-miR-21	1292	407	432	239	354
oan-miR-21-5p	1292	407	432	239	354
oha-miR-21-5p	1292	407	432	239	354
pal-miR-21-5p	1292	407	432	239	354
ppa-miR-21	1292	407	432	239	354
ppy-miR-21	1292	407	432	239	354
ptr-miR-21	1292	407	432	239	354
rno-miR-21-5p	1292	407	432	239	354
ssc-miR-21-5p	1292	407	432	239	354
tch-miR-21-5p	1292	407	432	239	354
tgu-miR-21-5p	1292	407	432	239	354
efu-miR-34a	175	95	221	65	86
ami-miR-34a-5p	174	95	220	65	86
cja-miR-34a	174	95	220	65	86
gga-miR-34a-5p	174	95	220	65	86

mdo-miR-34a-5p	174	95	220	65	86
oha-miR-34a-5p	174	95	220	65	86
tch-miR-34a-5p	174	95	220	65	86
xtr-miR-34a	174	95	220	65	86
ame-let-7-5p	80	75	204	53	63
bdo-let-7	80	75	204	53	63
bmo-let-7-5p	80	75	204	53	63
cte-let-7	80	75	204	53	63
dan-let-7	80	75	204	53	63
der-let-7	80	75	204	53	63
dgr-let-7	80	75	204	53	63
dme-let-7-5p	80	75	204	53	63
dmo-let-7	80	75	204	53	63
dpe-let-7	80	75	204	53	63
dps-let-7	80	75	204	53	63
dqu-let-7-5p	80	75	204	53	63
dse-let-7	80	75	204	53	63
dsi-let-7	80	75	204	53	63
dvi-let-7	80	75	204	53	63
dwi-let-7	80	75	204	53	63
dya-let-7	80	75	204	53	63
ggo-let-7a	80	75	204	53	63
isc-let-7	80	75	204	53	63
ngi-let-7	80	75	204	53	63
nvi-let-7	80	75	204	53	63
ola-let-7a-5p	80	75	204	53	63
sha-let-7a	80	75	204	53	63
hme-let-7	80	75	204	53	64
pca-let-7-5p	80	75	204	53	64
abu-miR-34	134	76	189	56	75
age-miR-34a	134	76	189	56	75
bta-miR-34a	134	76	189	56	75
ccr-miR-34	134	76	189	56	75
cfa-miR-34a	134	76	189	56	75
cgr-miR-34a	134	76	189	56	75
chi-miR-34a	134	76	189	56	75
cli-miR-34a-5p	134	76	189	56	75
cpi-miR-34a-5p	134	76	189	56	75
cpo-miR-34a-5p	134	76	189	56	75
dno-miR-34a-5p	134	76	189	56	75
dre-miR-34a	134	76	189	56	75
eca-miR-34a	134	76	189	56	75
ggo-miR-34a	134	76	189	56	75

gmo-miR-34-5p	134	76	189	56	75
hsa-miR-34a-5p	134	76	189	56	75
ipu-miR-34a	134	76	189	56	75
lla-miR-34a	134	76	189	56	75
mml-miR-34a-5p	134	76	189	56	75
mmr-miR-34a	134	76	189	56	75
mmu-miR-34a-5p	134	76	189	56	75
mne-miR-34a	134	76	189	56	75
mze-miR-34	134	76	189	56	75
nbr-miR-34	134	76	189	56	75
nle-miR-34a	134	76	189	56	75
ocu-miR-34a-5p	134	76	189	56	75
oga-miR-34a	134	76	189	56	75
oni-miR-34	134	76	189	56	75
pal-miR-34a-5p	134	76	189	56	75
pbv-miR-34a-5p	134	76	189	56	75
pny-miR-34	134	76	189	56	75
ppa-miR-34a	134	76	189	56	75
ppy-miR-34a	134	76	189	56	75
ptr-miR-34a	134	76	189	56	75
rno-miR-34a-5p	134	76	189	56	75
sla-miR-34a	134	76	189	56	75
ssc-miR-34a	134	76	189	56	75
tgu-miR-34a	134	76	189	56	75
prd-let-7-5p	283	201	540	169	186
abu-let-7a	276	195	528	165	184
aca-let-7a-5p	276	195	528	165	184
ami-let-7a-5p	276	195	528	165	184
asu-let-7-5p	276	195	528	165	184
bbe-let-7a-5p	276	195	528	165	184
bfl-let-7a-5p	276	195	528	165	184
bma-let-7	276	195	528	165	184
bta-let-7a-5p	276	195	528	165	184
cbn-let-7	276	195	528	165	184
cbr-let-7	276	195	528	165	184
ccr-let-7a	276	195	528	165	184
cel-let-7-5p	276	195	528	165	184
cfa-let-7a	276	195	528	165	184
cgr-let-7a	276	195	528	165	184
chi-let-7a-5p	276	195	528	165	184
cja-let-7a	276	195	528	165	184
cli-let-7a-5p	276	195	528	165	184
cpi-let-7a-5p	276	195	528	165	184

cpo-let-7a-5p	276	195	528	165	184
crm-let-7	276	195	528	165	184
dma-let-7a	276	195	528	165	184
dno-let-7a-5p	276	195	528	165	184
dre-let-7a	276	195	528	165	184
eca-let-7a	276	195	528	165	184
fru-let-7a	276	195	528	165	184
gga-let-7a-5p	276	195	528	165	184
gga-let-7j-5p	276	195	528	165	184
gmo-let-7a-5p	276	195	528	165	184
hpo-let-7-5p	276	195	528	165	184
hsa-let-7a-5p	276	195	528	165	184
ipu-let-7a	276	195	528	165	184
lgi-let-7	276	195	528	165	184
mdo-let-7a-5p	276	195	528	165	184
mml-let-7a-5p	276	195	528	165	184
mmr-let-7a	276	195	528	165	184
mmu-let-7a-5p	276	195	528	165	184
mze-let-7a	276	195	528	165	184
nbr-let-7a	276	195	528	165	184
nle-let-7a	276	195	528	165	184
oar-let-7a	276	195	528	165	184
ocu-let-7a-5p	276	195	528	165	184
oga-let-7a	276	195	528	165	184
oha-let-7a	276	195	528	165	184
oha-let-7a-5p	276	195	528	165	184
ola-let-7a	276	195	528	165	184
oni-let-7a	276	195	528	165	184
pal-let-7a-5p	276	195	528	165	184
pbv-let-7a-5p	276	195	528	165	184
pha-let-7a	276	195	528	165	184
pma-let-7a	276	195	528	165	184
pny-let-7a	276	195	528	165	184
ppa-let-7a	276	195	528	165	184
ppc-let-7	276	195	528	165	184
ppy-let-7a	276	195	528	165	184
pte-let-7-5p	276	195	528	165	184
ptr-let-7a	276	195	528	165	184
rno-let-7a-5p	276	195	528	165	184
sbo-let-7a	276	195	528	165	184
sko-let-7	276	195	528	165	184
ssa-let-7a-5p	276	195	528	165	184
ssc-let-7a	276	195	528	165	184

tgu-let-7a-5p	276	195	528	165	184
tni-let-7a	276	195	528	165	184
xla-let-7a-5p	276	195	528	165	184
xtr-let-7a	276	195	528	165	184
abu-miR-429b	9	37	167	23	39
aca-miR-429-3p	9	37	167	23	39
bta-miR-429	9	37	167	23	39
ccr-miR-429	9	37	167	23	39
cfa-miR-429	9	37	167	23	39
cgr-miR-429	9	37	167	23	39
cli-miR-429-3p	9	37	167	23	39
cpi-miR-429-3p	9	37	167	23	39
cpo-miR-429-3p	9	37	167	23	39
dno-miR-429-3p	9	37	167	23	39
dre-miR-429a	9	37	167	23	39
efu-miR-429	9	37	167	23	39
fru-miR-429	9	37	167	23	39
gga-miR-429-3p	9	37	167	23	39
gmo-miR-429-3p	9	37	167	23	39
mmu-miR-429-3p	9	37	167	23	39
mze-miR-429b	9	37	167	23	39
nbr-miR-429b	9	37	167	23	39
oan-miR-429-3p	9	37	167	23	39
oha-miR-429-3p	9	37	167	23	39
oni-miR-429b	9	37	167	23	39
pal-miR-429-3p	9	37	167	23	39
pbv-miR-429-3p	9	37	167	23	39
pny-miR-429b	9	37	167	23	39
rno-miR-429	9	37	167	23	39
ssc-miR-429	9	37	167	23	39
tni-miR-429	9	37	167	23	39
xla-miR-429-3p	9	37	167	23	39
xtr-miR-429	9	37	167	23	39
aof-miR166c	101	1840	1341	461	530
ath-miR165a-3p	101	1840	1341	461	530
ath-miR165b	101	1840	1341	461	530
bna-miR166f	101	1840	1341	461	530
cas-miR165a	101	1840	1341	461	530
lus-miR166b	101	1840	1341	461	530
cli-let-7i-5p	203	105	205	74	111
abu-let-7i	201	103	204	74	111
aca-let-7i-5p	201	103	204	74	111
bta-let-7i	201	103	204	74	111

chi-let-7i-5p	201	103	204	74	111
cja-let-7i	201	103	204	74	111
cpi-let-7i-5p	201	103	204	74	111
cpo-let-7i-5p	201	103	204	74	111
dno-let-7i-5p	201	103	204	74	111
dre-let-7i	201	103	204	74	111
fru-let-7i	201	103	204	74	111
gmo-let-7i-5p	201	103	204	74	111
hsa-let-7i-5p	201	103	204	74	111
ipu-let-7i	201	103	204	74	111
mml-let-7i-5p	201	103	204	74	111
mmu-let-7i-5p	201	103	204	74	111
mze-let-7i	201	103	204	74	111
nbr-let-7i	201	103	204	74	111
nle-let-7i	201	103	204	74	111
oar-let-7i	201	103	204	74	111
ocu-let-7i-5p	201	103	204	74	111
oga-let-7i	201	103	204	74	111
oha-let-7i-5p	201	103	204	74	111
oni-let-7i	201	103	204	74	111
pal-let-7i-5p	201	103	204	74	111
pbv-let-7i-5p	201	103	204	74	111
pha-let-7i	201	103	204	74	111
pny-let-7i	201	103	204	74	111
ppa-let-7i	201	103	204	74	111
ppy-let-7i	201	103	204	74	111
ptr-let-7i	201	103	204	74	111
rno-let-7i-5p	201	103	204	74	111
ssa-let-7i-5p	201	103	204	74	111
tch-let-7i-5p	201	103	204	74	111
tgu-let-7i-5p	201	103	204	74	111
tni-let-7i	201	103	204	74	111
ami-miR-30d-5p	75	82	136	31	60
bta-miR-30d	75	82	136	31	60
cfa-miR-30d	75	82	136	31	60
cli-miR-30d-5p	75	82	136	31	60
cpo-miR-30d-5p	75	82	136	31	60
dno-miR-30d-5p	75	82	136	31	60
gmo-miR-30a-5p	75	82	136	31	60
nle-miR-30d	75	82	136	31	60
ocu-miR-30d-5p	75	82	136	31	60
oga-miR-30d	75	82	136	31	60
oha-miR-30d-5p	75	82	136	31	60

pal-miR-30d-5p	75	82	136	31	60
pbv-miR-30d-5p	75	82	136	31	60
pha-miR-30d	75	82	136	31	60
ssa-miR-30b-5p	75	82	136	31	60
ssc-miR-30d	75	82	136	31	60
tgu-miR-30d-5p	75	82	136	31	60
xla-miR-30d-5p	75	82	136	31	60
cgr-miR-29a-3p	88	63	108	32	67
chi-miR-29a-3p	88	63	108	32	67
oar-miR-29a	88	63	108	32	67
tch-miR-29a-3p	88	63	108	32	67
ssa-miR-23b-3p	101	31	58	21	45
ami-miR-23b-3p	98	30	57	21	45
bta-miR-10174-3p	98	30	57	21	45
bta-miR-23b-3p	98	30	57	21	45
cpo-miR-23b-3p	98	30	57	21	45
dno-miR-23b-3p	98	30	57	21	45
dre-miR-23b-3p	98	30	57	21	45
efu-miR-23b	98	30	57	21	45
hsa-miR-23b-3p	98	30	57	21	45
ocu-miR-23b-3p	98	30	57	21	45
oga-miR-23b	98	30	57	21	45
oha-miR-23b-3p	98	30	57	21	45
ola-miR-23b	98	30	57	21	45
pbv-miR-23b-3p	98	30	57	21	45
pma-miR-23b	98	30	57	21	45
ppa-miR-23b	98	30	57	21	45
ppy-miR-23b	98	30	57	21	45
ptr-miR-23b	98	30	57	21	45
tch-miR-23b-3p	98	30	57	21	45
cfa-miR-29a	117	82	137	45	82
cja-miR-29a	117	82	137	45	82
cpo-miR-29a-3p	117	82	137	45	82
dma-miR-29a	117	82	137	45	82
dno-miR-29a-3p	117	82	137	45	82
eca-miR-29a	117	82	137	45	82
hsa-miR-29a-3p	117	82	137	45	82
mmr-miR-29a	117	82	137	45	82
mmu-miR-29a-3p	117	82	137	45	82
nle-miR-29a	117	82	137	45	82
ocu-miR-29a-3p	117	82	137	45	82
oga-miR-29a	117	82	137	45	82
pal-miR-29a-3p	117	82	137	45	82

pha-miR-29a	117	82	137	45	82
rno-miR-29a-3p	117	82	137	45	82
cli-miR-23b-3p	99	30	57	22	45
age-miR-29a	170	93	148	58	108
ggo-miR-29a	170	93	148	58	108
lla-miR-29a	170	93	148	58	108
mml-miR-29a-3p	170	93	148	58	108
mne-miR-29a	170	93	148	58	108
ppa-miR-29a	170	93	148	58	108
ppy-miR-29a	170	93	148	58	108
ptr-miR-29a	170	93	148	58	108
sbo-miR-29a	170	93	148	58	108
sla-miR-29a	170	93	148	58	108
gga-miR-126-3p	752	501	671	291	487
bta-miR-200c	2	59	226	29	53
cfa-miR-200c	2	59	226	29	53
cgr-miR-200c	2	59	226	29	53
chi-miR-200c	2	59	226	29	53
cja-miR-200c	2	59	226	29	53
cpo-miR-200c-3p	2	59	226	29	53
eca-miR-200c	2	59	226	29	53
efu-miR-200c	2	59	226	29	53
hsa-miR-200c-3p	2	59	226	29	53
mmu-miR-200c-3p	2	59	226	29	53
ocu-miR-200c-3p	2	59	226	29	53
pal-miR-200c-3p	2	59	226	29	53
ptr-miR-200c	2	59	226	29	53
tch-miR-200c-3p	2	59	226	29	53
aca-miR-126-3p	752	499	671	291	487
ami-miR-126-3p	752	499	671	291	487
cgr-miR-126a	752	499	671	291	487
cja-miR-126	752	499	671	291	487
cli-miR-126-3p	752	499	671	291	487
cpi-miR-126-3p	752	499	671	291	487
cpo-miR-126-3p	752	499	671	291	487
dno-miR-126-3p	752	499	671	291	487
eca-miR-126-3p	752	499	671	291	487
hsa-miR-126-3p	752	499	671	291	487
mdo-miR-126-3p	752	499	671	291	487
mml-miR-126	752	499	671	291	487
mmu-miR-126a-3p	752	499	671	291	487
oan-miR-126-3p	752	499	671	291	487
pbv-miR-126-3p	752	499	671	291	487

ppy-miR-126	752	499	671	291	487
ptr-miR-126	752	499	671	291	487
rno-miR-126a-3p	752	499	671	291	487
ssc-miR-126-3p	752	499	671	291	487
tgu-miR-126-3p	752	499	671	291	487
ccr-miR-30d	46	49	94	18	34
cja-miR-30d	46	49	94	18	34
cpi-miR-30d-5p	46	49	94	18	34
oan-miR-30d-5p	46	49	94	18	34
ola-miR-30d-5p	46	49	94	18	34
efu-miR-126	756	506	678	291	498
ccr-miR-100	126	30	25	38	32
cgr-miR-100-5p	126	30	25	38	32
chi-miR-100-5p	126	30	25	38	32
cpi-miR-100-5p	126	30	25	38	32
dma-miR-100	126	30	25	38	32
mdo-miR-100-5p	126	30	25	38	32
pmi-miR-100-5p	126	30	25	38	32
sbo-miR-100	126	30	25	38	32
sha-miR-100	126	30	25	38	32
tgu-miR-100-5p	126	30	25	38	32
efu-miR-29a	207	117	182	73	128
gga-let-7g-5p	27	68	130	39	56
ggo-let-7g	27	68	130	39	56
mdo-let-7g-5p	27	68	130	39	56
oar-let-7g	27	68	130	39	56
sha-let-7g	27	68	130	39	56
bta-miR-29a	200	114	179	73	124
ssc-miR-29a-3p	200	114	179	73	124
cpo-miR-16b-5p	401	204	217	133	202
dno-miR-16b-5p	401	204	217	133	202
efu-miR-16	401	204	217	133	202
ocu-miR-16b-5p	401	204	217	133	202
bta-miR-375	12	470	1593	199	498
efu-miR-375	12	470	1593	199	498
mdo-miR-375	12	470	1593	199	498
cfa-miR-375	12	464	1564	196	491
cpo-miR-375-3p	12	464	1564	196	491
dno-miR-375-3p	12	464	1564	196	491
ggo-miR-375	12	464	1564	196	491
hsa-miR-375-3p	12	464	1564	196	491
mml-miR-375	12	464	1564	196	491
mmu-miR-375-3p	12	464	1564	196	491

ocu-miR-375-3p	12	464	1564	196	491
pal-miR-375-3p	12	464	1564	196	491
ppy-miR-375	12	464	1564	196	491
ptr-miR-375	12	464	1564	196	491
rno-miR-375-3p	12	464	1564	196	491
ssc-miR-375	12	464	1564	196	491
gma-miR390a-3p	6474	6483	8058	5160	4809
gma-miR390c	6474	6483	8058	5160	4809
mes-miR390	6474	6483	8058	5160	4809
nle-miR-148a	0	84	241	41	76
oga-miR-148a	0	84	241	41	76
pha-miR-148a	0	84	241	41	76
ppa-miR-148a	0	84	241	41	76
abu-miR-26a	519	374	526	243	334
aca-miR-26-3-5p	519	374	526	243	334
ami-miR-26-5p	519	374	526	243	334
bta-miR-26a	519	374	526	243	334
ccr-miR-26a	519	374	526	243	334
cfa-miR-26a	519	374	526	243	334
chi-miR-26a-5p	519	374	526	243	334
cja-miR-26a	519	374	526	243	334
cli-miR-26-5p	519	374	526	243	334
cpi-miR-26-5p	519	374	526	243	334
cpo-miR-26a-5p	519	374	526	243	334
dma-miR-26a	519	374	526	243	334
dno-miR-26a-5p	519	374	526	243	334
dre-miR-26a-5p	519	374	526	243	334
eca-miR-26a	519	374	526	243	334
fru-miR-26	519	374	526	243	334
gga-miR-26a-2-5p	519	374	526	243	334
ggo-miR-26a	519	374	526	243	334
gmo-miR-26a-5p	519	374	526	243	334
hsa-miR-26a-5p	519	374	526	243	334
ipu-miR-26a	519	374	526	243	334
lla-miR-26a	519	374	526	243	334
mml-miR-26a-5p	519	374	526	243	334
mmr-miR-26a	519	374	526	243	334
mmu-miR-26a-5p	519	374	526	243	334
mne-miR-26a	519	374	526	243	334
mze-miR-26a	519	374	526	243	334
nbr-miR-26a	519	374	526	243	334
nle-miR-26a	519	374	526	243	334
oan-miR-26-5p	519	374	526	243	334

oar-miR-26a	519	374	526	243	334
ocu-miR-26a-5p	519	374	526	243	334
oga-miR-26a	519	374	526	243	334
oha-miR-26-5p	519	374	526	243	334
oni-miR-26a	519	374	526	243	334
pal-miR-26a-5p	519	374	526	243	334
pbv-miR-26-5p	519	374	526	243	334
pha-miR-26a	519	374	526	243	334
pma-miR-26a-5p	519	374	526	243	334
pny-miR-26a	519	374	526	243	334
ppa-miR-26a	519	374	526	243	334
ppy-miR-26a	519	374	526	243	334
ptr-miR-26a	519	374	526	243	334
rno-miR-26a-5p	519	374	526	243	334
sbo-miR-26a	519	374	526	243	334
ssa-miR-26a-5p	519	374	526	243	334
ssc-miR-26a	519	374	526	243	334
tch-miR-26a-5p	519	374	526	243	334
tgu-miR-26-5p	519	374	526	243	334
tni-miR-26	519	374	526	243	334
xla-miR-26-5p	519	374	526	243	334
efu-miR-26a	521	375	527	243	334
efu-miR-26c	521	375	527	243	334
gma-miR391-5p	85	196	96	86	109
aca-let-7g	85	147	289	94	135
ami-let-7g-5p	85	147	289	94	135
bta-let-7g	85	147	289	94	135
cfa-let-7g	85	147	289	94	135
cgr-let-7g-5p	85	147	289	94	135
chi-let-7g-5p	85	147	289	94	135
cja-let-7g	85	147	289	94	135
cli-let-7g-5p	85	147	289	94	135
cpi-let-7g-5p	85	147	289	94	135
cpo-let-7g-5p	85	147	289	94	135
dma-let-7g	85	147	289	94	135
dno-let-7g-5p	85	147	289	94	135
eca-let-7g	85	147	289	94	135
hsa-let-7g-5p	85	147	289	94	135
mml-let-7g-5p	85	147	289	94	135
mmr-let-7g	85	147	289	94	135
mmu-let-7g-5p	85	147	289	94	135
nle-let-7g	85	147	289	94	135
oan-let-7g-5p	85	147	289	94	135

ocu-let-7g-5p	85	147	289	94	135
oga-let-7g	85	147	289	94	135
oha-let-7g-5p	85	147	289	94	135
pal-let-7g-5p	85	147	289	94	135
pbv-let-7g-5p	85	147	289	94	135
pha-let-7g	85	147	289	94	135
ppa-let-7g	85	147	289	94	135
ppy-let-7g	85	147	289	94	135
ptr-let-7g	85	147	289	94	135
rno-let-7g-5p	85	147	289	94	135
ssc-let-7g	85	147	289	94	135
tch-let-7g-5p	85	147	289	94	135
tgu-let-7g-5p	85	147	289	94	135
aly-miR390a-3p	7408	7479	8969	5907	5712
ath-miR390a-3p	7408	7479	8969	5907	5712
cas-miR390a-3p	7408	7479	8969	5907	5712
csi-miR390a-3p	7408	7479	8969	5907	5712
lja-miR390a-3p	7408	7479	8969	5907	5712
lja-miR390b-3p	7408	7479	8969	5907	5712
sly-miR390b-3p	7408	7479	8969	5907	5712
pal-miR-126-3p	144	117	122	63	112
xla-miR-126-3p	144	117	122	63	112
aof-miR166a	7981	8169	8133	5956	6604
atr-miR166b	7981	8169	8133	5956	6604
bdi-miR166f	7981	8169	8133	5956	6604
csi-miR166b-3p	7981	8169	8133	5956	6604
csi-miR166d-3p	7981	8169	8133	5956	6604
csi-miR166g-3p	7981	8169	8133	5956	6604
gma-miR166h-3p	7981	8169	8133	5956	6604
gma-miR166k	7981	8169	8133	5956	6604
pab-miR166e	7981	8169	8133	5956	6604
abu-let-7b	225	214	386	156	214
ami-let-7b-5p	225	214	386	156	214
bta-let-7b	225	214	386	156	214
ccr-let-7b	225	214	386	156	214
cfa-let-7b	225	214	386	156	214
cgr-let-7b	225	214	386	156	214
chi-let-7b-5p	225	214	386	156	214
cja-let-7b	225	214	386	156	214
cpi-let-7b-5p	225	214	386	156	214
cpo-let-7b-5p	225	214	386	156	214
dma-let-7b	225	214	386	156	214
dno-let-7b-5p	225	214	386	156	214

dre-let-7b	225	214	386	156	214
fru-let-7b	225	214	386	156	214
gga-let-7b	225	214	386	156	214
hsa-let-7b-5p	225	214	386	156	214
mdo-let-7b	225	214	386	156	214
mml-let-7b-5p	225	214	386	156	214
mmr-let-7b	225	214	386	156	214
mmu-let-7b-5p	225	214	386	156	214
mze-let-7b	225	214	386	156	214
nbr-let-7b	225	214	386	156	214
oan-let-7b-5p	225	214	386	156	214
ocu-let-7b-5p	225	214	386	156	214
oga-let-7b	225	214	386	156	214
oha-let-7b-5p	225	214	386	156	214
oni-let-7b	225	214	386	156	214
pbv-let-7b-5p	225	214	386	156	214
pha-let-7b	225	214	386	156	214
pny-let-7b	225	214	386	156	214
pol-let-7b-5p	225	214	386	156	214
ppa-let-7b	225	214	386	156	214
ppy-let-7b	225	214	386	156	214
ptr-let-7b	225	214	386	156	214
rno-let-7b-5p	225	214	386	156	214
sbo-let-7b	225	214	386	156	214
ssa-let-7b-5p	225	214	386	156	214
tgu-let-7b-5p	225	214	386	156	214
tni-let-7b	225	214	386	156	214
bta-miR-126-3p	144	115	122	63	112
xla-miR-126-2-3p	144	115	122	63	112
efu-miR-22	1415	908	1298	714	916
xla-miR-22-3p	1415	908	1298	714	916
ama-miR156	4349	4087	2522	2892	2048
aly-miR156a-5p	4346	4087	2521	2892	2048
aly-miR156b-5p	4346	4087	2521	2892	2048
aly-miR156c-5p	4346	4087	2521	2892	2048
aly-miR156d-5p	4346	4087	2521	2892	2048
aly-miR156e-5p	4346	4087	2521	2892	2048
aly-miR156f-5p	4346	4087	2521	2892	2048
aof-miR156a	4346	4087	2521	2892	2048
ata-miR156a-5p	4346	4087	2521	2892	2048
ata-miR156b-5p	4346	4087	2521	2892	2048
ata-miR156c-5p	4346	4087	2521	2892	2048
ata-miR156d-5p	4346	4087	2521	2892	2048

ata-miR156e-5p	4346	4087	2521	2892	2048
ath-miR156a-5p	4346	4087	2521	2892	2048
ath-miR156b-5p	4346	4087	2521	2892	2048
ath-miR156c-5p	4346	4087	2521	2892	2048
ath-miR156d-5p	4346	4087	2521	2892	2048
ath-miR156e	4346	4087	2521	2892	2048
ath-miR156f-5p	4346	4087	2521	2892	2048
atr-miR156b	4346	4087	2521	2892	2048
atr-miR156d	4346	4087	2521	2892	2048
bdi-miR156b-5p	4346	4087	2521	2892	2048
bdi-miR156c	4346	4087	2521	2892	2048
bdi-miR156d-5p	4346	4087	2521	2892	2048
bdi-miR156e-5p	4346	4087	2521	2892	2048
bdi-miR156f-5p	4346	4087	2521	2892	2048
bdi-miR156g-5p	4346	4087	2521	2892	2048
bdi-miR156h-5p	4346	4087	2521	2892	2048
bdi-miR156i-5p	4346	4087	2521	2892	2048
bna-miR156d	4346	4087	2521	2892	2048
bna-miR156e	4346	4087	2521	2892	2048
bna-miR156f	4346	4087	2521	2892	2048
bra-miR156a-5p	4346	4087	2521	2892	2048
bra-miR156b-5p	4346	4087	2521	2892	2048
bra-miR156c-5p	4346	4087	2521	2892	2048
bra-miR156d-5p	4346	4087	2521	2892	2048
bra-miR156e-5p	4346	4087	2521	2892	2048
bra-miR156f-5p	4346	4087	2521	2892	2048
bra-miR156g-5p	4346	4087	2521	2892	2048
cas-miR156a	4346	4087	2521	2892	2048
cas-miR156b-5p	4346	4087	2521	2892	2048
cas-miR156c-5p	4346	4087	2521	2892	2048
cas-miR156d-5p	4346	4087	2521	2892	2048
cas-miR156e-5p	4346	4087	2521	2892	2048
cas-miR156f-5p	4346	4087	2521	2892	2048
cas-miR156k-5p	4346	4087	2521	2892	2048
cca-miR156a	4346	4087	2521	2892	2048
cme-miR156a	4346	4087	2521	2892	2048
cme-miR156c	4346	4087	2521	2892	2048
cme-miR156d	4346	4087	2521	2892	2048
cme-miR156i	4346	4087	2521	2892	2048
cpa-miR156a	4346	4087	2521	2892	2048
cpa-miR156b	4346	4087	2521	2892	2048
cpa-miR156c	4346	4087	2521	2892	2048
cpa-miR156d	4346	4087	2521	2892	2048

csi-miR156a-5p	4346	4087	2521	2892	2048
csi-miR156b-5p	4346	4087	2521	2892	2048
csi-miR156c-5p	4346	4087	2521	2892	2048
ctr-miR156	4346	4087	2521	2892	2048
dpr-miR156b	4346	4087	2521	2892	2048
fve-miR156d	4346	4087	2521	2892	2048
ghr-miR156a	4346	4087	2521	2892	2048
ghr-miR156b	4346	4087	2521	2892	2048
ghr-miR156d	4346	4087	2521	2892	2048
gma-miR156a	4346	4087	2521	2892	2048
gma-miR156h	4346	4087	2521	2892	2048
gma-miR156u	4346	4087	2521	2892	2048
gma-miR156v	4346	4087	2521	2892	2048
gma-miR156w	4346	4087	2521	2892	2048
gma-miR156x	4346	4087	2521	2892	2048
gma-miR156y	4346	4087	2521	2892	2048
han-miR156a	4346	4087	2521	2892	2048
han-miR156b	4346	4087	2521	2892	2048
har-miR156a	4346	4087	2521	2892	2048
htu-miR156a	4346	4087	2521	2892	2048
lus-miR156a	4346	4087	2521	2892	2048
lus-miR156g	4346	4087	2521	2892	2048
mdm-miR156a	4346	4087	2521	2892	2048
mdm-miR156b	4346	4087	2521	2892	2048
mdm-miR156c	4346	4087	2521	2892	2048
mdm-miR156d	4346	4087	2521	2892	2048
mdm-miR156e	4346	4087	2521	2892	2048
mdm-miR156f	4346	4087	2521	2892	2048
mdm-miR156g	4346	4087	2521	2892	2048
mdm-miR156h	4346	4087	2521	2892	2048
mdm-miR156i	4346	4087	2521	2892	2048
mdm-miR156j	4346	4087	2521	2892	2048
mdm-miR156k	4346	4087	2521	2892	2048
mdm-miR156l	4346	4087	2521	2892	2048
mdm-miR156m	4346	4087	2521	2892	2048
mdm-miR156n	4346	4087	2521	2892	2048
mdm-miR156o	4346	4087	2521	2892	2048
mes-miR156a	4346	4087	2521	2892	2048
mes-miR156b	4346	4087	2521	2892	2048
mes-miR156c	4346	4087	2521	2892	2048
mes-miR156d	4346	4087	2521	2892	2048
mes-miR156e	4346	4087	2521	2892	2048
mes-miR156f	4346	4087	2521	2892	2048

mes-miR156g	4346	4087	2521	2892	2048
mtr-miR156b-5p	4346	4087	2521	2892	2048
mtr-miR156c-5p	4346	4087	2521	2892	2048
mtr-miR156d-5p	4346	4087	2521	2892	2048
mtr-miR156i-5p	4346	4087	2521	2892	2048
nta-miR156a	4346	4087	2521	2892	2048
nta-miR156b	4346	4087	2521	2892	2048
nta-miR156c	4346	4087	2521	2892	2048
nta-miR156d	4346	4087	2521	2892	2048
nta-miR156e	4346	4087	2521	2892	2048
osa-miR156a	4346	4087	2521	2892	2048
osa-miR156b-5p	4346	4087	2521	2892	2048
osa-miR156c-5p	4346	4087	2521	2892	2048
osa-miR156d	4346	4087	2521	2892	2048
osa-miR156e	4346	4087	2521	2892	2048
osa-miR156f-5p	4346	4087	2521	2892	2048
osa-miR156g-5p	4346	4087	2521	2892	2048
osa-miR156h-5p	4346	4087	2521	2892	2048
osa-miR156i	4346	4087	2521	2892	2048
osa-miR156j-5p	4346	4087	2521	2892	2048
pab-miR156a	4346	4087	2521	2892	2048
pab-miR156l	4346	4087	2521	2892	2048
ppe-miR156c	4346	4087	2521	2892	2048
ppe-miR156d	4346	4087	2521	2892	2048
ppe-miR156e	4346	4087	2521	2892	2048
ppt-miR156a	4346	4087	2521	2892	2048
ppt-miR156b	4346	4087	2521	2892	2048
ppt-miR156c	4346	4087	2521	2892	2048
ptc-miR156a	4346	4087	2521	2892	2048
ptc-miR156b	4346	4087	2521	2892	2048
ptc-miR156c	4346	4087	2521	2892	2048
ptc-miR156d	4346	4087	2521	2892	2048
ptc-miR156e	4346	4087	2521	2892	2048
ptc-miR156f	4346	4087	2521	2892	2048
sbi-miR156a	4346	4087	2521	2892	2048
sbi-miR156b	4346	4087	2521	2892	2048
sbi-miR156c	4346	4087	2521	2892	2048
sbi-miR156f	4346	4087	2521	2892	2048
sbi-miR156g	4346	4087	2521	2892	2048
sbi-miR156h	4346	4087	2521	2892	2048
sbi-miR156i	4346	4087	2521	2892	2048
sly-miR156d-5p	4346	4087	2521	2892	2048
sof-miR156	4346	4087	2521	2892	2048

stu-miR156e	4346	4087	2521	2892	2048
stu-miR156g-5p	4346	4087	2521	2892	2048
stu-miR156h-5p	4346	4087	2521	2892	2048
stu-miR156i-5p	4346	4087	2521	2892	2048
stu-miR156j-5p	4346	4087	2521	2892	2048
stu-miR156k-5p	4346	4087	2521	2892	2048
tcc-miR156b	4346	4087	2521	2892	2048
tcc-miR156c	4346	4087	2521	2892	2048
tcc-miR156d	4346	4087	2521	2892	2048
tcc-miR156g	4346	4087	2521	2892	2048
vca-miR156a-5p	4346	4087	2521	2892	2048
vun-miR156a	4346	4087	2521	2892	2048
vvi-miR156b	4346	4087	2521	2892	2048
vvi-miR156c	4346	4087	2521	2892	2048
vvi-miR156d	4346	4087	2521	2892	2048
zma-miR156a-5p	4346	4087	2521	2892	2048
zma-miR156b-5p	4346	4087	2521	2892	2048
zma-miR156c	4346	4087	2521	2892	2048
zma-miR156d-5p	4346	4087	2521	2892	2048
zma-miR156e-5p	4346	4087	2521	2892	2048
zma-miR156f-5p	4346	4087	2521	2892	2048
zma-miR156g-5p	4346	4087	2521	2892	2048
zma-miR156h-5p	4346	4087	2521	2892	2048
zma-miR156i-5p	4346	4087	2521	2892	2048
zma-miR156l-5p	4346	4087	2521	2892	2048
cme-miR156j	4473	4226	2603	2978	2127
fve-miR156a	4473	4226	2603	2978	2127
fve-miR156b	4473	4226	2603	2978	2127
fve-miR156c	4473	4226	2603	2978	2127
fve-miR156e	4473	4226	2603	2978	2127
gma-miR156k	4473	4226	2603	2978	2127
gma-miR156n	4473	4226	2603	2978	2127
gma-miR156o	4473	4226	2603	2978	2127
bna-miR156a	4370	4109	2532	2903	2073
hvu-miR156a	4370	4109	2532	2903	2073
hvu-miR156b	4370	4109	2532	2903	2073
rco-miR156a	4370	4109	2532	2903	2073
rco-miR156b	4370	4109	2532	2903	2073
rco-miR156c	4370	4109	2532	2903	2073
rco-miR156d	4370	4109	2532	2903	2073
ssl-miR156	4370	4109	2532	2903	2073
ssp-miR156	4370	4109	2532	2903	2073
tae-miR156	4370	4109	2532	2903	2073

gma-miR156q	4361	4101	2529	2913	2052
gma-miR156s	4361	4101	2529	2913	2052
aca-miR-148a-3p	0	61	174	33	60
bta-miR-148a	0	61	174	33	60
cfa-miR-148a	0	61	174	33	60
cgr-miR-148a	0	61	174	33	60
chi-miR-148a-3p	0	61	174	33	60
cja-miR-148a	0	61	174	33	60
cli-miR-148a-3p	0	61	174	33	60
cpi-miR-148a-3p	0	61	174	33	60
cpo-miR-148a-3p	0	61	174	33	60
dno-miR-148a-3p	0	61	174	33	60
eca-miR-148a	0	61	174	33	60
gga-miR-148a-3p	0	61	174	33	60
hsa-miR-148a-3p	0	61	174	33	60
mdo-miR-148-3p	0	61	174	33	60
mml-miR-148a-3p	0	61	174	33	60
mmu-miR-148a-3p	0	61	174	33	60
oan-miR-148-3p	0	61	174	33	60
oar-miR-148a	0	61	174	33	60
ocu-miR-148a-3p	0	61	174	33	60
pal-miR-148a-3p	0	61	174	33	60
pbv-miR-148a-3p	0	61	174	33	60
ppy-miR-148a	0	61	174	33	60
ptr-miR-148a	0	61	174	33	60
sbo-miR-148a	0	61	174	33	60
ssc-miR-148a-3p	0	61	174	33	60
tch-miR-148a-3p	0	61	174	33	60
tgu-miR-148a-3p	0	61	174	33	60
xtr-miR-148a	0	61	174	33	60
age-miR-22	1379	886	1272	702	902
aja-miR-22	1379	886	1272	702	902
cfa-miR-22	1379	886	1272	702	902
cgr-miR-22-3p	1379	886	1272	702	902
cja-miR-22	1379	886	1272	702	902
cli-miR-22-3p	1379	886	1272	702	902
cpi-miR-22-3p	1379	886	1272	702	902
cpo-miR-22-3p	1379	886	1272	702	902
dma-miR-22	1379	886	1272	702	902
dno-miR-22-3p	1379	886	1272	702	902
eca-miR-22	1379	886	1272	702	902
gga-miR-22-3p	1379	886	1272	702	902
hsa-miR-22-3p	1379	886	1272	702	902

lca-miR-22	1379	886	1272	702	902
lla-miR-22	1379	886	1272	702	902
mml-miR-22	1379	886	1272	702	902
mmr-miR-22	1379	886	1272	702	902
mmu-miR-22-3p	1379	886	1272	702	902
mne-miR-22	1379	886	1272	702	902
nle-miR-22	1379	886	1272	702	902
oan-miR-22-3p	1379	886	1272	702	902
ocu-miR-22-3p	1379	886	1272	702	902
oga-miR-22	1379	886	1272	702	902
oha-miR-22a	1379	886	1272	702	902
pal-miR-22-3p	1379	886	1272	702	902
pbv-miR-22-3p	1379	886	1272	702	902
pha-miR-22	1379	886	1272	702	902
ppa-miR-22	1379	886	1272	702	902
ppy-miR-22	1379	886	1272	702	902
ptr-miR-22	1379	886	1272	702	902
rno-miR-22-3p	1379	886	1272	702	902
sbo-miR-22	1379	886	1272	702	902
sla-miR-22	1379	886	1272	702	902
ssc-miR-22-3p	1379	886	1272	702	902
tch-miR-22-3p	1379	886	1272	702	902
xtr-miR-22-3p	1379	886	1272	702	902
aly-miR170-5p	8021	6868	7105	4211	6540
aly-miR171a-5p	8021	6868	7105	4211	6540
ath-miR170-5p	8021	6868	7105	4211	6540
ath-miR171a-5p	8021	6868	7105	4211	6540
cas-miR170	8021	6868	7105	4211	6540
cas-miR171a-5p	8021	6868	7105	4211	6540
csi-miR171f-5p	8021	6868	7105	4211	6540
gma-miR171j-5p	8021	6868	7105	4211	6540
sly-miR171f	8021	6868	7105	4211	6540
stu-miR171a-5p	8021	6868	7105	4211	6540
stu-miR171c-5p	8021	6868	7105	4211	6540
age-miR-16	266	163	163	103	156
cfa-miR-16	266	163	163	103	156
cgr-miR-16-5p	266	163	163	103	156
cja-miR-16	266	163	163	103	156
cpi-miR-16a-5p	266	163	163	103	156
dma-miR-16	266	163	163	103	156
eca-miR-16	266	163	163	103	156
ggo-miR-16	266	163	163	103	156
hsa-miR-16-5p	266	163	163	103	156

lla-miR-16	266	163	163	103	156
mdo-miR-16-5p	266	163	163	103	156
mml-miR-16-5p	266	163	163	103	156
mmu-miR-16-5p	266	163	163	103	156
mne-miR-16	266	163	163	103	156
mze-miR-16a	266	163	163	103	156
nle-miR-16	266	163	163	103	156
oan-miR-16a-5p	266	163	163	103	156
oga-miR-16	266	163	163	103	156
oni-miR-16a	266	163	163	103	156
pal-miR-16-5p	266	163	163	103	156
pha-miR-16	266	163	163	103	156
ppa-miR-16	266	163	163	103	156
ptr-miR-16	266	163	163	103	156
rno-miR-16-5p	266	163	163	103	156
sbo-miR-16	266	163	163	103	156
sla-miR-16	266	163	163	103	156
ssa-miR-16c-5p	266	163	163	103	156
ssc-miR-16	266	163	163	103	156
xla-miR-148a-3p	0	61	177	34	60
efu-miR-133-3p	331	233	127	128	219
chi-miR-133a-3p	324	223	125	127	212
cli-miR-133a-3p	324	223	125	127	212
cpi-miR-133a-3p	324	223	125	127	212
cpo-miR-133a-3p	324	223	125	127	212
dno-miR-133a-3p	324	223	125	127	212
ocu-miR-133a-3p	324	223	125	127	212
pbv-miR-133a-3p	324	223	125	127	212
aca-miR-200a-3p	2	58	166	41	61
ami-miR-200a-3p	2	58	166	41	61
dre-miR-200a-3p	2	58	166	41	61
eca-miR-200a	2	58	166	41	61
fru-miR-200a	2	58	166	41	61
gga-miR-200a-3p	2	58	166	41	61
ggo-miR-200a	2	58	166	41	61
gmo-miR-200a-3p	2	58	166	41	61
hsa-miR-200a-3p	2	58	166	41	61
mdo-miR-200a-3p	2	58	166	41	61
mml-miR-200a-3p	2	58	166	41	61
mmu-miR-200a-3p	2	58	166	41	61
ppy-miR-200a	2	58	166	41	61
ptr-miR-200a	2	58	166	41	61
rno-miR-200a-3p	2	58	166	41	61

tni-miR-200a	2	58	166	41	61
xtr-miR-200a	2	58	166	41	61
osa-miR159f	1487	3915	3203	2104	1946
aof-miR171b	340	402	379	288	323
fve-miR171f-3p	340	402	379	288	323
gma-miR171k-3p	340	402	379	288	323
lja-miR171d-5p	340	402	379	288	323
mdm-miR171j	340	402	379	288	323
mdm-miR171k	340	402	379	288	323
mdm-miR171l	340	402	379	288	323
mes-miR171e	340	402	379	288	323
nta-miR171b	340	402	379	288	323
pab-miR171b	340	402	379	288	323
pab-miR171c	340	402	379	288	323
ppe-miR171b	340	402	379	288	323
ssl-miR171b	340	402	379	288	323
vvi-miR171f	340	402	379	288	323
abu-miR-200a	16	197	535	142	189
bta-miR-200a	16	197	535	142	189
cgr-miR-200a	16	197	535	142	189
cli-miR-200a-3p	16	197	535	142	189
cpi-miR-200a-3p	16	197	535	142	189
cpo-miR-200a-3p	16	197	535	142	189
efu-miR-200a	16	197	535	142	189
mze-miR-200a	16	197	535	142	189
nbr-miR-200a	16	197	535	142	189
oan-miR-200a-3p	16	197	535	142	189
oha-miR-200a	16	197	535	142	189
oni-miR-200a	16	197	535	142	189
pal-miR-200a-3p	16	197	535	142	189
pbv-miR-200a-3p	16	197	535	142	189
pny-miR-200a	16	197	535	142	189
ssa-miR-200b-3p	16	197	535	142	189
tch-miR-200a-3p	16	197	535	142	189
tgu-miR-200a-3p	16	197	535	142	189
xla-miR-200a-3p	16	197	535	142	189
aca-miR-181a	221	179	302	129	188
ami-miR-181a-5p	221	179	302	129	188
cgr-miR-181a-5p	221	179	302	129	188
cja-miR-181a	221	179	302	129	188
cpi-miR-181a-5p	221	179	302	129	188
dma-miR-181a	221	179	302	129	188
dre-miR-181a-5p	221	179	302	129	188

eca-miR-181a	221	179	302	129	188
fru-miR-181a-5p	221	179	302	129	188
gga-miR-181a-5p	221	179	302	129	188
ggo-miR-181a-5p	221	179	302	129	188
gmo-miR-181a-5p	221	179	302	129	188
hsa-miR-181a-5p	221	179	302	129	188
lla-miR-181a-5p	221	179	302	129	188
mdo-miR-181a-5p	221	179	302	129	188
mml-miR-181a-5p	221	179	302	129	188
mmu-miR-181a-5p	221	179	302	129	188
mne-miR-181a-5p	221	179	302	129	188
nle-miR-181a	221	179	302	129	188
oan-miR-181a-5p	221	179	302	129	188
oar-miR-181a	221	179	302	129	188
oga-miR-181a	221	179	302	129	188
pha-miR-181a	221	179	302	129	188
pma-miR-181a-5p	221	179	302	129	188
ppa-miR-181a-5p	221	179	302	129	188
ppy-miR-181a-5p	221	179	302	129	188
ptr-miR-181a-5p	221	179	302	129	188
rno-miR-181a-5p	221	179	302	129	188
sla-miR-181a	221	179	302	129	188
ssa-miR-181a-5p	221	179	302	129	188
tch-miR-181a-5p	221	179	302	129	188
tgu-miR-181a-5p	221	179	302	129	188
tni-miR-181a-5p	221	179	302	129	188
xtr-miR-181a-5p	221	179	302	129	188
bta-miR-181a	264	202	337	151	211
cli-miR-181a-5p	264	202	337	151	211
cpo-miR-181a-5p	264	202	337	151	211
dno-miR-181a-5p	264	202	337	151	211
ocu-miR-181a-5p	264	202	337	151	211
oha-miR-181a-5p	264	202	337	151	211
pal-miR-181a-5p	264	202	337	151	211
pbv-miR-181a-5p	264	202	337	151	211
ssc-miR-181a	264	202	337	151	211
abu-miR-221	90	49	41	42	43
ami-miR-221-3p	90	49	41	42	43
cgr-miR-221-3p	90	49	41	42	43
cpo-miR-221-3p	90	49	41	42	43
dma-miR-221	90	49	41	42	43
dno-miR-221-3p	90	49	41	42	43
dre-miR-221-3p	90	49	41	42	43

eca-miR-221	90	49	41	42	43
fru-miR-221	90	49	41	42	43
gga-miR-221-3p	90	49	41	42	43
ggo-miR-221	90	49	41	42	43
hsa-miR-221-3p	90	49	41	42	43
mdo-miR-221-3p	90	49	41	42	43
mml-miR-221-3p	90	49	41	42	43
mmr-miR-221	90	49	41	42	43
mmu-miR-221-3p	90	49	41	42	43
mze-miR-221	90	49	41	42	43
nbr-miR-221	90	49	41	42	43
nle-miR-221	90	49	41	42	43
ocu-miR-221-3p	90	49	41	42	43
oga-miR-221	90	49	41	42	43
oha-miR-221-3p	90	49	41	42	43
ola-miR-221	90	49	41	42	43
oni-miR-221	90	49	41	42	43
pha-miR-221	90	49	41	42	43
pny-miR-221	90	49	41	42	43
ppa-miR-221	90	49	41	42	43
ppy-miR-221	90	49	41	42	43
ptr-miR-221	90	49	41	42	43
rno-miR-221-3p	90	49	41	42	43
sbo-miR-221	90	49	41	42	43
tgu-miR-221-3p	90	49	41	42	43
tni-miR-221	90	49	41	42	43
xtr-miR-221	90	49	41	42	43
gma-miR159e-5p	2364	1927	1599	1667	1619
cli-miR-199-3p	191	104	103	82	111
efu-miR-199	191	104	103	82	111
dre-miR-199-3p	182	97	95	75	108
oha-miR-199c-3p	182	97	95	75	108
ssc-miR-199b-3p	182	97	95	75	108
xtr-miR-199a-3p	182	97	95	75	108
aca-miR-23a-3p	177	117	122	81	117
age-miR-23a	177	117	122	81	117
ccr-miR-23a	177	117	122	81	117
cgr-miR-23a-3p	177	117	122	81	117
chi-miR-23a	177	117	122	81	117
cpi-miR-23a-3p	177	117	122	81	117
eca-miR-23a	177	117	122	81	117
ggo-miR-23a	177	117	122	81	117
hsa-miR-23a-3p	177	117	122	81	117

ipu-miR-23a	177	117	122	81	117
lca-miR-23a	177	117	122	81	117
mml-miR-23a-3p	177	117	122	81	117
mmu-miR-23a-3p	177	117	122	81	117
mne-miR-23a	177	117	122	81	117
pbv-miR-23a-3p	177	117	122	81	117
pha-miR-23a	177	117	122	81	117
pny-miR-23a	177	117	122	81	117
ppa-miR-23a	177	117	122	81	117
ppy-miR-23a	177	117	122	81	117
ptr-miR-23a	177	117	122	81	117
rno-miR-23a-3p	177	117	122	81	117
sla-miR-23a	177	117	122	81	117
ssa-miR-23a-3p	177	117	122	81	117
ssc-miR-23a	177	117	122	81	117
xla-miR-23a	177	117	122	81	117
xtr-miR-23a	177	117	122	81	117
aly-miR168a-5p	28942	22785	27536	20618	22487
aly-miR168b-5p	28942	22785	27536	20618	22487
aof-miR168a	28942	22785	27536	20618	22487
ath-miR168a-5p	28942	22785	27536	20618	22487
ath-miR168b-5p	28942	22785	27536	20618	22487
atr-miR168	28942	22785	27536	20618	22487
bna-miR168a	28942	22785	27536	20618	22487
bra-miR168a-5p	28942	22785	27536	20618	22487
cca-miR168a	28942	22785	27536	20618	22487
ccl-miR168	28942	22785	27536	20618	22487
crt-miR168	28942	22785	27536	20618	22487
csi-miR168-5p	28942	22785	27536	20618	22487
fve-miR168-5p	28942	22785	27536	20618	22487
gma-miR168a	28942	22785	27536	20618	22487
lus-miR168a	28942	22785	27536	20618	22487
lus-miR168b	28942	22785	27536	20618	22487
mdm-miR168a	28942	22785	27536	20618	22487
mdm-miR168b	28942	22785	27536	20618	22487
mes-miR168a	28942	22785	27536	20618	22487
mtr-miR168b	28942	22785	27536	20618	22487
mtr-miR168c-5p	28942	22785	27536	20618	22487
nta-miR168d	28942	22785	27536	20618	22487
nta-miR168e	28942	22785	27536	20618	22487
pab-miR168a	28942	22785	27536	20618	22487
ppe-miR168	28942	22785	27536	20618	22487
ptc-miR168a-5p	28942	22785	27536	20618	22487

ptc-miR168b-5p	28942	22785	27536	20618	22487
rco-miR168	28942	22785	27536	20618	22487
tcc-miR168	28942	22785	27536	20618	22487
vca-miR168a-5p	28942	22785	27536	20618	22487
vca-miR168b-5p	28942	22785	27536	20618	22487
vun-miR168	28942	22785	27536	20618	22487
vvi-miR168	28942	22785	27536	20618	22487
lja-miR168-5p	29003	22843	27583	20701	22538
oha-miR-1a-3p	135	103	63	65	98
pma-miR-1c-3p	135	103	63	65	98
ami-miR-27b-3p	67	83	148	54	80
dma-miR-27b	67	83	148	54	80
gmo-miR-27b-3p	67	83	148	54	80
nle-miR-27b	67	83	148	54	80
oga-miR-27b	67	83	148	54	80
pha-miR-27b	67	83	148	54	80
csi-miR167c-3p	377	359	421	357	328
aae-miR-133	206	143	77	83	146
abu-miR-133a	206	143	77	83	146
aga-miR-133	206	143	77	83	146
age-miR-133a	206	143	77	83	146
ame-miR-133-3p	206	143	77	83	146
bbe-miR-133-5p	206	143	77	83	146
bmo-miR-133	206	143	77	83	146
ccr-miR-133a-3p	206	143	77	83	146
cfa-miR-133a	206	143	77	83	146
cja-miR-133a	206	143	77	83	146
cqu-miR-133	206	143	77	83	146
cte-miR-133	206	143	77	83	146
dan-miR-133	206	143	77	83	146
der-miR-133	206	143	77	83	146
dgr-miR-133	206	143	77	83	146
dme-miR-133-3p	206	143	77	83	146
dmo-miR-133	206	143	77	83	146
dpe-miR-133	206	143	77	83	146
dps-miR-133	206	143	77	83	146
dpu-miR-133	206	143	77	83	146
dqu-miR-133-3p	206	143	77	83	146
dse-miR-133	206	143	77	83	146
dsi-miR-133	206	143	77	83	146
dvi-miR-133-3p	206	143	77	83	146
dwi-miR-133	206	143	77	83	146
dya-miR-133	206	143	77	83	146

gga-miR-133a-3p	206	143	77	83	146
ggo-miR-133a	206	143	77	83	146
gmo-miR-133a-3p	206	143	77	83	146
ipu-miR-133a	206	143	77	83	146
isc-miR-133	206	143	77	83	146
lgi-miR-133-3p	206	143	77	83	146
lla-miR-133a	206	143	77	83	146
mdo-miR-133a-3p	206	143	77	83	146
mne-miR-133a	206	143	77	83	146
mse-miR-133	206	143	77	83	146
mze-miR-133a	206	143	77	83	146
nbr-miR-133a	206	143	77	83	146
ngi-miR-133	206	143	77	83	146
nlo-miR-133	206	143	77	83	146
nvi-miR-133	206	143	77	83	146
oan-miR-133a-3p	206	143	77	83	146
oar-miR-133	206	143	77	83	146
oni-miR-133a	206	143	77	83	146
pal-miR-133a-3p	206	143	77	83	146
pca-miR-133-3p	206	143	77	83	146
ppa-miR-133a	206	143	77	83	146
sko-miR-133	206	143	77	83	146
sla-miR-133a	206	143	77	83	146
ssa-miR-133a-3p	206	143	77	83	146
tca-miR-133-3p	206	143	77	83	146
tcf-miR-133	206	143	77	83	146
tur-miR-133-3p	206	143	77	83	146
xla-miR-133a	206	143	77	83	146
xtr-miR-133a	206	143	77	83	146
ami-miR-199-3p	152	98	96	73	100
bta-miR-199a-3p	152	98	96	73	100
cpi-miR-199-3p	152	98	96	73	100
cpo-miR-199-3p	152	98	96	73	100
dno-miR-199-3p	152	98	96	73	100
eca-miR-199a-3p	152	98	96	73	100
eca-miR-199b-3p	152	98	96	73	100
gmo-miR-199-3p	152	98	96	73	100
hsa-miR-199a-3p	152	98	96	73	100
hsa-miR-199b-3p	152	98	96	73	100
mml-miR-199a-3p	152	98	96	73	100
mmu-miR-199a-3p	152	98	96	73	100
mmu-miR-199b-3p	152	98	96	73	100
ocu-miR-199a-3p	152	98	96	73	100

oha-miR-199a-3p	152	98	96	73	100
ola-miR-199a-3p	152	98	96	73	100
pol-miR-199a-3p	152	98	96	73	100
ptr-miR-199a-3p	152	98	96	73	100
ptr-miR-199b	152	98	96	73	100
rno-miR-199a-3p	152	98	96	73	100
ssc-miR-199a-3p	152	98	96	73	100
xla-miR-199-3p	152	98	96	73	100
bdi-miR166e-3p	1001	1255	1211	1048	894
atr-miR319a	4040	3144	2272	2517	2469
atr-miR319c	4040	3144	2272	2517	2469
cme-miR319a	4040	3144	2272	2517	2469
cme-miR319b	4040	3144	2272	2517	2469
ctr-miR319	4040	3144	2272	2517	2469
gma-miR319a	4040	3144	2272	2517	2469
gma-miR319b	4040	3144	2272	2517	2469
gma-miR319e	4040	3144	2272	2517	2469
lus-miR319b	4040	3144	2272	2517	2469
mtr-miR319a-3p	4040	3144	2272	2517	2469
mtr-miR319b-3p	4040	3144	2272	2517	2469
pab-miR319a	4040	3144	2272	2517	2469
pab-miR319b	4040	3144	2272	2517	2469
pab-miR319c	4040	3144	2272	2517	2469
pab-miR319f	4040	3144	2272	2517	2469
pab-miR319g	4040	3144	2272	2517	2469
pab-miR319i	4040	3144	2272	2517	2469
pab-miR319k	4040	3144	2272	2517	2469
pab-miR319l	4040	3144	2272	2517	2469
pab-miR319m	4040	3144	2272	2517	2469
pab-miR319n	4040	3144	2272	2517	2469
ppe-miR319a	4040	3144	2272	2517	2469
ptc-miR319a	4040	3144	2272	2517	2469
ptc-miR319b	4040	3144	2272	2517	2469
ptc-miR319c	4040	3144	2272	2517	2469
ptc-miR319d	4040	3144	2272	2517	2469
mes-miR166i	65	161	139	108	79
csi-miR159c-3p	4060	3182	2307	2548	2498
ppt-miR319c	4060	3182	2307	2548	2498
ppt-miR319d-3p	4060	3182	2307	2548	2498
ppt-miR319e	4060	3182	2307	2548	2498
abu-miR-199-3p	144	91	88	66	97
ccr-miR-199-3p	144	91	88	66	97
cfa-miR-199	144	91	88	66	97

cgr-miR-199a-3p	144	91	88	66	97
chi-miR-199a-3p	144	91	88	66	97
chi-miR-199b-3p	144	91	88	66	97
chi-miR-199c-3p	144	91	88	66	97
cja-miR-199	144	91	88	66	97
dma-miR-199	144	91	88	66	97
gmo-miR-199-4-3p	144	91	88	66	97
ipu-miR-199a-3p	144	91	88	66	97
mdo-miR-199b-3p	144	91	88	66	97
mmr-miR-199	144	91	88	66	97
mze-miR-199	144	91	88	66	97
nbr-miR-199	144	91	88	66	97
nle-miR-199a	144	91	88	66	97
nle-miR-199b	144	91	88	66	97
oan-miR-199-3p	144	91	88	66	97
oar-miR-199a-3p	144	91	88	66	97
oga-miR-199	144	91	88	66	97
oni-miR-199a	144	91	88	66	97
pal-miR-199-3p	144	91	88	66	97
pbv-miR-199-3p	144	91	88	66	97
pha-miR-199	144	91	88	66	97
pny-miR-199	144	91	88	66	97
ppa-miR-199b	144	91	88	66	97
sbo-miR-199	144	91	88	66	97
sha-miR-199a	144	91	88	66	97
ssa-miR-199a-3p	144	91	88	66	97
tch-miR-199a-3p	144	91	88	66	97
tch-miR-199b-3p	144	91	88	66	97
tgu-miR-199-3p	144	91	88	66	97
mtr-miR319c-3p	4046	3147	2279	2525	2473
vvi-miR319g	4046	3147	2279	2525	2473
csi-miR396f-3p	870	702	698	707	569
gma-miR396b-3p	870	702	698	707	569
gma-miR396k-3p	870	702	698	707	569
mtr-miR396a-3p	870	702	698	707	569
cpo-miR-23a-3p	264	180	170	131	175
dno-miR-23a-3p	264	180	170	131	175
efu-miR-23a	270	183	174	134	177
abu-miR-92a	107	89	126	64	97
aca-miR-92a	107	89	126	64	97
age-miR-92	107	89	126	64	97
ami-miR-92a-3p	107	89	126	64	97
bta-miR-92a	107	89	126	64	97

ccr-miR-92a	107	89	126	64	97
cfa-miR-92a	107	89	126	64	97
cgr-miR-92a-3p	107	89	126	64	97
chi-miR-92a-3p	107	89	126	64	97
chi-miR-92b	107	89	126	64	97
cja-miR-92a	107	89	126	64	97
cli-miR-92-3p	107	89	126	64	97
cpo-miR-92a-3p	107	89	126	64	97
dma-miR-92a	107	89	126	64	97
dno-miR-92a-3p	107	89	126	64	97
dre-miR-92a-3p	107	89	126	64	97
eca-miR-92a	107	89	126	64	97
efu-miR-92a	107	89	126	64	97
fru-miR-92	107	89	126	64	97
ggo-miR-92	107	89	126	64	97
hsa-miR-92a-3p	107	89	126	64	97
ipu-miR-92a	107	89	126	64	97
lca-miR-92	107	89	126	64	97
lla-miR-92	107	89	126	64	97
mdo-miR-92a-3p	107	89	126	64	97
mml-miR-92a-3p	107	89	126	64	97
mmr-miR-92a	107	89	126	64	97
mmr-miR-92b	107	89	126	64	97
mne-miR-92	107	89	126	64	97
mze-miR-92a	107	89	126	64	97
nbr-miR-92a	107	89	126	64	97
nle-miR-92a	107	89	126	64	97
oan-miR-92a-3p	107	89	126	64	97
ocu-miR-92a-3p	107	89	126	64	97
oga-miR-92a	107	89	126	64	97
oha-miR-92a	107	89	126	64	97
oha-miR-92a-3p	107	89	126	64	97
oni-miR-92a	107	89	126	64	97
pal-miR-92a-3p	107	89	126	64	97
pbv-miR-92a-3p	107	89	126	64	97
pha-miR-92a	107	89	126	64	97
pny-miR-92	107	89	126	64	97
ppa-miR-92a	107	89	126	64	97
ppy-miR-92	107	89	126	64	97
ptr-miR-92	107	89	126	64	97
sbo-miR-92a	107	89	126	64	97
sla-miR-92	107	89	126	64	97
ssa-miR-92a-3p	107	89	126	64	97

ssc-miR-92a	107	89	126	64	97
tch-miR-92a-3p	107	89	126	64	97
tgu-miR-92-3p	107	89	126	64	97
tni-miR-92	107	89	126	64	97
xla-miR-92a-3p	107	89	126	64	97
aau-miR319	5644	4160	3002	3409	3391
aly-miR319a-3p	5644	4160	3002	3409	3391
aly-miR319b-3p	5644	4160	3002	3409	3391
amg-miR319	5644	4160	3002	3409	3391
aof-miR319a	5644	4160	3002	3409	3391
aqc-miR319	5644	4160	3002	3409	3391
ath-miR319a	5644	4160	3002	3409	3391
ath-miR319b	5644	4160	3002	3409	3391
bra-miR319-3p	5644	4160	3002	3409	3391
cca-miR319	5644	4160	3002	3409	3391
gma-miR319h	5644	4160	3002	3409	3391
gma-miR319j	5644	4160	3002	3409	3391
gma-miR319k	5644	4160	3002	3409	3391
gma-miR319m	5644	4160	3002	3409	3391
hbr-miR319	5644	4160	3002	3409	3391
lus-miR319a	5644	4160	3002	3409	3391
mdm-miR319a	5644	4160	3002	3409	3391
mdm-miR319b-3p	5644	4160	3002	3409	3391
mes-miR319a	5644	4160	3002	3409	3391
mes-miR319b	5644	4160	3002	3409	3391
mes-miR319c	5644	4160	3002	3409	3391
mes-miR319d	5644	4160	3002	3409	3391
mes-miR319e	5644	4160	3002	3409	3391
mtr-miR319d-3p	5644	4160	3002	3409	3391
nta-miR319a	5644	4160	3002	3409	3391
nta-miR319b	5644	4160	3002	3409	3391
rco-miR319a	5644	4160	3002	3409	3391
rco-miR319b	5644	4160	3002	3409	3391
rco-miR319c	5644	4160	3002	3409	3391
sly-miR319b	5644	4160	3002	3409	3391
stu-miR319a-3p	5644	4160	3002	3409	3391
tae-miR319	5644	4160	3002	3409	3391
vun-miR319a	5644	4160	3002	3409	3391
vvi-miR319b	5644	4160	3002	3409	3391
vvi-miR319c	5644	4160	3002	3409	3391
vvi-miR319f	5644	4160	3002	3409	3391
gma-miR5374-5p	200	176	217	147	170
abu-miR-23a	257	176	161	129	171

ami-miR-23a-3p	257	176	161	129	171
bta-miR-23a	257	176	161	129	171
cja-miR-23a	257	176	161	129	171
dre-miR-23a-3p	257	176	161	129	171
fru-miR-23a	257	176	161	129	171
gmo-miR-23a-3p	257	176	161	129	171
hhi-miR-23a	257	176	161	129	171
mze-miR-23a	257	176	161	129	171
nbr-miR-23a	257	176	161	129	171
oan-miR-23a-3p	257	176	161	129	171
oar-miR-23a	257	176	161	129	171
oga-miR-23a	257	176	161	129	171
oha-miR-23a-3p	257	176	161	129	171
ola-miR-23a	257	176	161	129	171
oni-miR-23a	257	176	161	129	171
pal-miR-23a-3p	257	176	161	129	171
tni-miR-23a	257	176	161	129	171
xla-miR-23a-3p	257	176	161	129	171
aly-miR171b-3p	717	906	916	769	739
aly-miR171c-3p	717	906	916	769	739
ata-miR171c-3p	717	906	916	769	739
ath-miR171b-3p	717	906	916	769	739
ath-miR171c-3p	717	906	916	769	739
bna-miR171a	717	906	916	769	739
bna-miR171b	717	906	916	769	739
bna-miR171c	717	906	916	769	739
bna-miR171d	717	906	916	769	739
bna-miR171e	717	906	916	769	739
bol-miR171a	717	906	916	769	739
bra-miR171a	717	906	916	769	739
bra-miR171b	717	906	916	769	739
bra-miR171c	717	906	916	769	739
bra-miR171d	717	906	916	769	739
cas-miR171b	717	906	916	769	739
cas-miR171c-3p	717	906	916	769	739
cme-miR171b	717	906	916	769	739
cme-miR171d	717	906	916	769	739
gma-miR171i-3p	717	906	916	769	739
lus-miR171i	717	906	916	769	739
mdm-miR171f-3p	717	906	916	769	739
mes-miR171b	717	906	916	769	739
mes-miR171c	717	906	916	769	739
mtr-miR171f	717	906	916	769	739

ptc-miR171a-3p	717	906	916	769	739
ptc-miR171b	717	906	916	769	739
rco-miR171a	717	906	916	769	739
rco-miR171b	717	906	916	769	739
sly-miR171b-3p	717	906	916	769	739
ssl-miR171a	717	906	916	769	739
stu-miR171d-3p	717	906	916	769	739
tae-miR171b	717	906	916	769	739
ptc-miR396e-3p	559	463	485	488	383
aly-miR390a-5p	4718	5643	4258	4695	3692
aly-miR390b-5p	4718	5643	4258	4695	3692
aof-miR390	4718	5643	4258	4695	3692
ata-miR390-5p	4718	5643	4258	4695	3692
ath-miR390a-5p	4718	5643	4258	4695	3692
ath-miR390b-5p	4718	5643	4258	4695	3692
atr-miR390.2	4718	5643	4258	4695	3692
bdi-miR390a-5p	4718	5643	4258	4695	3692
bna-miR390a	4718	5643	4258	4695	3692
bna-miR390b	4718	5643	4258	4695	3692
bna-miR390c	4718	5643	4258	4695	3692
bra-miR390-5p	4718	5643	4258	4695	3692
cas-miR390a-5p	4718	5643	4258	4695	3692
cas-miR390b	4718	5643	4258	4695	3692
cme-miR390a	4718	5643	4258	4695	3692
cme-miR390b	4718	5643	4258	4695	3692
cme-miR390c	4718	5643	4258	4695	3692
cme-miR390d	4718	5643	4258	4695	3692
cpa-miR390a	4718	5643	4258	4695	3692
cpa-miR390b	4718	5643	4258	4695	3692
csi-miR390a-5p	4718	5643	4258	4695	3692
fve-miR390a	4718	5643	4258	4695	3692
fve-miR390b	4718	5643	4258	4695	3692
ghr-miR390a	4718	5643	4258	4695	3692
ghr-miR390b	4718	5643	4258	4695	3692
ghr-miR390c	4718	5643	4258	4695	3692
gma-miR390a-5p	4718	5643	4258	4695	3692
gma-miR390f	4718	5643	4258	4695	3692
gma-miR390g	4718	5643	4258	4695	3692
hex-miR390a	4718	5643	4258	4695	3692
hex-miR390b	4718	5643	4258	4695	3692
lja-miR390a-5p	4718	5643	4258	4695	3692
lja-miR390b-5p	4718	5643	4258	4695	3692
lus-miR390a	4718	5643	4258	4695	3692

lus-miR390b	4718	5643	4258	4695	3692
lus-miR390c	4718	5643	4258	4695	3692
lus-miR390d	4718	5643	4258	4695	3692
mdm-miR390a	4718	5643	4258	4695	3692
mdm-miR390b	4718	5643	4258	4695	3692
mdm-miR390c	4718	5643	4258	4695	3692
mdm-miR390d	4718	5643	4258	4695	3692
mdm-miR390e	4718	5643	4258	4695	3692
mdm-miR390f	4718	5643	4258	4695	3692
mes-miR390b	4718	5643	4258	4695	3692
mtr-miR390	4718	5643	4258	4695	3692
nta-miR390b	4718	5643	4258	4695	3692
nta-miR390c	4718	5643	4258	4695	3692
osa-miR390-5p	4718	5643	4258	4695	3692
pab-miR390a	4718	5643	4258	4695	3692
pab-miR390b	4718	5643	4258	4695	3692
ppe-miR390	4718	5643	4258	4695	3692
ppt-miR390a	4718	5643	4258	4695	3692
ppt-miR390b	4718	5643	4258	4695	3692
ptc-miR390a	4718	5643	4258	4695	3692
ptc-miR390b	4718	5643	4258	4695	3692
ptc-miR390c	4718	5643	4258	4695	3692
ptc-miR390d-5p	4718	5643	4258	4695	3692
rco-miR390a	4718	5643	4258	4695	3692
rco-miR390b	4718	5643	4258	4695	3692
sbi-miR390	4718	5643	4258	4695	3692
sly-miR390b-5p	4718	5643	4258	4695	3692
tcc-miR390a	4718	5643	4258	4695	3692
tcc-miR390b	4718	5643	4258	4695	3692
vvi-miR390	4718	5643	4258	4695	3692
zma-miR390a-5p	4718	5643	4258	4695	3692
zma-miR390b-5p	4718	5643	4258	4695	3692
aae-miR-125-5p	89	54	61	42	55
abu-miR-125b	89	54	61	42	55
aca-miR-125b	89	54	61	42	55
aga-miR-125	89	54	61	42	55
age-miR-125b	89	54	61	42	55
ami-miR-125b-5p	89	54	61	42	55
bbe-miR-125a-5p	89	54	61	42	55
bdo-miR-125	89	54	61	42	55
bfl-miR-125a-5p	89	54	61	42	55
bta-miR-125b	89	54	61	42	55
ccr-miR-125b	89	54	61	42	55

cfa-miR-125b	89	54	61	42	55
cgr-miR-125b-5p	89	54	61	42	55
cja-miR-125	89	54	61	42	55
cja-miR-125b	89	54	61	42	55
cli-miR-125-5p	89	54	61	42	55
cpi-miR-125b-5p	89	54	61	42	55
cpo-miR-125b-5p	89	54	61	42	55
cqu-miR-125-5p	89	54	61	42	55
cte-miR-125	89	54	61	42	55
dan-miR-125	89	54	61	42	55
der-miR-125	89	54	61	42	55
dgr-miR-125	89	54	61	42	55
dma-miR-125b	89	54	61	42	55
dme-miR-125-5p	89	54	61	42	55
dmo-miR-125	89	54	61	42	55
dno-miR-125b-5p	89	54	61	42	55
dpe-miR-125	89	54	61	42	55
dps-miR-125	89	54	61	42	55
dqu-miR-125-5p	89	54	61	42	55
dre-miR-125b-5p	89	54	61	42	55
dse-miR-125	89	54	61	42	55
dsi-miR-125	89	54	61	42	55
dwi-miR-125	89	54	61	42	55
dya-miR-125	89	54	61	42	55
eca-miR-125b-5p	89	54	61	42	55
efu-miR-125b	89	54	61	42	55
fru-miR-125b	89	54	61	42	55
gga-miR-125b-5p	89	54	61	42	55
ggo-miR-125b	89	54	61	42	55
gmo-miR-125b-5p	89	54	61	42	55
hsa-miR-125b-5p	89	54	61	42	55
ipu-miR-125b	89	54	61	42	55
lca-miR-125b	89	54	61	42	55
lla-miR-125b	89	54	61	42	55
lva-miR-125-5p	89	54	61	42	55
mdo-miR-125b-5p	89	54	61	42	55
mml-miR-125b-5p	89	54	61	42	55
mmr-miR-125a	89	54	61	42	55
mmu-miR-125b-5p	89	54	61	42	55
mne-miR-125b	89	54	61	42	55
mze-miR-125b	89	54	61	42	55
nbr-miR-125b	89	54	61	42	55
nle-miR-125b	89	54	61	42	55

nlo-miR-125	89	54	61	42	55
nvi-miR-125	89	54	61	42	55
oan-miR-125-5p	89	54	61	42	55
ocu-miR-125b-5p	89	54	61	42	55
oga-miR-125b	89	54	61	42	55
oha-miR-125b-5p	89	54	61	42	55
ola-miR-125b	89	54	61	42	55
ola-miR-125c	89	54	61	42	55
oni-miR-125b	89	54	61	42	55
pal-miR-125b-5p	89	54	61	42	55
pbv-miR-125b-5p	89	54	61	42	55
pha-miR-125b	89	54	61	42	55
pma-miR-125-5p	89	54	61	42	55
pmi-miR-125-5p	89	54	61	42	55
pny-miR-125b	89	54	61	42	55
ppa-miR-125b	89	54	61	42	55
ppy-miR-125b	89	54	61	42	55
ptr-miR-125b	89	54	61	42	55
rno-miR-125b-5p	89	54	61	42	55
sha-miR-125a	89	54	61	42	55
sko-miR-125a	89	54	61	42	55
sla-miR-125b	89	54	61	42	55
spu-miR-125-5p	89	54	61	42	55
ssa-miR-125a-5p	89	54	61	42	55
ssc-miR-125b	89	54	61	42	55
tca-miR-125-5p	89	54	61	42	55
tcf-miR-125	89	54	61	42	55
tch-miR-125b-5p	89	54	61	42	55
tgu-miR-125-5p	89	54	61	42	55
tni-miR-125b	89	54	61	42	55
xla-miR-125b-5p	89	54	61	42	55
xtr-miR-125b	89	54	61	42	55
cpa-miR166d	9876	9912	11328	9107	9264
gma-miR166j-3p	9876	9912	11328	9107	9264
crt-miR166a	9887	9917	11339	9118	9271
mes-miR166h	9887	9917	11339	9118	9271
atr-miR171b	613	340	332	360	408
gma-miR171c-3p	613	340	332	360	408
gma-miR171o-3p	613	340	332	360	408
gma-miR171q	613	340	332	360	408
mdm-miR171m	613	340	332	360	408
mdm-miR171n	613	340	332	360	408
zma-miR171f-3p	613	340	332	360	408

gma-miR169e	561	651	624	465	600
mtr-miR169e-5p	565	652	625	467	602
vvi-miR169m	565	652	625	467	602
vvi-miR169n	565	652	625	467	602
vvi-miR169p	565	652	625	467	602
vvi-miR169q	565	652	625	467	602
ata-miR169h-5p	566	657	625	469	603
bdi-miR169b	566	657	625	469	603
mes-miR169f	566	657	625	469	603
osa-miR169e	566	657	625	469	603
sbi-miR169e	566	657	625	469	603
sbi-miR169j	566	657	625	469	603
ssp-miR169	566	657	625	469	603
zma-miR169p-5p	566	657	625	469	603
cme-miR168	953	1082	894	850	845
bra-miR168b-5p	965	1101	912	870	854
bra-miR168c-5p	965	1101	912	870	854
nta-miR168a	965	1101	912	870	854
nta-miR168b	965	1101	912	870	854
nta-miR168c	965	1101	912	870	854
sly-miR168a-5p	965	1101	912	870	854
sly-miR168b-5p	965	1101	912	870	854
aof-miR167b	10888	9933	10539	8743	9558
ata-miR167b-5p	10888	9933	10539	8743	9558
ata-miR167d-5p	10888	9933	10539	8743	9558
bdi-miR167c-5p	10888	9933	10539	8743	9558
bdi-miR167d-5p	10888	9933	10539	8743	9558
bdi-miR167e-5p	10888	9933	10539	8743	9558
bdi-miR167g	10888	9933	10539	8743	9558
ccl-miR167a	10888	9933	10539	8743	9558
ccl-miR167b	10888	9933	10539	8743	9558
cpa-miR167d	10888	9933	10539	8743	9558
ctr-miR167	10888	9933	10539	8743	9558
eun-miR167a-5p	10888	9933	10539	8743	9558
gma-miR167g	10888	9933	10539	8743	9558
mes-miR167d	10888	9933	10539	8743	9558
mes-miR167e	10888	9933	10539	8743	9558
mes-miR167f	10888	9933	10539	8743	9558
ppe-miR167c	10888	9933	10539	8743	9558
vca-miR167a-5p	10888	9933	10539	8743	9558
vca-miR167b-5p	10888	9933	10539	8743	9558
aof-miR167c	10502	9647	10322	8511	9280
atr-miR167	10502	9647	10322	8511	9280

cme-miR167d	10502	9647	10322	8511	9280
cme-miR167f	10502	9647	10322	8511	9280
csi-miR167a-5p	10502	9647	10322	8511	9280
csi-miR167c-5p	10502	9647	10322	8511	9280
dpr-miR167c	10502	9647	10322	8511	9280
gma-miR167c	10502	9647	10322	8511	9280
gma-miR167j	10502	9647	10322	8511	9280
gso-miR167a	10502	9647	10322	8511	9280
lja-miR167	10502	9647	10322	8511	9280
lus-miR167f	10502	9647	10322	8511	9280
lus-miR167g	10502	9647	10322	8511	9280
lus-miR167i	10502	9647	10322	8511	9280
mes-miR167a	10502	9647	10322	8511	9280
mtr-miR167b-5p	10502	9647	10322	8511	9280
osa-miR167d-5p	10502	9647	10322	8511	9280
osa-miR167e-5p	10502	9647	10322	8511	9280
osa-miR167f	10502	9647	10322	8511	9280
osa-miR167g	10502	9647	10322	8511	9280
osa-miR167h-5p	10502	9647	10322	8511	9280
osa-miR167i-5p	10502	9647	10322	8511	9280
osa-miR167j	10502	9647	10322	8511	9280
ptc-miR167e	10502	9647	10322	8511	9280
sbi-miR167c	10502	9647	10322	8511	9280
sbi-miR167d	10502	9647	10322	8511	9280
sbi-miR167e	10502	9647	10322	8511	9280
sbi-miR167f	10502	9647	10322	8511	9280
sbi-miR167g	10502	9647	10322	8511	9280
sbi-miR167h	10502	9647	10322	8511	9280
sof-miR167a	10502	9647	10322	8511	9280
sof-miR167b	10502	9647	10322	8511	9280
ssp-miR167b	10502	9647	10322	8511	9280
vvi-miR167a	10502	9647	10322	8511	9280
zma-miR167e-5p	10502	9647	10322	8511	9280
zma-miR167f-5p	10502	9647	10322	8511	9280
zma-miR167g-5p	10502	9647	10322	8511	9280
zma-miR167h-5p	10502	9647	10322	8511	9280
zma-miR167i-5p	10502	9647	10322	8511	9280
zma-miR167j-5p	10502	9647	10322	8511	9280
aca-let-7b-5p	28	71	150	47	82
ggo-let-7b	28	71	150	47	82
ipu-let-7b	28	71	150	47	82
oar-let-7b	28	71	150	47	82
ola-let-7b	28	71	150	47	82

ata-miR167f-5p	10504	9649	10324	8514	9284
tae-miR167c-5p	10504	9649	10324	8514	9284
ppt-miR390c-5p	278	325	186	285	168
efu-miR-99a	203	319	406	196	297
aof-miR166b	356	315	387	316	314
csi-miR390b-5p	275	324	186	285	167
gma-miR390e	275	324	186	285	167
abu-miR-27b	109	114	188	89	124
bta-miR-27b	109	114	188	89	124
cfa-miR-27b	109	114	188	89	124
cgr-miR-27b-3p	109	114	188	89	124
chi-miR-27b-3p	109	114	188	89	124
cja-miR-27b	109	114	188	89	124
cli-miR-27b-3p	109	114	188	89	124
cpi-miR-27b-3p	109	114	188	89	124
cpo-miR-27b-3p	109	114	188	89	124
dno-miR-27b-3p	109	114	188	89	124
eca-miR-27b	109	114	188	89	124
gga-miR-27b-3p	109	114	188	89	124
ggo-miR-27b	109	114	188	89	124
hsa-miR-27b-3p	109	114	188	89	124
ipu-miR-27b	109	114	188	89	124
mdo-miR-27b-3p	109	114	188	89	124
mml-miR-27b-3p	109	114	188	89	124
mmr-miR-27b	109	114	188	89	124
mmu-miR-27b-3p	109	114	188	89	124
mze-miR-27b	109	114	188	89	124
nbr-miR-27b	109	114	188	89	124
oan-miR-27b-3p	109	114	188	89	124
ocu-miR-27b-3p	109	114	188	89	124
oni-miR-27b	109	114	188	89	124
pal-miR-27b-3p	109	114	188	89	124
pbv-miR-27b-3p	109	114	188	89	124
pma-miR-27b-3p	109	114	188	89	124
pny-miR-27b	109	114	188	89	124
ppa-miR-27b	109	114	188	89	124
ppy-miR-27b	109	114	188	89	124
ptr-miR-27b	109	114	188	89	124
rno-miR-27b-3p	109	114	188	89	124
sbo-miR-27b	109	114	188	89	124
sha-miR-27b	109	114	188	89	124
ssa-miR-27b-3p	109	114	188	89	124
ssc-miR-27b-3p	109	114	188	89	124

tch-miR-27b-3p	109	114	188	89	124
tgu-miR-27-3p	109	114	188	89	124
xtr-miR-27b	109	114	188	89	124
aca-miR-27b-3p	116	124	192	94	134
dre-miR-27b-3p	116	124	192	94	134
fru-miR-27b	116	124	192	94	134
oha-miR-27b-3p	116	124	192	94	134
tni-miR-27b	116	124	192	94	134
xla-miR-27b-3p	116	124	192	94	134
efu-miR-378	167	180	151	115	162
ggo-miR-378a	166	180	151	115	162
gma-miR169n-5p	387	611	589	332	607
mtr-miR169c	387	611	589	332	607
aca-miR-99a-5p	201	311	402	194	294
ami-miR-99a-5p	201	311	402	194	294
cli-miR-99-5p	201	311	402	194	294
cpi-miR-99a-5p	201	311	402	194	294
cpo-miR-99a-5p	201	311	402	194	294
dno-miR-99a-5p	201	311	402	194	294
dre-miR-99	201	311	402	194	294
eca-miR-99a	201	311	402	194	294
gga-miR-99a-5p	201	311	402	194	294
ggo-miR-99a	201	311	402	194	294
gmo-miR-99-5p	201	311	402	194	294
hsa-miR-99a-5p	201	311	402	194	294
ipu-miR-99a	201	311	402	194	294
lla-miR-99a	201	311	402	194	294
mml-miR-99a-5p	201	311	402	194	294
mmr-miR-99a	201	311	402	194	294
mmu-miR-99a-5p	201	311	402	194	294
mne-miR-99a	201	311	402	194	294
mze-miR-99b	201	311	402	194	294
nbr-miR-99b	201	311	402	194	294
ocu-miR-99a-5p	201	311	402	194	294
oga-miR-99a	201	311	402	194	294
oha-miR-99a-5p	201	311	402	194	294
oni-miR-99b	201	311	402	194	294
pbv-miR-99a-5p	201	311	402	194	294
pha-miR-99a	201	311	402	194	294
pny-miR-99b	201	311	402	194	294
ppa-miR-99a	201	311	402	194	294
ppy-miR-99a	201	311	402	194	294
ptr-miR-99a	201	311	402	194	294

rno-miR-99a-5p	201	311	402	194	294
ssa-miR-99-5p	201	311	402	194	294
ssc-miR-99a-5p	201	311	402	194	294
tch-miR-99a-5p	201	311	402	194	294
xtr-miR-99	201	311	402	194	294
bna-miR167d	7576	6868	7151	6109	6451
fve-miR167a	7576	6868	7151	6109	6451
fve-miR167b	7576	6868	7151	6109	6451
fve-miR167c	7576	6868	7151	6109	6451
gma-miR167l	7576	6868	7151	6109	6451
lja-miR167a	7576	6868	7151	6109	6451
lja-miR167b	7576	6868	7151	6109	6451
lja-miR167c	7576	6868	7151	6109	6451
mes-miR167b	7576	6868	7151	6109	6451
lus-miR167a	7648	6940	7218	6183	6514
vvi-miR167c	7648	6940	7218	6183	6514
fve-miR167d	7696	6976	7256	6211	6559
aca-miR-191-5p	250	146	156	119	176
bta-miR-191	250	146	156	119	176
cgr-miR-191-5p	250	146	156	119	176
cja-miR-191	250	146	156	119	176
cpo-miR-191-5p	250	146	156	119	176
dma-miR-191	250	146	156	119	176
dno-miR-191-5p	250	146	156	119	176
eca-miR-191a	250	146	156	119	176
gga-miR-191-5p	250	146	156	119	176
hsa-miR-191-5p	250	146	156	119	176
mml-miR-191-5p	250	146	156	119	176
mmr-miR-191	250	146	156	119	176
mmu-miR-191-5p	250	146	156	119	176
nle-miR-191	250	146	156	119	176
ocu-miR-191-5p	250	146	156	119	176
oga-miR-191	250	146	156	119	176
oha-miR-191-5p	250	146	156	119	176
pbv-miR-191-5p	250	146	156	119	176
pha-miR-191	250	146	156	119	176
ppa-miR-191	250	146	156	119	176
ppy-miR-191	250	146	156	119	176
ptr-miR-191	250	146	156	119	176
rno-miR-191a-5p	250	146	156	119	176
sbo-miR-191	250	146	156	119	176
ssc-miR-191	250	146	156	119	176
bta-miR-378	166	179	151	115	162

cfa-miR-378	166	179	151	115	162
cgr-miR-378-3p	166	179	151	115	162
chi-miR-378-3p	166	179	151	115	162
cja-miR-378	166	179	151	115	162
cpo-miR-378-3p	166	179	151	115	162
dno-miR-378-3p	166	179	151	115	162
hsa-miR-378a-3p	166	179	151	115	162
nle-miR-378a	166	179	151	115	162
ocu-miR-378-3p	166	179	151	115	162
oga-miR-378	166	179	151	115	162
pal-miR-378-3p	166	179	151	115	162
pha-miR-378	166	179	151	115	162
ppa-miR-378a	166	179	151	115	162
ssc-miR-378	166	179	151	115	162
tch-miR-378a-3p	166	179	151	115	162
ipu-miR-99b	220	333	441	213	320
abu-miR-99b	90	189	250	100	172
bta-miR-99a-5p	90	189	250	100	172
ccr-miR-99	90	189	250	100	172
cfa-miR-99a	90	189	250	100	172
cgr-miR-99a-5p	90	189	250	100	172
chi-miR-99a-5p	90	189	250	100	172
cja-miR-99	90	189	250	100	172
nle-miR-99a	90	189	250	100	172
oan-miR-99-5p	90	189	250	100	172
pal-miR-99a-5p	90	189	250	100	172
sbo-miR-99a	90	189	250	100	172
tgu-miR-99-5p	90	189	250	100	172
xla-miR-99-5p	90	189	250	100	172
abu-miR-30d	42	53	90	31	65
aca-miR-30b-5p	42	53	90	31	65
ami-miR-30b-5p	42	53	90	31	65
bta-miR-30b-5p	42	53	90	31	65
ccr-miR-30b	42	53	90	31	65
cfa-miR-30b	42	53	90	31	65
cgr-miR-30b-5p	42	53	90	31	65
chi-miR-30b-5p	42	53	90	31	65
cja-miR-30b	42	53	90	31	65
cpi-miR-30b-5p	42	53	90	31	65
cpo-miR-30b-5p	42	53	90	31	65
dno-miR-30b-5p	42	53	90	31	65
dre-miR-30b	42	53	90	31	65
eca-miR-30b	42	53	90	31	65

fru-miR-30b	42	53	90	31	65
gga-miR-30b-5p	42	53	90	31	65
gmo-miR-30c-5p	42	53	90	31	65
hsa-miR-30b-5p	42	53	90	31	65
ipu-miR-30b	42	53	90	31	65
mdo-miR-30b-5p	42	53	90	31	65
mmu-miR-30b-5p	42	53	90	31	65
mze-miR-30d	42	53	90	31	65
nbr-miR-30d	42	53	90	31	65
nle-miR-30b	42	53	90	31	65
oan-miR-30b-5p	42	53	90	31	65
ocu-miR-30b-5p	42	53	90	31	65
oga-miR-30b	42	53	90	31	65
oha-miR-30b-5p	42	53	90	31	65
oni-miR-30d	42	53	90	31	65
pal-miR-30b-5p	42	53	90	31	65
pbv-miR-30b-5p	42	53	90	31	65
pny-miR-30d	42	53	90	31	65
ppy-miR-30b	42	53	90	31	65
rno-miR-30b-5p	42	53	90	31	65
ssa-miR-30e-5p	42	53	90	31	65
ssc-miR-30b-5p	42	53	90	31	65
tch-miR-30b-5p	42	53	90	31	65
tgu-miR-30e	42	53	90	31	65
tni-miR-30b	42	53	90	31	65
xla-miR-30b-5p	42	53	90	31	65
xtr-miR-30b	42	53	90	31	65
mdo-miR-22-3p	55	48	121	42	82
crt-miR166b	1477	1442	1546	1462	1248
cas-miR166e	1471	1437	1540	1457	1243
csi-miR166f-3p	1471	1437	1540	1457	1243
osa-miR166m	1471	1437	1540	1457	1243
aly-miR166a-5p	5486	4533	6616	5391	4363
aly-miR166c-5p	5486	4533	6616	5391	4363
aly-miR166d-5p	5486	4533	6616	5391	4363
bdi-miR166e-5p	5486	4533	6616	5391	4363
cas-miR166a	5486	4533	6616	5391	4363
csi-miR166a-5p	5486	4533	6616	5391	4363
csi-miR166e-5p	5486	4533	6616	5391	4363
eun-miR166-5p	5486	4533	6616	5391	4363
gma-miR166a-5p	5486	4533	6616	5391	4363
gma-miR166c-5p	5486	4533	6616	5391	4363
gma-miR166l	5486	4533	6616	5391	4363

mtr-miR166g-5p	5486	4533	6616	5391	4363
osa-miR166d-5p	5486	4533	6616	5391	4363
stu-miR166a-5p	5486	4533	6616	5391	4363
vca-miR166b-5p	5486	4533	6616	5391	4363
zma-miR166c-5p	5486	4533	6616	5391	4363
gma-miR169d	678	740	699	522	697
aly-miR167d-5p	14528	13834	15655	12374	13711
ath-miR167d	14528	13834	15655	12374	13711
cca-miR167	14528	13834	15655	12374	13711
eun-miR167b-5p	14528	13834	15655	12374	13711
nta-miR167a	14528	13834	15655	12374	13711
nta-miR167b	14528	13834	15655	12374	13711
nta-miR167c	14528	13834	15655	12374	13711
pab-miR167b	14528	13834	15655	12374	13711
rco-miR167c	14528	13834	15655	12374	13711
mes-miR394c	20373	13190	6876	10560	9404
vvi-miR394a	20373	13190	6876	10560	9404
vvi-miR394c	20373	13190	6876	10560	9404
ahy-miR394	20361	13174	6869	10551	9394
aly-miR394a-5p	20361	13174	6869	10551	9394
aly-miR394b-5p	20361	13174	6869	10551	9394
aof-miR394	20361	13174	6869	10551	9394
ata-miR394-5p	20361	13174	6869	10551	9394
ath-miR394a	20361	13174	6869	10551	9394
ath-miR394b-5p	20361	13174	6869	10551	9394
atr-miR394	20361	13174	6869	10551	9394
bdi-miR394	20361	13174	6869	10551	9394
bna-miR394a	20361	13174	6869	10551	9394
bna-miR394b	20361	13174	6869	10551	9394
cca-miR394	20361	13174	6869	10551	9394
cme-miR394a	20361	13174	6869	10551	9394
cme-miR394b	20361	13174	6869	10551	9394
cpa-miR394a	20361	13174	6869	10551	9394
cpa-miR394b	20361	13174	6869	10551	9394
csi-miR394a	20361	13174	6869	10551	9394
csi-miR394b-5p	20361	13174	6869	10551	9394
fve-miR394	20361	13174	6869	10551	9394
ghr-miR394a	20361	13174	6869	10551	9394
ghr-miR394b	20361	13174	6869	10551	9394
gma-miR394a-5p	20361	13174	6869	10551	9394
gma-miR394b-5p	20361	13174	6869	10551	9394
gma-miR394c-5p	20361	13174	6869	10551	9394
gma-miR394d	20361	13174	6869	10551	9394

gma-miR394e	20361	13174	6869	10551	9394
gma-miR394f	20361	13174	6869	10551	9394
gma-miR394g	20361	13174	6869	10551	9394
lus-miR394a	20361	13174	6869	10551	9394
lus-miR394b	20361	13174	6869	10551	9394
mdm-miR394a	20361	13174	6869	10551	9394
mdm-miR394b	20361	13174	6869	10551	9394
mes-miR394a	20361	13174	6869	10551	9394
mes-miR394b	20361	13174	6869	10551	9394
nta-miR394	20361	13174	6869	10551	9394
osa-miR394	20361	13174	6869	10551	9394
pab-miR394c	20361	13174	6869	10551	9394
ppe-miR394a	20361	13174	6869	10551	9394
ppe-miR394b	20361	13174	6869	10551	9394
ptc-miR394a-5p	20361	13174	6869	10551	9394
ptc-miR394b-5p	20361	13174	6869	10551	9394
sbi-miR394a	20361	13174	6869	10551	9394
sbi-miR394b	20361	13174	6869	10551	9394
sly-miR394-5p	20361	13174	6869	10551	9394
ssl-miR394	20361	13174	6869	10551	9394
stu-miR384-5p	20361	13174	6869	10551	9394
tcc-miR394a	20361	13174	6869	10551	9394
tcc-miR394b	20361	13174	6869	10551	9394
vvi-miR394b	20361	13174	6869	10551	9394
zma-miR394a-5p	20361	13174	6869	10551	9394
zma-miR394b-5p	20361	13174	6869	10551	9394
aly-miR396a-3p	248	215	161	180	207
ath-miR396a-3p	248	215	161	180	207
csi-miR396b-3p	248	215	161	180	207
eun-miR396a-3p	248	215	161	180	207
fve-miR396a-3p	248	215	161	180	207
fve-miR396c-3p	248	215	161	180	207
gma-miR396i-3p	248	215	161	180	207
mtr-miR396b-3p	248	215	161	180	207
sly-miR396a-3p	248	215	161	180	207
cas-miR394	20411	13198	6897	10582	9441
bna-miR167a	13781	13587	11418	10576	12688
bna-miR167b	13781	13587	11418	10576	12688
aly-miR167a-5p	13768	13581	11415	10571	12683
aly-miR167b-5p	13768	13581	11415	10571	12683
aof-miR167a	13768	13581	11415	10571	12683
ata-miR167a-5p	13768	13581	11415	10571	12683
ata-miR167c-5p	13768	13581	11415	10571	12683

ata-miR167e-5p	13768	13581	11415	10571	12683
ath-miR167a-5p	13768	13581	11415	10571	12683
ath-miR167b	13768	13581	11415	10571	12683
bdi-miR167a	13768	13581	11415	10571	12683
bdi-miR167b	13768	13581	11415	10571	12683
bdi-miR167f	13768	13581	11415	10571	12683
bna-miR167c	13768	13581	11415	10571	12683
bra-miR167a	13768	13581	11415	10571	12683
bra-miR167b	13768	13581	11415	10571	12683
bra-miR167c	13768	13581	11415	10571	12683
bra-miR167d	13768	13581	11415	10571	12683
cme-miR167a	13768	13581	11415	10571	12683
cme-miR167b	13768	13581	11415	10571	12683
cpa-miR167a	13768	13581	11415	10571	12683
cpa-miR167b	13768	13581	11415	10571	12683
csi-miR167d-5p	13768	13581	11415	10571	12683
csi-miR167e-5p	13768	13581	11415	10571	12683
dpr-miR167a	13768	13581	11415	10571	12683
dpr-miR167b	13768	13581	11415	10571	12683
ghr-miR167a	13768	13581	11415	10571	12683
ghr-miR167b	13768	13581	11415	10571	12683
gma-miR167a	13768	13581	11415	10571	12683
gma-miR167b	13768	13581	11415	10571	12683
gma-miR167d	13768	13581	11415	10571	12683
lus-miR167c	13768	13581	11415	10571	12683
lus-miR167d	13768	13581	11415	10571	12683
lus-miR167e	13768	13581	11415	10571	12683
lus-miR167h	13768	13581	11415	10571	12683
mdm-miR167b	13768	13581	11415	10571	12683
mdm-miR167c	13768	13581	11415	10571	12683
mdm-miR167d	13768	13581	11415	10571	12683
mdm-miR167e	13768	13581	11415	10571	12683
mdm-miR167f	13768	13581	11415	10571	12683
mdm-miR167g	13768	13581	11415	10571	12683
mes-miR167c	13768	13581	11415	10571	12683
mtr-miR167a	13768	13581	11415	10571	12683
nta-miR167d	13768	13581	11415	10571	12683
nta-miR167e	13768	13581	11415	10571	12683
osa-miR167a-5p	13768	13581	11415	10571	12683
osa-miR167b	13768	13581	11415	10571	12683
osa-miR167c-5p	13768	13581	11415	10571	12683
ppe-miR167a	13768	13581	11415	10571	12683
ppe-miR167b	13768	13581	11415	10571	12683

ptc-miR167a	13768	13581	11415	10571	12683
ptc-miR167b	13768	13581	11415	10571	12683
ptc-miR167c	13768	13581	11415	10571	12683
ptc-miR167d	13768	13581	11415	10571	12683
rco-miR167a	13768	13581	11415	10571	12683
rco-miR167b	13768	13581	11415	10571	12683
sbi-miR167a	13768	13581	11415	10571	12683
sbi-miR167b	13768	13581	11415	10571	12683
sbi-miR167i	13768	13581	11415	10571	12683
sly-miR167a	13768	13581	11415	10571	12683
stu-miR167a-5p	13768	13581	11415	10571	12683
stu-miR167b-5p	13768	13581	11415	10571	12683
stu-miR167c-5p	13768	13581	11415	10571	12683
stu-miR167d-5p	13768	13581	11415	10571	12683
tae-miR167a	13768	13581	11415	10571	12683
tcc-miR167a	13768	13581	11415	10571	12683
tcc-miR167b	13768	13581	11415	10571	12683
vvi-miR167b	13768	13581	11415	10571	12683
vvi-miR167d	13768	13581	11415	10571	12683
vvi-miR167e	13768	13581	11415	10571	12683
zma-miR167a-5p	13768	13581	11415	10571	12683
zma-miR167b-5p	13768	13581	11415	10571	12683
zma-miR167c-5p	13768	13581	11415	10571	12683
zma-miR167d-5p	13768	13581	11415	10571	12683
efu-miR-27b	118	125	193	96	138
gma-miR166u	276	242	308	248	245
ami-miR-191-5p	140	88	106	70	105
cfa-miR-191	140	88	106	70	105
chi-miR-191-5p	140	88	106	70	105
cpi-miR-191-5p	140	88	106	70	105
mdo-miR-191-5p	140	88	106	70	105
oan-miR-191-5p	140	88	106	70	105
oar-miR-191	140	88	106	70	105
pal-miR-191-5p	140	88	106	70	105
tch-miR-191-5p	140	88	106	70	105
xla-miR-191-5p	140	88	106	70	105
xtr-miR-191	140	88	106	70	105
aly-miR166a-3p	117790	98898	110407	105198	91820
aly-miR166b-3p	117790	98898	110407	105198	91820
aly-miR166c-3p	117790	98898	110407	105198	91820
aly-miR166d-3p	117790	98898	110407	105198	91820
aly-miR166e-3p	117790	98898	110407	105198	91820
aly-miR166f-3p	117790	98898	110407	105198	91820

aly-miR166g-3p	117790	98898	110407	105198	91820
aly-miR166h-3p	117790	98898	110407	105198	91820
aof-miR166d	117790	98898	110407	105198	91820
aqc-miR166b	117790	98898	110407	105198	91820
aqc-miR166e	117790	98898	110407	105198	91820
ata-miR166a-3p	117790	98898	110407	105198	91820
ata-miR166b-3p	117790	98898	110407	105198	91820
ata-miR166d-3p	117790	98898	110407	105198	91820
ata-miR166e-3p	117790	98898	110407	105198	91820
ath-miR166a-3p	117790	98898	110407	105198	91820
ath-miR166b-3p	117790	98898	110407	105198	91820
ath-miR166c	117790	98898	110407	105198	91820
ath-miR166d	117790	98898	110407	105198	91820
ath-miR166e-3p	117790	98898	110407	105198	91820
ath-miR166f	117790	98898	110407	105198	91820
ath-miR166g	117790	98898	110407	105198	91820
atr-miR166a	117790	98898	110407	105198	91820
atr-miR166c	117790	98898	110407	105198	91820
gma-miR166i-3p	117790	98898	110407	105198	91820
hpa-miR166a	117790	98898	110407	105198	91820
hpe-miR166a	117790	98898	110407	105198	91820
hvu-miR166a	117790	98898	110407	105198	91820
hvu-miR166b	117790	98898	110407	105198	91820
hvu-miR166c	117790	98898	110407	105198	91820
lus-miR166a	117790	98898	110407	105198	91820
lus-miR166c	117790	98898	110407	105198	91820
lus-miR166d	117790	98898	110407	105198	91820
lus-miR166g	117790	98898	110407	105198	91820
lus-miR166h	117790	98898	110407	105198	91820
lus-miR166j	117790	98898	110407	105198	91820
mdm-miR166a	117790	98898	110407	105198	91820
mdm-miR166b	117790	98898	110407	105198	91820
mdm-miR166c	117790	98898	110407	105198	91820
mdm-miR166d	117790	98898	110407	105198	91820
mdm-miR166e	117790	98898	110407	105198	91820
mdm-miR166f	117790	98898	110407	105198	91820
mdm-miR166h	117790	98898	110407	105198	91820
mdm-miR166i	117790	98898	110407	105198	91820
mdm-miR166j	117790	98898	110407	105198	91820
mes-miR166a	117790	98898	110407	105198	91820
mes-miR166b	117790	98898	110407	105198	91820
mtr-miR166g-3p	117790	98898	110407	105198	91820
nta-miR166a	117790	98898	110407	105198	91820

nta-miR166b	117790	98898	110407	105198	91820
osa-miR166b-3p	117790	98898	110407	105198	91820
osa-miR166c-3p	117790	98898	110407	105198	91820
rco-miR166c	117790	98898	110407	105198	91820
atr-miR166d	117790	98898	110407	105198	91820
bdi-miR166a-3p	117790	98898	110407	105198	91820
bdi-miR166b-3p	117790	98898	110407	105198	91820
bdi-miR166c-3p	117790	98898	110407	105198	91820
bdi-miR166d-3p	117790	98898	110407	105198	91820
bdi-miR166i-3p	117790	98898	110407	105198	91820
bna-miR166a	117790	98898	110407	105198	91820
bna-miR166b	117790	98898	110407	105198	91820
bna-miR166c	117790	98898	110407	105198	91820
bna-miR166d	117790	98898	110407	105198	91820
bna-miR166e	117790	98898	110407	105198	91820
cme-miR166a	117790	98898	110407	105198	91820
cme-miR166b	117790	98898	110407	105198	91820
cme-miR166c	117790	98898	110407	105198	91820
cme-miR166d	117790	98898	110407	105198	91820
cme-miR166f	117790	98898	110407	105198	91820
cme-miR166h	117790	98898	110407	105198	91820
cpa-miR166a	117790	98898	110407	105198	91820
cpa-miR166b	117790	98898	110407	105198	91820
cpa-miR166c	117790	98898	110407	105198	91820
csi-miR166e-3p	117790	98898	110407	105198	91820
dpr-miR166b	117790	98898	110407	105198	91820
eun-miR166-3p	117790	98898	110407	105198	91820
fve-miR166a	117790	98898	110407	105198	91820
fve-miR166b	117790	98898	110407	105198	91820
fve-miR166c	117790	98898	110407	105198	91820
fve-miR166d-3p	117790	98898	110407	105198	91820
fve-miR166e	117790	98898	110407	105198	91820
fve-miR166f	117790	98898	110407	105198	91820
ghr-miR166b	117790	98898	110407	105198	91820
gma-miR166a-3p	117790	98898	110407	105198	91820
gma-miR166b	117790	98898	110407	105198	91820
gma-miR166c-3p	117790	98898	110407	105198	91820
gma-miR166d	117790	98898	110407	105198	91820
gma-miR166e	117790	98898	110407	105198	91820
gma-miR166f	117790	98898	110407	105198	91820
gma-miR166g	117790	98898	110407	105198	91820
gma-miR166n	117790	98898	110407	105198	91820
gma-miR166o	117790	98898	110407	105198	91820

mdm-miR166g	117790	98898	110407	105198	91820
mes-miR166c	117790	98898	110407	105198	91820
mes-miR166d	117790	98898	110407	105198	91820
mes-miR166e	117790	98898	110407	105198	91820
mes-miR166f	117790	98898	110407	105198	91820
mes-miR166g	117790	98898	110407	105198	91820
mtr-miR166a	117790	98898	110407	105198	91820
mtr-miR166e-3p	117790	98898	110407	105198	91820
nta-miR166c	117790	98898	110407	105198	91820
nta-miR166d	117790	98898	110407	105198	91820
nta-miR166e	117790	98898	110407	105198	91820
nta-miR166f	117790	98898	110407	105198	91820
nta-miR166g	117790	98898	110407	105198	91820
nta-miR166h	117790	98898	110407	105198	91820
osa-miR166a-3p	117790	98898	110407	105198	91820
osa-miR166d-3p	117790	98898	110407	105198	91820
osa-miR166f	117790	98898	110407	105198	91820
osa-miR166j-3p	117790	98898	110407	105198	91820
pab-miR166f	117790	98898	110407	105198	91820
pab-miR166g	117790	98898	110407	105198	91820
pab-miR166h	117790	98898	110407	105198	91820
pab-miR166i	117790	98898	110407	105198	91820
ppe-miR166a	117790	98898	110407	105198	91820
ppe-miR166b	117790	98898	110407	105198	91820
ppe-miR166c	117790	98898	110407	105198	91820
ppe-miR166d	117790	98898	110407	105198	91820
ppe-miR166e	117790	98898	110407	105198	91820
ppt-miR166a	117790	98898	110407	105198	91820
ppt-miR166b	117790	98898	110407	105198	91820
ppt-miR166c	117790	98898	110407	105198	91820
ppt-miR166d	117790	98898	110407	105198	91820
ppt-miR166e	117790	98898	110407	105198	91820
ppt-miR166f	117790	98898	110407	105198	91820
ppt-miR166g	117790	98898	110407	105198	91820
ppt-miR166h	117790	98898	110407	105198	91820
ppt-miR166i	117790	98898	110407	105198	91820
pta-miR166a	117790	98898	110407	105198	91820
pta-miR166b	117790	98898	110407	105198	91820
ptc-miR166a	117790	98898	110407	105198	91820
ptc-miR166b	117790	98898	110407	105198	91820
ptc-miR166c	117790	98898	110407	105198	91820
ptc-miR166d	117790	98898	110407	105198	91820
ptc-miR166e	117790	98898	110407	105198	91820

ptc-miR166f	117790	98898	110407	105198	91820
ptc-miR166g	117790	98898	110407	105198	91820
ptc-miR166h	117790	98898	110407	105198	91820
ptc-miR166i	117790	98898	110407	105198	91820
ptc-miR166j	117790	98898	110407	105198	91820
ptc-miR166k	117790	98898	110407	105198	91820
ptc-miR166l	117790	98898	110407	105198	91820
ptc-miR166m	117790	98898	110407	105198	91820
pvu-miR166a	117790	98898	110407	105198	91820
rco-miR166a	117790	98898	110407	105198	91820
rco-miR166b	117790	98898	110407	105198	91820
rco-miR166d	117790	98898	110407	105198	91820
rco-miR166e	117790	98898	110407	105198	91820
sly-miR166a	117790	98898	110407	105198	91820
sly-miR166b	117790	98898	110407	105198	91820
smo-miR166a	117790	98898	110407	105198	91820
smo-miR166b	117790	98898	110407	105198	91820
smo-miR166c	117790	98898	110407	105198	91820
ssl-miR166b	117790	98898	110407	105198	91820
ssp-miR166	117790	98898	110407	105198	91820
stu-miR166a-3p	117790	98898	110407	105198	91820
stu-miR166c-3p	117790	98898	110407	105198	91820
stu-miR166d-3p	117790	98898	110407	105198	91820
tcc-miR166a	117790	98898	110407	105198	91820
tcc-miR166d	117790	98898	110407	105198	91820
vca-miR166a-3p	117790	98898	110407	105198	91820
vca-miR166b-3p	117790	98898	110407	105198	91820
vca-miR166c-3p	117790	98898	110407	105198	91820
vvi-miR166c	117790	98898	110407	105198	91820
vvi-miR166d	117790	98898	110407	105198	91820
vvi-miR166e	117790	98898	110407	105198	91820
vvi-miR166f	117790	98898	110407	105198	91820
vvi-miR166g	117790	98898	110407	105198	91820
vvi-miR166h	117790	98898	110407	105198	91820
zma-miR166a-3p	117790	98898	110407	105198	91820
csi-miR166a-3p	117813	98934	110449	105238	91846
ctr-miR166	117813	98934	110449	105238	91846
hbr-miR166b	117813	98934	110449	105238	91846
lus-miR166i	117813	98934	110449	105238	91846
lus-miR166k	117813	98934	110449	105238	91846
cas-miR166c-3p	118539	99568	111102	105947	92546
cas-miR166d	118539	99568	111102	105947	92546
cas-miR166f-3p	118539	99568	111102	105947	92546

lja-miR166-3p	122067	102434	113916	109193	95425
bta-miR-22-3p	51	45	113	42	74
ggo-miR-22	51	45	113	42	74
oar-miR-22-3p	51	45	113	42	74
abu-miR-499	79	68	58	44	65
aca-miR-499-5p	79	68	58	44	65
ccr-miR-499	79	68	58	44	65
cgr-miR-499-5p	79	68	58	44	65
cpi-miR-499-5p	79	68	58	44	65
cpo-miR-499-5p	79	68	58	44	65
dno-miR-499-5p	79	68	58	44	65
dre-miR-499-5p	79	68	58	44	65
gmo-miR-499-5p	79	68	58	44	65
mze-miR-499	79	68	58	44	65
nbr-miR-499	79	68	58	44	65
ocu-miR-499-5p	79	68	58	44	65
oha-miR-499-5p	79	68	58	44	65
oni-miR-499	79	68	58	44	65
pbv-miR-499-5p	79	68	58	44	65
pny-miR-499	79	68	58	44	65
ssa-miR-499b-5p	79	68	58	44	65
xla-miR-499-5p	79	68	58	44	65
xtr-miR-499	79	68	58	44	65
cme-miR166g	954	916	1017	975	810
csi-miR166c-3p	954	916	1017	975	810
gma-miR166p	954	916	1017	975	810
gma-miR166q	954	916	1017	975	810
gma-miR166r	954	916	1017	975	810
gma-miR166s	954	916	1017	975	810
gma-miR166t	954	916	1017	975	810
sbi-miR166a	954	916	1017	975	810
sbi-miR166b	954	916	1017	975	810
sbi-miR166c	954	916	1017	975	810
sbi-miR166d	954	916	1017	975	810
sbi-miR166h	954	916	1017	975	810
sbi-miR166i	954	916	1017	975	810
sbi-miR166j	954	916	1017	975	810
tcc-miR166b	954	916	1017	975	810
zma-miR166b-3p	954	916	1017	975	810
zma-miR166c-3p	954	916	1017	975	810
zma-miR166d-3p	954	916	1017	975	810
zma-miR166e	954	916	1017	975	810
zma-miR166f	954	916	1017	975	810

zma-miR166g-3p	954	916	1017	975	810
zma-miR166h-3p	954	916	1017	975	810
zma-miR166i-3p	954	916	1017	975	810
ahy-miR156b-5p	494	477	394	447	305
aly-miR157a-5p	494	477	394	447	305
aly-miR157b-5p	494	477	394	447	305
aly-miR157c-5p	494	477	394	447	305
aof-miR156b	494	477	394	447	305
ath-miR157a-5p	494	477	394	447	305
ath-miR157b-5p	494	477	394	447	305
ath-miR157c-5p	494	477	394	447	305
atr-miR156a	494	477	394	447	305
atr-miR156c	494	477	394	447	305
bna-miR156b	494	477	394	447	305
bna-miR156c	494	477	394	447	305
bna-miR156g	494	477	394	447	305
bol-miR157a	494	477	394	447	305
bra-miR157a	494	477	394	447	305
cca-miR156c	494	477	394	447	305
cme-miR156b	494	477	394	447	305
cpa-miR156e	494	477	394	447	305
cpa-miR156f	494	477	394	447	305
fve-miR156f	494	477	394	447	305
fve-miR156g-5p	494	477	394	447	305
gma-miR156c	494	477	394	447	305
gma-miR156d	494	477	394	447	305
gma-miR156i	494	477	394	447	305
gma-miR156j	494	477	394	447	305
gma-miR156l	494	477	394	447	305
gma-miR156m	494	477	394	447	305
gra-miR157a	494	477	394	447	305
gra-miR157b	494	477	394	447	305
han-miR156c	494	477	394	447	305
lus-miR156b	494	477	394	447	305
lus-miR156c	494	477	394	447	305
lus-miR156e	494	477	394	447	305
lus-miR156f	494	477	394	447	305
lus-miR156h	494	477	394	447	305
lus-miR156i	494	477	394	447	305
mdm-miR156ab	494	477	394	447	305
mdm-miR156ac	494	477	394	447	305
mes-miR156h	494	477	394	447	305
mes-miR156i	494	477	394	447	305

mes-miR156j	494	477	394	447	305
mtr-miR156e	494	477	394	447	305
mtr-miR156f	494	477	394	447	305
mtr-miR156h-5p	494	477	394	447	305
ppe-miR156g	494	477	394	447	305
ppe-miR156h	494	477	394	447	305
ppe-miR156i	494	477	394	447	305
ptc-miR156g	494	477	394	447	305
ptc-miR156h	494	477	394	447	305
ptc-miR156i	494	477	394	447	305
ptc-miR156j	494	477	394	447	305
rco-miR156f	494	477	394	447	305
rco-miR156g	494	477	394	447	305
rco-miR156h	494	477	394	447	305
sly-miR156a	494	477	394	447	305
sly-miR156b	494	477	394	447	305
sly-miR156c	494	477	394	447	305
stu-miR156a	494	477	394	447	305
stu-miR156b	494	477	394	447	305
stu-miR156c	494	477	394	447	305
stu-miR156d-5p	494	477	394	447	305
tcc-miR156e	494	477	394	447	305
tcc-miR156f	494	477	394	447	305
vca-miR156b-5p	494	477	394	447	305
vun-miR156b	494	477	394	447	305
vvi-miR156f	494	477	394	447	305
vvi-miR156g	494	477	394	447	305
vvi-miR156i	494	477	394	447	305
gma-miR169s-5p	678	780	744	545	782
mtr-miR169d-5p	678	780	744	545	782
pab-miR166j	569	1967	1318	1082	984
asu-miR-100a-5p	531	277	204	309	269
prd-miR-100-5p	531	277	204	309	269
bcy-miR156	494	477	394	447	305
bgy-miR156	494	477	394	447	305
bfl-miR-100-5p	531	266	185	305	259
dpu-miR-100	531	266	185	305	259
hpo-miR-100-5p	531	266	185	305	259
isc-miR-100	531	266	185	305	259
efu-miR-499	80	69	58	45	68
aof-miR171a	9653	12047	12181	10431	10297
aqc-miR171a	9653	12047	12181	10431	10297
aqc-miR171b	9653	12047	12181	10431	10297

aqc-miR171d	9653	12047	12181	10431	10297
ata-miR171b-3p	9653	12047	12181	10431	10297
ata-miR171d-3p	9653	12047	12181	10431	10297
bdi-miR171b	9653	12047	12181	10431	10297
bdi-miR171c-3p	9653	12047	12181	10431	10297
bdi-miR171d-3p	9653	12047	12181	10431	10297
bdi-miR171e	9653	12047	12181	10431	10297
cme-miR171c	9653	12047	12181	10431	10297
cme-miR171f	9653	12047	12181	10431	10297
cpa-miR171a	9653	12047	12181	10431	10297
cpa-miR171b	9653	12047	12181	10431	10297
cpa-miR171c	9653	12047	12181	10431	10297
cpa-miR171d	9653	12047	12181	10431	10297
crt-miR171	9653	12047	12181	10431	10297
csi-miR171c-3p	9653	12047	12181	10431	10297
csi-miR171d-3p	9653	12047	12181	10431	10297
csi-miR171f-3p	9653	12047	12181	10431	10297
csi-miR171h-3p	9653	12047	12181	10431	10297
csi-miR171i-3p	9653	12047	12181	10431	10297
far-miR171	9653	12047	12181	10431	10297
fve-miR171a	9653	12047	12181	10431	10297
fve-miR171c-3p	9653	12047	12181	10431	10297
fve-miR171d	9653	12047	12181	10431	10297
fve-miR171e	9653	12047	12181	10431	10297
fve-miR171g	9653	12047	12181	10431	10297
gma-miR171e	9653	12047	12181	10431	10297
gma-miR171f	9653	12047	12181	10431	10297
gma-miR171g	9653	12047	12181	10431	10297
gma-miR171j-3p	9653	12047	12181	10431	10297
gma-miR171u	9653	12047	12181	10431	10297
hpa-miR171a	9653	12047	12181	10431	10297
htu-miR171b	9653	12047	12181	10431	10297
htu-miR171c	9653	12047	12181	10431	10297
hvu-miR171-3p	9653	12047	12181	10431	10297
lja-miR171a	9653	12047	12181	10431	10297
lus-miR171b	9653	12047	12181	10431	10297
lus-miR171c	9653	12047	12181	10431	10297
lus-miR171e	9653	12047	12181	10431	10297
mdm-miR171g	9653	12047	12181	10431	10297
mdm-miR171h	9653	12047	12181	10431	10297
mes-miR171g	9653	12047	12181	10431	10297
mes-miR171h	9653	12047	12181	10431	10297
mes-miR171i	9653	12047	12181	10431	10297

mes-miR171j	9653	12047	12181	10431	10297
mes-miR171k	9653	12047	12181	10431	10297
mtr-miR171d	9653	12047	12181	10431	10297
nta-miR171c	9653	12047	12181	10431	10297
osa-miR171b	9653	12047	12181	10431	10297
osa-miR171c-3p	9653	12047	12181	10431	10297
osa-miR171d-3p	9653	12047	12181	10431	10297
osa-miR171e-3p	9653	12047	12181	10431	10297
osa-miR171f-3p	9653	12047	12181	10431	10297
pde-miR171	9653	12047	12181	10431	10297
ppe-miR171a	9653	12047	12181	10431	10297
ppe-miR171c	9653	12047	12181	10431	10297
ppe-miR171f	9653	12047	12181	10431	10297
ppe-miR171g	9653	12047	12181	10431	10297
ptc-miR171e	9653	12047	12181	10431	10297
ptc-miR171f	9653	12047	12181	10431	10297
ptc-miR171g-3p	9653	12047	12181	10431	10297
ptc-miR171h-3p	9653	12047	12181	10431	10297
ptc-miR171i	9653	12047	12181	10431	10297
rco-miR171c	9653	12047	12181	10431	10297
rco-miR171d	9653	12047	12181	10431	10297
rco-miR171e	9653	12047	12181	10431	10297
rco-miR171f	9653	12047	12181	10431	10297
sbi-miR171a	9653	12047	12181	10431	10297
sbi-miR171b	9653	12047	12181	10431	10297
sbi-miR171d	9653	12047	12181	10431	10297
sbi-miR171i	9653	12047	12181	10431	10297
sbi-miR171k	9653	12047	12181	10431	10297
sly-miR171a	9653	12047	12181	10431	10297
stu-miR171a-3p	9653	12047	12181	10431	10297
stu-miR171e	9653	12047	12181	10431	10297
tae-miR171a	9653	12047	12181	10431	10297
tcc-miR171d	9653	12047	12181	10431	10297
tcc-miR171e	9653	12047	12181	10431	10297
tcc-miR171f	9653	12047	12181	10431	10297
tcc-miR171g	9653	12047	12181	10431	10297
tcc-miR171h	9653	12047	12181	10431	10297
vvi-miR171a	9653	12047	12181	10431	10297
vvi-miR171c	9653	12047	12181	10431	10297
vvi-miR171d	9653	12047	12181	10431	10297
vvi-miR171i	9653	12047	12181	10431	10297
vvi-miR171j	9653	12047	12181	10431	10297
zma-miR171d-3p	9653	12047	12181	10431	10297

zma-miR171e-3p	9653	12047	12181	10431	10297
zma-miR171i-3p	9653	12047	12181	10431	10297
zma-miR171j-3p	9653	12047	12181	10431	10297
gma-miR166m	458	1911	1254	1011	935
mdm-miR167h	332445	328666	280552	259175	328814
mdm-miR167i	332445	328666	280552	259175	328814
mdm-miR167j	332445	328666	280552	259175	328814
ppe-miR167d	332445	328666	280552	259175	328814
ahy-miR159	124202	95587	114081	103220	93839
aly-miR159a-3p	124202	95587	114081	103220	93839
aof-miR159	124202	95587	114081	103220	93839
ath-miR159a	124202	95587	114081	103220	93839
atr-miR159	124202	95587	114081	103220	93839
bna-miR159	124202	95587	114081	103220	93839
bra-miR159a	124202	95587	114081	103220	93839
cme-miR159a	124202	95587	114081	103220	93839
cpa-miR159a	124202	95587	114081	103220	93839
csi-miR159a-3p	124202	95587	114081	103220	93839
fve-miR159a-3p	124202	95587	114081	103220	93839
gma-miR159a-3p	124202	95587	114081	103220	93839
gma-miR159e-3p	124202	95587	114081	103220	93839
hbr-miR159a	124202	95587	114081	103220	93839
htu-miR159a	124202	95587	114081	103220	93839
mdm-miR159d	124202	95587	114081	103220	93839
mdm-miR159e	124202	95587	114081	103220	93839
mdm-miR159f	124202	95587	114081	103220	93839
mes-miR159a-3p	124202	95587	114081	103220	93839
mes-miR159b	124202	95587	114081	103220	93839
mtr-miR159a	124202	95587	114081	103220	93839
nta-miR159	124202	95587	114081	103220	93839
ppe-miR159	124202	95587	114081	103220	93839
ptc-miR159a	124202	95587	114081	103220	93839
ptc-miR159b	124202	95587	114081	103220	93839
pvu-miR159a.1	124202	95587	114081	103220	93839
rco-miR159	124202	95587	114081	103220	93839
sly-miR159	124202	95587	114081	103220	93839
vca-miR159-3p	124202	95587	114081	103220	93839
vvi-miR159c	124202	95587	114081	103220	93839
tca-miR-100-5p	477	244	170	288	241
oha-miR-100-5p	479	244	170	287	242
csi-miR393b-5p	200	229	175	202	173
gma-miR393h	200	229	175	202	173
gma-miR393i	200	229	175	202	173

gma-miR393j	200	229	175	202	173
gma-miR393k	200	229	175	202	173
aae-miR-100	476	244	170	287	241
abu-miR-100	476	244	170	287	241
aca-miR-100	476	244	170	287	241
aga-miR-100	476	244	170	287	241
age-miR-100	476	244	170	287	241
ame-miR-100-5p	476	244	170	287	241
ami-miR-100-5p	476	244	170	287	241
bbe-miR-100-5p	476	244	170	287	241
bma-miR-100b	476	244	170	287	241
bmo-miR-100	476	244	170	287	241
bta-miR-100	476	244	170	287	241
cja-miR-100	476	244	170	287	241
cli-miR-100-5p	476	244	170	287	241
cpo-miR-100-5p	476	244	170	287	241
cqu-miR-100-5p	476	244	170	287	241
dno-miR-100-5p	476	244	170	287	241
dre-miR-100-5p	476	244	170	287	241
eca-miR-100	476	244	170	287	241
fru-miR-100	476	244	170	287	241
gga-miR-100-5p	476	244	170	287	241
ggo-miR-100	476	244	170	287	241
gmo-miR-100a-5p	476	244	170	287	241
hsa-miR-100-5p	476	244	170	287	241
ipu-miR-100	476	244	170	287	241
lgi-miR-100	476	244	170	287	241
lla-miR-100	476	244	170	287	241
mml-miR-100-5p	476	244	170	287	241
mmr-miR-100	476	244	170	287	241
mmu-miR-100-5p	476	244	170	287	241
mse-miR-100	476	244	170	287	241
mze-miR-100	476	244	170	287	241
nbr-miR-100	476	244	170	287	241
nle-miR-100	476	244	170	287	241
nvi-miR-100	476	244	170	287	241
oan-miR-100-5p	476	244	170	287	241
ocu-miR-100-5p	476	244	170	287	241
oga-miR-100	476	244	170	287	241
oni-miR-100	476	244	170	287	241
pal-miR-100-5p	476	244	170	287	241
pbv-miR-100-5p	476	244	170	287	241
pha-miR-100	476	244	170	287	241

pma-miR-100a-5p	476	244	170	287	241
pny-miR-100	476	244	170	287	241
ppa-miR-100	476	244	170	287	241
ppy-miR-100	476	244	170	287	241
pte-miR-100b-5p	476	244	170	287	241
ptr-miR-100	476	244	170	287	241
rno-miR-100-5p	476	244	170	287	241
sko-miR-100	476	244	170	287	241
sla-miR-100	476	244	170	287	241
ssa-miR-100a-5p	476	244	170	287	241
ssc-miR-100	476	244	170	287	241
tcf-miR-100	476	244	170	287	241
tch-miR-100-5p	476	244	170	287	241
tni-miR-100	476	244	170	287	241
xla-miR-100-5p	476	244	170	287	241
xtr-miR-100	476	244	170	287	241
ahy-miR167-5p	125567	123159	109633	103163	121638
cme-miR167c	125567	123159	109633	103163	121638
cpa-miR167c	125567	123159	109633	103163	121638
csi-miR167b-5p	125567	123159	109633	103163	121638
gma-miR167e	125567	123159	109633	103163	121638
gma-miR167f	125567	123159	109633	103163	121638
lus-miR167b	125567	123159	109633	103163	121638
mes-miR167g	125567	123159	109633	103163	121638
mes-miR167h	125567	123159	109633	103163	121638
ptc-miR167f-5p	125567	123159	109633	103163	121638
ptc-miR167g-5p	125567	123159	109633	103163	121638
tcc-miR167c	125567	123159	109633	103163	121638
gma-miR171n	127	110	106	97	124
gma-miR171p	127	110	106	97	124
aly-miR169b-5p	6230	7972	6743	5589	7610
aly-miR169c-5p	6230	7972	6743	5589	7610
aqc-miR169c	6230	7972	6743	5589	7610
ata-miR169d-5p	6230	7972	6743	5589	7610
ath-miR169b-5p	6230	7972	6743	5589	7610
ath-miR169c	6230	7972	6743	5589	7610
bdi-miR169c-5p	6230	7972	6743	5589	7610
bdi-miR169f	6230	7972	6743	5589	7610
bna-miR169n	6230	7972	6743	5589	7610
cas-miR169b	6230	7972	6743	5589	7610
cme-miR169f	6230	7972	6743	5589	7610
cme-miR169h	6230	7972	6743	5589	7610
csi-miR169g-5p	6230	7972	6743	5589	7610

csi-miR169k-5p	6230	7972	6743	5589	7610
csi-miR169m-5p	6230	7972	6743	5589	7610
csi-miR169n-5p	6230	7972	6743	5589	7610
csi-miR169o-5p	6230	7972	6743	5589	7610
csi-miR169r-5p	6230	7972	6743	5589	7610
gma-miR169a	6230	7972	6743	5589	7610
gma-miR169f	6230	7972	6743	5589	7610
gma-miR169g	6230	7972	6743	5589	7610
gma-miR169m	6230	7972	6743	5589	7610
lus-miR169f	6230	7972	6743	5589	7610
lus-miR169h	6230	7972	6743	5589	7610
lus-miR169j	6230	7972	6743	5589	7610
mdm-miR169a	6230	7972	6743	5589	7610
mdm-miR169g	6230	7972	6743	5589	7610
mdm-miR169h	6230	7972	6743	5589	7610
mdm-miR169i	6230	7972	6743	5589	7610
mdm-miR169j	6230	7972	6743	5589	7610
mes-miR169a	6230	7972	6743	5589	7610
mes-miR169b	6230	7972	6743	5589	7610
mes-miR169c	6230	7972	6743	5589	7610
mes-miR169d	6230	7972	6743	5589	7610
mes-miR169e	6230	7972	6743	5589	7610
mtr-miR169b	6230	7972	6743	5589	7610
mtr-miR169g	6230	7972	6743	5589	7610
mtr-miR169l-5p	6230	7972	6743	5589	7610
nta-miR169q	6230	7972	6743	5589	7610
nta-miR169r	6230	7972	6743	5589	7610
nta-miR169s	6230	7972	6743	5589	7610
osa-miR169b	6230	7972	6743	5589	7610
osa-miR169c	6230	7972	6743	5589	7610
ppe-miR169a	6230	7972	6743	5589	7610
ppe-miR169b	6230	7972	6743	5589	7610
ppe-miR169c	6230	7972	6743	5589	7610
ptc-miR169d	6230	7972	6743	5589	7610
ptc-miR169e	6230	7972	6743	5589	7610
ptc-miR169f	6230	7972	6743	5589	7610
ptc-miR169g	6230	7972	6743	5589	7610
ptc-miR169h	6230	7972	6743	5589	7610
ptc-miR169p	6230	7972	6743	5589	7610
rco-miR169a	6230	7972	6743	5589	7610
rco-miR169b	6230	7972	6743	5589	7610
sbi-miR169b	6230	7972	6743	5589	7610
sbi-miR169k	6230	7972	6743	5589	7610

sly-miR169a	6230	7972	6743	5589	7610
tcc-miR169b	6230	7972	6743	5589	7610
tcc-miR169k	6230	7972	6743	5589	7610
tcc-miR169l	6230	7972	6743	5589	7610
vun-miR169	6230	7972	6743	5589	7610
vvi-miR169a	6230	7972	6743	5589	7610
vvi-miR169c	6230	7972	6743	5589	7610
vvi-miR169j	6230	7972	6743	5589	7610
vvi-miR169k	6230	7972	6743	5589	7610
vvi-miR169s	6230	7972	6743	5589	7610
vvi-miR169w	6230	7972	6743	5589	7610
zma-miR169c-5p	6230	7972	6743	5589	7610
zma-miR169r-5p	6230	7972	6743	5589	7610
gma-miR156f	2621	2691	2018	2315	1867
aly-miR164a-5p	7094	4921	2155	4855	3374
aly-miR164b-5p	7094	4921	2155	4855	3374
aof-miR164	7094	4921	2155	4855	3374
ata-miR164b-5p	7094	4921	2155	4855	3374
ata-miR164c-5p	7094	4921	2155	4855	3374
ath-miR164a	7094	4921	2155	4855	3374
ath-miR164b-5p	7094	4921	2155	4855	3374
atr-miR164a	7094	4921	2155	4855	3374
atr-miR164b	7094	4921	2155	4855	3374
bdi-miR164a-5p	7094	4921	2155	4855	3374
bdi-miR164b	7094	4921	2155	4855	3374
bdi-miR164e	7094	4921	2155	4855	3374
bna-miR164a	7094	4921	2155	4855	3374
bra-miR164a	7094	4921	2155	4855	3374
cas-miR164	7094	4921	2155	4855	3374
cme-miR164c	7094	4921	2155	4855	3374
cme-miR164d	7094	4921	2155	4855	3374
cpa-miR164a	7094	4921	2155	4855	3374
cpa-miR164b	7094	4921	2155	4855	3374
cpa-miR164c	7094	4921	2155	4855	3374
csi-miR164a-5p	7094	4921	2155	4855	3374
csi-miR164b-5p	7094	4921	2155	4855	3374
csi-miR164c-5p	7094	4921	2155	4855	3374
csi-miR164d-5p	7094	4921	2155	4855	3374
ctr-miR164	7094	4921	2155	4855	3374
fve-miR164a-5p	7094	4921	2155	4855	3374
fve-miR164b	7094	4921	2155	4855	3374
ghr-miR164	7094	4921	2155	4855	3374
gma-miR164a	7094	4921	2155	4855	3374

gma-miR164e	7094	4921	2155	4855	3374
gma-miR164f	7094	4921	2155	4855	3374
gma-miR164g	7094	4921	2155	4855	3374
gma-miR164h	7094	4921	2155	4855	3374
gma-miR164i	7094	4921	2155	4855	3374
gma-miR164j	7094	4921	2155	4855	3374
gma-miR164k	7094	4921	2155	4855	3374
lus-miR164a	7094	4921	2155	4855	3374
lus-miR164b	7094	4921	2155	4855	3374
lus-miR164c	7094	4921	2155	4855	3374
lus-miR164d	7094	4921	2155	4855	3374
lus-miR164e	7094	4921	2155	4855	3374
mdm-miR164b	7094	4921	2155	4855	3374
mdm-miR164c	7094	4921	2155	4855	3374
mdm-miR164d	7094	4921	2155	4855	3374
mdm-miR164e	7094	4921	2155	4855	3374
mdm-miR164f	7094	4921	2155	4855	3374
mes-miR164a	7094	4921	2155	4855	3374
mes-miR164b	7094	4921	2155	4855	3374
mes-miR164c	7094	4921	2155	4855	3374
mtr-miR164a	7094	4921	2155	4855	3374
mtr-miR164b	7094	4921	2155	4855	3374
mtr-miR164c	7094	4921	2155	4855	3374
nta-miR164a	7094	4921	2155	4855	3374
nta-miR164b	7094	4921	2155	4855	3374
osa-miR164a	7094	4921	2155	4855	3374
osa-miR164b	7094	4921	2155	4855	3374
osa-miR164f	7094	4921	2155	4855	3374
ppe-miR164a	7094	4921	2155	4855	3374
ppe-miR164b	7094	4921	2155	4855	3374
ppe-miR164c	7094	4921	2155	4855	3374
ptc-miR164a	7094	4921	2155	4855	3374
ptc-miR164b	7094	4921	2155	4855	3374
ptc-miR164c	7094	4921	2155	4855	3374
ptc-miR164d	7094	4921	2155	4855	3374
ptc-miR164e	7094	4921	2155	4855	3374
rco-miR164a	7094	4921	2155	4855	3374
rco-miR164b	7094	4921	2155	4855	3374
rco-miR164c	7094	4921	2155	4855	3374
sbi-miR164a	7094	4921	2155	4855	3374
sbi-miR164d	7094	4921	2155	4855	3374
sbi-miR164e	7094	4921	2155	4855	3374
sly-miR164a-5p	7094	4921	2155	4855	3374

sly-miR164b-5p	7094	4921	2155	4855	3374
ssl-miR164a	7094	4921	2155	4855	3374
ssl-miR164b	7094	4921	2155	4855	3374
tae-miR164	7094	4921	2155	4855	3374
tcc-miR164a	7094	4921	2155	4855	3374
tcc-miR164b	7094	4921	2155	4855	3374
vvi-miR164a	7094	4921	2155	4855	3374
vvi-miR164c	7094	4921	2155	4855	3374
vvi-miR164d	7094	4921	2155	4855	3374
zma-miR164a-5p	7094	4921	2155	4855	3374
zma-miR164b-5p	7094	4921	2155	4855	3374
zma-miR164c-5p	7094	4921	2155	4855	3374
zma-miR164d-5p	7094	4921	2155	4855	3374
zma-miR164g-5p	7094	4921	2155	4855	3374
bra-miR164e-5p	7101	4935	2160	4861	3386
ahy-miR156c	2606	2676	2010	2308	1861
far-miR156b	2606	2676	2010	2308	1861
mdm-miR156t	2606	2676	2010	2308	1861
mdm-miR156u	2606	2676	2010	2308	1861
mdm-miR156v	2606	2676	2010	2308	1861
mdm-miR156w	2606	2676	2010	2308	1861
mes-miR156k	2606	2676	2010	2308	1861
aly-miR166g-5p	364	304	383	343	358
cas-miR166f-5p	364	304	383	343	358
csi-miR166b-5p	364	304	383	343	358
gma-miR166h-5p	364	304	383	343	358
gma-miR166j-5p	364	304	383	343	358
stu-miR166c-5p	364	304	383	343	358
gma-miR159d	1575	1537	1275	1561	1314
aof-miR398	8721	10351	12418	9258	10489
aqc-miR398b	8721	10351	12418	9258	10489
bdi-miR398a	8721	10351	12418	9258	10489
cca-miR398	8721	10351	12418	9258	10489
cme-miR398a	8721	10351	12418	9258	10489
csi-miR398b-3p	8721	10351	12418	9258	10489
gma-miR398c	8721	10351	12418	9258	10489
gma-miR398d	8721	10351	12418	9258	10489
lus-miR398a	8721	10351	12418	9258	10489
mdm-miR398b	8721	10351	12418	9258	10489
mdm-miR398c	8721	10351	12418	9258	10489
mes-miR398	8721	10351	12418	9258	10489
mtr-miR398b	8721	10351	12418	9258	10489
mtr-miR398c	8721	10351	12418	9258	10489

nta-miR398	8721	10351	12418	9258	10489
osa-miR398b	8721	10351	12418	9258	10489
ppe-miR398a-3p	8721	10351	12418	9258	10489
ptc-miR398b	8721	10351	12418	9258	10489
ptc-miR398c-3p	8721	10351	12418	9258	10489
rco-miR398b	8721	10351	12418	9258	10489
tcc-miR398a	8721	10351	12418	9258	10489
vvi-miR398b	8721	10351	12418	9258	10489
vvi-miR398c	8721	10351	12418	9258	10489
abu-miR-222	350	182	148	265	177
age-miR-222	350	182	148	265	177
ami-miR-222a-3p	350	182	148	265	177
cgr-miR-222-3p	350	182	148	265	177
chi-miR-222-3p	350	182	148	265	177
cli-miR-222a-3p	350	182	148	265	177
cpo-miR-222-3p	350	182	148	265	177
dma-miR-222	350	182	148	265	177
dno-miR-222-3p	350	182	148	265	177
dre-miR-222a-3p	350	182	148	265	177
fru-miR-222	350	182	148	265	177
gga-miR-222a	350	182	148	265	177
mdo-miR-222a	350	182	148	265	177
mmr-miR-222	350	182	148	265	177
mze-miR-222	350	182	148	265	177
nbr-miR-222	350	182	148	265	177
nle-miR-222	350	182	148	265	177
ocu-miR-222-3p	350	182	148	265	177
oga-miR-222	350	182	148	265	177
oha-miR-222a-3p	350	182	148	265	177
oni-miR-222	350	182	148	265	177
pbv-miR-222a-3p	350	182	148	265	177
pha-miR-222	350	182	148	265	177
pny-miR-222	350	182	148	265	177
ppa-miR-222	350	182	148	265	177
ssa-miR-222a-3p	350	182	148	265	177
ssc-miR-222	350	182	148	265	177
tgu-miR-222-3p	350	182	148	265	177
tni-miR-222	350	182	148	265	177
xtr-miR-222	350	182	148	265	177
lja-miR1511-3p	49605	43469	45736	42592	43044
aly-miR170-3p	1478	1986	1879	1793	1706
ath-miR170-3p	1478	1986	1879	1793	1706
stu-miR171c-3p	1478	1986	1879	1793	1706

gma-miR159a-5p	3882	3147	2995	3451	3205
gma-miR319f	134	171	91	133	95
ahy-miR167-3p	1040	1379	1214	1227	1117
ptc-miR167f-3p	1040	1379	1214	1227	1117
ptc-miR167g-3p	1040	1379	1214	1227	1117
ptc-miR167h-3p	1040	1379	1214	1227	1117
aja-miR-143	282	344	295	207	331
bta-miR-143	282	344	295	207	331
chi-miR-143-3p	282	344	295	207	331
gga-miR-143-3p	282	344	295	207	331
mdo-miR-143-3p	282	344	295	207	331
tch-miR-143-3p	282	344	295	207	331
xtr-miR-143	282	344	295	207	331
eca-miR-378	96	126	95	78	112
mml-miR-378a	96	126	95	78	112
mmu-miR-378a-3p	96	126	95	78	112
ptr-miR-378a	96	126	95	78	112
rno-miR-378a-3p	96	126	95	78	112
efu-miR-143	283	345	298	208	334
abu-miR-143	281	342	295	207	331
aca-miR-143-3p	281	342	295	207	331
ami-miR-143-3p	281	342	295	207	331
cfa-miR-143	281	342	295	207	331
cgr-miR-143	281	342	295	207	331
cli-miR-143-3p	281	342	295	207	331
cpi-miR-143-3p	281	342	295	207	331
cpo-miR-143-3p	281	342	295	207	331
dno-miR-143-3p	281	342	295	207	331
dre-miR-143	281	342	295	207	331
eca-miR-143	281	342	295	207	331
hsa-miR-143-3p	281	342	295	207	331
ipu-miR-143	281	342	295	207	331
mml-miR-143-3p	281	342	295	207	331
mmu-miR-143-3p	281	342	295	207	331
nle-miR-143	281	342	295	207	331
oan-miR-143-3p	281	342	295	207	331
oar-miR-143	281	342	295	207	331
ocu-miR-143-3p	281	342	295	207	331
oga-miR-143	281	342	295	207	331
oni-miR-143	281	342	295	207	331
pal-miR-143-3p	281	342	295	207	331
pbv-miR-143-3p	281	342	295	207	331
pha-miR-143	281	342	295	207	331

ssa-miR-143-3p	281	342	295	207	331
ssc-miR-143-3p	281	342	295	207	331
xla-miR-143-3p	281	342	295	207	331
gma-miR171m	53026	54481	53808	50160	52786
gma-miR171t	53026	54481	53808	50160	52786
dma-miR-143	294	397	330	230	360
ggo-miR-143	294	397	330	230	360
lla-miR-143	294	397	330	230	360
oha-miR-143-3p	294	397	330	230	360
ppa-miR-143	294	397	330	230	360
ppy-miR-143	294	397	330	230	360
ptr-miR-143	294	397	330	230	360
rno-miR-143-3p	294	397	330	230	360
bta-miR-99b	96	69	60	61	73
cfa-miR-99b	96	69	60	61	73
chi-miR-99b-5p	96	69	60	61	73
cpo-miR-99b-5p	96	69	60	61	73
eca-miR-99b	96	69	60	61	73
efu-miR-99b	96	69	60	61	73
hsa-miR-99b-5p	96	69	60	61	73
mml-miR-99b-5p	96	69	60	61	73
mmu-miR-99b-5p	96	69	60	61	73
oga-miR-99b	96	69	60	61	73
pal-miR-99b-5p	96	69	60	61	73
ptr-miR-99b	96	69	60	61	73
rno-miR-99b-5p	96	69	60	61	73
ssc-miR-99b	96	69	60	61	73
tch-miR-99b-5p	96	69	60	61	73
bbe-miR-216-5p	0	53	196	23	82
bfl-miR-216-5p	0	53	196	23	82
cpo-miR-216a-5p	0	53	196	23	82
dno-miR-216a-5p	0	53	196	23	82
ocu-miR-216a-5p	0	53	196	23	82
oha-miR-216-5p	0	53	196	23	82
ssc-miR-216	0	53	196	23	82
xla-miR-216-5p	0	53	196	23	82
aca-miR-216a	0	52	194	22	82
bta-miR-216a	0	52	194	22	82
cja-miR-216a	0	52	194	22	82
cli-miR-216a-5p	0	52	194	22	82
cpi-miR-216a-5p	0	52	194	22	82
dre-miR-216a	0	52	194	22	82
eca-miR-216a	0	52	194	22	82

hsa-miR-216a-5p	0	52	194	22	82
ipu-miR-216a	0	52	194	22	82
mml-miR-216a-5p	0	52	194	22	82
mmu-miR-216a-5p	0	52	194	22	82
oan-miR-216a-5p	0	52	194	22	82
pbv-miR-216a-5p	0	52	194	22	82
rno-miR-216a-5p	0	52	194	22	82
ssa-miR-216b-5p	0	52	194	22	82
tgu-miR-216a-5p	0	52	194	22	82
ppt-miR160b	140	221	113	163	136
ppt-miR160i	140	221	113	163	136
gma-miR169k	6868	8249	7252	5755	8943
gma-miR169l-5p	6868	8249	7252	5755	8943
mes-miR169l	6868	8249	7252	5755	8943
mes-miR169m	6868	8249	7252	5755	8943
eun-miR167b-3p	57	82	78	57	90
aly-miR168a-3p	11285	8749	11690	11552	9913
ath-miR168a-3p	11285	8749	11690	11552	9913
bra-miR168b-3p	11285	8749	11690	11552	9913
bra-miR168c-3p	11285	8749	11690	11552	9913
cas-miR168	11285	8749	11690	11552	9913
csi-miR168-3p	11285	8749	11690	11552	9913
fve-miR168-3p	11285	8749	11690	11552	9913
mtr-miR168c-3p	11285	8749	11690	11552	9913
ptc-miR168a-3p	11285	8749	11690	11552	9913
ptc-miR168b-3p	11285	8749	11690	11552	9913
sly-miR168b-3p	11285	8749	11690	11552	9913
lja-miR168-3p	11316	8762	11718	11574	9938
bdi-miR159b-3p.1	7101	5451	6272	6828	5467
far-miR159	7101	5451	6272	6828	5467
hvu-miR159a	7101	5451	6272	6828	5467
hvu-miR159b	7101	5451	6272	6828	5467
osa-miR159a.1	7101	5451	6272	6828	5467
osa-miR159b	7101	5451	6272	6828	5467
sbi-miR159a	7101	5451	6272	6828	5467
sof-miR159a	7101	5451	6272	6828	5467
sof-miR159b	7101	5451	6272	6828	5467
sof-miR159d	7101	5451	6272	6828	5467
ssp-miR159a	7101	5451	6272	6828	5467
tae-miR159a	7101	5451	6272	6828	5467
tae-miR159b	7101	5451	6272	6828	5467
zma-miR159a-3p	7101	5451	6272	6828	5467
zma-miR159b-3p	7101	5451	6272	6828	5467

zma-miR159f-3p	7101	5451	6272	6828	5467
zma-miR159j-3p	7101	5451	6272	6828	5467
zma-miR159k-3p	7101	5451	6272	6828	5467
cfa-miR-24	315	341	375	296	362
cgr-miR-24-3p	315	341	375	296	362
ipu-miR-24	315	341	375	296	362
oga-miR-24	315	341	375	296	362
oha-miR-24-3p	315	341	375	296	362
cpo-miR-27a-3p	240	305	307	171	360
tch-miR-27a-3p	240	305	307	171	360
abu-miR-24b-3p	314	340	374	296	362
aca-miR-24-3p	314	340	374	296	362
ami-miR-24-3p	314	340	374	296	362
bta-miR-24-3p	314	340	374	296	362
ccr-miR-24	314	340	374	296	362
cja-miR-24	314	340	374	296	362
cpo-miR-24-3p	314	340	374	296	362
dno-miR-24a-3p	314	340	374	296	362
dre-miR-24	314	340	374	296	362
eca-miR-24	314	340	374	296	362
fru-miR-24-3p	314	340	374	296	362
gga-miR-24-3p	314	340	374	296	362
ggo-miR-24	314	340	374	296	362
hsa-miR-24-3p	314	340	374	296	362
mml-miR-24-3p	314	340	374	296	362
mmu-miR-24-3p	314	340	374	296	362
mne-miR-24-3p	314	340	374	296	362
nbr-miR-24a	314	340	374	296	362
oan-miR-24-3p	314	340	374	296	362
ocu-miR-24-3p	314	340	374	296	362
ola-miR-24a	314	340	374	296	362
oni-miR-24a	314	340	374	296	362
pbv-miR-24-3p	314	340	374	296	362
pma-miR-24	314	340	374	296	362
pny-miR-24a	314	340	374	296	362
ppa-miR-24-3p	314	340	374	296	362
ppy-miR-24-3p	314	340	374	296	362
ptr-miR-24	314	340	374	296	362
rno-miR-24-3p	314	340	374	296	362
ssc-miR-24-3p	314	340	374	296	362
tgu-miR-24-3p	314	340	374	296	362
tni-miR-24	314	340	374	296	362
xla-miR-24a-3p	314	340	374	296	362

xtr-miR-24a-3p	314	340	374	296	362
dre-miR-27a-3p	371	363	323	231	421
ipu-miR-27a	371	363	323	231	421
ssa-miR-27a-3p	371	363	323	231	421
gma-miR169u	194	322	243	235	264
aly-miR159b-3p	7112	5791	6708	7202	5808
ath-miR159b-3p	7112	5791	6708	7202	5808
cas-miR159b-3p	7112	5791	6708	7202	5808
cas-miR159c-3p	7112	5791	6708	7202	5808
lus-miR159c	7112	5791	6708	7202	5808
lus-miR159b	6733	5459	6276	6835	5464
age-miR-27a	322	338	307	213	395
ggo-miR-27a	322	338	307	213	395
lca-miR-27a	322	338	307	213	395
mml-miR-27a-3p	322	338	307	213	395
mne-miR-27a	322	338	307	213	395
oha-miR-27a-3p	322	338	307	213	395
ppa-miR-27a	322	338	307	213	395
ppy-miR-27a	322	338	307	213	395
ptr-miR-27a	322	338	307	213	395
sla-miR-27a	322	338	307	213	395
gma-miR1515a	8322	9086	9113	9201	9449
gma-miR1515b	8322	9086	9113	9201	9449
abu-miR-27a	321	336	307	212	395
aca-miR-27a-3p	321	336	307	212	395
ami-miR-27a-3p	321	336	307	212	395
ccr-miR-27a	321	336	307	212	395
cgr-miR-27a-3p	321	336	307	212	395
cja-miR-27a	321	336	307	212	395
cpi-miR-27a-3p	321	336	307	212	395
dno-miR-27a-3p	321	336	307	212	395
eca-miR-27a	321	336	307	212	395
hsa-miR-27a-3p	321	336	307	212	395
mdo-miR-27a-3p	321	336	307	212	395
mmu-miR-27a-3p	321	336	307	212	395
mze-miR-27a	321	336	307	212	395
nbr-miR-27a	321	336	307	212	395
oan-miR-27a-3p	321	336	307	212	395
oar-miR-27a	321	336	307	212	395
oni-miR-27a	321	336	307	212	395
pbv-miR-27a-3p	321	336	307	212	395
pny-miR-27a	321	336	307	212	395
rno-miR-27a-3p	321	336	307	212	395

sbo-miR-27a	321	336	307	212	395
ssc-miR-27a	321	336	307	212	395
xtr-miR-27a	321	336	307	212	395
mtr-miR171c	68	35	65	57	56
csi-miR160a-5p	143	213	110	176	127
htu-miR171a	66	32	63	54	54
bta-miR-27a-3p	186	259	253	146	314
cfa-miR-27a	186	259	253	146	314
chi-miR-27a-3p	186	259	253	146	314
gmo-miR-27d-3p	186	259	253	146	314
oga-miR-27a	186	259	253	146	314
ola-miR-27a	186	259	253	146	314
pal-miR-27a-3p	186	259	253	146	314
xla-miR-27a-3p	186	259	253	146	314
ppe-miR398b	90	204	173	190	132
pvu-miR1514a	6440	5014	5169	5730	6269
lja-miR398-3p	244	215	201	208	250
stu-miR398b-3p	244	215	201	208	250
aof-miR171c	558	594	556	633	559
csi-miR171e-3p	558	594	556	633	559
csi-miR171g-3p	558	594	556	633	559
ctr-miR171	558	594	556	633	559
fve-miR171h	558	594	556	633	559
mdm-miR171a	558	594	556	633	559
mdm-miR171b	558	594	556	633	559
mdm-miR171p	558	594	556	633	559
mes-miR171a	558	594	556	633	559
ppe-miR171h	558	594	556	633	559
gma-miR319p	782	300	384	525	514
cpi-miR-24-3p	113	167	178	134	178
sbo-miR-24	113	167	178	134	178
sly-miR171e	650	620	638	712	643
stu-miR171b-3p	650	620	638	712	643
gma-miR169l-3p	188	237	210	201	252
bta-miR-451	2138	3477	2414	2108	3233
cja-miR-451	2138	3477	2414	2108	3233
cpo-miR-451-5p	2138	3477	2414	2108	3233
dno-miR-451-5p	2138	3477	2414	2108	3233
gga-miR-451	2138	3477	2414	2108	3233
oan-miR-451	2138	3477	2414	2108	3233
ocu-miR-451-5p	2138	3477	2414	2108	3233
oha-miR-451-??	2138	3477	2414	2108	3233
tgu-miR-451	2138	3477	2414	2108	3233

aly-miR169a-5p	156	232	193	178	222
ata-miR169e-5p	156	232	193	178	222
ata-miR169f-5p	156	232	193	178	222
ata-miR169g-5p	156	232	193	178	222
ath-miR169a-5p	156	232	193	178	222
bdi-miR169a-5p	156	232	193	178	222
bna-miR169a	156	232	193	178	222
bna-miR169b	156	232	193	178	222
cas-miR169a	156	232	193	178	222
gma-miR169b	156	232	193	178	222
lus-miR169g	156	232	193	178	222
lus-miR169l	156	232	193	178	222
mes-miR169g	156	232	193	178	222
mtr-miR169a	156	232	193	178	222
nta-miR169a	156	232	193	178	222
nta-miR169b	156	232	193	178	222
nta-miR169c	156	232	193	178	222
nta-miR169d	156	232	193	178	222
nta-miR169e	156	232	193	178	222
nta-miR169f	156	232	193	178	222
nta-miR169g	156	232	193	178	222
nta-miR169h	156	232	193	178	222
nta-miR169i	156	232	193	178	222
nta-miR169j	156	232	193	178	222
nta-miR169k	156	232	193	178	222
nta-miR169l	156	232	193	178	222
nta-miR169m	156	232	193	178	222
nta-miR169o	156	232	193	178	222
nta-miR169p	156	232	193	178	222
osa-miR169a	156	232	193	178	222
ptc-miR169a	156	232	193	178	222
ptc-miR169b-5p	156	232	193	178	222
ptc-miR169c	156	232	193	178	222
sbi-miR169a	156	232	193	178	222
sly-miR169c	156	232	193	178	222
tcc-miR169a	156	232	193	178	222
tcc-miR169c	156	232	193	178	222
tcc-miR169e	156	232	193	178	222
vvi-miR169f	156	232	193	178	222
vvi-miR169g	156	232	193	178	222
zma-miR169a-5p	156	232	193	178	222
zma-miR169b-5p	156	232	193	178	222
lus-miR398f	83	201	178	192	134

sly-miR156e-3p	3491	2619	3494	3738	3412
stu-miR156g-3p	3491	2619	3494	3738	3412
cas-miR156k-3p	3496	2620	3499	3743	3418
mtr-miR156c-3p	3496	2620	3499	3743	3418
ptc-miR169s	152	230	188	178	217
gma-miR2118a-3p	4554	3424	4675	5118	4056
gma-miR2118b-3p	4554	3424	4675	5118	4056
cme-miR169t	55	85	57	55	76
cme-miR169r	55	85	56	55	74
mes-miR169i	55	85	56	55	74
mes-miR169j	55	85	56	55	74
mes-miR169k	55	85	56	55	74
ptc-miR169t	55	85	56	55	74
smo-miR171a	90	75	72	101	88
gso-miR2218	208359	92323	117761	205633	84468
pvu-miR2118	208359	92323	117761	205633	84468
vun-miR2118	208359	92323	117761	205633	84468
aly-miR164c-5p	162	120	47	149	74
ath-miR164c-5p	162	120	47	149	74
bna-miR164b	162	120	47	149	74
bna-miR164c	162	120	47	149	74
bna-miR164d	162	120	47	149	74
bra-miR164b-5p	162	120	47	149	74
bra-miR164c-5p	162	120	47	149	74
bra-miR164d-5p	162	120	47	149	74
cln-miR164	162	120	47	149	74
gma-miR403a	7423	9152	8806	11066	9104
gma-miR403b	7423	9152	8806	11066	9104
mes-miR319h	246	211	206	260	191
vun-miR319b	246	211	206	260	191
aly-miR319c-3p	249	223	210	269	192
aly-miR319d-3p	249	223	210	269	192
ath-miR319c	249	223	210	269	192
mes-miR319g	249	223	210	269	192
pvu-miR319c	249	223	210	269	192
rco-miR319d	249	223	210	269	192
sly-miR319c-3p	249	223	210	269	192
csi-miR858-3p	197	158	133	206	178
ppe-miR858	197	158	133	206	178
csi-miR171a	87	72	70	98	87
zma-miR171b-3p	87	72	70	98	87
cme-miR319c	236	200	198	246	186
cme-miR319d	236	200	198	246	186

gma-miR319c	236	200	198	246	186
ptc-miR319e	236	200	198	246	186
ptc-miR319f	236	200	198	246	186
ptc-miR319g	236	200	198	246	186
ptc-miR319h	236	200	198	246	186
stu-miR319b	236	200	198	246	186
gma-miR164b	161	118	44	147	74
gma-miR164c	161	118	44	147	74
gma-miR164d	161	118	44	147	74
aca-miR-451-5p	1022	2047	1417	1272	1853
cfa-miR-451	1022	2047	1417	1272	1853
cgr-miR-451a	1022	2047	1417	1272	1853
dre-miR-451	1022	2047	1417	1272	1853
hsa-miR-451a	1022	2047	1417	1272	1853
mml-miR-451	1022	2047	1417	1272	1853
mmu-miR-451a	1022	2047	1417	1272	1853
ppy-miR-451	1022	2047	1417	1272	1853
ptr-miR-451	1022	2047	1417	1272	1853
rno-miR-451-5p	1022	2047	1417	1272	1853
ssc-miR-451	1022	2047	1417	1272	1853
xtr-miR-451	1022	2047	1417	1272	1853
bta-miR-146b	10	54	85	44	70
chi-miR-146b-5p	10	54	85	44	70
cja-miR-146b	10	54	85	44	70
dno-miR-146b-5p	10	54	85	44	70
ggo-miR-146b	10	54	85	44	70
mmr-miR-146b	10	54	85	44	70
nle-miR-146b	10	54	85	44	70
pal-miR-146b-5p	10	54	85	44	70
pha-miR-146b	10	54	85	44	70
ppa-miR-146b	10	54	85	44	70
rno-miR-146b-5p	10	54	85	44	70
sbo-miR-146b	10	54	85	44	70
aqc-miR166a	53	98	104	113	82
aqc-miR166d	53	98	104	113	82
cme-miR166e	53	98	104	113	82
dpr-miR166a	53	98	104	113	82
lus-miR166e	53	98	104	113	82
mtr-miR166c	53	98	104	113	82
mtr-miR166f	53	98	104	113	82
osa-miR166g-3p	53	98	104	113	82
osa-miR166h-3p	53	98	104	113	82
pab-miR166a	53	98	104	113	82

sbi-miR166f	53	98	104	113	82
sly-miR166c-3p	53	98	104	113	82
ssl-miR166a	53	98	104	113	82
stu-miR166b	53	98	104	113	82
tcc-miR166c	53	98	104	113	82
zma-miR166l-3p	53	98	104	113	82
zma-miR166m-3p	53	98	104	113	82
cfa-miR-181a	37	83	114	49	106
ipu-miR-181a	37	83	114	49	106
mmr-miR-181a	37	83	114	49	106
oni-miR-181c	37	83	114	49	106
sbo-miR-181a	37	83	114	49	106
gma-miR169j-5p	52	92	58	58	81
ata-miR164a-5p	176	122	48	165	80
bdi-miR164c-5p	176	122	48	165	80
cme-miR164a	176	122	48	165	80
osa-miR164d	176	122	48	165	80
sbi-miR164b	176	122	48	165	80
zma-miR164f-5p	176	122	48	165	80
gma-miR319i	236	227	265	341	247
aof-miR319b	4672	2814	3138	4518	3420
atr-miR319b	4672	2814	3138	4518	3420
atr-miR319d	4672	2814	3138	4518	3420
atr-miR319e	4672	2814	3138	4518	3420
cas-miR319c	4672	2814	3138	4518	3420
csi-miR159d	4672	2814	3138	4518	3420
fve-miR319	4672	2814	3138	4518	3420
tcc-miR319	4672	2814	3138	4518	3420
vvi-miR319e	4672	2814	3138	4518	3420
gma-miR319d	227	215	254	333	240
gma-miR319o	227	215	254	333	240
efu-miR-93	47	76	69	48	88
ccr-miR-181a	16	73	83	36	79
xla-miR-181a-5p	16	73	83	36	79
eun-miR160-3p	61	100	57	105	75
gma-miR160a-3p	61	100	57	105	75
stu-miR160a-3p	61	100	57	105	75
gma-miR1511	7940	9451	8131	9671	9157
ami-miR-93-5p	43	75	65	46	87
cfa-miR-93	43	75	65	46	87
cgr-miR-93-5p	43	75	65	46	87
chi-miR-93-5p	43	75	65	46	87
cja-miR-93	43	75	65	46	87

cpo-miR-93-5p	43	75	65	46	87
dma-miR-93	43	75	65	46	87
dno-miR-93-5p	43	75	65	46	87
eca-miR-93	43	75	65	46	87
hsa-miR-93-5p	43	75	65	46	87
mmu-miR-93-5p	43	75	65	46	87
nle-miR-93	43	75	65	46	87
ocu-miR-93-5p	43	75	65	46	87
oga-miR-93	43	75	65	46	87
pal-miR-93-5p	43	75	65	46	87
pha-miR-93	43	75	65	46	87
rno-miR-93-5p	43	75	65	46	87
tch-miR-93-5p	43	75	65	46	87
xla-miR-93-5p	43	75	65	46	87
aau-miR162	7770	6558	7618	8453	10462
aly-miR162a-3p	7770	6558	7618	8453	10462
aly-miR162b-3p	7770	6558	7618	8453	10462
ath-miR162a-3p	7770	6558	7618	8453	10462
ath-miR162b-3p	7770	6558	7618	8453	10462
bra-miR162-3p	7770	6558	7618	8453	10462
cme-miR162	7770	6558	7618	8453	10462
cpa-miR162a	7770	6558	7618	8453	10462
csi-miR162-3p	7770	6558	7618	8453	10462
eun-miR162-3p	7770	6558	7618	8453	10462
fve-miR162-3p	7770	6558	7618	8453	10462
ghr-miR162a	7770	6558	7618	8453	10462
gma-miR162b	7770	6558	7618	8453	10462
gma-miR162c	7770	6558	7618	8453	10462
hpe-miR162a	7770	6558	7618	8453	10462
htu-miR162a	7770	6558	7618	8453	10462
lus-miR162a	7770	6558	7618	8453	10462
lus-miR162b	7770	6558	7618	8453	10462
mdm-miR162a	7770	6558	7618	8453	10462
mdm-miR162b	7770	6558	7618	8453	10462
mes-miR162	7770	6558	7618	8453	10462
mtr-miR162	7770	6558	7618	8453	10462
nta-miR162a	7770	6558	7618	8453	10462
nta-miR162b	7770	6558	7618	8453	10462
osa-miR162a	7770	6558	7618	8453	10462
pde-miR162	7770	6558	7618	8453	10462
ppe-miR162	7770	6558	7618	8453	10462
ptc-miR162a	7770	6558	7618	8453	10462
ptc-miR162b	7770	6558	7618	8453	10462

rco-miR162	7770	6558	7618	8453	10462
sbi-miR162	7770	6558	7618	8453	10462
sly-miR162	7770	6558	7618	8453	10462
stu-miR162a-3p	7770	6558	7618	8453	10462
stu-miR162b-3p	7770	6558	7618	8453	10462
tcc-miR162	7770	6558	7618	8453	10462
vun-miR162	7770	6558	7618	8453	10462
vvi-miR162	7770	6558	7618	8453	10462
aly-miR396b-5p	9275	5516	6221	9477	8412
ama-miR396-5p	9275	5516	6221	9477	8412
aqc-miR396b	9275	5516	6221	9477	8412
ata-miR396c-5p	9275	5516	6221	9477	8412
ath-miR396b-5p	9275	5516	6221	9477	8412
atr-miR396b	9275	5516	6221	9477	8412
atr-miR396c	9275	5516	6221	9477	8412
atr-miR396e	9275	5516	6221	9477	8412
bcy-miR396b	9275	5516	6221	9477	8412
bdi-miR396e-5p	9275	5516	6221	9477	8412
bgy-miR396b	9275	5516	6221	9477	8412
bna-miR396a	9275	5516	6221	9477	8412
bra-miR396-5p	9275	5516	6221	9477	8412
cas-miR396b	9275	5516	6221	9477	8412
cca-miR396a-5p	9275	5516	6221	9477	8412
ccl-miR396	9275	5516	6221	9477	8412
cme-miR396a	9275	5516	6221	9477	8412
cme-miR396c	9275	5516	6221	9477	8412
cme-miR396d	9275	5516	6221	9477	8412
csi-miR396f-5p	9275	5516	6221	9477	8412
fve-miR396b-5p	9275	5516	6221	9477	8412
gma-miR396b-5p	9275	5516	6221	9477	8412
gma-miR396c	9275	5516	6221	9477	8412
gma-miR396k-5p	9275	5516	6221	9477	8412
lus-miR396b	9275	5516	6221	9477	8412
lus-miR396e	9275	5516	6221	9477	8412
mdm-miR396c	9275	5516	6221	9477	8412
mdm-miR396d	9275	5516	6221	9477	8412
mdm-miR396e	9275	5516	6221	9477	8412
mes-miR396c	9275	5516	6221	9477	8412
mes-miR396d	9275	5516	6221	9477	8412
mes-miR396e	9275	5516	6221	9477	8412
mes-miR396f	9275	5516	6221	9477	8412
mtr-miR396a-5p	9275	5516	6221	9477	8412
nta-miR396b	9275	5516	6221	9477	8412

nta-miR396c	9275	5516	6221	9477	8412
osa-miR396c-5p	9275	5516	6221	9477	8412
pab-miR396g	9275	5516	6221	9477	8412
pab-miR396h	9275	5516	6221	9477	8412
ppe-miR396b	9275	5516	6221	9477	8412
pta-miR396	9275	5516	6221	9477	8412
ptc-miR396c	9275	5516	6221	9477	8412
ptc-miR396d	9275	5516	6221	9477	8412
ptc-miR396e-5p	9275	5516	6221	9477	8412
rco-miR396	9275	5516	6221	9477	8412
sbi-miR396c	9275	5516	6221	9477	8412
sly-miR396b	9275	5516	6221	9477	8412
stu-miR396-5p	9275	5516	6221	9477	8412
tcc-miR396c	9275	5516	6221	9477	8412
tcc-miR396e	9275	5516	6221	9477	8412
zma-miR396e-5p	9275	5516	6221	9477	8412
zma-miR396f-5p	9275	5516	6221	9477	8412
mes-miR160g	11771	13787	9505	15781	13869
mtr-miR160b	11715	13747	9463	15716	13825
mtr-miR160d	11715	13747	9463	15716	13825
mtr-miR160e	11715	13747	9463	15716	13825
nta-miR160a	11715	13747	9463	15716	13825
nta-miR160b	11715	13747	9463	15716	13825
nta-miR160c	11715	13747	9463	15716	13825
osa-miR160a-5p	11715	13747	9463	15716	13825
osa-miR160b-5p	11715	13747	9463	15716	13825
osa-miR160c-5p	11715	13747	9463	15716	13825
osa-miR160d-5p	11715	13747	9463	15716	13825
pab-miR160a	11715	13747	9463	15716	13825
pab-miR160b	11715	13747	9463	15716	13825
pab-miR160d	11715	13747	9463	15716	13825
ppe-miR160a	11715	13747	9463	15716	13825
ppe-miR160b	11715	13747	9463	15716	13825
ppt-miR160a	11715	13747	9463	15716	13825
ppt-miR160e	11715	13747	9463	15716	13825
ppt-miR160f	11715	13747	9463	15716	13825
ptc-miR160a	11715	13747	9463	15716	13825
ptc-miR160b-5p	11715	13747	9463	15716	13825
ptc-miR160c-5p	11715	13747	9463	15716	13825
ptc-miR160d	11715	13747	9463	15716	13825
rco-miR160a	11715	13747	9463	15716	13825
rco-miR160b	11715	13747	9463	15716	13825
sbi-miR160a	11715	13747	9463	15716	13825

sbi-miR160b	11715	13747	9463	15716	13825
sbi-miR160c	11715	13747	9463	15716	13825
sbi-miR160d	11715	13747	9463	15716	13825
sbi-miR160e	11715	13747	9463	15716	13825
sly-miR160a	11715	13747	9463	15716	13825
smo-miR160a	11715	13747	9463	15716	13825
smo-miR160b	11715	13747	9463	15716	13825
stu-miR160a-5p	11715	13747	9463	15716	13825
stu-miR160b	11715	13747	9463	15716	13825
tae-miR160	11715	13747	9463	15716	13825
tcc-miR160b	11715	13747	9463	15716	13825
ttu-miR160	11715	13747	9463	15716	13825
vun-miR160	11715	13747	9463	15716	13825
vvi-miR160c	11715	13747	9463	15716	13825
vvi-miR160d	11715	13747	9463	15716	13825
vvi-miR160e	11715	13747	9463	15716	13825
zma-miR160a-5p	11715	13747	9463	15716	13825
zma-miR160b-5p	11715	13747	9463	15716	13825
zma-miR160c-5p	11715	13747	9463	15716	13825
zma-miR160d-5p	11715	13747	9463	15716	13825
zma-miR160e	11715	13747	9463	15716	13825
zma-miR160g-5p	11715	13747	9463	15716	13825
aly-miR160a-5p	11715	13747	9463	15716	13825
aly-miR160b-5p	11715	13747	9463	15716	13825
aly-miR160c-5p	11715	13747	9463	15716	13825
aof-miR160c	11715	13747	9463	15716	13825
aqc-miR160b	11715	13747	9463	15716	13825
ata-miR160a-5p	11715	13747	9463	15716	13825
ata-miR160b-5p	11715	13747	9463	15716	13825
ata-miR160c-5p	11715	13747	9463	15716	13825
ath-miR160a-5p	11715	13747	9463	15716	13825
ath-miR160b	11715	13747	9463	15716	13825
ath-miR160c-5p	11715	13747	9463	15716	13825
atr-miR160	11715	13747	9463	15716	13825
bdi-miR160a-5p	11715	13747	9463	15716	13825
bdi-miR160b-5p	11715	13747	9463	15716	13825
bdi-miR160c-5p	11715	13747	9463	15716	13825
bdi-miR160d-5p	11715	13747	9463	15716	13825
bna-miR160a	11715	13747	9463	15716	13825
bna-miR160b	11715	13747	9463	15716	13825
bna-miR160c	11715	13747	9463	15716	13825
bna-miR160d	11715	13747	9463	15716	13825
bra-miR160a-5p	11715	13747	9463	15716	13825

cca-miR160b	11715	13747	9463	15716	13825
cme-miR160a	11715	13747	9463	15716	13825
cme-miR160b	11715	13747	9463	15716	13825
cme-miR160c	11715	13747	9463	15716	13825
cpa-miR160a	11715	13747	9463	15716	13825
cpa-miR160b	11715	13747	9463	15716	13825
cpa-miR160c-5p	11715	13747	9463	15716	13825
cpa-miR160e	11715	13747	9463	15716	13825
cpa-miR160f-5p	11715	13747	9463	15716	13825
eun-miR160-5p	11715	13747	9463	15716	13825
far-miR160	11715	13747	9463	15716	13825
fve-miR160a	11715	13747	9463	15716	13825
fve-miR160b	11715	13747	9463	15716	13825
gma-miR160a-5p	11715	13747	9463	15716	13825
gma-miR160f	11715	13747	9463	15716	13825
lus-miR160a	11715	13747	9463	15716	13825
lus-miR160b	11715	13747	9463	15716	13825
lus-miR160d	11715	13747	9463	15716	13825
lus-miR160e	11715	13747	9463	15716	13825
lus-miR160f	11715	13747	9463	15716	13825
lus-miR160h	11715	13747	9463	15716	13825
lus-miR160i	11715	13747	9463	15716	13825
lus-miR160j	11715	13747	9463	15716	13825
mdm-miR160a	11715	13747	9463	15716	13825
mdm-miR160b	11715	13747	9463	15716	13825
mdm-miR160c	11715	13747	9463	15716	13825
mdm-miR160d	11715	13747	9463	15716	13825
mdm-miR160e	11715	13747	9463	15716	13825
mes-miR160a	11715	13747	9463	15716	13825
mes-miR160b	11715	13747	9463	15716	13825
mes-miR160d	11715	13747	9463	15716	13825
mtr-miR160a	11715	13747	9463	15716	13825
mes-miR160h	11832	13835	9531	15859	13897
mtr-miR166e-5p	339	293	315	457	332
osa-miR166h-5p	339	293	315	457	332
zma-miR166m-5p	339	293	315	457	332
abu-miR-19b	19	71	82	57	84
ami-miR-19b-3p	19	71	82	57	84
cfa-miR-19b	19	71	82	57	84
cpi-miR-19b-3p	19	71	82	57	84
dma-miR-19b	19	71	82	57	84
mmr-miR-19b	19	71	82	57	84
mze-miR-19b	19	71	82	57	84

nbr-miR-19b	19	71	82	57	84
nle-miR-19b	19	71	82	57	84
oga-miR-19b	19	71	82	57	84
oni-miR-19b	19	71	82	57	84
pbv-miR-19b-3p	19	71	82	57	84
pha-miR-19b	19	71	82	57	84
pny-miR-19b	19	71	82	57	84
ssa-miR-19c-3p	19	71	82	57	84
bta-miR-93	32	63	53	40	75
gmo-miR-451-5p	273	833	548	505	753
cpa-miR169	110	134	151	133	168
cli-miR-451-5p	47	54	35	45	64
gma-miR319g	3386	2896	2088	3830	3074
gma-miR319l	3386	2896	2088	3830	3074
cpi-miR-93-5p	30	58	53	38	72
sha-miR-93	30	58	53	38	72
gma-miR319q	3108	2667	1865	3525	2844
csi-miR160b-5p	213	172	140	262	200
mes-miR160c	213	172	140	262	200
osa-miR160e-5p	213	172	140	262	200
zma-miR160f-5p	213	172	140	262	200
gma-miR482c-3p	526	292	405	598	453
gma-miR482a-3p	41395	12714	21203	36812	21935
vun-miR482	41395	12714	21203	36812	21935
age-miR-19b	22	77	92	65	95
bta-miR-19b	22	77	92	65	95
cgr-miR-19b-3p	22	77	92	65	95
chi-miR-19b-3p	22	77	92	65	95
cja-miR-19b	22	77	92	65	95
cli-miR-19b-3p	22	77	92	65	95
cpo-miR-19b-3p	22	77	92	65	95
dno-miR-19b-3p	22	77	92	65	95
dre-miR-19b-3p	22	77	92	65	95
eca-miR-19b	22	77	92	65	95
efu-miR-19	22	77	92	65	95
fru-miR-19b	22	77	92	65	95
gga-miR-19b-3p	22	77	92	65	95
ggo-miR-19b	22	77	92	65	95
gmo-miR-19b-3p	22	77	92	65	95
hsa-miR-19b-3p	22	77	92	65	95
lca-miR-19b	22	77	92	65	95
lla-miR-19b	22	77	92	65	95
mdo-miR-19b-3p	22	77	92	65	95

mml-miR-19b	22	77	92	65	95
mmu-miR-19b-3p	22	77	92	65	95
mne-miR-19b	22	77	92	65	95
oan-miR-19b-3p	22	77	92	65	95
oar-miR-19b	22	77	92	65	95
ocu-miR-19b-3p	22	77	92	65	95
oha-miR-19b-3p	22	77	92	65	95
pal-miR-19-3p	22	77	92	65	95
pma-miR-19b-3p	22	77	92	65	95
ppa-miR-19b	22	77	92	65	95
ppy-miR-19b	22	77	92	65	95
ptr-miR-19b	22	77	92	65	95
rno-miR-19b-3p	22	77	92	65	95
sha-miR-19b	22	77	92	65	95
sla-miR-19b	22	77	92	65	95
ssc-miR-19b	22	77	92	65	95
tch-miR-19b-3p	22	77	92	65	95
tgu-miR-19b-3p	22	77	92	65	95
tni-miR-19b	22	77	92	65	95
xla-miR-19b	22	77	92	65	95
xla-miR-19b-3p	22	77	92	65	95
xtr-miR-19b	22	77	92	65	95
dno-miR-146a-5p	100	162	130	106	197
vca-miR396-5p	391	229	265	455	360
vvi-miR396b	391	229	265	455	360
pab-miR396a-5p	398	229	275	467	366
vvi-miR396a	398	229	275	467	366
pvu-miR159a.2	134	136	90	158	147
bdi-miR160f	187	170	138	259	194
cas-miR160a	187	170	138	259	194
cas-miR160b-5p	187	170	138	259	194
gma-miR160b	187	170	138	259	194
gma-miR160c	187	170	138	259	194
gma-miR160d	187	170	138	259	194
gma-miR160e	187	170	138	259	194
htu-miR160a	187	170	138	259	194
pab-miR160c	187	170	138	259	194
pab-miR160e	187	170	138	259	194
pab-miR160f	187	170	138	259	194
ahy-miR408-3p	67	57	51	88	75
aly-miR408-3p	67	57	51	88	75
ath-miR408-3p	67	57	51	88	75
cas-miR408	67	57	51	88	75

cme-miR408	67	57	51	88	75
csi-miR408-3p	67	57	51	88	75
gma-miR408a-3p	67	57	51	88	75
gma-miR408b-3p	67	57	51	88	75
gma-miR408c-3p	67	57	51	88	75
lus-miR408a	67	57	51	88	75
mdm-miR408a	67	57	51	88	75
mes-miR408	67	57	51	88	75
mtr-miR408-3p	67	57	51	88	75
pta-miR408	67	57	51	88	75
ptc-miR408-3p	67	57	51	88	75
vun-miR408	67	57	51	88	75
vvi-miR408	67	57	51	88	75
ahy-miR160-5p	46	54	41	76	49
aof-miR160a	46	54	41	76	49
bdi-miR160e-5p	46	54	41	76	49
cme-miR160d	46	54	41	76	49
cpa-miR160d	46	54	41	76	49
mes-miR160e	46	54	41	76	49
mes-miR160f	46	54	41	76	49
mtr-miR160c	46	54	41	76	49
osa-miR160f-5p	46	54	41	76	49
ptc-miR160e-5p	46	54	41	76	49
ptc-miR160f	46	54	41	76	49
rco-miR160c	46	54	41	76	49
sbi-miR160f	46	54	41	76	49
tcc-miR160a	46	54	41	76	49
vca-miR160-5p	46	54	41	76	49
vvi-miR160a	46	54	41	76	49
vvi-miR160b	46	54	41	76	49
gma-miR396e	964	595	612	1072	1081
aau-miR396	963	594	611	1071	1079
aly-miR396a-5p	963	594	611	1071	1079
amg-miR396	963	594	611	1071	1079
aof-miR396b	963	594	611	1071	1079
aqc-miR396a	963	594	611	1071	1079
ata-miR396e-5p	963	594	611	1071	1079
ath-miR396a-5p	963	594	611	1071	1079
bcy-miR396a	963	594	611	1071	1079
bdi-miR396c-5p	963	594	611	1071	1079
bdi-miR396d-5p	963	594	611	1071	1079
bgy-miR396a	963	594	611	1071	1079
cas-miR396a	963	594	611	1071	1079

cme-miR396b	963	594	611	1071	1079
cpa-miR396	963	594	611	1071	1079
csi-miR396a-5p	963	594	611	1071	1079
csi-miR396b-5p	963	594	611	1071	1079
dpr-miR396	963	594	611	1071	1079
eun-miR396b-5p	963	594	611	1071	1079
fve-miR396a-5p	963	594	611	1071	1079
fve-miR396c-5p	963	594	611	1071	1079
fve-miR396d	963	594	611	1071	1079
ghr-miR396a	963	594	611	1071	1079
ghr-miR396b	963	594	611	1071	1079
gma-miR396a-5p	963	594	611	1071	1079
gma-miR396i-5p	963	594	611	1071	1079
hbr-miR396b	963	594	611	1071	1079
lja-miR396	963	594	611	1071	1079
lus-miR396a	963	594	611	1071	1079
lus-miR396c	963	594	611	1071	1079
mdm-miR396b	963	594	611	1071	1079
mes-miR396a	963	594	611	1071	1079
mes-miR396b	963	594	611	1071	1079
mtr-miR396b-5p	963	594	611	1071	1079
nta-miR396a	963	594	611	1071	1079
osa-miR396a-5p	963	594	611	1071	1079
osa-miR396b-5p	963	594	611	1071	1079
ptc-miR396a	963	594	611	1071	1079
ptc-miR396b	963	594	611	1071	1079
sbi-miR396a	963	594	611	1071	1079
sbi-miR396b	963	594	611	1071	1079
sly-miR396a-5p	963	594	611	1071	1079
sof-miR396	963	594	611	1071	1079
ssl-miR396	963	594	611	1071	1079
ssp-miR396	963	594	611	1071	1079
tcc-miR396a	963	594	611	1071	1079
tcc-miR396b	963	594	611	1071	1079
vvi-miR396c	963	594	611	1071	1079
vvi-miR396d	963	594	611	1071	1079
zma-miR396a-5p	963	594	611	1071	1079
zma-miR396b-5p	963	594	611	1071	1079
cli-miR-146a-5p	57	144	112	93	177
cpo-miR-146a-5p	57	144	112	93	177
ocu-miR-146a-5p	57	144	112	93	177
cfa-miR-146a	57	142	110	93	175
cgr-miR-146a	57	142	110	93	175

cja-miR-146a	57	142	110	93	175
eca-miR-146a	57	142	110	93	175
gga-miR-146a-5p	57	142	110	93	175
hsa-miR-146a-5p	57	142	110	93	175
mdo-miR-146a-5p	57	142	110	93	175
mml-miR-146a-5p	57	142	110	93	175
mmr-miR-146a	57	142	110	93	175
mmu-miR-146a-5p	57	142	110	93	175
nle-miR-146a	57	142	110	93	175
pal-miR-146a-5p	57	142	110	93	175
pha-miR-146a	57	142	110	93	175
ppy-miR-146a	57	142	110	93	175
ptr-miR-146a	57	142	110	93	175
rno-miR-146a-5p	57	142	110	93	175
ssc-miR-146a-5p	57	142	110	93	175
tch-miR-146a-5p	57	142	110	93	175
tgu-miR-146c	57	142	110	93	175
pvu-miR482-3p	324	179	265	440	347
gma-miR482b-3p	702	430	337	987	535
gma-miR482d-3p	702	430	337	987	535
cme-miR172a	183	184	189	324	359
gma-miR172c	183	184	189	324	359
lus-miR172e	183	184	189	324	359
lus-miR172i	183	184	189	324	359
mdm-miR172l	183	184	189	324	359
mes-miR172e	183	184	189	324	359
mes-miR172f	183	184	189	324	359
ppe-miR172d	183	184	189	324	359
ptc-miR172g-3p	183	184	189	324	359
ptc-miR172h-3p	183	184	189	324	359
rco-miR172	183	184	189	324	359
sly-miR172d	183	184	189	324	359
stu-miR172d-3p	183	184	189	324	359
vvi-miR172c	183	184	189	324	359
csi-miR172c-3p	183	184	189	324	360
gma-miR172d	187	185	189	328	359
gma-miR172e	187	185	189	328	359
ath-miR162a-5p	82	49	39	95	127
ath-miR162b-5p	82	49	39	95	127
csi-miR162-5p	82	49	39	95	127
ptc-miR6478	19612	41570	19446	47793	34975
ath-miR8175	64	22	33	60	95
csi-miR482d-3p	1692	0	0	1	0

ata-miR168-5p	1231	1	1	1	0
bdi-miR168-5p	1231	1	1	1	0
hvu-miR168-5p	1231	1	1	1	0
osa-miR168a-5p	1231	1	1	1	0
sbi-miR168	1231	1	1	1	0
sof-miR168a	1231	1	1	1	0
ssp-miR168a	1231	1	1	1	0
zma-miR168a-5p	1231	1	1	1	0
zma-miR168b-5p	1231	1	1	1	0
csi-miR482a-3p	370	0	0	0	0
csi-miR482g-3p	370	0	0	0	0
osa-miR444b.1	359	0	0	0	0
osa-miR444c.1	359	0	0	0	0

X24_3	norm.H24_1	norm.H24_2	norm.H24_3	norm.X24_1	norm.X24_2	norm.X24_3
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226	87	160	120	127	206	207
312	339	226	245	547	376	286
312	339	226	245	547	376	286
317	345	226	254	561	382	291
317	345	226	254	561	382	291
168	116	134	83	190	154	154
187	162	168	127	311	203	171
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187	162	168	127	311	203	171
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66	58	56	47	106	78	60
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199	49	142	103	112	185	182
199	49	142	103	112	185	182
199	49	142	103	112	185	182
198	49	140	102	112	183	181
198	49	140	102	112	183	181

198	49	140	102	112	183	181
198	49	140	102	112	183	181
198	49	140	102	112	183	181
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198	49	140	102	112	183	181
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198	49	140	102	112	183	181
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331	281	177	245	529	362	303
711	609	425	311	1186	559	652
711	609	425	311	1186	559	652
222	159	182	174	389	375	203
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222	159	182	174	389	376	203
226	162	183	174	394	375	207
226	162	183	174	394	375	207
53	71	48	36	114	133	49
53	71	48	36	114	133	49
53	71	48	36	114	133	49
61152	17008	41078	17947	57410	36531	56050
82	56	22	30	72	99	75
0	1467	0	0	1	0	0

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0	1068	1	1	1	0	0
0	321	0	0	0	0	0
0	321	0	0	0	0	0
0	311	0	0	0	0	0
0	311	0	0	0	0	0

baseMean	H2O	Xcf	FoldChange	log2FoldChan	stat	pvalue
71.47	142	1	0.992	-7.1497471	-1.983	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
46.12	91	1	0.993	-6.5077946	-2.123	NA
50.8	74	27	0.998	-1.4545659	-2.374	0.01758514
50.8	74	27	0.998	-1.4545659	-2.374	0.01758514
50.8	74	27	0.998	-1.4545659	-2.374	0.01758514
156.27	217	96	0.998	-1.1765887	-2.259	0.02385415
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
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148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
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148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
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148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
148.1	205	91	0.998	-1.1716855	-2.236	0.02535544
150.81	206	96	0.998	-1.101538	-2.472	0.01344867
149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
149.88	204	96	0.998	-1.0874628	-2.447	0.01439291
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393.96	534	254	0.997	-1.0720112	-2.789	0.00528842
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355.67	480	232	0.997	-1.0489096	-2.704	0.00684464
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355.52	480	232	0.997	-1.0489096	-2.701	0.00691441
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65.54	88	43	0.998	-1.0331669	-2.034	0.04198944
63.05	84	42	0.999	-1	-1.935	0.05293459
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63.05	84	42	0.999	-1	-1.935	0.05293459
63.05	84	42	0.999	-1	-1.935	0.05293459
63.05	84	42	0.999	-1	-1.935	0.05293459
63.05	84	42	0.999	-1	-1.935	0.05293459
63.05	84	42	0.999	-1	-1.935	0.05293459
63.05	84	42	0.999	-1	-1.935	0.05293459
63.05	84	42	0.999	-1	-1.935	0.05293459
63.05	84	42	0.999	-1	-1.935	0.05293459
201.09	267	136	0.997	-0.9732331	-2.801	0.00508989
2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824

2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
2883.54	3753	2014	0.997	-0.8979806	-2.626	0.00863824
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
2865.93	3729	2003	0.997	-0.8966264	-2.624	0.00868082
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
495.69	640	351	0.998	-0.8666009	-2.178	0.02938607
120.03	150	90	0.998	-0.7369656	-1.922	0.05465553
119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
119.73	149	90	0.998	-0.7273154	-1.908	0.05633446

119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
119.73	149	90	0.998	-0.7273154	-1.908	0.05633446
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.09	110	68	0.999	-0.6938969	-1.576	0.11491311
89.42	110	68	0.999	-0.6938969	-1.546	0.1220541
89.42	110	68	0.999	-0.6938969	-1.546	0.1220541
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525

99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
99.12	122	76	0.999	-0.6828098	-1.686	0.09188525
257.5	314	201	0.998	-0.6435691	-1.744	0.08120503
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
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251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366

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251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
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251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
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251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
251.74	306	197	0.998	-0.635336	-1.715	0.08641366
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251.74	306	197	0.998	-0.635336	-1.715	0.08641366
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54.25	66	43	1	-0.6181294	-0.883	0.37716247
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866.11	1048	685	1	-0.6134628	-0.588	0.5562651
866.11	1048	685	1	-0.6134628	-0.588	0.5562651
866.11	1048	685	1	-0.6134628	-0.588	0.5562651
866.11	1048	685	1	-0.6134628	-0.588	0.5562651
866.11	1048	685	1	-0.6134628	-0.588	0.5562651
866.11	1048	685	1	-0.6134628	-0.588	0.5562651
133.23	156	110	0.999	-0.5040425	-1.394	0.16338548
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296

132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
132.31	155	110	0.999	-0.4947647	-1.36	0.17387296
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745

77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
77.8	91	65	0.999	-0.4854268	-1.04	0.29854745
68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
68.32	79	57	0.999	-0.4708907	-1.121	0.26249418
49.52	58	42	0.999	-0.4656636	-0.875	0.38167002
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
48.62	56	41	0.999	-0.4498029	-0.82	0.4122912
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077

89.9	103	77	0.999	-0.419714	-1.087	0.27699077
89.9	103	77	0.999	-0.419714	-1.087	0.27699077
48.96	56	42	0.999	-0.4150375	-0.812	0.41681107
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
109.72	125	94	0.999	-0.4111954	-1.113	0.26587994
516.58	589	445	0.998	-0.4044623	-1.436	0.15106432
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
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78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
78.59	90	68	1	-0.4043903	-0.284	0.77668962
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999

516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
516.25	588	445	0.998	-0.4020108	-1.428	0.15317999
50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
50.92	58	44	0.999	-0.3985494	-0.774	0.43909009
522.35	594	451	0.998	-0.3973355	-1.395	0.16306794
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
47.66	54	41	1	-0.3973355	-0.662	0.50787169
135.93	155	118	0.999	-0.3934814	-1.118	0.26368155
62.13	70	54	1	-0.3743955	-0.704	0.48146024
62.13	70	54	1	-0.3743955	-0.704	0.48146024
62.13	70	54	1	-0.3743955	-0.704	0.48146024
62.13	70	54	1	-0.3743955	-0.704	0.48146024
62.13	70	54	1	-0.3743955	-0.704	0.48146024
133.11	150	116	0.999	-0.3708377	-1.073	0.2832042
133.11	150	116	0.999	-0.3708377	-1.073	0.2832042
222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
222.78	250	196	0.999	-0.3510744	-1.043	0.29680673
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579.63	648	511	1	-0.3426705	-0.238	0.8116487
579.63	648	511	1	-0.3426705	-0.238	0.8116487
579.63	648	511	1	-0.3426705	-0.238	0.8116487
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742

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570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
570.69	637	504	1	-0.3378696	-0.236	0.813742
5877.54	6486	5269	0.998	-0.2997998	-1.171	0.24161443
5877.54	6486	5269	0.998	-0.2997998	-1.171	0.24161443
5877.54	6486	5269	0.998	-0.2997998	-1.171	0.24161443
92.35	102	83	1	-0.2973859	-0.164	0.86953914
92.35	102	83	1	-0.2973859	-0.164	0.86953914
92.35	102	83	1	-0.2973859	-0.164	0.86953914
92.35	102	83	1	-0.2973859	-0.164	0.86953914
394.28	435	354	0.999	-0.297266	-1.046	0.29548296
394.28	435	354	0.999	-0.297266	-1.046	0.29548296
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395.34	436	355	0.999	-0.2965091	-1.045	0.29591636
395.34	436	355	0.999	-0.2965091	-1.045	0.29591636
108.97	119	99	1	-0.2654611	-0.603	0.5464287
148.63	162	135	1	-0.2630344	-0.591	0.55445819
148.63	162	135	1	-0.2630344	-0.591	0.55445819
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148.63	162	135	1	-0.2630344	-0.591	0.55445819
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6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539
6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539
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6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539
6750.85	7364	6138	0.999	-0.262721	-1.047	0.2951539
108.07	118	99	0.999	-0.2532864	-0.74	0.45937141
108.07	118	99	0.999	-0.2532864	-0.74	0.45937141
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
6901.32	7500	6303	0.999	-0.2508519	-0.969	0.33260102
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415

234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
234.27	254	214	0.999	-0.2472177	-0.74	0.45949415
107.74	117	99	0.999	-0.2410081	-0.716	0.47411965
107.74	117	99	0.999	-0.2410081	-0.716	0.47411965
1022.17	1107	937	0.999	-0.2405343	-0.929	0.35310181
1022.17	1107	937	0.999	-0.2405343	-0.929	0.35310181
3123.29	3380	2867	0.999	-0.2374813	-0.778	0.43684888
3122.71	3378	2867	0.999	-0.2366274	-0.776	0.43784626
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3122.71	3378	2867	0.999	-0.2366274	-0.776	0.43784626
3122.71	3378	2867	0.999	-0.2366274	-0.776	0.43784626
3223.27	3486	2961	0.999	-0.2354881	-0.775	0.43831798
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3140.49	3396	2885	0.999	-0.2352651	-0.773	0.4398146
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3140.49	3396	2885	0.999	-0.2352651	-0.773	0.4398146
3140.49	3396	2885	0.999	-0.2352651	-0.773	0.4398146

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197	211	183	0.999	-0.2053994	-0.563	0.57337155
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1733.99	1810	1658	0.999	-0.1265457	-0.455	0.64893761
116.02	121	111	1	-0.1244474	-0.354	0.72348885
116.02	121	111	1	-0.1244474	-0.354	0.72348885
109.35	114	105	1	-0.1186445	-0.316	0.75199545
109.35	114	105	1	-0.1186445	-0.316	0.75199545
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122.05	127	117	1	-0.11832	-0.359	0.71963611
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23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
23384.98	24342	22427	0.999	-0.1182111	-0.49	0.62417227
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96.62	99	94	1	-0.0747678	-0.195	0.84528898
96.62	99	94	1	-0.0747678	-0.195	0.84528898

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9468.94	9605	9333	1	-0.0414447	-0.16	0.87272051
9468.94	9605	9333	1	-0.0414447	-0.16	0.87272051
9477.23	9613	9341	1	-0.0414097	-0.16	0.8729265
9477.23	9613	9341	1	-0.0414097	-0.16	0.8729265
387.8	391	384	1	-0.0260623	-0.086	0.9317648
387.8	391	384	1	-0.0260623	-0.086	0.9317648
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563.55	569	559	1	-0.0255804	-0.096	0.92374405
565.2	570	560	1	-0.0255351	-0.098	0.92160242
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567.35	572	562	1	-0.025445	-0.094	0.92520655
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914.7	922	907	1	-0.0236642	-0.09	0.92849191
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9327.76	9389	9267	1	-0.0188691	-0.079	0.93684212
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9330.28	9391	9270	1	-0.0187095	-0.078	0.93755891
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243.3	245	242	1	-0.0177747	-0.047	0.96233375
287.67	289	286	1	-0.0150543	-0.025	0.98000584
324.32	326	323	1	-0.0133378	-0.048	0.96155246
242.53	243	241	1	-0.0119232	-0.033	0.97335829
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126.22	127	126	1	-0.0114048	-0.037	0.97014762
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133.31	134	133	1	-0.0108068	-0.003	0.99758817
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153.44	154	153	1	-0.0093987	-0.031	0.97526153
153.29	154	153	1	-0.0093987	-0.022	0.98223593
493.69	495	493	1	-0.0058409	-0.009	0.99246682
493.69	495	493	1	-0.0058409	-0.009	0.99246682
283.61	284	283	1	-0.0050889	-0.014	0.98870936
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6714.73	6717	6712	1	-0.0010743	-0.005	0.99606538
6714.73	6717	6712	1	-0.0010743	-0.005	0.99606538
6754.36	6755	6754	1	-0.0002136	-0.001	0.99929018
167.97	168	168	1	0	-0.02	0.98434459
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68.91	69	69	1	0	0.002	0.99831271
1377.91	1378	1378	1	0	0.001	0.99896527
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1372.67	1372	1373	1	0.00105114	0.001	0.99909475
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5121.43	5114	5129	1	0.00422541	0.014	0.98860733
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311.48	307	315	1	0.03711317	0.1	0.92051986
426.32	421	432	1	0.03721108	0.116	0.90750036
426.32	421	432	1	0.03721108	0.116	0.90750036
301.91	298	306	1	0.03821932	0.096	0.92346825
301.91	298	306	1	0.03821932	0.096	0.92346825
301.91	298	306	1	0.03821932	0.096	0.92346825
301.91	298	306	1	0.03821932	0.096	0.92346825
64.76	64	66	1	0.04439412	0.127	0.89859678
10687.68	10506	10869	1	0.04900572	0.187	0.85154364
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1169.81	1147	1192	1	0.05551884	0.129	0.89740317
297059.98	290668	303452	1	0.06209608	0.25	0.80278167
297059.98	290668	303452	1	0.06209608	0.25	0.80278167
297059.98	290668	303452	1	0.06209608	0.25	0.80278167
297059.98	290668	303452	1	0.06209608	0.25	0.80278167
104941.8	102484	107399	1	0.06758187	0.282	0.77831564
104941.8	102484	107399	1	0.06758187	0.282	0.77831564
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104941.8	102484	107399	1	0.06758187	0.282	0.77831564
104941.8	102484	107399	1	0.06758187	0.282	0.77831564
104941.8	102484	107399	1	0.06758187	0.282	0.77831564
277.05	271	284	1	0.06759808	0.177	0.85928993
277.32	271	284	1	0.06759808	0.168	0.86640625
191.44	187	196	1	0.06781538	0.201	0.8407443
191.44	187	196	1	0.06781538	0.201	0.8407443
191.44	187	196	1	0.06781538	0.201	0.8407443

191.44	187	196	1	0.06781538	0.201	0.8407443
191.44	187	196	1	0.06781538	0.201	0.8407443
276.71	270	283	1	0.06784265	0.176	0.86013823
276.71	270	283	1	0.06784265	0.176	0.86013823
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113431.6	110592	116271	1	0.07224428	0.295	0.76780776
113431.6	110592	116271	1	0.07224428	0.295	0.76780776
113431.6	110592	116271	1	0.07224428	0.295	0.76780776
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113431.6	110592	116271	1	0.07224428	0.295	0.76780776
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113431.6	110592	116271	1	0.07224428	0.295	0.76780776
113431.6	110592	116271	1	0.07224428	0.295	0.76780776
113431.6	110592	116271	1	0.07224428	0.295	0.76780776
108.6	106	112	1	0.07943447	0.232	0.81671774
108.6	106	112	1	0.07943447	0.232	0.81671774
6704.36	6501	6907	1	0.08739757	0.333	0.73887466
6704.36	6501	6907	1	0.08739757	0.333	0.73887466
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2339.63	2265	2414	1	0.09191463	0.342	0.73253296
4477.91	4335	4621	1	0.0921731	0.246	0.80583733
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4486.82	4343	4631	1	0.0926318	0.247	0.8051075
2329.79	2253	2406	1	0.09478933	0.352	0.72478177
2329.79	2253	2406	1	0.09478933	0.352	0.72478177
2329.79	2253	2406	1	0.09478933	0.352	0.72478177
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2329.79	2253	2406	1	0.09478933	0.352	0.72478177
2329.79	2253	2406	1	0.09478933	0.352	0.72478177
2329.79	2253	2406	1	0.09478933	0.352	0.72478177
334.44	323	346	1	0.09923787	0.32	0.7490803
334.44	323	346	1	0.09923787	0.32	0.7490803
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334.44	323	346	1	0.09923787	0.32	0.7490803
1403.77	1354	1454	1	0.10279953	0.361	0.71802608
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578

10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
10111.89	9751	10473	1.001	0.10305268	0.395	0.69267578
214.69	207	223	1	0.10741294	0.271	0.78662955
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214.69	207	223	1	0.10741294	0.271	0.78662955
44428.58	42728	46130	1.001	0.1105235	0.478	0.63249088
1730.1	1660	1801	1.001	0.11761494	0.419	0.67523204
1730.1	1660	1801	1.001	0.11761494	0.419	0.67523204
1730.1	1660	1801	1.001	0.11761494	0.419	0.67523204

3216.18	3080	3352	1.001	0.1220918	0.451	0.65179224
128.52	123	134	1	0.12357469	0.325	0.74501213
1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
1179.03	1128	1230	1.001	0.12489125	0.445	0.65648997
298.83	286	312	1	0.12553088	0.435	0.66325801
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298.83	286	312	1	0.12553088	0.435	0.66325801
102.99	99	108	1	0.12553088	0.364	0.71579102
102.99	99	108	1	0.12553088	0.364	0.71579102
102.99	99	108	1	0.12553088	0.364	0.71579102
102.99	99	108	1	0.12553088	0.364	0.71579102
102.99	99	108	1	0.12553088	0.364	0.71579102
300.48	287	314	1.001	0.12971382	0.437	0.662293
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
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298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
298.21	285	312	1.001	0.13058411	0.447	0.65469903
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298.21	285	312	1.001	0.13058411	0.447	0.65469903

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298.21	285	312	1.001	0.13058411	0.447	0.65469903
52297.91	49827	54769	1.001	0.13643182	0.577	0.56423435
52297.91	49827	54769	1.001	0.13643182	0.577	0.56423435
333.04	317	349	1.001	0.1387442	0.455	0.649012
333.04	317	349	1.001	0.1387442	0.455	0.649012
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333.04	317	349	1.001	0.1387442	0.455	0.649012
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72.37	69	76	1	0.13940306	0.36	0.71890701
72.37	69	76	1	0.13940306	0.36	0.71890701
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72.37	69	76	1	0.13940306	0.36	0.71890701
72.37	69	76	1	0.13940306	0.36	0.71890701
81.89	78	86	1	0.14086254	0.079	0.93685001
81.89	78	86	1	0.14086254	0.079	0.93685001
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81.07	77	85	1	0.1426044	0.082	0.93448171
81.07	77	85	1	0.1426044	0.082	0.93448171
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81.07	77	85	1	0.1426044	0.082	0.93448171
156.14	148	164	1	0.14809864	0.406	0.68495341
156.14	148	164	1	0.14809864	0.406	0.68495341
7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
7328.15	6933	7723	1.001	0.15568161	0.592	0.55378602
71.21	67	75	1	0.1627295	0.377	0.70593412
10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
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10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
10326.81	9741	10913	1.001	0.16390596	0.604	0.54561405
10349.39	9762	10937	1.001	0.16396841	0.604	0.54602043
6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
6146.58	5778	6515	1.001	0.17319497	0.666	0.50553672
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339.39	319	360	1.001	0.17444048	0.649	0.51662146
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281.14	264	298	1.001	0.1747744	0.534	0.59319238
281.14	264	298	1.001	0.1747744	0.534	0.59319238
338.78	318	360	1.001	0.17897014	0.659	0.50981709
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348.16	326	370	1.001	0.18265331	0.625	0.53224409
348.16	326	370	1.001	0.18265331	0.625	0.53224409
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253.77	237	271	1.001	0.19340579	0.6	0.54872062
6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
6459.69	6027	6892	1.001	0.19348264	0.75	0.4532886
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6097.27	5675	6519	1.001	0.20003028	0.772	0.43985612
321.48	299	344	1.001	0.20226308	0.686	0.49279709
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8828.39	8202	9455	1.001	0.20510171	0.788	0.43096626
8828.39	8202	9455	1.001	0.20510171	0.788	0.43096626
320.81	298	344	1.001	0.20709623	0.695	0.48723533
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55.15	51	59	1	0.21021771	0.471	0.63787349
156.59	145	168	1.001	0.21240833	0.554	0.57976616
52.81	49	57	1	0.21818017	0.461	0.64493481
236.49	217	256	1.001	0.23844877	0.706	0.48005851
236.49	217	256	1.001	0.23844877	0.706	0.48005851
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236.49	217	256	1.001	0.23844877	0.706	0.48005851
160.2	147	174	1.001	0.24327115	0.623	0.53310376
5602.86	5103	6102	1.001	0.25793654	1.016	0.30978276
223.27	203	243	1.001	0.25947659	0.91	0.36304605
223.27	203	243	1.001	0.25947659	0.91	0.36304605
581.23	528	634	1.001	0.26394491	0.982	0.32633394
581.23	528	634	1.001	0.26394491	0.982	0.32633394
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581.23	528	634	1.001	0.26394491	0.982	0.32633394
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487.58	443	532	1.001	0.26411955	0.75	0.45334014
157.14	142	172	1.001	0.27651764	0.81	0.41797895
157.14	142	172	1.001	0.27651764	0.81	0.41797895
651.94	589	716	1.001	0.28169195	1.071	0.28425623
651.94	589	716	1.001	0.28169195	1.071	0.28425623
218.97	197	241	1.001	0.29083752	0.969	0.33245343
2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
2785.92	2506	3066	1.001	0.29097128	0.975	0.32963083
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201.24	181	222	1.001	0.29456998	0.929	0.35291315
201.24	181	222	1.001	0.29456998	0.929	0.35291315
201.24	181	222	1.001	0.29456998	0.929	0.35291315
201.24	181	222	1.001	0.29456998	0.929	0.35291315
201.24	181	222	1.001	0.29456998	0.929	0.35291315
201.24	181	222	1.001	0.29456998	0.929	0.35291315
201.24	181	222	1.001	0.29456998	0.929	0.35291315
201.24	181	222	1.001	0.29456998	0.929	0.35291315
161.59	145	178	1.001	0.29582434	0.734	0.46316177

3282.22	2947	3618	1.001	0.29594535	1.093	0.27458295
3282.22	2947	3618	1.001	0.29594535	1.093	0.27458295
3286.22	2950	3622	1.001	0.29607159	1.093	0.27441971
3286.22	2950	3622	1.001	0.29607159	1.093	0.27441971
198.08	178	219	1.001	0.29905363	0.946	0.34430522
4349.45	3882	4816	1.001	0.31103527	1.15	0.25017723
4349.45	3882	4816	1.001	0.31103527	1.15	0.25017723
69.16	62	77	1.001	0.31259023	0.807	0.41980832
68.66	61	76	1.001	0.31719018	0.79	0.42972192
68.66	61	76	1.001	0.31719018	0.79	0.42972192
68.66	61	76	1.001	0.31719018	0.79	0.42972192
68.66	61	76	1.001	0.31719018	0.79	0.42972192
68.66	61	76	1.001	0.31719018	0.79	0.42972192
81.9	73	91	1.001	0.31797008	0.794	0.42711485
142731.01	126869	158593	1.001	0.3219895	0.851	0.394813
142731.01	126869	158593	1.001	0.3219895	0.851	0.394813
142731.01	126869	158593	1.001	0.3219895	0.851	0.394813
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
114.05	101	127	1.001	0.3304732	0.717	0.47345655
8886.21	7869	9903	1.001	0.33168533	1.106	0.26867058
8886.21	7869	9903	1.001	0.33168533	1.106	0.26867058
230.53	204	257	1.001	0.33319921	1.097	0.27269201
230.53	204	257	1.001	0.33319921	1.097	0.27269201
237.82	210	266	1.001	0.34103692	1.105	0.26908289
237.82	210	266	1.001	0.34103692	1.105	0.26908289
237.82	210	266	1.001	0.34103692	1.105	0.26908289
237.82	210	266	1.001	0.34103692	1.105	0.26908289
237.82	210	266	1.001	0.34103692	1.105	0.26908289
237.82	210	266	1.001	0.34103692	1.105	0.26908289
237.82	210	266	1.001	0.34103692	1.105	0.26908289
169.94	150	190	1.001	0.34103692	0.99	0.32201644
169.94	150	190	1.001	0.34103692	0.99	0.32201644
79.74	70	89	1.001	0.34645041	0.843	0.39933402
79.74	70	89	1.001	0.34645041	0.843	0.39933402
221.45	195	248	1.001	0.346866	1.142	0.25331815
221.45	195	248	1.001	0.346866	1.142	0.25331815

221.45	195	248	1.001	0.346866	1.142	0.25331815
221.45	195	248	1.001	0.346866	1.142	0.25331815
221.45	195	248	1.001	0.346866	1.142	0.25331815
221.45	195	248	1.001	0.346866	1.142	0.25331815
221.45	195	248	1.001	0.346866	1.142	0.25331815
221.45	195	248	1.001	0.346866	1.142	0.25331815
112.25	99	126	1.001	0.3479233	0.723	0.46958971
112.25	99	126	1.001	0.3479233	0.723	0.46958971
112.25	99	126	1.001	0.3479233	0.723	0.46958971
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
1608.78	1406	1812	1.001	0.36598636	1.132	0.25764727
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
54.03	47	61	1	0.37614849	0.647	0.51791658
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319

91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
91.51	80	104	1.001	0.37851162	0.908	0.36403319
83.91	73	95	1.001	0.38003105	0.793	0.42769265
83.91	73	95	1.001	0.38003105	0.793	0.42769265
83.91	73	95	1.001	0.38003105	0.793	0.42769265
83.91	73	95	1.001	0.38003105	0.793	0.42769265
83.91	73	95	1.001	0.38003105	0.793	0.42769265
72.27	63	82	1.001	0.38027208	0.89	0.37337613
122.03	106	138	1.001	0.380604	0.815	0.41490049
122.03	106	138	1.001	0.380604	0.815	0.41490049
122.03	106	138	1.001	0.380604	0.815	0.41490049
122.03	106	138	1.001	0.380604	0.815	0.41490049
122.03	106	138	1.001	0.380604	0.815	0.41490049
122.03	106	138	1.001	0.380604	0.815	0.41490049
259.73	225	295	1.001	0.39078995	1.2	0.23033198
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
3754.64	3243	4266	1.002	0.39555494	1.391	0.16417376
249.5	214	285	1.001	0.41335112	1.215	0.22435046
249.5	214	285	1.001	0.41335112	1.215	0.22435046
69.98	60	80	1.001	0.4150375	1.015	0.30994321
63.49	54	73	1	0.43493706	0.76	0.44723325
63.49	54	73	1	0.43493706	0.76	0.44723325
79.89	68	92	1.001	0.43609911	0.997	0.31868972
79.89	68	92	1.001	0.43609911	0.997	0.31868972
79.89	68	92	1.001	0.43609911	0.997	0.31868972
9348.17	7910	10787	1.002	0.44754409	1.79	0.07352049
67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926

67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
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67.43	57	78	1.001	0.4525122	1.045	0.29613926
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67.43	57	78	1.001	0.4525122	1.045	0.29613926
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67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
67.43	57	78	1.001	0.4525122	1.045	0.29613926
8011.87	6750	9274	1.002	0.45830422	1.711	0.08703002
8011.87	6750	9274	1.002	0.45830422	1.711	0.08703002
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7614.21	6412	8816	1.002	0.4593498	1.537	0.12426027
7614.21	6412	8816	1.002	0.4593498	1.537	0.12426027
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12940.38	10868	15013	1.002	0.46612582	1.612	0.10702652
12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
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12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
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12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
12891.99	10826	14958	1.002	0.466417	1.612	0.10685671
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12991.21	10909	15073	1.002	0.46644773	1.612	0.1068821
347.85	292	404	1.002	0.46838692	1.537	0.12436711
347.85	292	404	1.002	0.46838692	1.537	0.12436711
347.85	292	404	1.002	0.46838692	1.537	0.12436711
65	54	76	1.001	0.49304001	0.947	0.34369062
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55.67	46	65	1.001	0.49880586	1.08	0.28008841
631.99	522	742	1.001	0.50736938	1.305	0.19192189
148.38	122	174	1.002	0.51220616	1.588	0.11236333
51.3	42	60	1.001	0.51457317	1.215	0.22453308
3130.67	2575	3686	1.002	0.51748364	1.818	0.06903456
3130.67	2575	3686	1.002	0.51748364	1.818	0.06903456
53.33	44	63	1.001	0.5178483	1.101	0.27100359
53.33	44	63	1.001	0.5178483	1.101	0.27100359
2865.44	2350	3380	1.002	0.52436249	1.813	0.06981196
197.1	161	233	1.002	0.53326927	1.552	0.12064702
197.1	161	233	1.002	0.53326927	1.552	0.12064702
197.1	161	233	1.002	0.53326927	1.552	0.12064702
197.1	161	233	1.002	0.53326927	1.552	0.12064702
458.01	373	543	1.002	0.54177657	1.723	0.08487894
27927.58	22677	33178	1.001	0.54899713	1.459	0.14448767
27927.58	22677	33178	1.001	0.54899713	1.459	0.14448767
73.92	60	88	1.001	0.55254102	1.099	0.27171185
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73.92	60	88	1.001	0.55254102	1.099	0.27171185
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151.17	122	180	1.001	0.56111576	1.54	0.12348132
336.41	270	403	1.002	0.57782043	1.731	0.08345349
336.41	270	403	1.002	0.57782043	1.731	0.08345349
343.18	275	411	1.002	0.57970678	1.735	0.08276887
343.18	275	411	1.002	0.57970678	1.735	0.08276887
138.5	111	166	1.002	0.58062356	1.705	0.08827572
190.44	152	228	1.002	0.5849625	1.712	0.08682214
190.44	152	228	1.002	0.5849625	1.712	0.08682214
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861.57	662	1061	1.003	0.68052153	2.256	0.02408365
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861.57	662	1061	1.003	0.68052153	2.256	0.02408365
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861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
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861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
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861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
861.57	662	1061	1.003	0.68052153	2.256	0.02408365
129.01	98	160	1.001	0.70721825	1.667	0.09559944
129.01	98	160	1.001	0.70721825	1.667	0.09559944
129.01	98	160	1.001	0.70721825	1.667	0.09559944
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646

127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
127.88	97	159	1.001	0.71297011	1.697	0.08968646
316.13	234	398	1.003	0.7662599	2.333	0.01962831
623.47	448	799	1.002	0.83469677	2.31	0.02089101
623.47	448	799	1.002	0.83469677	2.31	0.02089101
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.1	172	322	1.003	0.90465212	2.733	0.0062736
247.27	172	323	1.003	0.9091256	2.737	0.00620793
249.25	173	325	1.003	0.90966768	2.752	0.00592535
249.25	173	325	1.003	0.90966768	2.752	0.00592535
75.15	52	99	1.002	0.9289169	1.963	0.04960358
75.15	52	99	1.002	0.9289169	1.963	0.04960358
75.15	52	99	1.002	0.9289169	1.963	0.04960358
37670.73	25344	49997	1.003	0.98019729	2.724	0.00644433
59.03	36	82	1.002	1.187627	2.575	0.0100373
244.76	489	0	0.958	#NUM!	-2.636	NA

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

padj	dispGeneEst	dispFit	dispMAP	dispersion	betaConv	maxCooks
NA	10	0.1354	1.1448	10	TRUE	32.7664
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
NA	5.9331	0.1753	1.0679	5.9331	TRUE	29.9634
0.99796172	0.4018	0.1649	0.2377	0.2377	TRUE	3.19
0.99796172	0.4018	0.1649	0.2377	0.2377	TRUE	3.19
0.99796172	0.4018	0.1649	0.2377	0.2377	TRUE	3.19
0.99796172	0.3943	0.096	0.1874	0.1874	TRUE	9.6964
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
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0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776

0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
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0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.4036	0.0979	0.1916	0.1916	TRUE	9.7776
0.99796172	0.2144	0.0972	0.1348	0.1348	TRUE	1.6992
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
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0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
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0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944

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0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
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0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
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0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.2177	0.0974	0.1359	0.1359	TRUE	1.6944
0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
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0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649

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0.99796172	0.1585	0.076	0.1024	0.1024	TRUE	0.9649
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0.99796172	0.1661	0.0774	0.1056	0.1056	TRUE	0.8728
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0.99796172	0.1663	0.0774	0.1057	0.1057	TRUE	0.8721
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0.99796172	0.2291	0.142	0.1705	0.1705	TRUE	1.3856
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.2481	0.1451	0.1786	0.1786	TRUE	3.107
0.99796172	0.0681	0.0886	0.0815	0.0815	TRUE	0.164
0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184

0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
0.99796172	0.1213	0.0646	0.0838	0.0838	TRUE	2.2184
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1211	0.0647	0.0838	0.0838	TRUE	2.2127
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.1938	0.0733	0.1122	0.1122	TRUE	5.095
0.99796172	0.0756	0.106	0.0955	0.0955	TRUE	0.1354
0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332

0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
0.99796172	0.0748	0.1062	0.0953	0.0953	TRUE	0.1332
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1593	0.121	0.1339	0.1339	TRUE	3.8289
0.99796172	0.1596	0.1208	0.1338	0.1338	TRUE	3.8289
0.99796172	0.1596	0.1208	0.1338	0.1338	TRUE	3.8289
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991

0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.0848	0.1152	0.1047	0.1047	TRUE	0.1991
0.99796172	0.1171	0.083	0.0946	0.0946	TRUE	1.9401
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884

0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884

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0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.1185	0.0834	0.0954	0.0954	TRUE	1.8884
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.8312	0.1584	0.3597	0.3597	TRUE	1.1668
0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
0.99796172	0.7843	0.0688	0.2642	0.7843	TRUE	0.3437
0.99796172	0.058	0.1018	0.0866	0.0866	TRUE	0.9103
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425

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0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
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0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
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0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
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0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
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0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.0595	0.102	0.0873	0.0873	TRUE	0.9425
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701

0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.1402	0.1295	0.134	0.134	TRUE	0.3701
0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
0.99796172	0.0553	0.1387	0.1114	0.1114	TRUE	0.4239
0.99796172	0.1779	0.1676	0.1709	0.1709	TRUE	0.2444
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.1756	0.1695	0.1712	0.1712	TRUE	0.2294
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931

0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.0475	0.1205	0.096	0.096	TRUE	0.2931
0.99796172	0.1709	0.1688	0.1695	0.1695	TRUE	0.2394
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.049	0.1101	0.0893	0.0893	TRUE	0.5532
0.99796172	0.0268	0.0729	0.0556	0.0556	TRUE	0.3966
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	1.4464	0.1288	0.478	1.4464	TRUE	0.6288
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966

0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.0272	0.0729	0.0557	0.0557	TRUE	0.3966
0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
0.99796172	0.2377	0.1647	0.1877	0.1877	TRUE	1.1534
0.99796172	0.0288	0.0728	0.0563	0.0563	TRUE	0.4409
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.3451	0.1716	0.2276	0.2276	TRUE	7.016
0.99796172	0.0442	0.101	0.0813	0.0813	TRUE	0.5065
0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
0.99796172	0.2763	0.1463	0.1877	0.1877	TRUE	0.1875
0.99796172	0.0416	0.1018	0.0809	0.0809	TRUE	0.5051
0.99796172	0.0416	0.1018	0.0809	0.0809	TRUE	0.5051
0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
0.99796172	0.0634	0.0861	0.0776	0.0776	TRUE	1.3263
0.99796172	1.4958	0.0718	0.4403	1.4958	TRUE	0.4815
0.99796172	1.4958	0.0718	0.4403	1.4958	TRUE	0.4815
0.99796172	1.4958	0.0718	0.4403	1.4958	TRUE	0.4815
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768

0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	1.4899	0.0719	0.439	1.4899	TRUE	0.4768
0.99796172	0.0222	0.0637	0.0471	0.0471	TRUE	0.2897
0.99796172	0.0222	0.0637	0.0471	0.0471	TRUE	0.2897
0.99796172	0.0222	0.0637	0.0471	0.0471	TRUE	0.2897
0.99796172	2.3298	0.119	0.5333	2.3298	TRUE	0.3198
0.99796172	2.3298	0.119	0.5333	2.3298	TRUE	0.3198
0.99796172	2.3298	0.119	0.5333	2.3298	TRUE	0.3198
0.99796172	2.3298	0.119	0.5333	2.3298	TRUE	0.3198
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101

0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0232	0.076	0.0561	0.0561	TRUE	0.3101
0.99796172	0.0225	0.076	0.0563	0.0563	TRUE	0.3261
0.99796172	0.0225	0.076	0.0563	0.0563	TRUE	0.3261
0.99796172	0.1429	0.1104	0.1212	0.1212	TRUE	3.0969
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334

0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.1949	0.0977	0.1292	0.1292	TRUE	0.334
0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
0.99796172	0.0171	0.0636	0.0453	0.0453	TRUE	0.2273
0.99796172	0.0113	0.1108	0.0768	0.0768	TRUE	0.3753
0.99796172	0.0113	0.1108	0.0768	0.0768	TRUE	0.3753
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0227	0.0636	0.0482	0.0482	TRUE	0.4924
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
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0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827

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0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
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0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0605	0.085	0.0755	0.0755	TRUE	1.3827
0.99796172	0.0116	0.111	0.077	0.077	TRUE	0.3753
0.99796172	0.0116	0.111	0.077	0.077	TRUE	0.3753
0.99796172	0.0166	0.0679	0.0476	0.0476	TRUE	0.3299
0.99796172	0.0166	0.0679	0.0476	0.0476	TRUE	0.3299
0.99796172	0.0705	0.0645	0.0667	0.0667	TRUE	0.739
0.99796172	0.0706	0.0645	0.0667	0.0667	TRUE	0.7389
0.99796172	0.0706	0.0645	0.0667	0.0667	TRUE	0.7389
0.99796172	0.0706	0.0645	0.0667	0.0667	TRUE	0.7389
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0.99796172	0.0706	0.0645	0.0667	0.0667	TRUE	0.7389

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0.99796172	0.0706	0.0645	0.0667	0.0667	TRUE	0.7389
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0.99796172	0.0695	0.0645	0.0663	0.0663	TRUE	0.7571
0.99796172	0.0695	0.0645	0.0663	0.0663	TRUE	0.7571
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0.99796172	0.0695	0.0645	0.0663	0.0663	TRUE	0.7571
0.99796172	0.0695	0.0645	0.0663	0.0663	TRUE	0.7571
0.99796172	0.0695	0.0645	0.0663	0.0663	TRUE	0.7571
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0.99796172	0.0697	0.0645	0.0664	0.0664	TRUE	0.7546
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0.99796172	0.0697	0.0645	0.0664	0.0664	TRUE	0.7546
0.99796172	0.0697	0.0645	0.0664	0.0664	TRUE	0.7546
0.99796172	0.0697	0.0645	0.0664	0.0664	TRUE	0.7546

0.99796172	0.0712	0.0645	0.0669	0.0669	TRUE	0.7062
0.99796172	0.0712	0.0645	0.0669	0.0669	TRUE	0.7062
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	2.1711	0.1389	0.5255	2.1711	TRUE	0.3291
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328

0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.0168	0.068	0.0478	0.0478	TRUE	0.3328
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.013	0.0637	0.0428	0.0428	TRUE	0.3011
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417

0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	0.0403	0.0936	0.0746	0.0746	TRUE	0.6417
0.99796172	2.1802	0.1376	0.526	2.1802	TRUE	0.3459
0.99796172	0.115	0.0892	0.0979	0.0979	TRUE	0.4416
0.99796172	0.1105	0.0898	0.0968	0.0968	TRUE	0.3573
0.99796172	0.1105	0.0898	0.0968	0.0968	TRUE	0.3573
0.99796172	0.1105	0.0898	0.0968	0.0968	TRUE	0.3573
0.99796172	0.1105	0.0898	0.0968	0.0968	TRUE	0.3573
0.99796172	0.1105	0.0898	0.0968	0.0968	TRUE	0.3573
0.99796172	0.1105	0.0898	0.0968	0.0968	TRUE	0.3573
0.99796172	0.1105	0.0898	0.0968	0.0968	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573

0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	1.2037	0.1409	0.4206	1.2037	TRUE	0.3573
0.99796172	0.1493	0.0649	0.0928	0.0928	TRUE	0.3897
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.0298	0.0787	0.0605	0.0605	TRUE	0.4691
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.9357	0.0864	0.3179	0.9357	TRUE	0.3363
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209

0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0431	0.0883	0.072	0.072	TRUE	0.7209
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0378	0.0851	0.0679	0.0679	TRUE	0.4546
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836

0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0576	0.1629	0.1268	0.1268	TRUE	0.836
0.99796172	0.0384	0.0658	0.0554	0.0554	TRUE	0.296
0.99796172	0.0454	0.1075	0.0855	0.0855	TRUE	1.0762
0.99796172	0.0454	0.1075	0.0855	0.0855	TRUE	1.0762
0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
0.99796172	0.0528	0.1103	0.0901	0.0901	TRUE	1.1846
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429

0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0191	0.1053	0.0745	0.0745	TRUE	0.3429
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152

0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.0419	0.0419	TRUE	0.2152
0.99796172	0.0105	0.0631	0.042	0.042	TRUE	0.2164
0.99796172	0.066	0.1212	0.1023	0.1023	TRUE	0.8714
0.99796172	0.066	0.1212	0.1023	0.1023	TRUE	0.8714
0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
0.99796172	0.1122	0.1213	0.1183	0.1183	TRUE	0.5918
0.99796172	0.0554	0.0779	0.0699	0.0699	TRUE	0.3326
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345

0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.1186	0.1041	0.1089	0.1089	TRUE	0.4345
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754

0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0193	0.1135	0.0798	0.0798	TRUE	0.4754
0.99796172	0.0389	0.0678	0.0569	0.0569	TRUE	0.57
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.0381	0.0647	0.0546	0.0546	TRUE	0.7126
0.99796172	0.1448	0.1097	0.1212	0.1212	TRUE	0.6215
0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
0.99796172	0.0371	0.0647	0.0542	0.0542	TRUE	0.6969
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453

0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0258	0.1169	0.0847	0.0847	TRUE	0.5453
0.99796172	0.0379	0.0647	0.0545	0.0545	TRUE	0.7025
0.99796172	0.0379	0.0647	0.0545	0.0545	TRUE	0.7025
0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
0.99796172	0.0339	0.0705	0.0567	0.0567	TRUE	0.7864
0.99796172	0.0193	0.0912	0.0647	0.0647	TRUE	0.4029
0.99796172	0.0193	0.0912	0.0647	0.0647	TRUE	0.4029
0.99796172	0.0199	0.0906	0.0645	0.0645	TRUE	0.4112
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365

0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365

0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0136	0.1165	0.0805	0.0805	TRUE	0.2365
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0.0434	0.0642	0.0564	0.0564	TRUE	0.3801
0.99796172	0	0.092	0.0568	0.0568	TRUE	0.0785
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298

0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.021	0.092	0.0659	0.0659	TRUE	0.4298
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881

0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0458	0.0696	0.0608	0.0608	TRUE	0.2881
0.99796172	0.0338	0.0742	0.0592	0.0592	TRUE	0.8544
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708

0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
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0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.041	0.064	0.0578	0.0578	TRUE	0.7708
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004

0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
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0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004

0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0256	0.1472	0.1054	0.1054	TRUE	0.4004
0.99796172	0.0245	0.0634	0.0481	0.0481	TRUE	0.4081
0.99796172	0.0245	0.0634	0.0481	0.0481	TRUE	0.4081
0.99796172	0.0246	0.0634	0.0481	0.0481	TRUE	0.4089
0.99796172	0.0246	0.0634	0.0481	0.0481	TRUE	0.4089
0.99796172	0.0649	0.0762	0.0722	0.0722	TRUE	1.1432
0.99796172	0.0649	0.0762	0.0722	0.0722	TRUE	1.1432
0.99796172	0.0649	0.0762	0.0722	0.0722	TRUE	1.1432
0.99796172	0.0649	0.0762	0.0722	0.0722	TRUE	1.1432
0.99796172	0.0649	0.0762	0.0722	0.0722	TRUE	1.1432
0.99796172	0.0649	0.0762	0.0722	0.0722	TRUE	1.1432
0.99796172	0.0649	0.0762	0.0722	0.0722	TRUE	1.1432

0.99796172	0.0156	0.072	0.05	0.05	TRUE	0.1884
0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
0.99796172	0.0154	0.072	0.0499	0.0499	TRUE	0.1797
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0155	0.072	0.0499	0.0499	TRUE	0.1833
0.99796172	0.0199	0.0686	0.0496	0.0496	TRUE	0.2919
0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
0.99796172	0.0207	0.0685	0.0498	0.0498	TRUE	0.2948
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0096	0.0634	0.0412	0.0412	TRUE	0.216
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084

0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2084
0.99796172	0.3288	0.1303	0.192	0.192	TRUE	0.3182
0.99796172	0.3288	0.1303	0.192	0.192	TRUE	0.3182
0.99796172	0.3288	0.1303	0.192	0.192	TRUE	0.3182
0.99796172	0.3288	0.1303	0.192	0.192	TRUE	0.3182
0.99796172	0.3288	0.1303	0.192	0.192	TRUE	0.3182

0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2087
0.99796172	0.0094	0.0634	0.0411	0.0411	TRUE	0.2087
0.99796172	0.1038	0.0842	0.0908	0.0908	TRUE	0.3848
0.99796172	0.0806	0.0809	0.0808	0.0808	TRUE	0.6606
0.99796172	0.0175	0.0788	0.0556	0.0556	TRUE	0.268
0.99796172	0.1042	0.0842	0.091	0.091	TRUE	0.4166
0.99796172	0.1042	0.0842	0.091	0.091	TRUE	0.4166
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724

0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99796172	0.0525	0.1039	0.0859	0.0859	TRUE	1.0724
0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
0.99803669	0.0446	0.1017	0.0815	0.0815	TRUE	0.7395
0.99796172	0.0074	0.0966	0.0638	0.0638	TRUE	0.1927
0.99796172	0.0076	0.0967	0.0639	0.0639	TRUE	0.1981
0.99803669	0.0729	0.0733	0.0731	0.0731	TRUE	0.9276
0.99803669	0.0729	0.0733	0.0731	0.0731	TRUE	0.9276
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497

0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0796	0.0811	0.0806	0.0806	TRUE	0.5497
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99796172	0.0065	0.0636	0.0398	0.0398	TRUE	0.1339
0.99803669	0.0066	0.0636	0.0399	0.0399	TRUE	0.135
0.99803669	0.0066	0.0636	0.0399	0.0399	TRUE	0.135
0.99929018	0.0064	0.0636	0.0398	0.0398	TRUE	0.1323
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0323	0.0937	0.0715	0.0715	TRUE	0.6903
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882

0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99796172	0.0071	0.0967	0.0638	0.0638	TRUE	0.1882
0.99803669	0.079	0.0796	0.0794	0.0794	TRUE	0.4261
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1646	0.0943	0.1171	0.1171	TRUE	0.7275
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842

0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99803669	0.1171	0.1536	0.1416	0.1416	TRUE	0.4842
0.99868672	0.1466	0.1381	0.1409	0.1409	TRUE	1.4945
0.99916959	0.0318	0.0666	0.0533	0.0533	TRUE	0.5013
0.99916959	0.0319	0.0666	0.0533	0.0533	TRUE	0.5022
0.99916959	0.0319	0.0666	0.0533	0.0533	TRUE	0.5022
0.99916959	0.0319	0.0666	0.0533	0.0533	TRUE	0.5022
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643

0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0323	0.0639	0.0539	0.0539	TRUE	0.643
0.99796172	0.0088	0.0707	0.046	0.046	TRUE	0.1231
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.0081	0.0632	0.0415	0.0415	TRUE	0.1902
0.99796172	0.1422	0.0633	0.0895	0.0895	TRUE	0.31
0.99796172	0.1422	0.0633	0.0895	0.0895	TRUE	0.31
0.99796172	0.1422	0.0633	0.0895	0.0895	TRUE	0.31
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
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0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
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0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
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0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089

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0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
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0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
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0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
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0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
0.99796172	0.1423	0.0633	0.0895	0.0895	TRUE	0.3089
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0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.0402	0.0898	0.072	0.072	TRUE	0.5037
0.99796172	0.1417	0.0633	0.0893	0.0893	TRUE	0.307
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2272
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2272
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
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0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273

0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
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0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
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0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
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0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
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0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0132	0.0633	0.0446	0.0446	TRUE	0.2273
0.99796172	0.0429	0.1012	0.0805	0.0805	TRUE	0.7913
0.99796172	0.0144	0.0832	0.0573	0.0573	TRUE	0.1868
0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
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0.99796172	0.0178	0.1135	0.0798	0.0798	TRUE	0.2788
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0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5561
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0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5562
0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5562
0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5562
0.99796172	0.02	0.0629	0.0474	0.0474	TRUE	0.5562
0.99796172	0.02	0.0629	0.0475	0.0475	TRUE	0.5564
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0.99796172	0.1357	0.1429	0.1405	0.1405	TRUE	2.663
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0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
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0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0	0.1446	0.0966	0.0966	TRUE	0.1828
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201

0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0344	0.0686	0.0556	0.0556	TRUE	0.6201
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327

0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2327
0.99796172	0.0181	0.0704	0.0499	0.0499	TRUE	0.256
0.99796172	0.0181	0.0704	0.0499	0.0499	TRUE	0.256
0.99796172	0.2192	0.067	0.115	0.115	TRUE	0.19
0.99796172	0.1072	0.0795	0.0889	0.0889	TRUE	0.6072
0.99796172	0.1072	0.0795	0.0889	0.0889	TRUE	0.6072
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2382
0.99796172	0.0391	0.075	0.0618	0.0618	TRUE	0.2382
0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
0.99796172	0.1306	0.08	0.0969	0.0969	TRUE	0.5889
0.99796172	0	0.1429	0.0963	0.0963	TRUE	0.2014
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863

0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863

0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
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0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863

0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.0279	0.0633	0.0494	0.0494	TRUE	0.3863
0.99796172	0.2731	0.0673	0.1304	0.1304	TRUE	0.2014
0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
0.99796172	0.0144	0.0629	0.0445	0.0445	TRUE	0.2332
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
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0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
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0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
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0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.01	0.0629	0.0415	0.0415	TRUE	0.2237
0.99796172	0.1275	0.0816	0.0969	0.0969	TRUE	0.5587
0.99796172	0.128	0.0815	0.0971	0.0971	TRUE	0.5664
0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622

0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
0.99796172	0.0319	0.0899	0.0689	0.0689	TRUE	0.4622
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
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0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
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0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
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0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
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0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554

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0.99796172	0.1266	0.0816	0.0967	0.0967	TRUE	0.554
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0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0121	0.0629	0.0431	0.0431	TRUE	0.2355
0.99796172	0.0116	0.1106	0.0751	0.0751	TRUE	0.3291
0.99796172	0.0116	0.1106	0.0751	0.0751	TRUE	0.3291
0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
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0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186

0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
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0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
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0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186

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0.99796172	0.0233	0.0636	0.0495	0.0495	TRUE	0.4186
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0.99796172	0.0313	0.0651	0.0521	0.0521	TRUE	0.2495
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0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
0.99796172	0.1802	0.064	0.1015	0.1015	TRUE	0.6495
0.99796172	0.1797	0.064	0.1013	0.1013	TRUE	0.6595
0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
0.99796172	0.0312	0.0651	0.052	0.052	TRUE	0.2496
0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
0.99796172	0.0329	0.0783	0.0615	0.0615	TRUE	0.6625
0.99796172	0.0417	0.0665	0.0572	0.0572	TRUE	0.4532
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709

0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.0266	0.0634	0.0489	0.0489	TRUE	0.4709
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.1398	0.087	0.1045	0.1045	TRUE	1.0026
0.99796172	0.0049	0.063	0.0385	0.0385	TRUE	0.1115
0.99796172	0.0407	0.0658	0.0563	0.0563	TRUE	0.287
0.99796172	0.0407	0.0658	0.0563	0.0563	TRUE	0.287
0.99796172	0.0407	0.0658	0.0563	0.0563	TRUE	0.287

0.99796172	0.0296	0.0645	0.0523	0.0523	TRUE	0.1731
0.99796172	0.0809	0.1032	0.0956	0.0956	TRUE	0.4046
0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
0.99796172	0.0354	0.0672	0.0552	0.0552	TRUE	0.2307
0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
0.99796172	0.0272	0.0802	0.0606	0.0606	TRUE	0.3502
0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
0.99796172	0.0218	0.1132	0.081	0.081	TRUE	0.5211
0.99796172	0.0272	0.0801	0.0605	0.0605	TRUE	0.3524
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474

0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0268	0.0802	0.0604	0.0604	TRUE	0.3474
0.99796172	0.0085	0.0629	0.0403	0.0403	TRUE	0.1069
0.99796172	0.0085	0.0629	0.0403	0.0403	TRUE	0.1069
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.038	0.0784	0.0636	0.0636	TRUE	0.4617
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	0.0081	0.1345	0.0905	0.0905	TRUE	0.2606
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4515	0.1262	0.5752	2.4515	TRUE	0.6447
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631

0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	2.4595	0.1268	0.5782	2.4595	TRUE	0.631
0.99796172	0.0857	0.0961	0.0925	0.0925	TRUE	1.8099
0.99796172	0.0857	0.0961	0.0925	0.0925	TRUE	1.8099
0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
0.99796172	0.0273	0.0636	0.0496	0.0496	TRUE	0.4101
0.99796172	0.0419	0.1357	0.1036	0.1036	TRUE	0.5118
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4247
0.99796172	0.036	0.0633	0.053	0.053	TRUE	0.4216
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251

0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0271	0.0637	0.0486	0.0486	TRUE	0.6251
0.99796172	0.0064	0.0781	0.0502	0.0502	TRUE	0.1802
0.99796172	0.0064	0.0781	0.0502	0.0502	TRUE	0.1802
0.99796172	0.0064	0.0781	0.0502	0.0502	TRUE	0.1802
0.99796172	0.0064	0.0781	0.0502	0.0502	TRUE	0.1802
0.99796172	0.0064	0.0781	0.0502	0.0502	TRUE	0.1802
0.99796172	0.0597	0.0813	0.0737	0.0737	TRUE	0.3435
0.99796172	0.0597	0.0813	0.0737	0.0737	TRUE	0.3435
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807

0.99796172	0.0065	0.0782	0.0502	0.0502	TRUE	0.1807
0.99796172	0.0283	0.0777	0.0594	0.0594	TRUE	0.5387
0.99796172	0.0283	0.0777	0.0594	0.0594	TRUE	0.5387
0.99796172	0.0283	0.0777	0.0594	0.0594	TRUE	0.5387
0.99796172	0.048	0.0833	0.0706	0.0706	TRUE	0.4425
0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
0.99796172	0.0252	0.0636	0.0478	0.0478	TRUE	0.6077
0.99796172	0.0259	0.0637	0.0481	0.0481	TRUE	0.6277
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0305	0.079	0.0611	0.0611	TRUE	0.518
0.99796172	0.0248	0.0634	0.0487	0.0487	TRUE	0.4237
0.99796172	0.0248	0.0634	0.0487	0.0487	TRUE	0.4237
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265

0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0308	0.079	0.0613	0.0613	TRUE	0.5265
0.99796172	0.0355	0.1569	0.1167	0.1167	TRUE	0.6572
0.99796172	0.0927	0.096	0.095	0.095	TRUE	1.2452
0.99796172	0.0425	0.161	0.1221	0.1221	TRUE	0.7749
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.071	0.0848	0.08	0.08	TRUE	0.2533
0.99796172	0.1354	0.0952	0.1084	0.1084	TRUE	0.5894
0.99796172	0.0188	0.0638	0.0463	0.0463	TRUE	0.3773
0.99796172	0.0031	0.0861	0.0543	0.0543	TRUE	0.0864
0.99796172	0.0031	0.0861	0.0543	0.0543	TRUE	0.0864
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.0174	0.0718	0.0506	0.0506	TRUE	0.3515
0.99796172	0.1128	0.0735	0.0869	0.0869	TRUE	1.4026
0.99796172	0.0373	0.0958	0.0751	0.0751	TRUE	0.7971
0.99796172	0.0373	0.0958	0.0751	0.0751	TRUE	0.7971
0.99796172	0.0135	0.0708	0.0483	0.0483	TRUE	0.3424
0.99796172	0.0135	0.0708	0.0483	0.0483	TRUE	0.3424
0.99796172	0.0162	0.0865	0.0603	0.0603	TRUE	0.296
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781
0.99796172	0.0581	0.0647	0.0639	0.0639	TRUE	1.2781

0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.0297	0.0886	0.0673	0.0673	TRUE	0.288
0.99796172	0.15	0.0949	0.1129	0.1129	TRUE	1.0385

0.99796172	0.033	0.0644	0.0525	0.0525	TRUE	0.1969
0.99796172	0.033	0.0644	0.0525	0.0525	TRUE	0.1969
0.99796172	0.0332	0.0644	0.0526	0.0526	TRUE	0.1952
0.99796172	0.0332	0.0644	0.0526	0.0526	TRUE	0.1952
0.99796172	0.0316	0.089	0.0683	0.0683	TRUE	0.3234
0.99796172	0.0358	0.064	0.0524	0.0524	TRUE	0.7117
0.99796172	0.0358	0.064	0.0524	0.0524	TRUE	0.7117
0.99796172	0.0406	0.1378	0.1049	0.1049	TRUE	0.8973
0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
0.99796172	0.0417	0.1384	0.1056	0.1056	TRUE	0.9298
0.99796172	0.0532	0.1262	0.1011	0.1011	TRUE	0.1735
0.99796172	0.1875	0.0629	0.1032	0.1032	TRUE	0.4253
0.99796172	0.1875	0.0629	0.1032	0.1032	TRUE	0.4253
0.99796172	0.1875	0.0629	0.1032	0.1032	TRUE	0.4253
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.2351	0.1083	0.1481	0.1481	TRUE	0.3329
0.99796172	0.0665	0.0634	0.0646	0.0646	TRUE	0.2512
0.99796172	0.0665	0.0634	0.0646	0.0646	TRUE	0.2512
0.99796172	0.0222	0.0853	0.062	0.062	TRUE	0.1748
0.99796172	0.0222	0.0853	0.062	0.062	TRUE	0.1748
0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
0.99796172	0.0263	0.0846	0.0632	0.0632	TRUE	0.2498
0.99796172	0.0517	0.0934	0.0786	0.0786	TRUE	0.1983
0.99796172	0.0517	0.0934	0.0786	0.0786	TRUE	0.1983
0.99796172	0.0505	0.1279	0.1013	0.1013	TRUE	0.1939
0.99796172	0.0505	0.1279	0.1013	0.1013	TRUE	0.1939
0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439

0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
0.99796172	0.019	0.0863	0.0613	0.0613	TRUE	0.2439
0.99796172	0.247	0.109	0.1521	0.1521	TRUE	0.3882
0.99796172	0.247	0.109	0.1521	0.1521	TRUE	0.3882
0.99796172	0.247	0.109	0.1521	0.1521	TRUE	0.3882
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.0917	0.0661	0.075	0.075	TRUE	0.516
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.4456	0.1588	0.2432	0.2432	TRUE	0.5712
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262

0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.1015	0.1195	0.1136	0.1136	TRUE	1.3262
0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
0.99796172	0.2102	0.1246	0.1517	0.1517	TRUE	0.7639
0.99796172	0.0623	0.1346	0.1103	0.1103	TRUE	1.2936
0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
0.99796172	0.2517	0.1053	0.151	0.151	TRUE	0.3797
0.99796172	0.0571	0.0828	0.073	0.073	TRUE	1.1198
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0512	0.0642	0.058	0.058	TRUE	0.6887
0.99796172	0.0633	0.0836	0.0759	0.0759	TRUE	0.8119
0.99796172	0.0633	0.0836	0.0759	0.0759	TRUE	0.8119
0.99796172	0.063	0.137	0.1124	0.1124	TRUE	0.7054
0.99796172	0.3796	0.1445	0.2152	0.2152	TRUE	3.7357
0.99796172	0.3796	0.1445	0.2152	0.2152	TRUE	3.7357
0.99796172	0.1042	0.1278	0.1199	0.1199	TRUE	1.3928
0.99796172	0.1042	0.1278	0.1199	0.1199	TRUE	1.3928
0.99796172	0.1042	0.1278	0.1199	0.1199	TRUE	1.3928
0.99796172	0.0179	0.0634	0.045	0.045	TRUE	0.3052
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077

0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0755	0.1397	0.1185	0.1185	TRUE	0.5077
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
0.99796172	0.0295	0.0635	0.0516	0.0516	TRUE	0.6982
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0.99796172	0.0662	0.0635	0.0642	0.0642	TRUE	0.1438
0.99796172	0.0662	0.0635	0.0642	0.0642	TRUE	0.1438
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0.99796172	0.0567	0.0632	0.0602	0.0602	TRUE	0.2543
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0.99796172	0.0568	0.0632	0.0602	0.0602	TRUE	0.2523
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0.99796172	0.0443	0.0778	0.0648	0.0648	TRUE	1.1141
0.99796172	0.0443	0.0778	0.0648	0.0648	TRUE	1.1141
0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
0.99796172	0.2604	0.1426	0.1785	0.1785	TRUE	3.2665
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0.99796172	0.0871	0.156	0.1336	0.1336	TRUE	0.5158
0.99796172	0.1861	0.071	0.1079	0.1079	TRUE	0.3378
0.99796172	0.0156	0.0978	0.0683	0.0683	TRUE	0.3906
0.99796172	0.0124	0.1639	0.1142	0.1142	TRUE	0.4142
0.99796172	0.0464	0.0645	0.058	0.058	TRUE	0.5885
0.99796172	0.0464	0.0645	0.058	0.058	TRUE	0.5885
0.99796172	0.0873	0.1601	0.1365	0.1365	TRUE	1.0664
0.99796172	0.0873	0.1601	0.1365	0.1365	TRUE	1.0664
0.99796172	0.0504	0.0647	0.0598	0.0598	TRUE	0.6657
0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
0.99796172	0.0569	0.0892	0.0782	0.0782	TRUE	0.7662
0.99796172	0.0614	0.0742	0.069	0.069	TRUE	0.589
0.99796172	0.1744	0.063	0.102	0.102	TRUE	0.5408
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0.99796172	0.0769	0.078	0.0771	0.0771	TRUE	0.3403
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0.99796172	0.156	0.103	0.12	0.12	TRUE	0.4998
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0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
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0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0601	0.0838	0.0754	0.0754	TRUE	1.2015
0.99796172	0.0604	0.0838	0.0754	0.0754	TRUE	1.206
0.99796172	0.0577	0.0836	0.0743	0.0743	TRUE	1.1646
0.99796172	0.0577	0.0836	0.0743	0.0743	TRUE	1.1646
0.99796172	0.17	0.1319	0.1443	0.1443	TRUE	0.8127
0.99796172	0.17	0.1319	0.1443	0.1443	TRUE	0.8127
0.99796172	0.17	0.1319	0.1443	0.1443	TRUE	0.8127
0.99796172	0.172	0.063	0.0933	0.0933	TRUE	3.6096
0.99796172	0.0992	0.1507	0.1347	0.1347	TRUE	1.7485
NA	10	0.084	1.2226	10	TRUE	36.0827

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

mean	5%	1%
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53	1	1
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53.8333333	1	1
53.8333333	1	1
164.166667	1	1
155.5	1	1
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miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
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ugagguaguaga	Phvul.002G267400.1	2	-1	1	22
ugagguaguagg	Phvul.002G071800.1	2.5	-1	1	22
ugagguaguagg	Phvul.002G071800.1	2.5	-1	1	22
ugagguaguagg	Phvul.002G071800.1	2.5	-1	1	22
ugagguaguagg	Phvul.002G071800.1	2.5	-1	1	22
agagguaguagg	Phvul.006G201700.1	2.5	-1	1	24
ugagguaguaga	Phvul.009G057800.1	2.5	-1	1	22
ugagguaguaga	Phvul.009G057800.1	2.5	-1	1	22
agagguaguagg	Phvul.009G086800.1	2.5	-1	1	24
ugagguaguagg	Phvul.010G116400.1	2.5	-1	1	22
ugagguaguagg	Phvul.010G116400.1	2.5	-1	1	22
ugagguaguagg	Phvul.010G116400.1	2.5	-1	1	22
ugagguaguagg	Phvul.010G116400.1	2.5	-1	1	22
ugagguaguagg	Phvul.L009543.1	2.5	-1	1	22
ugagguaguagg	Phvul.L009543.1	2.5	-1	1	22
ugagguaguagg	Phvul.L009543.1	2.5	-1	1	22
ugagguaguagg	Phvul.L009543.1	2.5	-1	1	22
ugagguaguagg	Phvul.001G077200.2	3	-1	1	22
ugagguaguagg	Phvul.001G077200.2	3	-1	1	22
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ugagguaguagg	Phvul.001G077200.2	3	-1	1	22
ugagguaguaga	Phvul.001G215300.1	3	-1	1	22
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ugagguaguagg	Phvul.002G281100.1	3	-1	1	22
agagguaguagg	Phvul.004G044900.1	3	-1	1	24
agagguaguagg	Phvul.006G158900.1	3	-1	1	24
ugagguaguagg	Phvul.008G071966.1	3	-1	1	22
ugagguaguagg	Phvul.008G071966.1	3	-1	1	22
ugagguaguagg	Phvul.008G071966.1	3	-1	1	22
ugagguaguagg	Phvul.008G071966.1	3	-1	1	22
agagguaguagg	Phvul.008G110200.1	3	-1	1	24
agagguaguagg	Phvul.008G110500.1	3	-1	1	24

ugagguaguagg	Phvul.008G163350.4	3	-1	1	22
ugagguaguagg	Phvul.008G163350.3	3	-1	1	22
ugagguaguagg	Phvul.008G163350.2	3	-1	1	22
ugagguaguagg	Phvul.008G163350.1	3	-1	1	22
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ugagguaguagg	Phvul.008G163350.2	3	-1	1	22
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ugagguaguaga	Phvul.001G077200.2	3.5	-1	1	22
ugagguaguaga	Phvul.001G077200.2	3.5	-1	1	22
ugagguaguaga	Phvul.001G077700.1	3.5	-1	1	22
ugagguaguaga	Phvul.001G077700.1	3.5	-1	1	22
ugagguaguagg	Phvul.001G086466.1	3.5	-1	1	22
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ugagguaguagg	Phvul.001G089600.1	3.5	-1	1	22
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ugagguaguagg	Phvul.001G091100.1	3.5	-1	1	22
agagguaguagg	Phvul.001G121000.1	3.5	-1	1	24
agagguaguagg	Phvul.001G121000.2	3.5	-1	1	24
ugagguaguagg	Phvul.001G131150.1	3.5	-1	1	22

ugagguaguagg	Phvul.001G131150.2	3.5	-1	1	22
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ugagguaguaga	Phvul.002G042000.8	3.5	-1	1	22
ugagguaguaga	Phvul.002G042000.7	3.5	-1	1	22
ugagguaguaga	Phvul.002G042000.6	3.5	-1	1	22
ugagguaguaga	Phvul.002G042000.5	3.5	-1	1	22
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agagguaguagg	Phvul.002G185150.2	3.5	-1	1	24
agagguaguagg	Phvul.002G185150.1	3.5	-1	1	24
agagguaguagg	Phvul.002G185150.3	3.5	-1	1	24

agagguaguagg	Phvul.002G304500.1	3.5	-1	1	24
ugagguaguaga	Phvul.003G103100.2	3.5	-1	1	22
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agagguaguagg	Phvul.005G087300.1	3.5	-1	1	24
ugagguaguaga	Phvul.005G116100.2	3.5	-1	1	22
ugagguaguaga	Phvul.005G116100.1	3.5	-1	1	22
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ugagguaguaga	Phvul.005G116100.1	3.5	-1	1	22
ugagguaguaga	Phvul.005G180200.1	3.5	-1	1	22
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agagguaguagg	Phvul.006G106900.2	3.5	-1	1	24
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agagguaguagg	Phvul.006G137200.2	3.5	-1	1	24
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agagguaguagg	Phvul.001G036800.1	4	-1	1	24
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ugagguaguagg	Phvul.001G153600.2	4	-1	1	22
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agagguaguagg	Phvul.002G004100.1	4	-1	1	24
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agagguaguagg	Phvul.002G212900.1	4	-1	1	24
ugagguaguaga	Phvul.002G253200.1	4	-1	1	22
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agagguaguagg	Phvul.004G163200.1	4	-1	1	24
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ugagguaguaga	Phvul.005G097200.3	4	-1	1	22
ugagguaguaga	Phvul.005G097200.6	4	-1	1	22
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agagguaguag	Phvul.007G058400.2	4	-1	1	24
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ugagguaguaga	Phvul.002G216700.2	4.5	-1	1	22
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ugagguaguaga	Phvul.002G309100.1	4.5	-1	1	22
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ugagguaguaga	Phvul.003G032300.1	4.5	-1	1	22
ugagguaguaga	Phvul.003G057700.1	4.5	-1	1	22
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agagguaguagg	Phvul.007G064700.1	4.5	-1	1	24
ugagguaguagg	Phvul.007G064700.1	4.5	-1	1	22
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ugagguaguaga	Phvul.009G121300.1	4.5	-1	1	22
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ugagguaguaga	Phvul.010G043700.4	4.5	-1	1	22
ugagguaguaga	Phvul.010G043700.1	4.5	-1	1	22
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ugagguaguaga	Phvul.010G043700.9	4.5	-1	1	22
ugagguaguaga	Phvul.010G043700.8	4.5	-1	1	22
ugagguaguaga	Phvul.010G043700.7	4.5	-1	1	22
ugagguaguaga	Phvul.010G043700.5	4.5	-1	1	22

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ugagguaguaga	Phvul.010G043700.9	4.5	-1	1	22
ugagguaguaga	Phvul.010G043700.8	4.5	-1	1	22
ugagguaguaga	Phvul.010G043700.7	4.5	-1	1	22
agagguaguagg	Phvul.010G070600.1	4.5	-1	1	24
agagguaguagg	Phvul.010G089200.1	4.5	-1	1	24
agagguaguagg	Phvul.010G089200.2	4.5	-1	1	24
ugagguaguagg	Phvul.010G089200.1	4.5	-1	1	22
ugagguaguagg	Phvul.010G089200.2	4.5	-1	1	22
ugagguaguagg	Phvul.010G089200.1	4.5	-1	1	22
ugagguaguagg	Phvul.010G089200.2	4.5	-1	1	22
ugagguaguagg	Phvul.010G089200.1	4.5	-1	1	22
ugagguaguagg	Phvul.010G089200.2	4.5	-1	1	22
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ugagguaguagg	Phvul.010G089200.2	4.5	-1	1	22
ugagguaguagg	Phvul.010G135701.1	4.5	-1	1	22
ugagguaguagg	Phvul.010G135701.1	4.5	-1	1	22
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ugagguaguagg	Phvul.010G135701.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G013900.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G013900.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G013900.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G013900.1	4.5	-1	1	22
ugagguaguaga	Phvul.011G050300.1	4.5	-1	1	22
ugagguaguaga	Phvul.011G050300.2	4.5	-1	1	22
ugagguaguaga	Phvul.011G050300.1	4.5	-1	1	22
ugagguaguaga	Phvul.011G050300.2	4.5	-1	1	22
ugagguaguaga	Phvul.011G061600.1	4.5	-1	1	22
ugagguaguaga	Phvul.011G061600.1	4.5	-1	1	22
agagguaguagg	Phvul.011G114700.1	4.5	-1	1	24
agagguaguagg	Phvul.011G123000.1	4.5	-1	1	24
ugagguaguaga	Phvul.011G123701.1	4.5	-1	1	22
ugagguaguaga	Phvul.011G123701.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.3	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.2	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.3	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.2	4.5	-1	1	22

ugagguaguagg	Phvul.011G160800.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.3	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.2	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.1	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.3	4.5	-1	1	22
ugagguaguagg	Phvul.011G160800.2	4.5	-1	1	22
ugagguaguagg	Phvul.011G202700.1	4.5	-1	1	22
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ugagguaguagg	Phvul.L002051.1	4.5	-1	1	22
ugagguaguagg	Phvul.L002051.2	4.5	-1	1	22
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agagguaguagg	Phvul.L007343.1	4.5	-1	1	24
ugagguaguaga	Phvul.008G004400.1	4.75	-1	1	22
ugagguaguaga	Phvul.008G004400.1	4.75	-1	1	22
agagguaguagg	Phvul.001G020300.1	5	-1	1	24
agagguaguagg	Phvul.001G020350.1	5	-1	1	24
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agagguaguagg	Phvul.001G036800.1	5	-1	1	24
ugagguaguaga	Phvul.001G057800.1	5	-1	1	22
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ugagguaguaga	Phvul.001G077700.1	5	-1	1	22
ugagguaguaga	Phvul.001G077700.1	5	-1	1	22
ugagguaguaga	Phvul.001G097800.1	5	-1	1	22
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ugagguaguaga	Phvul.001G109300.1	5	-1	1	22
ugagguaguaga	Phvul.001G114900.1	5	-1	1	22
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ugagguaguaga	Phvul.001G123000.2	5	-1	1	22
ugagguaguaga	Phvul.001G123000.2	5	-1	1	22
ugagguaguagg	Phvul.001G134100.2	5	-1	1	22
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agagguaguagg	Phvul.001G159300.1	5	-1	1	24
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agagguaguagg	Phvul.001G214300.1	5	-1	1	24
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ugagguaguaga	Phvul.002G253100.1	5	-1	1	22
agagguaguagg	Phvul.002G262600.1	5	-1	1	24
ugagguaguaga	Phvul.002G290000.3	5	-1	1	22
ugagguaguaga	Phvul.002G290000.3	5	-1	1	22
ugagguaguaga	Phvul.003G022200.1	5	-1	1	22
ugagguaguaga	Phvul.003G022200.1	5	-1	1	22
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agagguaguagg	Phvul.003G119100.2	5	-1	1	24
agagguaguagg	Phvul.003G119100.1	5	-1	1	24
agagguaguagg	Phvul.003G169700.1	5	-1	1	24
agagguaguagg	Phvul.003G292000.1	5	-1	1	24
agagguaguagg	Phvul.004G058600.1	5	-1	1	24
ugagguaguagg	Phvul.004G121666.1	5	-1	1	22
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ugagguaguaga	Phvul.004G176700.1	5	-1	1	22
ugagguaguaga	Phvul.004G176700.1	5	-1	1	22
ugagguaguaga	Phvul.005G056400.1	5	-1	1	22
ugagguaguaga	Phvul.005G056400.1	5	-1	1	22
agagguaguagg	Phvul.005G088800.1	5	-1	1	24
agagguaguagg	Phvul.005G095600.1	5	-1	1	24
ugagguaguagg	Phvul.005G097200.3	5	-1	1	22

ugagguaguagg	Phvul.005G097200.6	5	-1	1	22
ugagguaguagg	Phvul.005G097200.5	5	-1	1	22
ugagguaguagg	Phvul.005G097200.3	5	-1	1	22
ugagguaguagg	Phvul.005G097200.6	5	-1	1	22
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ugagguaguagg	Phvul.007G035900.2	5	-1	1	22
ugagguaguagg	Phvul.007G035900.2	5	-1	1	22
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ugagguaguagg	Phvul.007G069900.5	5	-1	1	22
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ugagguaguagg	Phvul.007G069900.3	5	-1	1	22
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ugagguaguagg	Phvul.007G069900.3	5	-1	1	22
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ugagguaguagg	Phvul.007G069900.1	5	-1	1	22
ugagguaguagg	Phvul.007G069900.4	5	-1	1	22
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ugagguaguagg	Phvul.007G069900.4	5	-1	1	22
agagguaguagg	Phvul.007G099300.1	5	-1	1	24
ugagguaguagg	Phvul.007G114100.1	5	-1	1	22
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agagguaguagg	Phvul.007G192300.1	5	-1	1	24
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agagguaguagg	Phvul.007G251800.1	5	-1	1	24
agagguaguagg	Phvul.008G043400.1	5	-1	1	24
agagguaguagg	Phvul.008G043400.1	5	-1	1	24
ugagguaguaga	Phvul.008G067300.1	5	-1	1	22
ugagguaguaga	Phvul.008G067300.1	5	-1	1	22
ugagguaguagg	Phvul.008G110100.1	5	-1	1	22
ugagguaguagg	Phvul.008G110100.1	5	-1	1	22
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ugagguaguaga	Phvul.008G125400.2	5	-1	1	22
ugagguaguaga	Phvul.008G125400.1	5	-1	1	22
agagguaguagg	Phvul.008G229100.1	5	-1	1	24
ugagguaguaga	Phvul.008G279750.1	5	-1	1	22
ugagguaguaga	Phvul.008G279750.1	5	-1	1	22
ugagguaguaga	Phvul.009G010800.1	5	-1	1	22
ugagguaguaga	Phvul.009G010800.1	5	-1	1	22
agagguaguagg	Phvul.009G034800.1	5	-1	1	24
ugagguaguagg	Phvul.009G060200.1	5	-1	1	22
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agagguaguagg	Phvul.009G203100.1	5	-1	1	24
ugagguaguagg	Phvul.009G232500.1	5	-1	1	22
ugagguaguagg	Phvul.009G232500.1	5	-1	1	22
ugagguaguagg	Phvul.009G232500.1	5	-1	1	22
ugagguaguagg	Phvul.009G232500.1	5	-1	1	22
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ugagguaguaga	Phvul.009G255100.2	5	-1	1	22
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ugagguaguaga	Phvul.009G255100.2	5	-1	1	22
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ugagguaguagg	Phvul.010G026500.1	5	-1	1	22
ugagguaguaga	Phvul.010G028900.2	5	-1	1	22
ugagguaguaga	Phvul.010G028900.1	5	-1	1	22
ugagguaguaga	Phvul.010G028900.2	5	-1	1	22
ugagguaguaga	Phvul.010G028900.1	5	-1	1	22
ugagguaguagg	Phvul.010G067900.1	5	-1	1	22
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ugagguaguag	Phvul.010G067900.1	5	-1	1	22
ugagguaguag	Phvul.010G089200.1	5	-1	1	22
ugagguaguag	Phvul.010G089200.2	5	-1	1	22
ugagguaguag	Phvul.010G089200.1	5	-1	1	22
ugagguaguag	Phvul.010G089200.2	5	-1	1	22
ugagguaguag	Phvul.010G089200.1	5	-1	1	22
ugagguaguag	Phvul.010G089200.2	5	-1	1	22
ugagguaguag	Phvul.010G089200.1	5	-1	1	22
ugagguaguag	Phvul.010G089200.2	5	-1	1	22
ugagguaguag	Phvul.010G094450.1	5	-1	1	22
ugagguaguag	Phvul.010G094450.1	5	-1	1	22
ugagguaguag	Phvul.010G094450.1	5	-1	1	22
ugagguaguag	Phvul.010G094450.1	5	-1	1	22
ugagguaguag	Phvul.011G001200.2	5	-1	1	22
ugagguaguag	Phvul.011G001200.1	5	-1	1	22
ugagguaguag	Phvul.011G001200.2	5	-1	1	22
ugagguaguag	Phvul.011G001200.1	5	-1	1	22
ugagguaguag	Phvul.011G001200.2	5	-1	1	22
ugagguaguag	Phvul.011G001200.1	5	-1	1	22
ugagguaguag	Phvul.011G001200.2	5	-1	1	22
ugagguaguag	Phvul.011G001200.1	5	-1	1	22
agagguaguag	Phvul.011G004200.1	5	-1	1	24
ugagguaguag	Phvul.011G203450.1	5	-1	1	22
ugagguaguag	Phvul.011G203450.1	5	-1	1	22
ugagguaguag	Phvul.011G203450.1	5	-1	1	22
ugagguaguag	Phvul.011G203450.1	5	-1	1	22
ugagguaguag	Phvul.L001679.1	5	-1	1	22
ugagguaguag	Phvul.L001679.1	5	-1	1	22
ugagguaguag	Phvul.L002537.1	5	-1	1	22
ugagguaguag	Phvul.L002537.1	5	-1	1	22
ugagguaguag	Phvul.L009843.2	5	-1	1	22
ugagguaguag	Phvul.L009843.1	5	-1	1	22
ugagguaguag	Phvul.L009843.2	5	-1	1	22
ugagguaguag	Phvul.L009843.1	5	-1	1	22

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

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

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

256	279	AGAGGUAGU	.:: :.::...:::.::::.:	UGAAGUGUG	Cleavage	pacid=371749
3469	3490	UGAGGUAGU	: : .:: :::::..:::::::	ACCAGUAGA	Cleavage	pacid=371472
3469	3490	UGAGGUAGU	: : .:: :::::..:::::::	ACCAGUAGA	Cleavage	pacid=371472
2097	2120	AGAGGUAGU	:. :::::.::. ::.::.::	CAGUCUAUG	Translation	pacid=371618
891	914	AGAGGUAGU	.::::::.:::: :...:	CUUGCUAUG	Cleavage	pacid=371618
2005	2026	UGAGGUAGU	:.::..:::: :::.:::	GUGUGUAUG	Cleavage	pacid=371626
2005	2026	UGAGGUAGU	:.::..:::: :::.:::	GUGUGUAUG	Cleavage	pacid=371626
972	993	UGAGGUAGU	.:::..::.: :::::.:::	GCUCAUGUA	Translation	pacid=371622
972	993	UGAGGUAGU	.:::..::.: :::::.:::	GCUCAUGUA	Translation	pacid=371622
972	993	UGAGGUAGU	.:::..::.: :::::.:::	GCUCAUGUA	Translation	pacid=371622
972	993	UGAGGUAGU	.:::..::.: :::::.:::	GCUCAUGUA	Translation	pacid=371622
417	440	AGAGGUAGU	:.::::::.::: ::::...:	CCCAUUAUG	Cleavage	pacid=371542
735	756	UGAGGUAGU	:...:: :.:::.: :::::::	AGUUAGAUA	Cleavage	pacid=371529
825	846	UGAGGUAGU	:...:: :.:::.: :::::::	AGUUAGAUA	Cleavage	pacid=371529
735	756	UGAGGUAGU	:...:: :.:::.: :::::::	AGUUAGAUA	Cleavage	pacid=371529
825	846	UGAGGUAGU	:...:: :.:::.: :::::::	AGUUAGAUA	Cleavage	pacid=371529
2997	3018	UGAGGUAGU	: :: :.::::::.::: ::::	ACCUCUGCA	Cleavage	pacid=371532
2997	3018	UGAGGUAGU	: :: :.::::::.::: ::::	ACCUCUGCA	Cleavage	pacid=371532
126	147	UGAGGUAGU	: ::::::...: ::.:.:::	CAGCAUACA	Cleavage	pacid=371723
126	147	UGAGGUAGU	: ::::::...: ::.:.:::	CAGCAUACA	Cleavage	pacid=371723
126	147	UGAGGUAGU	: ::::::...: ::.:.:::	CAGCAUACA	Cleavage	pacid=371723
126	147	UGAGGUAGU	: ::::::...: ::.:.:::	CAGCAUACA	Cleavage	pacid=371723
3724	3745	UGAGGUAGU	:..::::::::..:....:::	UUCUGUACA	Cleavage	pacid=371728
3724	3745	UGAGGUAGU	:..::::::::..:....:::	UUCUGUACA	Cleavage	pacid=371728
3724	3745	UGAGGUAGU	:..::::::::..:....:::	UUCUGUACA	Cleavage	pacid=371728
3724	3745	UGAGGUAGU	:..::::::::..:....:::	UUCUGUACA	Cleavage	pacid=371728
1362	1385	AGAGGUAGU	:.:: :.::::::: ::::	UUCAUUACG	Cleavage	pacid=371720
1380	1403	AGAGGUAGU	:.:: :.::::::: ::::	UUCAUUACG	Cleavage	pacid=371720
7	30	AGAGGUAGU	: ::::::::. ::::::	CUAUCUAUG	Translation	pacid=371716
7	30	AGAGGUAGU	: ::::::::. ::::::	CUAUCUAUG	Translation	pacid=371716
459	480	UGAGGUAGU	.: ::: :::: :::::.::.	GAAUAUUCA	Translation	pacid=371672
459	480	UGAGGUAGU	.: ::: :::: :::::.::.	GAAUAUUCA	Translation	pacid=371672
588	609	UGAGGUAGU	:.::: ::::::::...:.	CAUUAUUCA	Cleavage	pacid=371667
588	609	UGAGGUAGU	:.::: ::::::::...:.	CAUUAUUCA	Cleavage	pacid=371667
495	516	UGAGGUAGU	: .:.:: :::.::.:::.:.:	AUUUGUAGA	Cleavage	pacid=371662
495	516	UGAGGUAGU	: .:.:: :::.::.:::.:.:	AUUUGUAGA	Cleavage	pacid=371662
3299	3320	UGAGGUAGU	: :::.:::::::: .::::	UUCCAUAUA	Cleavage	pacid=371576
3299	3320	UGAGGUAGU	: :::.:::::::: .::::	UUCCAUAUA	Cleavage	pacid=371576
44	65	UGAGGUAGU	: ::::::::.:...:. ::::	CAAUAUACA	Cleavage	pacid=371601
44	65	UGAGGUAGU	: ::::::::.:...:. ::::	CAAUAUACA	Cleavage	pacid=371601
270	291	UGAGGUAGU	:.:.:.:: :::::.::::	CGGUGUGCG	Translation	pacid=371580
270	291	UGAGGUAGU	:.:.:.:: :::::.::::	CGGUGUGCG	Translation	pacid=371580
1032	1053	UGAGGUAGU	::. :.:::.:..::::::	UUCUGCAUA	Cleavage	pacid=371582

1053	1074	UGAGGUAGU	::. :.:::.:..::::::	UUCUGCAUA	Cleavage	pacid=371582
1032	1053	UGAGGUAGU	::. :.:::.:..::::::	UUCUGCAUA	Cleavage	pacid=371582
1053	1074	UGAGGUAGU	::. :.:::.:..::::::	UUCUGCAUA	Cleavage	pacid=371582
1669	1692	AGAGGUAGU	::.:::: :.:::.::..:	UUAAUUAUG	Cleavage	pacid=371575
2280	2303	AGAGGUAGU	.::::::.: :::::...:	GUUGCUAUG	Cleavage	pacid=371580
852	873	UGAGGUAGU	:. :::.:.:::::::...:..	AGGCAUGCG	Cleavage	pacid=371519
852	873	UGAGGUAGU	:. :::.:.:::::::...:..	AGGCAUGCG	Cleavage	pacid=371519
852	873	UGAGGUAGU	:. :::.:.:::::::...:..	AGGCAUGCG	Cleavage	pacid=371519
852	873	UGAGGUAGU	:. :::.:.:::::::...:..	AGGCAUGCG	Cleavage	pacid=371519
615	636	UGAGGUAGU	.:::::::.:.::.: :.:::	UGCCAUACA	Cleavage	pacid=371516
615	636	UGAGGUAGU	.:::::::.:.::.: :.:::	UGCCAUACA	Cleavage	pacid=371516
615	636	UGAGGUAGU	.:::::::.:.::.: :.:::	UGCCAUACA	Cleavage	pacid=371516
615	636	UGAGGUAGU	.:::::::.:.::.: :.:::	UGCCAUACA	Cleavage	pacid=371516
1826	1847	UGAGGUAGU	::.::::.::: ::::::	UGGAAUGCA	Cleavage	pacid=371428
1826	1847	UGAGGUAGU	::.::::.::: ::::::	UGGAAUGCA	Cleavage	pacid=371428
1826	1847	UGAGGUAGU	::.::::.::: ::::::	UGGAAUGCA	Cleavage	pacid=371428
1826	1847	UGAGGUAGU	::.::::.::: ::::::	UGGAAUGCA	Cleavage	pacid=371428
510	531	UGAGGUAGU	: :::.::.:::.::. ::::	CAAUAUGCA	Cleavage	pacid=371574
510	531	UGAGGUAGU	: :::.::.:::.::. ::::	CAAUAUGCA	Cleavage	pacid=371574
9552	9573	UGAGGUAGU	: :.::::::::.::.. :::	CAAUGUACA	Cleavage	pacid=371548
9552	9573	UGAGGUAGU	: :.::::::::.::.. :::	CAAUGUACA	Cleavage	pacid=371548
9552	9573	UGAGGUAGU	: :.::::::::.::.. :::	CAAUGUACA	Cleavage	pacid=371548
9552	9573	UGAGGUAGU	: :.::::::::.::.. :::	CAAUGUACA	Cleavage	pacid=371548
81	102	UGAGGUAGU	::.:.: .:::.::::.:::	GUCUGUGCU	Cleavage	pacid=371789
81	102	UGAGGUAGU	::.:.: .:::.::::.:::	GUCUGUGCU	Cleavage	pacid=371789
2388	2409	UGAGGUAGU	:: : :..::::::.: :::::	AAAUCUGUA	Cleavage	pacid=371676
2388	2409	UGAGGUAGU	:: : :..::::::.: :::::	AAAUCUGUA	Cleavage	pacid=371676
2019	2042	AGAGGUAGU	::: :::.::.:.:.:	AUGCAAAUG	Cleavage	pacid=371711
1753	1774	UGAGGUAGU	:: ::::.:::.::.:. .:::	AAAUAUAUA	Cleavage	pacid=371710
1753	1774	UGAGGUAGU	:: ::::.:::.::.:. .:::	AAAUAUAUA	Cleavage	pacid=371710
678	699	UGAGGUAGU	:.:::::::::.:: .:::	CUCUAUACA	Cleavage	pacid=371699
678	699	UGAGGUAGU	:.:::::::::.:: .:::	CUCUAUACA	Cleavage	pacid=371699
678	699	UGAGGUAGU	:.:::::::::.:: .:::	CUCUAUACA	Cleavage	pacid=371699
678	699	UGAGGUAGU	:.:::::::::.:: .:::	CUCUAUACA	Cleavage	pacid=371699
495	518	AGAGGUAGU	::. :: :::: ::.::::.:	AAGCCUUUG	Cleavage	pacid=371701
601	624	AGAGGUAGU	..:.::.::... ::.:::::	GGAGCUGUG	Cleavage	pacid=371753
615	636	UGAGGUAGU	..:::::::::.:: : :.:::	GGCUAUACA	Cleavage	pacid=371766
615	636	UGAGGUAGU	..:::::::::.:: : :.:::	GGCUAUACA	Cleavage	pacid=371766
709	732	AGAGGUAGU	:: ::::.::. :..:.:::	UCAAAUAUG	Translation	pacid=371778
935	956	UGAGGUAGU	::.::::::: :::::::. :.	AAUUAUACA	Cleavage	pacid=371754
935	956	UGAGGUAGU	::.::::::: :::::::. :.	AAUUAUACA	Cleavage	pacid=371754
160	184	AGAGGUAGU	:.: ::: ::::.:::.:.:.	CAGAGUAUC	Cleavage	pacid=371476
160	184	AGAGGUAGU	:.: ::: ::::.:::.:.:.	CAGAGUAUC	Cleavage	pacid=371476

1287	1308	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
1360	1381	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
1287	1308	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
1360	1381	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
1287	1308	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
1360	1381	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
1287	1308	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
1360	1381	UGAGGUAGU	::::.:: :.::::::.:..	CUCCAUGCA	Cleavage	pacid=371474
575	596	UGAGGUAGU	:.:::::::::.::: ...:.:	AGCUAUACA	Cleavage	pacid=371471
575	596	UGAGGUAGU	:.:::::::::.::: ...:.:	AGCUAUACA	Cleavage	pacid=371471
1400	1421	UGAGGUAGU	:.:.::. ::.::.:..::::	CAUUGUAUC	Cleavage	pacid=371474
1400	1421	UGAGGUAGU	:.:.::. ::.::.:..::::	CAUUGUAUC	Cleavage	pacid=371474
1154	1175	UGAGGUAGU	:: .:::...:.:.::..::::	AAAUAUAUG	Cleavage	pacid=371474
1154	1175	UGAGGUAGU	:: .:::...:.:.::..::::	AAAUAUAUG	Cleavage	pacid=371474
1154	1175	UGAGGUAGU	:: .:::...:.:.::..::::	AAAUAUAUG	Cleavage	pacid=371474
1154	1175	UGAGGUAGU	:: .:::...:.:.::..::::	AAAUAUAUG	Cleavage	pacid=371474
389	412	AGAGGUAGU	:.: :::::::::.::.:.	CUAGCCAUG	Cleavage	pacid=371474
1354	1377	AGAGGUAGU	:.: :::::::::.::.:.	CUAGCCAUG	Cleavage	pacid=371451
1492	1515	AGAGGUAGU	:.: :::::::::.::.:.	CUAGCCAUG	Cleavage	pacid=371451
763	784	UGAGGUAGU	::: :: :::::..:.::::.:	CACCUUAAAA	Cleavage	pacid=371631
763	784	UGAGGUAGU	::: :: :::::..:.::::.:	CACCUUAAAA	Cleavage	pacid=371631
763	784	UGAGGUAGU	::: :: :::::..:.::::.:	CACCUUAAAA	Cleavage	pacid=371631
763	784	UGAGGUAGU	::: :: :::::..:.::::.:	CACCUUAAAA	Cleavage	pacid=371631
724	747	AGAGGUAGU	: :: :::::::::::...::	CAUACAAUG	Cleavage	pacid=371634
1991	2012	UGAGGUAGU	::::.:::: ::.::.:::	GUCUAUGCA	Translation	pacid=371619
1991	2012	UGAGGUAGU	::::.:::: ::.::.:::	GUCUAUGCA	Translation	pacid=371619
1035	1057	AGAGGUAGU	: ::::::::::: :.:.:::	UAUACUAUG	Translation	pacid=371623
1488	1511	AGAGGUAGU	::::::::..: .:::::::.:	UCAACUAUG	Cleavage	pacid=371545
1497	1518	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
1539	1560	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
1497	1518	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
1539	1560	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
1497	1518	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
1539	1560	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
1497	1518	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
1539	1560	UGAGGUAGU	:.::: ::::.:..:.::::	UAUCAUCCA	Cleavage	pacid=371529
854	875	UGAGGUAGU	.: ::::::.:. .:::..:::	GAAUAUACA	Translation	pacid=371522
854	875	UGAGGUAGU	.: ::::::.:. .:::..:::	GAAUAUACA	Translation	pacid=371522
10	32	UGAGGUAGU	::::: : ::::::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	::::: : ::::::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	::::: : ::::::::::..::	AACUACAACA	Cleavage	pacid=371524
10	32	UGAGGUAGU	::::: : ::::::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	::::: : ::::::::::..::	AACUACAACA	Cleavage	pacid=371524

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

805	826	UGAGGUAGU	..:: .:::::::: .:.:::	UGUUAGGCA	Cleavage	pacid=371587
593	614	UGAGGUAGU	:.. :: :::: :.::::::::	AGUGAUUCA	Translation	pacid=371587
805	826	UGAGGUAGU	..:: .:::::::: .:.:::	UGUUAGGCA	Cleavage	pacid=371587
972	995	AGAGGUAGU	:::.:.: .::..::.:::::	CAAAUUGUC	Cleavage	pacid=371580
1025	1046	UGAGGUAGU	::.:.:..:::.:.:::::.	AAUUGUGUA	Cleavage	pacid=371614
1025	1046	UGAGGUAGU	::.:.:..:::.:.:::::.	AAUUGUGUA	Cleavage	pacid=371614
840	863	AGAGGUAGU	:::.:.: .::..:.::::::	CAAAUUGUC	Cleavage	pacid=371613
929	950	UGAGGUAGU	::.:.:..:::.:.:::::.	AAUUGUGUA	Cleavage	pacid=371601
929	950	UGAGGUAGU	::.:.:..:::.:.:::::.	AAUUGUGUA	Cleavage	pacid=371601
251	274	AGAGGUAGU	: ..:::: :.:::: ::.:.:	AUGGCUAUU	Cleavage	pacid=371584
628	649	UGAGGUAGU	::::.:..:: ::::::::	UCCCAUGCG	Translation	pacid=371592
628	649	UGAGGUAGU	::::.:..:: ::::::::	UCCCAUGCG	Translation	pacid=371592
628	649	UGAGGUAGU	::::.:..:: ::::::::	UCCCAUGCG	Translation	pacid=371592
628	649	UGAGGUAGU	::::.:..:: ::::::::	UCCCAUGCG	Translation	pacid=371592
297	318	UGAGGUAGU	::.: ::...:.::::::.::.	AAUUCUAUG	Cleavage	pacid=371519
297	318	UGAGGUAGU	::.: ::...:.::::::.::.	AAUUCUAUG	Cleavage	pacid=371519
2076	2099	AGAGGUAGU	.....:.::. :.::.::.:.:	GGGGUUGUG	Cleavage	pacid=371509
2163	2186	AGAGGUAGU	.....:.::. :.::.::.:.:	GGGGUUGUG	Cleavage	pacid=371509
1812	1835	AGAGGUAGU	.....:.::. :.::.::.:.:	GGGGUUGUG	Cleavage	pacid=371509
2873	2894	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
2905	2926	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
2873	2894	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
2905	2926	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
2873	2894	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
2905	2926	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
2873	2894	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
2905	2926	UGAGGUAGU	: .:::::::.::..:::::	AUUCAUACA	Cleavage	pacid=371488
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
642	663	UGAGGUAGU	:: ::::::::.::::... .:	AAGUAUACA	Cleavage	pacid=371500
886	907	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371426
892	913	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371425
886	907	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371425
892	913	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371425
886	907	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371426
892	913	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371425
886	907	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371425
892	913	UGAGGUAGU	..::::.:::::::::. : ::	GGCCAUGCA	Cleavage	pacid=371425

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

1614	1635	UGAGGUAGU	.:::: :.:.:::: :::::	GACCAAAUA	Cleavage	pacid=371703
1617	1638	UGAGGUAGU	.:::: :.:.:::: :::::	GACCAAAUA	Cleavage	pacid=371703
1670	1691	UGAGGUAGU	.:::: :.:.:::: :::::	GACCAAAUA	Cleavage	pacid=371703
1608	1629	UGAGGUAGU	.:::: :.:.:::: :::::	GACCAAAUA	Cleavage	pacid=371703
1614	1635	UGAGGUAGU	.:::: :.:.:::: :::::	GACCAAAUA	Cleavage	pacid=371703
1617	1638	UGAGGUAGU	.:::: :.:.:::: :::::	GACCAAAUA	Cleavage	pacid=371703
1670	1691	UGAGGUAGU	.:::: :.:.:::: :::::	GACCAAAUA	Cleavage	pacid=371703
1388	1412	AGAGGUAGU	:..:::::::::. ::.::::	UAGGCUAUG	Translation	pacid=371689
12	33	UGAGGUAGU	:.::: : ::.::.:::: :::	AGCCACAGAA	Cleavage	pacid=371689
12	33	UGAGGUAGU	:.::: : ::.::.:::: :::	AGCCACAGAA	Cleavage	pacid=371689
12	33	UGAGGUAGU	:.::: : ::.::.:::: :::	AGCCACAGAA	Cleavage	pacid=371689
12	33	UGAGGUAGU	:.::: : ::.::.:::: :::	AGCCACAGAA	Cleavage	pacid=371689
145	166	UGAGGUAGU	.:.:.:.::. ::..::.::::	GAUUGUGCA	Cleavage	pacid=371689
145	166	UGAGGUAGU	.:.:.:.::. ::..::.::::	GAUUGUGCA	Cleavage	pacid=371689
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
1118	1139	UGAGGUAGU	:.:::::::: ::.:...:: :	UAUCAUACA	Translation	pacid=371696
40	63	AGAGGUAGU	..:: :.::.:.::.: .::	GGAAAUGUG	Cleavage	pacid=371689
1077	1098	UGAGGUAGU	.::.:.::.::..::.:......	CGCUGUGCA	Cleavage	pacid=371690
1077	1098	UGAGGUAGU	.::.:.::.::..::.:......	CGCUGUGCA	Cleavage	pacid=371690
1175	1196	UGAGGUAGU	:.. ::::: :::::: ..:	AGUGAUACA	Cleavage	pacid=371755
1175	1196	UGAGGUAGU	:.. ::::: :::::: ..:	AGUGAUACA	Cleavage	pacid=371755
615	636	UGAGGUAGU	:: ..::::.:::::. :..	AAGUGUACA	Cleavage	pacid=371771
615	636	UGAGGUAGU	:: ..::::.:::::. :..	AAGUGUACA	Cleavage	pacid=371771
615	636	UGAGGUAGU	:: ..::::.:::::. :..	AAGUGUACA	Cleavage	pacid=371771
615	636	UGAGGUAGU	:: ..::::.:::::. :..	AAGUGUACA	Cleavage	pacid=371771
958	979	UGAGGUAGU	::.: ::::::.: .:::.:.:	AAUUCUACA	Cleavage	pacid=371766
958	979	UGAGGUAGU	::.: ::::::.: .:::.:.:	AAUUCUACA	Cleavage	pacid=371766
1506	1527	UGAGGUAGU	:::: : :::.:.::...::.:	AACCAAAGAA	Cleavage	pacid=371744
1506	1527	UGAGGUAGU	:::: : :::.:.::...::.:	AACCAAAGAA	Cleavage	pacid=371744
1506	1527	UGAGGUAGU	:::: : :::.:.::...::.:	AACCAAAGAA	Cleavage	pacid=371744
1506	1527	UGAGGUAGU	:::: : :::.:.::...::.:	AACCAAAGAA	Cleavage	pacid=371744
102	123	UGAGGUAGU	:: ::::.:: ::.::.:.::	AAAUAUAUA	Cleavage	pacid=371753
102	123	UGAGGUAGU	:: ::::.:: ::.::.:.::	AAAUAUAUA	Cleavage	pacid=371753
102	123	UGAGGUAGU	:: ::::.:: ::.::.:.::	AAAUAUAUA	Cleavage	pacid=371753
102	123	UGAGGUAGU	:: ::::.:: ::.::.:.::	AAAUAUAUA	Cleavage	pacid=371753
628	649	UGAGGUAGU	..:.:::..:: : :::::.:::	GAUUAUGUA	Translation	pacid=371766
628	649	UGAGGUAGU	..:.:::..:: : :::::.:::	GAUUAUGUA	Translation	pacid=371766

935	956	UGAGGUAGU	::..:::::: ::::::. :.	AAUUAUACA	Cleavage	pacid=371754
935	956	UGAGGUAGU	::..:::::: ::::::. :.	AAUUAUACA	Cleavage	pacid=371754
935	956	UGAGGUAGU	::..:::::: ::::::. :.	AAUUAUACA	Cleavage	pacid=371754
935	956	UGAGGUAGU	::..:::::: ::::::. :.	AAUUAUACA	Cleavage	pacid=371754
342	363	UGAGGUAGU	: :.:::.:::.::.:..: ::	AUCUAUAUA	Cleavage	pacid=371773
342	363	UGAGGUAGU	: :.:::.:::.::.:..: ::	AUCUAUAUA	Cleavage	pacid=371773
342	363	UGAGGUAGU	: :.:::.:::.::.:..: ::	AUCUAUAUA	Cleavage	pacid=371773
342	363	UGAGGUAGU	: :.:::.:::.::.:..: ::	AUCUAUAUA	Cleavage	pacid=371773
1025	1046	UGAGGUAGU	.:::. ::::.:.::.:.:..	GACUGAACA	Cleavage	pacid=371764
1025	1046	UGAGGUAGU	.:::. ::::.:.::.:.:..	GACUGAACA	Cleavage	pacid=371764
1036	1057	UGAGGUAGU	::. .:: .:::::::.::::	AAUGGUAGG	Cleavage	pacid=371752
1036	1057	UGAGGUAGU	::. .:: .:::::::.::::	AAUGGUAGG	Cleavage	pacid=371752
21	42	UGAGGUAGU	:.:::: ::::.::::::	UUCUAUACC	Cleavage	pacid=371762
21	42	UGAGGUAGU	:.:::: ::::.::::::	UUCUAUACC	Cleavage	pacid=371762
21	42	UGAGGUAGU	:.:::: ::::.::::::	UUCUAUACC	Cleavage	pacid=371762
21	42	UGAGGUAGU	:.:::: ::::.::::::	UUCUAUACC	Cleavage	pacid=371762
706	727	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
726	747	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
706	727	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
726	747	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
706	727	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
726	747	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
706	727	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
726	747	UGAGGUAGU	:::::. :.::::.:...:.:	CACCAUGAA	Cleavage	pacid=371776
12	33	UGAGGUAGU	:::. .:::::::::.:. ::	CACUGGGCA	Cleavage	pacid=371445
12	33	UGAGGUAGU	:::. .:::::::::.:. ::	CACUGGGCA	Cleavage	pacid=371445
1022	1043	UGAGGUAGU	::.:::::::.::.: :.::	UUCUGUACA	Cleavage	pacid=371454
1022	1043	UGAGGUAGU	::.:::::::.::.: :.::	UUCUGUACA	Cleavage	pacid=371454
883	904	UGAGGUAGU	.::: :: :::: ::::::::	GACCCUAAAA	Translation	pacid=371470
883	904	UGAGGUAGU	.::: :: :::: ::::::::	GACCCUAAAA	Translation	pacid=371470
883	904	UGAGGUAGU	.::: :: :::: ::::::::	GACCCUAAAA	Translation	pacid=371470
883	904	UGAGGUAGU	.::: :: :::: ::::::::	GACCCUAAAA	Translation	pacid=371470
1371	1392	UGAGGUAGU	.:: :::..::::: ::::..	GACAAUAUG	Cleavage	pacid=371453
1371	1392	UGAGGUAGU	.:: :::..::::: ::::..	GACAAUAUG	Cleavage	pacid=371453
1371	1392	UGAGGUAGU	.:: :::..::::: ::::..	GACAAUAUG	Cleavage	pacid=371453
1371	1392	UGAGGUAGU	.:: :::..::::: ::::..	GACAAUAUG	Cleavage	pacid=371453
306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468
306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468
306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468
306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468
306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468
306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468
306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468

306	327	UGAGGUAGU	.:::: ::::..:..::..::.	GACCAAACAA	Cleavage	pacid=371468
125	146	UGAGGUAGU	.::::::.:.:. :.::..:::	GACUAUAUA	Translation	pacid=371466
125	146	UGAGGUAGU	.::::::.:.:. :.::..:::	GACUAUAUA	Translation	pacid=371466
391	412	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371474
391	412	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371474
391	412	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371474
391	412	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371474
1356	1377	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
1494	1515	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
1356	1377	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
1494	1515	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
1356	1377	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
1494	1515	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
1356	1377	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
1494	1515	UGAGGUAGU	:.::::.::::::.::.:. :	AGCCAUGCAA	Cleavage	pacid=371451
726	747	UGAGGUAGU	:: ::.:::::::::.:: :	UACAAUGCA	Cleavage	pacid=371634
726	747	UGAGGUAGU	:: ::.:::::::::.:: :	UACAAUGCA	Cleavage	pacid=371634
726	747	UGAGGUAGU	:: ::.:::::::::.:: :	UACAAUGCA	Cleavage	pacid=371634
726	747	UGAGGUAGU	:: ::.:::::::::.:: :	UACAAUGCA	Cleavage	pacid=371634
2099	2120	UGAGGUAGU	::::..::: ::.::.:::	GUCUAUGUA	Translation	pacid=371618
2099	2120	UGAGGUAGU	::::..::: ::.::.:::	GUCUAUGUA	Translation	pacid=371618
3322	3343	UGAGGUAGU	:::::.::::::.::. .:...	CACCAUGCAA	Cleavage	pacid=371632
3322	3343	UGAGGUAGU	::::.::::::.::. .:...	CACCAUGCAA	Cleavage	pacid=371632
3322	3343	UGAGGUAGU	::::.::::::.::. .:...	CACCAUGCAA	Cleavage	pacid=371632
3322	3343	UGAGGUAGU	::::.::::::.::. .:...	CACCAUGCAA	Cleavage	pacid=371632
616	637	UGAGGUAGU	:::::: : :::::::.:: :	CACCAUAAAC	Cleavage	pacid=371624
616	637	UGAGGUAGU	:::::: : :::::::.:: :	CACCAUAAAC	Cleavage	pacid=371624
616	637	UGAGGUAGU	:::::: : :::::::.:: :	CACCAUAAAC	Cleavage	pacid=371624
616	637	UGAGGUAGU	:::::: : :::::::.:: :	CACCAUAAAC	Cleavage	pacid=371624
1251	1272	UGAGGUAGU	:::::: ::..:..::.:::	CACCAUAGAA	Cleavage	pacid=371543
1251	1272	UGAGGUAGU	:::::: ::..:..::.:::	CACCAUAGAA	Cleavage	pacid=371543
1251	1272	UGAGGUAGU	:::::: ::..:..::.:::	CACCAUAGAA	Cleavage	pacid=371543
1251	1272	UGAGGUAGU	:::::: ::..:..::.:::	CACCAUAGAA	Cleavage	pacid=371543
1073	1096	AGAGGUAGU	.: ::::::::::.:.: :::	GACACUAUG	Cleavage	pacid=371538
2517	2540	AGAGGUAGU	::.: ::::.:::: ::::	UAAGCGCUG	Cleavage	pacid=371540
3256	3279	AGAGGUAGU	.::.: ::.:::::::::. :	GAAGCAUUG	Cleavage	pacid=371545
196	219	AGAGGUAGU	: ::.:.::::.. ::.:.:.:	ACAAUUGUG	Translation	pacid=371528
735	756	UGAGGUAGU	:...: :.::..: :::::::	AGUUAGAUA	Cleavage	pacid=371529
825	846	UGAGGUAGU	:...: :.::..: :::::::	AGUUAGAUA	Cleavage	pacid=371529
735	756	UGAGGUAGU	:...: :.::..: :::::::	AGUUAGAUA	Cleavage	pacid=371529
825	846	UGAGGUAGU	:...: :.::..: :::::::	AGUUAGAUA	Cleavage	pacid=371529
735	756	UGAGGUAGU	:...: :.::..: :::::::	AGUUAGAUA	Cleavage	pacid=371529
825	846	UGAGGUAGU	:...: :.::..: :::::::	AGUUAGAUA	Cleavage	pacid=371529

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

381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
381	402	UGAGGUAGU	:...:::: :::::::: :	AGUUAUACA	Cleavage	pacid=371660
607	630	AGAGGUAGU	.::::::: : ::..:::::	CCGACUAUG	Cleavage	pacid=371662
609	630	UGAGGUAGU	.::.::.: : ::..::::::	GACUAUGCC	Cleavage	pacid=371662
609	630	UGAGGUAGU	.::.::.: : ::..::::::	GACUAUGCC	Cleavage	pacid=371662
609	630	UGAGGUAGU	.::.::.: : ::..::::::	GACUAUGCC	Cleavage	pacid=371662
609	630	UGAGGUAGU	.::.::.: : ::..::::::	GACUAUGCC	Cleavage	pacid=371662
914	935	UGAGGUAGU	::.:::.... ::.::::::.:	AAUCAUGUG	Cleavage	pacid=371654
914	935	UGAGGUAGU	::.:::.... ::.::::::.:	AAUCAUGUG	Cleavage	pacid=371654
914	935	UGAGGUAGU	::.:::.... ::.::::::.:	AAUCAUGUG	Cleavage	pacid=371654
914	935	UGAGGUAGU	::.:::.... ::.::::::.:	AAUCAUGUG	Cleavage	pacid=371654
48	69	UGAGGUAGU	::.:::.. :.::.:::.::	AAUCAUGUC	Cleavage	pacid=371676
48	69	UGAGGUAGU	::.:::.. :.::.:::.::	AAUCAUGUC	Cleavage	pacid=371676
48	69	UGAGGUAGU	::.:::.. :.::.:::.::	AAUCAUGUC	Cleavage	pacid=371676
48	69	UGAGGUAGU	::.:::.. :.::.:::.::	AAUCAUGUC	Cleavage	pacid=371676
42	63	UGAGGUAGU	:::::.:.: :::::.:.::	CACCAUGCGA	Cleavage	pacid=371666
42	63	UGAGGUAGU	:::::.:.: :::::.:.::	CACCAUGCGA	Cleavage	pacid=371666
42	63	UGAGGUAGU	:::::.:.: :::::.:.::	CACCAUGCGA	Cleavage	pacid=371666
42	63	UGAGGUAGU	:::::.:.: :::::.:.::	CACCAUGCGA	Cleavage	pacid=371666
559	580	UGAGGUAGU	:... :::.::.::::..::	AGUUUUACG	Cleavage	pacid=371662
559	580	UGAGGUAGU	:... :::.::.::::..::	AGUUUUACG	Cleavage	pacid=371662
559	580	UGAGGUAGU	:... :::.::.::::..::	AGUUUUACG	Cleavage	pacid=371662
559	580	UGAGGUAGU	:... :::.::.::::..::	AGUUUUACG	Cleavage	pacid=371662
337	358	UGAGGUAGU	.:::::.: .:.:::::::	UGCUAUAUA	Cleavage	pacid=371643
337	358	UGAGGUAGU	.:::::.: .:.:::::::	UGCUAUAUA	Cleavage	pacid=371643
496	516	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
833	853	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
496	516	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
833	853	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
496	516	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
833	853	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
496	516	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
833	853	UGAGGUAGU	:..::::.: :::::..:::	AGUCAUAUA-	Cleavage	pacid=371669
1110	1133	AGAGGUAGU	::.:: :::::: ::.:::::	AAGACAAUG	Cleavage	pacid=371653
29	50	UGAGGUAGU	.:::::. :.::::.: :.:::	GACUAUGAA	Cleavage	pacid=371643
29	50	UGAGGUAGU	.:::::. :.::::.: :.:::	GACUAUGAA	Cleavage	pacid=371643
37	58	UGAGGUAGU	.:::::. :.::::.: :.:::	GACUAUGAA	Cleavage	pacid=371660

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

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

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

405	426	UGAGGUAGU	.:.:::::: .:.::.:.:.:	UGCUAUACA	Cleavage	pacid=371559
410	431	UGAGGUAGU	.:.:::::: .:.::.:.:.:	UGCUAUACA	Cleavage	pacid=371559
405	426	UGAGGUAGU	.:.:::::: .:.::.:.:.:	UGCUAUACA	Cleavage	pacid=371559
405	426	UGAGGUAGU	.:.:::::: .:.::.:.:.:	UGCUAUACA	Cleavage	pacid=371559
410	431	UGAGGUAGU	.:.:::::: .:.::.:.:.:	UGCUAUACA	Cleavage	pacid=371559
405	426	UGAGGUAGU	.:.:::::: .:.::.:.:.:	UGCUAUACA	Cleavage	pacid=371559
294	315	UGAGGUAGU	::.. ::::::::::..:.	UACUGAACA	Cleavage	pacid=371569
294	315	UGAGGUAGU	::.. ::::::::::..:.	UACUGAACA	Cleavage	pacid=371569
294	315	UGAGGUAGU	::.. ::::::::::..:.	UACUGAACA	Cleavage	pacid=371569
294	315	UGAGGUAGU	::.. ::::::::::..:.	UACUGAACA	Cleavage	pacid=371569
3916	3937	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
2706	2727	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
3916	3937	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
2706	2727	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
3916	3937	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
2706	2727	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
3916	3937	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
2706	2727	UGAGGUAGU	:..: :.:::.:::::: .:	AGUCCUGCA	Cleavage	pacid=371443
1727	1749	AGAGGUAGU	::.::.: :::..::.::.::	CAAGCUGU-C	Cleavage	pacid=371575
1223	1245	UGAGGUAGU	:::::: :::: ::::::::	UACUAUAAC	Translation	pacid=371575
1223	1245	UGAGGUAGU	:::::: :::: ::::::::	UACUAUAAC	Translation	pacid=371575
79	102	AGAGGUAGU	:::. ::.::: ..::.::::.:	AAGUCUGUG	Cleavage	pacid=371789
986	1009	UGAGGU--AG	.: ::::::::.::.: ::::	GAAUAUACA	Cleavage	pacid=371577
986	1009	UGAGGU--AG	.: ::::::::.::.: ::::	GAAUAUACA	Cleavage	pacid=371577
753	776	AGAGGUAGU	:::. :::::::::: :.: ...:	AAGUCUAUG	Translation	pacid=371678
695	718	AGAGGUAGU	:::. :::::::::: :.: ...:	AAGUCUAUG	Translation	pacid=371680
2388	2409	UGAGGUAGU	:: . :..::.:::.: :::::	AAAUCUGUA	Cleavage	pacid=371676
2388	2409	UGAGGUAGU	:: . :..::.:::.: :::::	AAAUCUGUA	Cleavage	pacid=371676
2388	2409	UGAGGUAGU	:: . :..::.:::.: :::::	AAAUCUGUA	Cleavage	pacid=371676
2388	2409	UGAGGUAGU	:: . :..::.:::.: :::::	AAAUCUGUA	Cleavage	pacid=371676
1918	1941	AGAGGUAGU	.: :::::::: ..::..:...:	AUAACUAUG	Cleavage	pacid=371711
1601	1622	UGAGGUAGU	:::.: :.::.:.:..: :::::	AAUUUUGCA	Cleavage	pacid=371696
1601	1622	UGAGGUAGU	:::.: :.::.:.:..: :::::	AAUUUUGCA	Cleavage	pacid=371696
1983	2004	UGAGGUAGU	:. :.::. :::: ::.::::	AGGUGUAUC	Cleavage	pacid=371684
1983	2004	UGAGGUAGU	:. :.::. :::: ::.::::	AGGUGUAUC	Cleavage	pacid=371684
2640	2661	UGAGGUAGU	::.:::.. .::::.::: :.:	AAUUAUGUU	Cleavage	pacid=371712
2640	2661	UGAGGUAGU	::.:::.. .::::.::: :.:	AAUUAUGUU	Cleavage	pacid=371712
876	897	UGAGGUAGU	::::.::::.:. :.:::::.	AACUGUACA	Translation	pacid=371709
876	897	UGAGGUAGU	::::.::::.:. :.:::::.	AACUGUACA	Translation	pacid=371709
876	897	UGAGGUAGU	::::.::::.:. :.:::::.	AACUGUACA	Translation	pacid=371709
876	897	UGAGGUAGU	::::.::::.:. :.:::::.	AACUGUACA	Translation	pacid=371709
2372	2393	UGAGGUAGU	:::.:.:: :.:::: :::.:	UACUGUGCA	Cleavage	pacid=371700
2372	2393	UGAGGUAGU	:::.:.:: :.:::: :::.:	UACUGUGCA	Cleavage	pacid=371700

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

628	649	UGAGGUAGU	.:..::..:: : :::::.::::	GAUUAUGUA	Translation	pacid=371766
868	889	UGAGGUAGU	.:.:::::: :::::... :.	GAUUAUACA	Cleavage	pacid=371774
868	889	UGAGGUAGU	.:.:::::: :::::... :.	GAUUAUACA	Cleavage	pacid=371774
169	192	AGAGGUAGU	:::: .:::::: ::::: :	AAAAAGGUG	Translation	pacid=371764
300	321	UGAGGUAGU	:::.:..:::.:..: ::::.:	CACUGUGUA	Cleavage	pacid=371760
300	321	UGAGGUAGU	:::.:..:::.:..: ::::.:	CACUGUGUA	Cleavage	pacid=371760
2595	2616	UGAGGUAGU	..:.::.::::::: ..:.	CGUUGUAUA	Cleavage	pacid=371445
2595	2616	UGAGGUAGU	..:.::.::::::: ..:.	CGUUGUAUA	Cleavage	pacid=371445
2031	2052	UGAGGUAGU	.:.:::.::: :::::::. :	GAUCAUGCA	Cleavage	pacid=371470
2031	2052	UGAGGUAGU	.:.:::.::: :::::::. :	GAUCAUGCA	Cleavage	pacid=371470
2031	2052	UGAGGUAGU	.:.:::.::: :::::::. :	GAUCAUGCA	Cleavage	pacid=371470
2031	2052	UGAGGUAGU	.:.:::.::: :::::::. :	GAUCAUGCA	Cleavage	pacid=371470
165	187	UGAGGUAGU	..::::. :::.: :::::::	GGCCAUGAA	Cleavage	pacid=371454
165	187	UGAGGUAGU	..::::. :::.: :::::::	GGCCAUGAA	Cleavage	pacid=371454
165	187	UGAGGUAGU	..::::. :::.: :::::::	GGCCAUGAA	Cleavage	pacid=371454
165	187	UGAGGUAGU	..::::. :::.: :::::::	GGCCAUGAA	Cleavage	pacid=371454
1526	1547	UGAGGUAGU	.:::.:: :: ::..:..::::	GACUGUAAA	Cleavage	pacid=371467
1526	1547	UGAGGUAGU	.:::.:: :: ::..:..::::	GACUGUAAA	Cleavage	pacid=371467
575	596	UGAGGUAGU	:.:.:::::..::: ...:.:	AGCUAUACA	Cleavage	pacid=371471
575	596	UGAGGUAGU	:.:.:::::..::: ...:.:	AGCUAUACA	Cleavage	pacid=371471
575	596	UGAGGUAGU	:.:.:::::..::: ...:.:	AGCUAUACA	Cleavage	pacid=371471
575	596	UGAGGUAGU	:.:.:::::..::: ...:.:	AGCUAUACA	Cleavage	pacid=371471
9208	9231	AGAGGUAGU	:. :::.:::: :::. :..:	AGCACUGUG	Cleavage	pacid=371454
9208	9231	AGAGGUAGU	:. :::.:::: :::. :..:	AGCACUGUG	Cleavage	pacid=371454
9208	9231	AGAGGUAGU	:. :::.:::: :::. :..:	AGCACUGUG	Cleavage	pacid=371454
143	166	AGAGGUAGU	::::. :::. ::::::: .:	AAAAUCAUG	Cleavage	pacid=371469
420	443	AGAGGUAGU	.::::. . :::::::: :.:::	GAAAUGGAG	Cleavage	pacid=371446
349	373	AGAGGUAGU	:..::::::..: ::.:::.	CUAGUUAUG	Translation	pacid=371637
4084	4104	UGAGGUAGU	::.:::.:. ::::.:.::::	AAUCAUGCG-	Cleavage	pacid=371622
4084	4104	UGAGGUAGU	::.:::.:. ::::.:.::::	AAUCAUGCG-	Cleavage	pacid=371622
4084	4104	UGAGGUAGU	::.:::.:. ::::.:.::::	AAUCAUGCG-	Cleavage	pacid=371622
4084	4104	UGAGGUAGU	::.:::.:. ::::.:.::::	AAUCAUGCG-	Cleavage	pacid=371622
2603	2624	UGAGGUAGU	::::: :::..::::::.: :	AACCAACCAA	Cleavage	pacid=371635
2603	2624	UGAGGUAGU	::::: :::..::::::.: :	AACCAACCAA	Cleavage	pacid=371635
2603	2624	UGAGGUAGU	::::: :::..::::::.: :	AACCAACCAA	Cleavage	pacid=371635
2603	2624	UGAGGUAGU	::::: :::..::::::.: :	AACCAACCAA	Cleavage	pacid=371635
971	993	UGAGGUAGU	:.:: ::..:::: :::::.::	AGCUCAUGU	Translation	pacid=371622
971	993	UGAGGUAGU	:.:: ::..:::: :::::.::	AGCUCAUGU	Translation	pacid=371622
2918	2939	UGAGGUAGU	:.:::: .::::::: ::: .:	AGCUAUUUA	Cleavage	pacid=371540
2918	2939	UGAGGUAGU	:.:::: .::::::: ::: .:	AGCUAUUUA	Cleavage	pacid=371540
297	320	AGAGGUAGU	:::..:.: ....:::: ::::	AAAGUUGUU	Cleavage	pacid=371538
1539	1562	AGAGGUAGU	::::.:::::::.:..:.:	AAAAUUAUG	Cleavage	pacid=371546
10	32	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524

190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
10	32	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
10	32	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
10	32	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
190	212	UGAGGUAGU	:::.: : :::.::::::..::	AACUACAACA	Cleavage	pacid=371524
2173	2194	UGAGGUAGU	::::::.:.. . :::::::::	AACUAUGCG(	Translation	pacid=371530
2213	2234	UGAGGUAGU	::::::.:.. . :::::::::	AACUAUGCG(	Translation	pacid=371530
2421	2442	UGAGGUAGU	::::::.:.. . :::::::::	AACUAUGCG(	Translation	pacid=371530
2173	2194	UGAGGUAGU	::::::.:.. . :::::::::	AACUAUGCG(	Translation	pacid=371530
2213	2234	UGAGGUAGU	::::::.:.. . :::::::::	AACUAUGCG(	Translation	pacid=371530
2421	2442	UGAGGUAGU	::::::.:.. . :::::::::	AACUAUGCG(	Translation	pacid=371530
362	383	UGAGGUAGU	:.:.. :::: .::.:.::::	AGCUGAACA/	Cleavage	pacid=371534
362	383	UGAGGUAGU	:.:.. :::: .::.:.::::	AGCUGAACA/	Cleavage	pacid=371534
362	383	UGAGGUAGU	:.:.. :::: .::.:.::::	AGCUGAACA/	Cleavage	pacid=371534
362	383	UGAGGUAGU	:.:.. :::: .::.:.::::	AGCUGAACA/	Cleavage	pacid=371534
197	219	UGAGGUAGU	:.::::. ::::::: :..::	AGCCAUGGC/	Cleavage	pacid=371522
197	219	UGAGGUAGU	:.::::. ::::::: :..::	AGCCAUGGC/	Cleavage	pacid=371522
197	219	UGAGGUAGU	:.::::. ::::::: :..::	AGCCAUGGC/	Cleavage	pacid=371522
197	219	UGAGGUAGU	:.::::. ::::::: :..::	AGCCAUGGC/	Cleavage	pacid=371522
44	65	UGAGGUAGU	:.::::.:::..:: :.:.::	AGCCAUGCA/	Cleavage	pacid=371713
44	65	UGAGGUAGU	:.::::.:::..:: :.:.::	AGCCAUGCA/	Cleavage	pacid=371713
44	65	UGAGGUAGU	:.::::.:::..:: :.:.::	AGCCAUGCA/	Cleavage	pacid=371713
44	65	UGAGGUAGU	:.::::.:::..:: :.:.::	AGCCAUGCA/	Cleavage	pacid=371713
267	288	UGAGGUAGU	: .:: :.::::::.:::	GUGCAGGCA(	Cleavage	pacid=371730
267	288	UGAGGUAGU	: .:: :.::::::.:::	GUGCAGGCA(	Cleavage	pacid=371730
1870	1891	UGAGGUAGU	::.:::::::::: :..::.	CACUAUACA/	Cleavage	pacid=371645
1870	1891	UGAGGUAGU	::.:::::::::: :..::.	CACUAUACA/	Cleavage	pacid=371645
1870	1891	UGAGGUAGU	::.:::::::::: :..::.	CACUAUACA/	Cleavage	pacid=371645
1870	1891	UGAGGUAGU	::.:::::::::: :..::.	CACUAUACA/	Cleavage	pacid=371645
1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648
1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648
1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648
1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCA(	Cleavage	pacid=371648

1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
1971	1992	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
2125	2146	UGAGGUAGU	:.:::: ::...:.::.:: ::	AGCCAUUCAG	Cleavage	pacid=371648
46	69	AGAGGUAGU	.::::. :::. :.::.::::.:	AAAAUCAUGU	Cleavage	pacid=371676
165	186	UGAGGUAGU	:::: : ::.::: :::...:::	AACCUUCCAG	Cleavage	pacid=371643
165	186	UGAGGUAGU	:::: : ::.::: :::...:::	AACCUUCCAG	Cleavage	pacid=371643
165	186	UGAGGUAGU	:::: : ::.::: :::...:::	AACCUUCCAG	Cleavage	pacid=371643
165	186	UGAGGUAGU	:::: : ::.::: :::...:::	AACCUUCCAG	Cleavage	pacid=371643
833	854	UGAGGUAGU	::.:. :::: ::.:.:.:.:	AAUUGCACAA	Translation	pacid=371669
833	854	UGAGGUAGU	::.:. :::: ::.:.:.:.:	AAUUGCACAA	Translation	pacid=371669
365	388	AGAGGUAGU	:::: ::: :::::.. ::::	CAAACAAUGA	Cleavage	pacid=371643
1112	1133	UGAGGUAGU	.:: ::.::: ::.:::::.	GACAAUGCAA	Cleavage	pacid=371653
1112	1133	UGAGGUAGU	.:: ::.::: ::.:::::.	GACAAUGCAA	Cleavage	pacid=371653
1112	1133	UGAGGUAGU	.:: ::.::: ::.:::::.	GACAAUGCAA	Cleavage	pacid=371653
1112	1133	UGAGGUAGU	.:: ::.::: ::.:::::.	GACAAUGCAA	Cleavage	pacid=371653
1112	1133	UGAGGUAGU	.:: ::.::: ::.:::::.	GACAAUGCAA	Cleavage	pacid=371653
1112	1133	UGAGGUAGU	.:: ::.::: ::.:::::.	GACAAUGCAA	Cleavage	pacid=371653
1919	1940	UGAGGUAGU	::::: .:...::.:.::::	AACCAAUUAG	Cleavage	pacid=371670
1919	1940	UGAGGUAGU	::::: .:...::.:.::::	AACCAAUUAG	Cleavage	pacid=371670
1919	1940	UGAGGUAGU	::::: .:...::.:.::::	AACCAAUUAG	Cleavage	pacid=371670
1919	1940	UGAGGUAGU	::::: .:...::.:.::::	AACCAAUUAG	Cleavage	pacid=371670
2013	2037	AGAGGUAGU	.:::::: :: ::::::.::..	GAAACUAAUC	Cleavage	pacid=371654
2548	2571	AGAGGUAGU	::: ::::::...:.:::: :	CAAAAUAUGC	Cleavage	pacid=371606
1653	1676	AGAGGUAGU	.: :: ::::::..:. :.::	ACAAAUAUGC	Cleavage	pacid=371606
1200	1221	UGAGGUAGU	::.:::: ..::: ::::::.	AAUUAUAGGC	Cleavage	pacid=371586
1200	1221	UGAGGUAGU	::.:::: ..::: ::::::.	AAUUAUAGGC	Cleavage	pacid=371586
1025	1046	UGAGGUAGU	::.: :..::..:.:::::.	AAUCCUGUAA	Cleavage	pacid=371596
1025	1046	UGAGGUAGU	::.: :..::..:.:::::.	AAUCCUGUAA	Cleavage	pacid=371596
1025	1046	UGAGGUAGU	::.: :..::..:.:::::.	AAUCCUGUAA	Cleavage	pacid=371596
1025	1046	UGAGGUAGU	::.: :..::..:.:::::.	AAUCCUGUAA	Cleavage	pacid=371596
1025	1046	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371614
1025	1046	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371614
1025	1046	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371614
1025	1046	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371614
929	950	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371601
929	950	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371601
929	950	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371601
929	950	UGAGGUAGU	::...:..::...:.:::::.	AAUUGUGUA	Cleavage	pacid=371601

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

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

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

1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.4	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.3	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.2	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.008G163350.1	Phvul.008G163350	Phvul.008G163350		0
1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072	
1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072	
1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072	
1	Phvul.009G057800.1	Phvul.009G057800	Phvul.009G057800	PF04072	
1	Phvul.010G058700.1	Phvul.010G058700	Phvul.010G058700		0
1	Phvul.010G058700.1	Phvul.010G058700	Phvul.010G058700		0
1	Phvul.001G022400.1	Phvul.001G022400	Phvul.001G022400	PF00497,PF0	
1	Phvul.001G022400.1	Phvul.001G022400	Phvul.001G022400	PF00497,PF0	
1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170	
1	Phvul.001G077200.2	Phvul.001G077200	Phvul.001G077200	PF00170	
2	Phvul.001G077700.1	Phvul.001G077700	Phvul.001G077700	PF10509,PF0	
2	Phvul.001G077700.1	Phvul.001G077700	Phvul.001G077700	PF10509,PF0	
1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022	
1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022	
1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022	
1	Phvul.001G086466.1	Phvul.001G086466	Phvul.001G086466	PF00022	
1	Phvul.001G089600.1	Phvul.001G089600	Phvul.001G089600		0
1	Phvul.001G089600.1	Phvul.001G089600	Phvul.001G089600		0
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1	Phvul.001G089600.1	Phvul.001G089600	Phvul.001G089600		0
1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365	
1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365	
1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365	
1	Phvul.001G091100.1	Phvul.001G091100	Phvul.001G091100	PF02365	
1	Phvul.001G121000.1	Phvul.001G121000	Phvul.001G121000	PF00682	
1	Phvul.001G121000.2	Phvul.001G121000	Phvul.001G121000	PF00682	
1	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF0	

1	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF0
1	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF0
1	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF0
1	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF0
1	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF0
1	Phvul.001G131150.1	Phvul.001G131150	Phvul.001G131150	PF13304,PF0
1	Phvul.001G131150.2	Phvul.001G131150	Phvul.001G131150	PF13304,PF0
1	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
1	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
1	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
1	Phvul.001G141000.1	Phvul.001G141000	Phvul.001G141000	PF03110
1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01
1	Phvul.002G042000.2	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.8	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.7	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.6	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.5	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.3	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.4	Phvul.002G042000	Phvul.002G042000	0
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1	Phvul.002G042000.2	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.8	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.7	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.6	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.5	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.3	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.4	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G042000.1	Phvul.002G042000	Phvul.002G042000	0
1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085
1	Phvul.002G071800.1	Phvul.002G071800	Phvul.002G071800	PF06075
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1	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF0
1	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF0
1	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF0
1	Phvul.002G076600.1	Phvul.002G076600	Phvul.002G076600	PF01471,PF0
1	Phvul.002G185150.2	Phvul.002G185150	Phvul.002G185150	PF00999
1	Phvul.002G185150.1	Phvul.002G185150	Phvul.002G185150	PF00999
1	Phvul.002G185150.3	Phvul.002G185150	Phvul.002G185150	PF00999

1	Phvul.002G304500.1	Phvul.002G304500	Phvul.002G304500	PF07714
1	Phvul.003G103100.2	Phvul.003G103100	Phvul.003G103100	PF07496
1	Phvul.003G103100.2	Phvul.003G103100	Phvul.003G103100	PF07496
1	Phvul.004G044800.1	Phvul.004G044800	Phvul.004G044800	PF08263,PF0
1	Phvul.004G106000.1	Phvul.004G106000	Phvul.004G106000	PF01535
1	Phvul.004G133400.1	Phvul.004G133400	Phvul.004G133400	PF00571,PF0
1	Phvul.004G133400.1	Phvul.004G133400	Phvul.004G133400	PF00571,PF0
1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
1	Phvul.004G176700.1	Phvul.004G176700	Phvul.004G176700	PF00085
1	Phvul.005G087300.1	Phvul.005G087300	Phvul.005G087300	PF12609
1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G180200.1	Phvul.005G180200	Phvul.005G180200	PF16987
1	Phvul.005G180200.1	Phvul.005G180200	Phvul.005G180200	PF16987
1	Phvul.006G019800.1	Phvul.006G019800	Phvul.006G019800	PF00736
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1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
1	Phvul.006G067700.1	Phvul.006G067700	Phvul.006G067700	PF14510,PF08
1	Phvul.006G106900.2	Phvul.006G106900	Phvul.006G106900	PF14365,PF03
1	Phvul.006G106900.1	Phvul.006G106900	Phvul.006G106900	PF14365,PF03
1	Phvul.006G137200.3	Phvul.006G137200	Phvul.006G137200	PF03765
1	Phvul.006G137200.2	Phvul.006G137200	Phvul.006G137200	PF03765
1	Phvul.007G113800.1	Phvul.007G113800	Phvul.007G113800	PF12697
1	Phvul.007G113800.1	Phvul.007G113800	Phvul.007G113800	PF12697
1	Phvul.007G211400.1	Phvul.007G211400	Phvul.007G211400	PF00295
1	Phvul.007G211400.1	Phvul.007G211400	Phvul.007G211400	PF00295
1	Phvul.007G219400.1	Phvul.007G219400	Phvul.007G219400	PF02519
1	Phvul.007G219400.1	Phvul.007G219400	Phvul.007G219400	PF02519
1	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
1	Phvul.008G071966.1	Phvul.008G071966	Phvul.008G071966	0
1	Phvul.008G107300.1	Phvul.008G107300	Phvul.008G107300	0
1	Phvul.008G107300.1	Phvul.008G107300	Phvul.008G107300	0
1	Phvul.008G115900.1	Phvul.008G115900	Phvul.008G115900	PF08659
1	Phvul.008G115900.1	Phvul.008G115900	Phvul.008G115900	PF08659
1	Phvul.008G257700.2	Phvul.008G257700	Phvul.008G257700	PF01370

1	Phvul.008G257700.1	Phvul.008G257700	Phvul.008G257700	PF01370
1	Phvul.008G257700.2	Phvul.008G257700	Phvul.008G257700	PF01370
1	Phvul.008G257700.1	Phvul.008G257700	Phvul.008G257700	PF01370
1	Phvul.008G282700.1	Phvul.008G282700	Phvul.008G282700	PF02628
1	Phvul.008G289600.1	Phvul.008G289600	Phvul.008G289600	PF02990
1	Phvul.009G127300.1	Phvul.009G127300	Phvul.009G127300	PF12937
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1	Phvul.009G160700.1	Phvul.009G160700	Phvul.009G160700	PF03016
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1	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
1	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
1	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
1	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G064700	PF00931
1	Phvul.011G047100.1	Phvul.011G047100	Phvul.011G047100	PF00170
1	Phvul.011G047100.1	Phvul.011G047100	Phvul.011G047100	PF00170
2	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
2	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
2	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
2	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
1	Phvul.L007343.1	Phvul.L007343	Phvul.L007343	PF07731,PF07
1	Phvul.L007343.1	Phvul.L007343	Phvul.L007343	PF07731,PF07
1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
2	Phvul.001G036800.1	Phvul.001G036800	Phvul.001G036800	PF08244,PF00
1	Phvul.001G100700.2	Phvul.001G100700	Phvul.001G100700	PF00076
1	Phvul.001G100700.2	Phvul.001G100700	Phvul.001G100700	PF00076
1	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
1	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
1	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
1	Phvul.001G153600.2	Phvul.001G153600	Phvul.001G153600	PF14368
1	Phvul.001G247000.1	Phvul.001G247000	Phvul.001G247000	PF00364
1	Phvul.002G004100.1	Phvul.002G004100	Phvul.002G004100	PF03330,PF01
1	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
1	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
1	Phvul.002G212900.1	Phvul.002G212900	Phvul.002G212900	PF12689
1	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
1	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
1	Phvul.003G029000.2	Phvul.003G029000	Phvul.003G029000	PF13646,PF02
1	Phvul.003G029000.1	Phvul.003G029000	Phvul.003G029000	PF13646,PF02

1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G087600.2	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G087600.1	Phvul.003G087600	Phvul.003G087600	PF02803,PF0C
1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
1	Phvul.003G141700.1	Phvul.003G141700	Phvul.003G141700	PF00566
1	Phvul.003G141700.1	Phvul.003G141700	Phvul.003G141700	PF00566
1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF0C
1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF0C
1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF0C
1	Phvul.003G231500.1	Phvul.003G231500	Phvul.003G231500	PF03953,PF0C
1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601	PF00076
1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
1	Phvul.004G015500.1	Phvul.004G015500	Phvul.004G015500	PF00646,PF08
1	Phvul.004G032100.1	Phvul.004G032100	Phvul.004G032100	0
1	Phvul.004G044900.1	Phvul.004G044900	Phvul.004G044900	PF08263,PF0C
1	Phvul.004G044900.1	Phvul.004G044900	Phvul.004G044900	PF08263,PF0C
1	Phvul.004G163200.1	Phvul.004G163200	Phvul.004G163200	PF00225
1	Phvul.005G010700.2	Phvul.005G010700	Phvul.005G010700	PF11717,PF01
1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G015800.2	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G015800.1	Phvul.005G015800	Phvul.005G015800	PF00067
1	Phvul.005G081600.1	Phvul.005G081600	Phvul.005G081600	PF13692,PF13
1	Phvul.005G081600.1	Phvul.005G081600	Phvul.005G081600	PF13692,PF13
1	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
1	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
1	Phvul.005G097200.5	Phvul.005G097200	Phvul.005G097200	PF03634
1	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634
1	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634

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

2	Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800	0
2	Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800	0
2	Phvul.008G108800.2	Phvul.008G108800	Phvul.008G108800	0
1	Phvul.008G110000.1	Phvul.008G110000	Phvul.008G110000	PF05056
1	Phvul.008G110200.1	Phvul.008G110200	Phvul.008G110200	PF05056
1	Phvul.008G110200.1	Phvul.008G110200	Phvul.008G110200	PF05056
1	Phvul.008G110400.1	Phvul.008G110400	Phvul.008G110400	PF05056
1	Phvul.008G110500.1	Phvul.008G110500	Phvul.008G110500	PF05056
1	Phvul.008G110500.1	Phvul.008G110500	Phvul.008G110500	PF05056
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1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
1	Phvul.008G290300.1	Phvul.008G290300	Phvul.008G290300	PF00201
1	Phvul.009G026200.1	Phvul.009G026200	Phvul.009G026200	PF02362,PF06
1	Phvul.009G026200.1	Phvul.009G026200	Phvul.009G026200	PF02362,PF06
1	Phvul.009G040800.3	Phvul.009G040800	Phvul.009G040800	0
1	Phvul.009G040800.1	Phvul.009G040800	Phvul.009G040800	0
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1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G246900.4	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.009G246900.3	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.009G246900.1	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.009G246900.2	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.009G246900.4	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.009G246900.3	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.009G246900.1	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.009G246900.2	Phvul.009G246900	Phvul.009G246900	PF00153
1	Phvul.010G048400.4	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.3	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.4	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.3	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879

1	Phvul.010G048400.4	Phvul.010G048400	Phvul.010G048400	PF08879
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1	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.4	Phvul.010G048400	Phvul.010G048400	PF08879
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1	Phvul.010G048400.1	Phvul.010G048400	Phvul.010G048400	PF08879
1	Phvul.010G048400.2	Phvul.010G048400	Phvul.010G048400	PF08879
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1	Phvul.011G013800.1	Phvul.011G013800	Phvul.011G013800	PF00642,PF00
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1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
1	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
1	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
1	Phvul.011G173000.1	Phvul.011G173000	Phvul.011G173000	PF01641
1	Phvul.011G190200.3	Phvul.011G190200	Phvul.011G190200	PF05033,PF00
1	Phvul.011G190200.2	Phvul.011G190200	Phvul.011G190200	PF05033,PF00
1	Phvul.001G098600.1	Phvul.001G098600	Phvul.001G098600	PF05553
1	Phvul.001G098600.1	Phvul.001G098600	Phvul.001G098600	PF05553
1	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818
1	Phvul.001G102901.2	Phvul.001G102901	Phvul.001G102901	PF04818

1	Phvul.001G102901.4	Phvul.001G102901	Phvul.001G102901	PF04818	
1	Phvul.001G102901.3	Phvul.001G102901	Phvul.001G102901	PF04818	
1	Phvul.001G102901.1	Phvul.001G102901	Phvul.001G102901	PF04818	
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1	Phvul.001G173900.1	Phvul.001G173900	Phvul.001G173900	PF13911	
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1	Phvul.001G179700.1	Phvul.001G179700	Phvul.001G179700	PF00994,PF01	
1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G200700.3	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G200700.1	Phvul.001G200700	Phvul.001G200700	PF15801,PF03	
1	Phvul.001G260300.1	Phvul.001G260300	Phvul.001G260300	PF04564	
1	Phvul.001G268700.1	Phvul.001G268700	Phvul.001G268700	PF08100,PF0C	
1	Phvul.001G268700.1	Phvul.001G268700	Phvul.001G268700	PF08100,PF0C	
2	Phvul.002G058900.1	Phvul.002G058900	Phvul.002G058900	PF13912	
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1	Phvul.002G068200.1	Phvul.002G068200	Phvul.002G068200	PF00085	
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1	Phvul.002G163400.1	Phvul.002G163400	Phvul.002G163400	PF03106	
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1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738	
1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738	
1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738	
1	Phvul.002G165300.1	Phvul.002G165300	Phvul.002G165300	PF07738	
1	Phvul.002G216700.3	Phvul.002G216700	Phvul.002G216700	PF00010	
1	Phvul.002G216700.2	Phvul.002G216700	Phvul.002G216700	PF00010	
1	Phvul.002G216700.3	Phvul.002G216700	Phvul.002G216700	PF00010	
1	Phvul.002G216700.2	Phvul.002G216700	Phvul.002G216700	PF00010	
1	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657	
1	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657	

1	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
1	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
1	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
1	Phvul.002G253200.1	Phvul.002G253200	Phvul.002G253200	PF00415
1	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
1	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
1	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
1	Phvul.002G283800.1	Phvul.002G283800	Phvul.002G283800	PF03083
1	Phvul.002G290904.1	Phvul.002G290904	Phvul.002G290904	PF11940
1	Phvul.002G290904.1	Phvul.002G290904	Phvul.002G290904	PF11940
1	Phvul.002G309100.1	Phvul.002G309100	Phvul.002G309100	PF00481
1	Phvul.002G309100.1	Phvul.002G309100	Phvul.002G309100	PF00481
1	Phvul.002G320900.1	Phvul.002G320900	Phvul.002G320900	PF03152
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1	Phvul.002G320900.1	Phvul.002G320900	Phvul.002G320900	PF03152
1	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.002G329900.2	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.002G329900.1	Phvul.002G329900	Phvul.002G329900	PF00153
1	Phvul.003G032300.1	Phvul.003G032300	Phvul.003G032300	PF15628
1	Phvul.003G032300.1	Phvul.003G032300	Phvul.003G032300	PF15628
1	Phvul.003G057700.1	Phvul.003G057700	Phvul.003G057700	PF13641
1	Phvul.003G057700.1	Phvul.003G057700	Phvul.003G057700	PF13641
1	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
1	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
1	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
1	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
1	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
1	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
1	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
1	Phvul.003G137000.1	Phvul.003G137000	Phvul.003G137000	PF02140,PF01
1	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF0
1	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF0
1	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF0
1	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF0
1	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF0
1	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF0
1	Phvul.003G247200.2	Phvul.003G247200	Phvul.003G247200	PF05659,PF0

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1	Phvul.003G247200.1	Phvul.003G247200	Phvul.003G247200	PF05659,PF00
1	Phvul.003G280100.2	Phvul.003G280100	Phvul.003G280100	PF03141
1	Phvul.003G280100.2	Phvul.003G280100	Phvul.003G280100	PF03141
1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601	PF00076
1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601	PF00076
1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601	PF00076
1	Phvul.003G294601.1	Phvul.003G294601	Phvul.003G294601	PF00076
1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.4	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.003G294800.3	Phvul.003G294800	Phvul.003G294800	PF00076
1	Phvul.004G032100.1	Phvul.004G032100	Phvul.004G032100	0
1	Phvul.004G032100.1	Phvul.004G032100	Phvul.004G032100	0
1	Phvul.004G032100.1	Phvul.004G032100	Phvul.004G032100	0
1	Phvul.004G032100.1	Phvul.004G032100	Phvul.004G032100	0
1	Phvul.004G044800.1	Phvul.004G044800	Phvul.004G044800	PF08263,PF00
1	Phvul.004G044800.1	Phvul.004G044800	Phvul.004G044800	PF08263,PF00
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G050550	PF13650
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G050550	PF13650
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G050550	PF13650
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G050550	PF13650
1	Phvul.004G173101.1	Phvul.004G173101	Phvul.004G173101	PF06376
1	Phvul.004G173101.1	Phvul.004G173101	Phvul.004G173101	PF06376
1	Phvul.004G173101.1	Phvul.004G173101	Phvul.004G173101	PF06376
1	Phvul.004G173101.1	Phvul.004G173101	Phvul.004G173101	PF06376
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1	Phvul.005G006400.1	Phvul.005G006400	Phvul.005G006400	PF12796
1	Phvul.005G006400.1	Phvul.005G006400	Phvul.005G006400	PF12796
1	Phvul.005G014300.2	Phvul.005G014300	Phvul.005G014300	PF00808
1	Phvul.005G056400.1	Phvul.005G056400	Phvul.005G056400	PF00651
1	Phvul.005G095300.1	Phvul.005G095300	Phvul.005G095300	PF00311
1	Phvul.005G100300.1	Phvul.005G100300	Phvul.005G100300	PF10551
1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.2	Phvul.005G116100	Phvul.005G116100	PF01738
1	Phvul.005G116100.1	Phvul.005G116100	Phvul.005G116100	PF01738

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

1	Phvul.007G058400.1	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G058400.1	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G058400.1	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G058400.1	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G058400.2	Phvul.007G058400	Phvul.007G058400	PF04570
1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
1	Phvul.007G064700.1	Phvul.007G064700	Phvul.007G064700	PF12695
1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
1	Phvul.007G073800.1	Phvul.007G073800	Phvul.007G073800	PF01794,PF08
1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
1	Phvul.007G099300.1	Phvul.007G099300	Phvul.007G099300	PF12646
1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
1	Phvul.007G107200.1	Phvul.007G107200	Phvul.007G107200	PF00043,PF02
1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
1	Phvul.007G182300.2	Phvul.007G182300	Phvul.007G182300	0
1	Phvul.007G189000.1	Phvul.007G189000	Phvul.007G189000	0
1	Phvul.007G189000.1	Phvul.007G189000	Phvul.007G189000	0
1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
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1	Phvul.007G204300.2	Phvul.007G204300	Phvul.007G204300	PF00069
1	Phvul.007G204300.1	Phvul.007G204300	Phvul.007G204300	PF00069
1	Phvul.007G210400.1	Phvul.007G210400	Phvul.007G210400	PF04043,PF01
1	Phvul.007G275700.1	Phvul.007G275700	Phvul.007G275700	PF00045
1	Phvul.007G275700.1	Phvul.007G275700	Phvul.007G275700	PF00045
1	Phvul.007G276200.1	Phvul.007G276200	Phvul.007G276200	PF00045

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

1	Phvul.008G206400.1	Phvul.008G206400	Phvul.008G206400	PF01575
1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
1	Phvul.008G225900.1	Phvul.008G225900	Phvul.008G225900	0
1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
1	Phvul.008G227600.1	Phvul.008G227600	Phvul.008G227600	PF01490
1	Phvul.008G274900.1	Phvul.008G274900	Phvul.008G274900	PF00076
1	Phvul.008G274900.2	Phvul.008G274900	Phvul.008G274900	PF00076
1	Phvul.008G274900.3	Phvul.008G274900	Phvul.008G274900	PF00076
1	Phvul.008G282700.1	Phvul.008G282700	Phvul.008G282700	PF02628
1	Phvul.008G282700.1	Phvul.008G282700	Phvul.008G282700	PF02628
1	Phvul.009G106700.1	Phvul.009G106700	Phvul.009G106700	PF00249
1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.1	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G121300.2	Phvul.009G121300	Phvul.009G121300	PF15413,PF01
1	Phvul.009G173100.1	Phvul.009G173100	Phvul.009G173100	PF00069
1	Phvul.009G173100.3	Phvul.009G173100	Phvul.009G173100	PF00069
1	Phvul.009G173100.1	Phvul.009G173100	Phvul.009G173100	PF00069
1	Phvul.009G173100.3	Phvul.009G173100	Phvul.009G173100	PF00069
1	Phvul.009G232500.1	Phvul.009G232500	Phvul.009G232500	PF01301
1	Phvul.009G232500.1	Phvul.009G232500	Phvul.009G232500	PF01301
1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
1	Phvul.009G259000.1	Phvul.009G259000	Phvul.009G259000	PF08100,PF00
1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
1	Phvul.010G032400.1	Phvul.010G032400	Phvul.010G032400	0
1	Phvul.010G043700.5	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.6	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.4	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.1	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.3	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.2	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.9	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.8	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.7	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.5	Phvul.010G043700	Phvul.010G043700	PF02847,PF02

1	Phvul.010G043700.6	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.4	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.1	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.3	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.2	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.9	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.8	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G043700.7	Phvul.010G043700	Phvul.010G043700	PF02847,PF02
1	Phvul.010G070600.1	Phvul.010G070600	Phvul.010G070600	PF00010
1	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
1	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
2	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
2	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
2	Phvul.010G089200.1	Phvul.010G089200	Phvul.010G089200	PF08610
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2	Phvul.010G089200.2	Phvul.010G089200	Phvul.010G089200	PF08610
1	Phvul.010G135701.1	Phvul.010G135701	Phvul.010G135701	PF00305
1	Phvul.010G135701.1	Phvul.010G135701	Phvul.010G135701	PF00305
1	Phvul.010G135701.1	Phvul.010G135701	Phvul.010G135701	PF00305
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1	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
1	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
1	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
1	Phvul.011G013900.1	Phvul.011G013900	Phvul.011G013900	PF00690,PF12
2	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
2	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
2	Phvul.011G050300.1	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
2	Phvul.011G050300.2	Phvul.011G050300	Phvul.011G050300	PF02260,PF15
1	Phvul.011G061600.1	Phvul.011G061600	Phvul.011G061600	PF05368
1	Phvul.011G061600.1	Phvul.011G061600	Phvul.011G061600	PF05368
1	Phvul.011G114700.1	Phvul.011G114700	Phvul.011G114700	PF05938
1	Phvul.011G123000.1	Phvul.011G123000	Phvul.011G123000	PF05938
1	Phvul.011G123701.1	Phvul.011G123701	Phvul.011G123701	0
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1	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112

1	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.1	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.3	Phvul.011G160800	Phvul.011G160800	PF01112
1	Phvul.011G160800.2	Phvul.011G160800	Phvul.011G160800	PF01112
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1	Phvul.011G202700.1	Phvul.011G202700	Phvul.011G202700	0
1	Phvul.011G202700.1	Phvul.011G202700	Phvul.011G202700	0
1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002051.1	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002051.2	Phvul.L002051	Phvul.L002051	PF01434,PF00
1	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
2	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
2	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF00
1	Phvul.L007343.1	Phvul.L007343	Phvul.L007343	PF07731,PF07
1	Phvul.008G004400.1	Phvul.008G004400	Phvul.008G004400	PF00107,PF16
1	Phvul.008G004400.1	Phvul.008G004400	Phvul.008G004400	PF00107,PF16
1	Phvul.001G020300.1	Phvul.001G020300	Phvul.001G020300	PF01734
1	Phvul.001G020350.1	Phvul.001G020350	Phvul.001G020350	PF01734
1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
1	Phvul.001G022700.1	Phvul.001G022700	Phvul.001G022700	PF03763
2	Phvul.001G036800.1	Phvul.001G036800	Phvul.001G036800	PF08244,PF00
1	Phvul.001G057800.1	Phvul.001G057800	Phvul.001G057800	PF10058
1	Phvul.001G057800.1	Phvul.001G057800	Phvul.001G057800	PF10058
2	Phvul.001G077700.1	Phvul.001G077700	Phvul.001G077700	PF10509,PF00
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1	Phvul.001G097800.1	Phvul.001G097800	Phvul.001G097800	PF16177,PF13
1	Phvul.001G097800.1	Phvul.001G097800	Phvul.001G097800	PF16177,PF13
1	Phvul.001G109300.2	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
1	Phvul.001G109300.1	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
1	Phvul.001G109300.2	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
1	Phvul.001G109300.1	Phvul.001G109300	Phvul.001G109300	PF04153,PF04
1	Phvul.001G114900.1	Phvul.001G114900	Phvul.001G114900	PF01042,PF01
1	Phvul.001G114900.1	Phvul.001G114900	Phvul.001G114900	PF01042,PF01

1	Phvul.001G123000.2	Phvul.001G123000	Phvul.001G123000	PF01055
1	Phvul.001G123000.2	Phvul.001G123000	Phvul.001G123000	PF01055
1	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
1	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
1	Phvul.001G134100.2	Phvul.001G134100	Phvul.001G134100	PF00931
1	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
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1	Phvul.001G134100.1	Phvul.001G134100	Phvul.001G134100	PF00931
1	Phvul.001G159300.1	Phvul.001G159300	Phvul.001G159300	PF03195
1	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
1	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
1	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
1	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
1	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
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1	Phvul.001G163900.2	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
1	Phvul.001G163900.1	Phvul.001G163900	Phvul.001G163900	PF00249,PF14
1	Phvul.001G214300.2	Phvul.001G214300	Phvul.001G214300	PF05691
1	Phvul.001G214300.1	Phvul.001G214300	Phvul.001G214300	PF05691
1	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
1	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
1	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
1	Phvul.001G220900.1	Phvul.001G220900	Phvul.001G220900	PF01926,PF11
1	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
1	Phvul.002G013866.1	Phvul.002G013866	Phvul.002G013866	PF13414
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1	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
1	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
1	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
1	Phvul.002G043500.1	Phvul.002G043500	Phvul.002G043500	PF14432,PF01
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2	Phvul.002G058900.1	Phvul.002G058900	Phvul.002G058900	PF13912
1	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
1	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
1	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
1	Phvul.002G152900.1	Phvul.002G152900	Phvul.002G152900	PF03330,PF01
1	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
1	Phvul.002G243300.1	Phvul.002G243300	Phvul.002G243300	PF00657
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1	Phvul.002G253100.1	Phvul.002G253100	Phvul.002G253100	PF00415
1	Phvul.002G262600.1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0
1	Phvul.002G290000.3	Phvul.002G290000	Phvul.002G290000	PF00010
1	Phvul.002G290000.3	Phvul.002G290000	Phvul.002G290000	PF00010
1	Phvul.003G022200.1	Phvul.003G022200	Phvul.003G022200	PF10508
1	Phvul.003G022200.1	Phvul.003G022200	Phvul.003G022200	PF10508
1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
1	Phvul.003G035400.1	Phvul.003G035400	Phvul.003G035400	PF16863,PF01
1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
1	Phvul.003G050600.1	Phvul.003G050600	Phvul.003G050600	PF02458
1	Phvul.003G088200.1	Phvul.003G088200	Phvul.003G088200	PF02893,PF0
1	Phvul.003G088200.1	Phvul.003G088200	Phvul.003G088200	PF02893,PF0
1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
1	Phvul.003G104200.1	Phvul.003G104200	Phvul.003G104200	PF00153
1	Phvul.003G119100.3	Phvul.003G119100	Phvul.003G119100	PF00169,PF06
1	Phvul.003G119100.2	Phvul.003G119100	Phvul.003G119100	PF00169,PF06
1	Phvul.003G119100.1	Phvul.003G119100	Phvul.003G119100	PF00169,PF06
1	Phvul.003G169700.1	Phvul.003G169700	Phvul.003G169700	PF03016
1	Phvul.003G292000.1	Phvul.003G292000	Phvul.003G292000	PF00852
1	Phvul.004G058600.1	Phvul.004G058600	Phvul.004G058600	PF04193
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1	Phvul.005G088800.1	Phvul.005G088800	Phvul.005G088800	PF11883,PF08
1	Phvul.005G095600.1	Phvul.005G095600	Phvul.005G095600	PF13419
1	Phvul.005G097200.3	Phvul.005G097200	Phvul.005G097200	PF03634

1	Phvul.005G097200.6	Phvul.005G097200	Phvul.005G097200	PF03634
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1	Phvul.L001679.1	Phvul.L001679	Phvul.L001679	PF00168	
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2	Phvul.L002537.1	Phvul.L002537	Phvul.L002537	PF16131,PF0	
1	Phvul.L009843.2	Phvul.L009843	Phvul.L009843	PF00153	
1	Phvul.L009843.1	Phvul.L009843	Phvul.L009843	PF00153	
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Panther	KOG	KEGG	KOG	GO	Best-hit-arabi
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PTHR13451,P	0	0	K10882	GO:0004518,(	AT2G22140.1
PTHR31928,P	0	0	0	0	AT1G70340.1
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PTHR27004,P	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
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PTHR33463,P	KOG1947	0	0	0	AT1G61300.1
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PTHR33103,P	0	0	0	0	AT5G01150.1
PTHR33103,P	0	0	0	0	AT5G01120.1

PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR12663,P	KOG1525	0	0	0	AT1G77600.2
PTHR13600,P	0	0	0	GO:0032259,(	AT5G42760.1
PTHR13600,P	0	0	0	GO:0032259,(	AT5G42760.1
PTHR13600,P	0	0	0	GO:0032259,(	AT5G42760.1
PTHR13600,P	0	0	0	GO:0032259,(	AT5G42760.1
PTHR31949,P	0	0	0	0	AT3G08670.1
PTHR31949,P	0	0	0	0	AT3G08670.1
PTHR18966,P	KOG1052	0	K05387	GO:0016020,(	AT4G35290.1
PTHR18966,P	KOG1052	0	K05387	GO:0016020,(	AT4G35290.1
PTHR22952,P	0	0	0	GO:0043565,(	AT5G24800.1
PTHR22952,P	0	0	0	GO:0043565,(	AT5G24800.1
PTHR10457,P	KOG0631	2.7.1.46	K12446	GO:0005524	AT4G16130.1
PTHR10457,P	KOG0631	2.7.1.46	K12446	GO:0005524	AT4G16130.1
PTHR11937,P	0	0	0	GO:0034314,(	AT3G27000.1
PTHR11937,P	0	0	0	GO:0034314,(	AT3G27000.1
PTHR11937,P	0	0	0	GO:0034314,(	AT3G27000.1
PTHR11937,P	0	0	0	GO:0034314,(	AT3G27000.1
PTHR11937,P	0	0	K17260	GO:0034314,(	AT3G27000.1
PTHR11937,P	0	0	K17260	GO:0034314,(	AT3G27000.1
PTHR11937,P	0	0	K17260	GO:0034314,(	AT3G27000.1
PTHR11937,P	0	0	K17260	GO:0034314,(	AT3G27000.1
PTHR31719,P	0	0	0	GO:0006355,(	AT2G33480.2
PTHR31719,P	0	0	0	GO:0006355,(	AT2G33480.2
PTHR31719,P	0	0	0	GO:0006355,(	AT2G33480.2
PTHR31719,P	0	0	0	GO:0006355,(	AT2G33480.2
PTHR10277,P	0	4.1.3.4	0	GO:0003824	AT2G26800.1
PTHR10277,P	0	4.1.3.4	0	GO:0003824	AT2G26800.1
PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1

PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1
PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1
PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1
PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1
PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1
PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1
PTHR19229,P	KOG0059	3.6.3.25	K05643	GO:0005524,(	AT2G41700.1
PTHR31251,P	0	0	0	GO:0005634,(	AT2G42200.1
PTHR31251,P	0	0	0	GO:0005634,(	AT2G42200.1
PTHR31251,P	0	0	0	GO:0005634,(	AT2G42200.1
PTHR31251,P	0	0	0	GO:0005634,(	AT2G42200.1
PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(	AT5G03430.1
PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(	AT5G03430.1
PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(	AT5G03430.1
PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(	AT5G03430.1
PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(	AT5G03430.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR13115,P	0	0	0	0	AT5G43630.1
PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(	AT5G39950.1
PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(	AT5G39950.1
PTHR31928,P	0	0	0	0	AT1G70340.1
PTHR31928,P	0	0	0	0	AT1G70340.1
PTHR10201,P	0	3.4.24.23	0	GO:0031012,(	AT1G70170.1
PTHR10201,P	0	3.4.24.23	0	GO:0031012,(	AT1G70170.1
PTHR10201,P	0	3.4.24.23	0	GO:0031012,(	AT1G70170.1
PTHR10201,P	0	3.4.24.23	0	GO:0031012,(	AT1G70170.1
PTHR10110,P	KOG1965	0	0	GO:0055085,(	AT2G01980.1
PTHR10110,P	KOG1965	0	0	GO:0055085,(	AT2G01980.1
PTHR10110,P	KOG1965	0	0	GO:0055085,(	AT2G01980.1

PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT3G13690.1
PTHR23336,P	0	0	0	GO:0008270	AT3G62900.1
PTHR23336,P	0	0	0	GO:0008270	AT3G62900.1
PTHR27004,P	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
PTHR24015,P	0	0	0	0	AT4G21190.1
PTHR11689,P	0	0	K05016	GO:0055085,(	AT5G49890.1
PTHR11689,P	0	0	K05016	GO:0055085,(	AT5G49890.1
PTHR10438,P	KOG0907	3.5.1.52	0	GO:0045454,(	AT4G29670.1
PTHR10438,P	KOG0907	3.5.1.52	0	GO:0045454,(	AT4G29670.1
PTHR10438,P	KOG0907	3.5.1.52	0	GO:0045454,(	AT4G29670.1
PTHR10438,P	KOG0907	3.5.1.52	0	GO:0045454,(	AT4G29670.1
PTHR33090	0	0	0	0	AT4G10265.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR33137,P	0	0	K14972	0	AT1G15780.1
PTHR33137,P	0	0	K14972	0	AT1G15780.1
PTHR11595,P	KOG1668	0	K03232	GO:0006414,(	AT5G12110.1
PTHR11595,P	KOG1668	0	K03232	GO:0006414,(	AT5G12110.1
PTHR11595,P	KOG1668	0	K03232	GO:0006414,(	AT5G12110.1
PTHR11595,P	KOG1668	0	K03232	GO:0006414,(	AT5G12110.1
PTHR19241,P	0	3.6.3.34	0	GO:0016887,(	AT2G29940.1
PTHR19241,P	0	3.6.3.34	0	GO:0016887,(	AT2G29940.1
PTHR19241,P	0	3.6.3.34	0	GO:0016887,(	AT2G29940.1
PTHR19241,P	0	3.6.3.34	0	GO:0016887,(	AT2G29940.1
PTHR31589,P	0	0	0	0	AT5G18460.1
PTHR31589,P	0	0	0	0	AT5G18460.1
PTHR23324,P	0	0	0	0	AT5G47730.1
PTHR23324,P	0	0	0	0	AT5G47730.1
PTHR10992,P	KOG1454	0	0	0	AT5G38520.1
PTHR10992,P	KOG1454	0	0	0	AT5G38520.1
PTHR31375,P	0	3.2.1.15	0	GO:0005975,(	AT1G02460.1
PTHR31375,P	0	3.2.1.15	0	GO:0005975,(	AT1G02460.1
PTHR31374,P	0	0	K14488	GO:0009733	AT3G09870.1
PTHR31374,P	0	0	K14488	GO:0009733	AT3G09870.1
PTHR33463,P	KOG1947	0	0	0	AT1G61300.1
PTHR33463,P	KOG1947	0	0	0	AT1G61300.1
PTHR35731,P	0	0	0	0	AT3G09050.1
PTHR35731,P	0	0	0	0	AT3G09050.1
PTHR24322,P	KOG0725	1.1.1.206	K08081	0	AT5G06060.1
PTHR24322,P	KOG0725	1.1.1.206	K08081	0	AT5G06060.1
PTHR10366,P	KOG1502	1.2.1.44	0	GO:0050662,(	AT5G58490.1

PTHR10366,P	KOG1502	1.2.1.44	0	GO:0050662,(	AT5G58490.1
PTHR10366,P	KOG1502	1.2.1.44	0	GO:0050662,(	AT5G58490.1
PTHR10366,P	KOG1502	1.2.1.44	0	GO:0050662,(	AT5G58490.1
PTHR23289,P	0	0	K02259	GO:0055114,(	AT5G56090.1
PTHR10766,P	0	0	K17086	GO:0016021	AT4G12650.1
PTHR12874	KOG2997	0	K10295	GO:0005515	AT1G21760.1
PTHR12874	KOG2997	0	K10295	GO:0005515	AT1G21760.1
PTHR12874	KOG2997	0	K10295	GO:0005515	AT1G21760.1
PTHR12874	KOG2997	0	K10295	GO:0005515	AT1G21760.1
PTHR11062,P	KOG1021	2.4.2.41	0	0	AT5G61840.1
PTHR11062,P	KOG1021	2.4.2.41	0	0	AT5G61840.1
PTHR11062,P	KOG1021	2.4.2.41	0	0	AT5G61840.1
PTHR11062,P	KOG1021	2.4.2.41	0	0	AT5G61840.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
0	0	0	0	GO:0043565,(	AT4G36730.1
0	0	0	0	GO:0043565,(	AT4G36730.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR11709,P	0	1.10.3.2	K05909	GO:0055114,(	AT2G29130.1
PTHR11709,P	0	1.10.3.2	K05909	GO:0055114,(	AT2G29130.1
PTHR31471,P	0	0	0	0	AT1G45207.2
PTHR31471,P	0	0	0	0	AT1G45207.2
PTHR31953,P	0	3.2.1.153,3.2.	K01193	0	AT3G13790.1
PTHR16105,P	0	0	K13157	GO:0003676	AT1G09230.1
PTHR16105,P	0	0	K13157	GO:0003676	AT1G09230.1
PTHR33044,P	0	0	0	0	AT2G48140.1
PTHR33044,P	0	0	0	0	AT2G48140.1
PTHR33044,P	0	0	0	0	AT2G48140.1
PTHR33044,P	0	0	0	0	AT2G48140.1
PTHR18866,P	0	0	0	0	AT3G56130.1
PTHR31692,P	0	0	0	0	AT4G17030.1
PTHR23083,P	0	0	0	0	AT4G37460.1
PTHR23083,P	0	0	0	0	AT4G37460.1
PTHR17901,P	KOG4549	3.1.3.48	K17619	GO:0016791	AT2G14110.1
PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR10648,P	0	0	K03456	GO:0005515	AT3G25800.1
PTHR10648,P	0	0	K03456	GO:0005515	AT3G25800.1

PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR18919,P	0	2.3.1.9	K00626	GO:0016747,(	AT5G47720.2
PTHR24089,P	KOG0752	0	K15108	0	AT5G48970.1
PTHR24089,P	KOG0752	0	K15108	0	AT5G48970.1
PTHR22957,P	KOG1091	0	K18469	0	AT4G29950.1
PTHR22957,P	KOG1091	0	K18469	0	AT4G29950.1
PTHR11588,P	0	0	K07374	GO:0003924,(	AT1G04820.1
PTHR11588,P	0	0	K07374	GO:0003924,(	AT1G04820.1
PTHR11588,P	0	0	K07374	GO:0003924,(	AT1G04820.1
PTHR11588,P	0	0	K07374	GO:0003924,(	AT1G04820.1
PTHR24012,P	0	0	0	GO:0003676	AT1G49600.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR32212,P	0	0	0	GO:0005515	AT3G49030.1
PTHR32212,P	0	0	0	GO:0005515	AT3G49030.1
PTHR32212,P	0	0	0	GO:0005515	AT3G49030.1
PTHR32212,P	0	0	0	GO:0005515	AT3G49030.1
0	0	0	0	0	0
PTHR27004,P	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
PTHR27004,P	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
PTHR24115,P	0	3.6.4.4	K10393	GO:0008017,(	AT3G16060.1
PTHR10615,P	KOG2747	2.3.1.48	K11308	GO:0016747,(	AT5G64610.1
PTHR24286,P	KOG0157	0	0	GO:0055114,(	AT3G14620.1
PTHR24286,P	KOG0157	0	0	GO:0055114,(	AT3G14620.1
PTHR24286,P	KOG0157	0	0	GO:0055114,(	AT3G14620.1
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PTHR24286,P	KOG0157	0	0	GO:0055114,(	AT3G14620.1
PTHR12526,P	KOG0853	2.4.1.132,2.4.	K03843	0	AT1G78800.1
PTHR12526,P	KOG0853	2.4.1.132,2.4.	K03843	0	AT1G78800.1
PTHR31072,P	0	0	0	0	AT3G15030.2
PTHR31072,P	0	0	0	0	AT3G15030.2
PTHR31072,P	0	0	0	0	AT3G15030.2
PTHR31072,P	0	0	0	0	AT3G15030.2
PTHR31072,P	0	0	0	0	AT3G15030.2

PTHR31072,P	0	0	0	0	AT3G15030.2
PTHR37716,P	0	0	0	0	AT2G01870.1
PTHR37716,P	0	0	0	0	AT2G01870.1
PTHR11999,P	0	4.1.1.28,4.1.1	K01592	GO:0030170,(	AT2G20340.1
PTHR11999,P	0	4.1.1.28,4.1.1	K01592	GO:0030170,(	AT2G20340.1
PTHR12381,P	0	0	K15047	GO:0005515	0
PTHR12381,P	0	0	K15047	GO:0005515	0
PTHR12381,P	0	0	K15047	GO:0005515	0
PTHR12381,P	0	0	K15047	GO:0005515	0
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G62180.1
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G62180.1
PTHR37764,P	0	0	0	0	AT5G27390.1
0	0	0	0	0	AT3G05625.1
0	0	0	0	0	AT3G05625.1
PTHR33416,P	0	0	0	0	AT3G10650.1
PTHR33416,P	0	0	0	0	AT3G10650.1
PTHR33416,P	0	0	0	0	AT3G10650.1
PTHR33416,P	0	0	0	0	AT3G10650.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR23240,P	KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1
PTHR23240,P	KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1
PTHR23240,P	KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1
PTHR23240,P	KOG1361	6.5.1.1	K10747	GO:0006310,(	AT1G66730.1
PTHR10783,P	0	0	0	GO:0016021	AT3G29060.1
PTHR10783,P	0	0	0	GO:0016021	AT3G29060.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR13480	KOG2932	0	K15685	0	AT5G01160.1

PTHR13480	KOG2932	0	K15685	0	AT5G01160.1
PTHR13480	KOG2932	0	K15685	0	AT5G01160.1
PTHR13480	KOG2932	0	K15685	0	AT5G01160.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR33103,P	0	0	0	0	AT5G01150.1
PTHR33103,P	0	0	0	0	AT5G01150.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR13343,P	0	0	0	0	AT3G59300.1
PTHR11926,P	KOG1192	0	0	GO:0016758,(	AT3G21780.1
PTHR11926,P	KOG1192	0	0	GO:0016758,(	AT3G21780.1
PTHR11926,P	KOG1192	0	0	GO:0016758,(	AT3G21780.1
PTHR11926,P	KOG1192	0	0	GO:0016758,(	AT3G21780.1
PTHR31384,P	0	0	0	GO:0003677,(	AT1G77850.1
PTHR31384,P	0	0	0	GO:0003677,(	AT1G77850.1
PTHR31851,P	0	0	0	0	AT4G27860.1
PTHR31851,P	0	0	0	0	AT4G27860.1
PTHR31851,P	0	0	0	0	AT4G27860.1
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR24089,P	0	0	0	0	AT5G48970.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
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PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
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PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1
PTHR22849,P	0	6.3.2.19	0	GO:0016567,(	AT1G76390.1
PTHR22849,P	0	6.3.2.19	0	GO:0016567,(	AT1G76390.1
PTHR22849,P	0	6.3.2.19	0	GO:0016567,(	AT1G76390.1
PTHR22849,P	0	6.3.2.19	0	GO:0016567,(	AT1G76390.1
PTHR24009,P	0	0	0	GO:0046872,(	AT3G51950.2
PTHR24009,P	0	0	0	GO:0046872,(	AT3G51950.2
PTHR24009,P	0	0	0	GO:0046872,(	AT3G51950.2
PTHR24009,P	0	0	0	GO:0046872,(	AT3G51950.2
0	0	0	0	0	AT3G06985.1
0	0	0	0	0	AT3G06985.1
0	0	0	0	0	AT3G06985.1
0	0	0	0	0	AT3G06985.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10173,P	KOG0856	1.8.4.12	K07305	GO:0055114,(	AT1G53670.1
PTHR10173,P	KOG0856	1.8.4.12	K07305	GO:0055114,(	AT1G53670.1
PTHR10173,P	KOG0856	1.8.4.12	K07305	GO:0055114,(	AT1G53670.1
PTHR10173,P	KOG0856	1.8.4.12	K07305	GO:0055114,(	AT1G53670.1
PTHR22884,P	KOG1082	2.1.1.43	K11420	GO:0034968,(	AT5G04940.2
PTHR22884,P	KOG1082	2.1.1.43	K11420	GO:0034968,(	AT5G04940.2
PTHR33265,P	0	0	0	0	AT1G52140.1
PTHR33265,P	0	0	0	0	AT1G52140.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
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PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR12460	KOG2669	0	K15559	0	AT5G65180.1
PTHR31447,P	KOG4176	0	0	0	AT4G02940.1
PTHR28630,P	KOG4498	0	0	0	AT2G37240.1
PTHR28630,P	KOG4498	0	0	0	AT2G37240.1
PTHR28630,P	KOG4498	0	0	0	AT2G37240.1
PTHR28630,P	KOG4498	0	0	0	AT2G37240.1
PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(	AT5G03430.1
PTHR23293,P	KOG2644	2.7.7.2	0	GO:0008152,(	AT5G03430.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR12121,P	KOG0620	3.1.13.4	K12603	0	AT3G58580.1
PTHR22849,P	0	6.3.2.19	0	GO:0016567,(	AT1G24330.1
PTHR11746,P	KOG3178	0	0	GO:0046983,(	AT4G35160.1
PTHR11746,P	KOG3178	0	0	GO:0046983,(	AT4G35160.1
PTHR26374,P	0	0	0	0	AT3G60580.1
PTHR26374,P	0	0	0	0	AT3G60580.1
PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(	AT5G39950.1
PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(	AT5G39950.1
PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(	AT5G39950.1
PTHR10438,P	KOG0907	1.6.5.4	K03671	GO:0045454,(	AT5G39950.1
PTHR32096,P	0	0	0	GO:0043565,(	AT4G11070.1
PTHR32096,P	0	0	0	GO:0043565,(	AT4G11070.1
PTHR12953	KOG1396	0	0	0	AT4G23950.1
PTHR12953	KOG1396	0	0	0	AT4G23950.1
PTHR12953	KOG1396	0	0	0	AT4G23950.1
PTHR12953	KOG1396	0	0	0	AT4G23950.1
PTHR23042,P	0	0	0	GO:0046983	AT4G37850.1
PTHR23042,P	0	0	0	GO:0046983	AT4G37850.1
PTHR23042,P	0	0	0	GO:0046983	AT4G37850.1
PTHR23042,P	0	0	0	GO:0046983	AT4G37850.1
PTHR22835,P	0	3.1.1.3	0	GO:0016788	AT1G29670.1
PTHR22835,P	0	3.1.1.3	0	GO:0016788	AT1G29670.1

PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR10791,P	KOG1623	0	K15382	GO:0016021	AT5G50800.1
PTHR10791,P	KOG1623	0	K15382	GO:0016021	AT5G50800.1
PTHR10791,P	KOG1623	0	K15382	GO:0016021	AT5G50800.1
PTHR10791,P	KOG1623	0	K15382	GO:0016021	AT5G50800.1
PTHR11533,P	0	3.4.11.14	K01256	GO:0006508	AT1G63770.3
PTHR11533,P	0	3.4.11.14	K01256	GO:0006508	AT1G63770.3
PTHR13832,P	KOG0698	3.1.3.16	K14497	GO:0003824,(	AT4G26080.1
PTHR13832,P	KOG0698	3.1.3.16	K14497	GO:0003824,(	AT4G26080.1
PTHR12555,P	KOG1816	0	K14016	GO:0006511	AT2G21270.3
PTHR12555,P	KOG1816	0	K14016	GO:0006511	AT2G21270.3
PTHR12555,P	KOG1816	0	K14016	GO:0006511	AT2G21270.3
PTHR12555,P	KOG1816	0	K14016	GO:0006511	AT2G21270.3
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR24089,P	KOG0749	0	K05863	0	AT5G17400.1
PTHR10359,P	0	4.2.99.18	0	0	AT5G04560.2
PTHR10359,P	0	4.2.99.18	0	0	AT5G04560.2
PTHR10859	KOG2978	2.4.1.83	K00721	0	AT1G20575.1
PTHR10859	KOG2978	2.4.1.83	K00721	0	AT1G20575.1
PTHR34775,P	0	0	0	0	AT2G16270.1
PTHR34775,P	0	0	0	0	AT2G16270.1
PTHR34775,P	0	0	0	0	AT2G16270.1
PTHR34775,P	0	0	0	0	AT2G16270.1
PTHR23421,P	0	3.2.1.23	0	GO:0030246,(	AT3G13750.1
PTHR23421,P	0	3.2.1.23	0	GO:0030246,(	AT3G13750.1
PTHR23421,P	0	3.2.1.23	0	GO:0030246,(	AT3G13750.1
PTHR23421,P	0	3.2.1.23	0	GO:0030246,(	AT3G13750.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT5G66900.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT5G66900.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT5G66900.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT5G66900.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT5G66900.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT5G66900.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT5G66900.1

PTHR23155,P	KOG4658	0		GO:0043531	AT5G66900.1
PTHR10108,P	0	2.1.1.41	0	GO:0008168	AT1G31850.2
PTHR10108,P	0	2.1.1.41	0	GO:0008168	AT1G31850.2
PTHR24012,P	0	0	0	GO:0003676	AT1G49600.1
PTHR24012,P	0	0	0	GO:0003676	AT1G49600.1
PTHR24012,P	0	0	0	GO:0003676	AT1G49600.1
PTHR24012,P	0	0	0	GO:0003676	AT1G49600.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
PTHR24012,P	KOG0148	0	0	GO:0003676	AT3G19130.1
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
PTHR27004,P	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
PTHR27004,P	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
PTHR34482,P	0	0	0	0	AT3G29750.1
PTHR34482,P	0	0	0	0	AT3G29750.1
PTHR34482,P	0	0	0	0	AT3G29750.1
PTHR34482,P	0	0	0	0	AT3G29750.1
PTHR33374,P	0	0	0	0	AT3G61640.1
PTHR33374,P	0	0	0	0	AT3G61640.1
PTHR33374,P	0	0	0	0	AT3G61640.1
PTHR33374,P	0	0	0	0	AT3G61640.1
PTHR24193,P	KOG4214	0	0	0	AT2G17390.1
PTHR24193,P	KOG4214	0	0	0	AT2G17390.1
PTHR24193,P	KOG4214	0	0	0	AT2G17390.1
PTHR24193,P	KOG4214	0	0	0	AT2G17390.1
PTHR10252,P	0	0	0	0	AT3G12480.1
PTHR35918,P	0	0	0	GO:0005515	AT1G04390.1
PTHR30523,P	0	4.1.1.31	K01595	GO:0015977,(	AT2G42600.2
PTHR31973,P	0	0	0	0	AT1G64260.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043	3.1.1.45	0	GO:0016787	AT2G32520.1

PTHR17630	KOG3043		3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR17630	KOG3043		3.1.1.45	0	GO:0016787	AT2G32520.1
PTHR10593,P		0	0	0	0	AT5G22890.1
PTHR10593,P		0	0	0	0	AT5G22890.1
PTHR14095,P		0	0	K11583	0	AT5G28850.2
PTHR13215,P		0	0	0	GO:0006355,(	AT4G00980.1
PTHR13215,P		0	0	0	GO:0006355,(	AT4G00980.1
PTHR13215,P		0	0	0	GO:0006355,(	AT4G00980.1
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PTHR13215,P		0	0	0	GO:0006355,(	AT4G00980.1
PTHR13215,P		0	0	0	GO:0006355,(	AT4G00980.1
PTHR11453,P		0	0	0	GO:0016021,(	AT3G62270.1
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PTHR11453,P		0	0	0	GO:0016021,(	AT3G62270.1
PTHR11453,P		0	0	0	GO:0016021,(	AT3G62270.1
PTHR33670,P		0	0	0	0	AT3G21570.1
PTHR11802,P	KOG1282		0	K16296	GO:0006508,(	AT5G09640.1
PTHR11802,P	KOG1282		0	K16296	GO:0006508,(	AT5G09640.1
PTHR11802,P	KOG1282		0	K16296	GO:0006508,(	AT5G09640.1
PTHR11802,P	KOG1282		0	K16296	GO:0006508,(	AT5G09640.1
PTHR13063,P	KOG3039		0	K13125	GO:0050999	AT1G61620.1
PTHR13063,P	KOG3039		0	K13125	GO:0050999	AT1G61620.1
PTHR11757,P		0	3.4.21.83	K01354	GO:0008236,(	AT1G50380.1
PTHR11757,P		0	3.4.21.83	K01354	GO:0008236,(	AT1G50380.1
PTHR11757,P		0	3.4.21.83	K01354	GO:0008236,(	AT1G50380.1
PTHR11757,P		0	3.4.21.83	K01354	GO:0008236,(	AT1G50380.1
PTHR31072,P		0	0	0	0	AT5G23280.1
PTHR31072,P		0	0	0	0	AT5G23280.1
PTHR15362,P		0	2.7.8.8	K08730	GO:0006659	AT1G15110.1
PTHR27002	KOG1187		2.7.10.2	0	GO:0006468,(	AT4G05200.1
PTHR27002	KOG1187		2.7.10.2	0	GO:0006468,(	AT4G05200.1
PTHR27002	KOG1187		2.7.10.2	0	GO:0006468,(	AT4G05200.1
PTHR27002	KOG1187		2.7.10.2	0	GO:0006468,(	AT4G05200.1
PTHR10638,P		0	0	K00276	GO:0055114,(	AT4G14940.1
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PTHR10638,P		0	0	K00276	GO:0055114,(	AT4G14940.1

PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR33059,P	0	0	0	0	AT3G22550.1
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G62180.1
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G62180.1
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G62180.1
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G62180.1
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G62180.1
PTHR11972,P	KOG0039	1.16.1.7	0	GO:0055114,(	AT1G01580.1
PTHR11972,P	KOG0039	1.16.1.7	0	GO:0055114,(	AT1G01580.1
PTHR11972,P	KOG0039	1.16.1.7	0	GO:0055114,(	AT1G01580.1
PTHR11972,P	KOG0039	1.16.1.7	0	GO:0055114,(	AT1G01580.1
PTHR35732,P	0	0	0	0	AT3G10405.1
PTHR35732,P	0	0	0	0	AT3G10405.1
PTHR35732,P	0	0	0	0	AT3G10405.1
PTHR35732,P	0	0	0	0	AT3G10405.1
PTHR11260,P	KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
PTHR11260,P	KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
PTHR11260,P	KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
PTHR11260,P	KOG0867	2.5.1.18	K00799	GO:0005515	AT1G02920.1
PTHR37764,P	0	0	0	0	AT5G27390.1
PTHR37764,P	0	0	0	0	AT5G27390.1
PTHR37764,P	0	0	0	0	AT5G27390.1
PTHR37764,P	0	0	0	0	AT5G27390.1
PTHR33592	0	0	0	0	AT2G31345.1
PTHR33592	0	0	0	0	AT2G31345.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT1G56720.1
PTHR31707,P	0	3.1.1.11	K01051	GO:0004857,(	AT3G05610.1
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0	0	0	0	0	0

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0	0	0	0	0	0
0	0	0	0	0	0
PTHR35313,P	0	0	0	0	AT5G13390.1
PTHR35313,P	0	0	0	0	AT5G13390.1
PTHR35313,P	0	0	0	0	AT5G13390.1
PTHR35313,P	0	0	0	0	AT5G13390.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR32059,P	0	0	0	0	AT5G16210.1
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1
PTHR13068,P	0	0	K15032	GO:0006355,(	AT3G18870.1
PTHR35410,P	0	0	0	0	0
PTHR35410,P	0	0	0	0	0
PTHR35410,P	0	0	0	0	0
PTHR35410,P	0	0	0	0	0
PTHR33463,P	KOG1947	0	0	0	AT1G61300.1
PTHR33463,P	KOG1947	0	0	0	AT1G61300.1
PTHR33463,P	KOG1947	0	0	0	AT1G61300.1
PTHR33463,P	KOG1947	0	0	0	AT1G61300.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR33103,P	0	0	0	0	AT5G01120.1
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT5G02190.1
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT5G02190.1
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0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
PTHR13078	0	4.2.1.119	0	0	AT5G60335.1
PTHR13078	0	4.2.1.119	0	0	AT5G60335.1
PTHR13078	0	4.2.1.119	0	0	AT5G60335.1

PTHR13078	0	4.2.1.119	0	0	AT5G60335.1
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
PTHR22950,P	KOG1303	0	0	0	AT2G39890.1
PTHR22950,P	KOG1303	0	0	0	AT2G39890.1
PTHR22950,P	KOG1303	0	0	0	AT2G39890.1
PTHR22950,P	KOG1303	0	0	0	AT2G39890.1
PTHR24012,P	KOG4205	0	K14411	GO:0003676	AT3G07810.1
PTHR24012,P	KOG4205	0	K14411	GO:0003676	AT3G07810.1
PTHR24012,P	KOG4205	0	K14411	GO:0003676	AT3G07810.1
PTHR23289,P	0	0	K02259	GO:0055114,(	AT5G56090.1
PTHR23289,P	0	0	K02259	GO:0055114,(	AT5G56090.1
PTHR10641,P	KOG0048	0	0	0	AT4G32730.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR10972,P	0	0	0	0	AT4G08180.2
PTHR13902	KOG0198	2.7.11.1	0	GO:0006468,(	AT3G48260.1
PTHR13902	KOG0198	2.7.11.1	0	GO:0006468,(	AT3G48260.1
PTHR13902	KOG0198	2.7.11.1	0	GO:0006468,(	AT3G48260.1
PTHR13902	KOG0198	2.7.11.1	0	GO:0006468,(	AT3G48260.1
PTHR23421,P	0	3.2.1.23	0	GO:0005975,(	AT4G26140.1
PTHR23421,P	0	3.2.1.23	0	GO:0005975,(	AT4G26140.1
PTHR11746,P	KOG3178	2.1.1.68	K13066	GO:0046983,(	AT5G54160.1
PTHR11746,P	KOG3178	2.1.1.68	K13066	GO:0046983,(	AT5G54160.1
PTHR11746,P	KOG3178	2.1.1.68	K13066	GO:0046983,(	AT5G54160.1
PTHR11746,P	KOG3178	2.1.1.68	K13066	GO:0046983,(	AT5G54160.1
PTHR32387,P	0	0	K17592	0	AT3G48770.1
PTHR32387,P	0	0	K17592	0	AT3G48770.1
PTHR32387,P	0	0	K17592	0	AT3G48770.1
PTHR32387,P	0	0	K17592	0	AT3G48770.1
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
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PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4

PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR23253,P	KOG0401	0	0	GO:0005515,(	AT3G60240.4
PTHR12565,P	0	0	0	GO:0046983	AT4G00050.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR13299,P	KOG4546	0	0	0	AT2G45690.1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,(	AT1G55020.1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,(	AT1G55020.1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,(	AT1G55020.1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,(	AT1G55020.1
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT3G57330.1
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT3G57330.1
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT3G57330.1
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT3G57330.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR11139,P	0	2.7.11.1	K08873	GO:0005515,(	AT1G50030.1
PTHR14194,P	KOG1203	0	0	0	AT3G46780.1
PTHR14194,P	KOG1203	0	0	0	AT3G46780.1
PTHR31232	0	0	0	0	AT1G04645.1
PTHR31232	0	0	0	0	AT4G16195.1
0	0	0	0	0	AT3G06985.1
0	0	0	0	0	AT3G06985.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1

PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
PTHR10188,P	KOG1592	3.4.19.5,3.5.1	0	GO:0016787	AT4G00590.1
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR23076,P	KOG0737	0	0	GO:0006508,(	AT3G04340.1
PTHR14089,P	0	0	K12872	GO:0003676	AT1G07360.1
PTHR14089,P	0	0	K12872	GO:0003676	AT1G07360.1
PTHR14089,P	0	0	K12872	GO:0003676	AT1G07360.1
PTHR11709,P	0	1.10.3.2	K05909	GO:0055114,(	AT2G29130.1
PTHR11695,P	0	1.1.1.54,1.3.1	0	GO:0055114,(	AT1G65560.1
PTHR11695,P	0	1.1.1.54,1.3.1	0	GO:0055114,(	AT1G65560.1
PTHR32176	KOG0513	0	0	GO:0006629	AT2G26560.1
PTHR32176	KOG0513	0	0	GO:0006629	AT2G26560.1
PTHR31471,P	0	0	0	0	AT1G45207.2
PTHR31471,P	0	0	0	0	AT1G45207.2
PTHR31471,P	0	0	0	0	AT1G45207.2
PTHR31471,P	0	0	0	0	AT1G45207.2
PTHR31953,P	0	3.2.1.153,3.2.	K01193	0	AT3G13790.1
PTHR22166,P	KOG2846	0	0	0	AT4G31080.1
PTHR22166,P	KOG2846	0	0	0	AT4G31080.1
PTHR10457,P	KOG0631	2.7.1.46	K12446	GO:0005524	AT4G16130.1
PTHR10457,P	KOG0631	2.7.1.46	K12446	GO:0005524	AT4G16130.1
PTHR24095,P	0	6.2.1.1	K01895	GO:0008152,(	AT5G36880.2
PTHR24095,P	0	6.2.1.1	K01895	GO:0008152,(	AT5G36880.2
PTHR23326,P	KOG2150	0	K12580	GO:0006355,(	AT5G18230.1
PTHR23326,P	KOG2150	0	K12580	GO:0006355,(	AT5G18230.1
PTHR23326,P	KOG2150	0	K12580	GO:0006355,(	AT5G18230.1
PTHR23326,P	KOG2150	0	K12580	GO:0006355,(	AT5G18230.1
PTHR12196	KOG2316	6.3.1.14	K06927	0	AT3G04480.1
PTHR12196	KOG2316	6.3.1.14	K06927	0	AT3G04480.1

PTHR22762,P	0	3.2.1.20	0	GO:0005975,(	AT5G63840.1
PTHR22762,P	0	3.2.1.20	0	GO:0005975,(	AT5G63840.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1
PTHR31529,P	0	0	0	0	AT2G42430.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31314,P	0	0	0	0	AT4G28610.1
PTHR31268,P	0	2.4.1.67	K06611	0	AT4G01970.1
PTHR31268,P	0	2.4.1.67	K06611	0	AT4G01970.1
PTHR23115,P	0	3.6.5.3	K02519	GO:0005525	AT4G11160.1
PTHR23115,P	0	3.6.5.3	K02519	GO:0005525	AT4G11160.1
PTHR23115,P	0	3.6.5.3	K02519	GO:0005525	AT4G11160.1
PTHR23115,P	0	3.6.5.3	K02519	GO:0005525	AT4G11160.1
PTHR23083,P	0	0	0	0	AT4G37460.1
PTHR23083,P	0	0	0	0	AT4G37460.1
PTHR23083,P	0	0	0	0	AT4G37460.1
PTHR23083,P	0	0	0	0	AT4G37460.1
PTHR24015,P	0	0	0	0	AT3G22690.2
PTHR24015,P	0	0	0	0	AT3G22690.2
PTHR24015,P	0	0	0	0	AT3G22690.2
PTHR24015,P	0	0	0	0	AT3G22690.2
PTHR26374,P	0	0	0	0	AT3G60580.1
PTHR26374,P	0	0	0	0	AT3G60580.1
PTHR31867,P	0	0	0	0	AT1G12560.1
PTHR31867,P	0	0	0	0	AT1G12560.1
PTHR31867,P	0	0	0	0	AT1G12560.1
PTHR31867,P	0	0	0	0	AT1G12560.1
PTHR10366,P	0	1.1.1.133	K12451	0	AT1G63000.1
PTHR22835,P	0	3.1.1.3	0	GO:0016788	AT1G29670.1
PTHR22835,P	0	3.1.1.3	0	GO:0016788	AT1G29670.1
PTHR22835,P	0	3.1.1.3	0	GO:0016788	AT1G29670.1

PTHR22835,P	0	3.1.1.3	0	GO:0016788	AT1G29670.1
PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR22870,P	0	0	0	0	AT3G26100.2
PTHR23315,P	0	0	0	GO:0005515	AT2G22125.1
PTHR11514,P	0	0	0	GO:0046983	AT5G41315.1
PTHR11514,P	0	0	0	GO:0046983	AT5G41315.1
PTHR23315,P	0	0	0	GO:0043248	AT1G23180.1
PTHR23315,P	0	0	0	GO:0043248	AT1G23180.1
PTHR22762,P	0	3.2.1.177,3.2.	K15925	GO:0005975,(	AT1G68560.1
PTHR22762,P	0	3.2.1.177,3.2.	K15925	GO:0005975,(	AT1G68560.1
PTHR22762,P	0	3.2.1.177,3.2.	K15925	GO:0005975,(	AT1G68560.1
PTHR22762,P	0	3.2.1.177,3.2.	K15925	GO:0005975,(	AT1G68560.1
PTHR31642,P	0	2.3.1.99	0	GO:0016747	AT4G13840.1
PTHR31642,P	0	2.3.1.99	0	GO:0016747	AT4G13840.1
PTHR31642,P	0	2.3.1.99	0	GO:0016747	AT4G13840.1
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PTHR10774,P	KOG1032	0	0	GO:0005515	AT1G03370.1
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PTHR33624,P	0	0	0	0	AT3G56710.1
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arabi-symbol	arabi-defline	ID
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
0	Plant protein of unknown function (DUF936)	Phvul.002G07
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EX1	Protein of unknown function (DUF3506)	Phvul.006G20
0	Leucine carboxyl methyltransferase	Phvul.009G05
0	Leucine carboxyl methyltransferase	Phvul.009G05
0	Endomembrane protein 70 protein family	Phvul.009G08
0	ARM repeat superfamily protein	Phvul.010G11
0	ARM repeat superfamily protein	Phvul.010G11
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ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L00954
ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L00954
ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L00954
ATXDH1,XDH1	xanthine dehydrogenase 1	Phvul.L00954
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
AtGolS1,GolS1	galactinol synthase 1	Phvul.001G21
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
ATEME1B,EME1B	essential meiotic endonuclease 1B	Phvul.002G26
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GUT1	Exostosin family protein	Phvul.002G28
GUT1	Exostosin family protein	Phvul.002G28
GUT1	Exostosin family protein	Phvul.002G28
GUT1	Exostosin family protein	Phvul.002G28
0	disease resistance family protein / LRR family protein	Phvul.004G04
0	0	Phvul.006G15
0	LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
0	LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
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0	Protein of unknown function (DUF674)	Phvul.008G11
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ATGLR3.2,ATGLUR2,GLR3.2,	glutamate receptor 2	Phvul.001G02
ATBZIP9,BZIP9,BZO2H2	basic leucine zipper 9	Phvul.001G07
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ARA1,ATISA1,ISA1	arabinose kinase	Phvul.001G07
ARA1,ATISA1,ISA1	arabinose kinase	Phvul.001G07
ARP2,ATARP2,WRM	actin related protein 2	Phvul.001G08
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ANAC041,NAC041	NAC domain containing protein 41	Phvul.001G09
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ANAC041,NAC041	NAC domain containing protein 41	Phvul.001G09
ANAC041,NAC041	NAC domain containing protein 41	Phvul.001G09
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ABCA1,AtABCA1	ATP-binding cassette A1	Phvul.001G13

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

0	Protein kinase protein with adenine nucleotide alpha	Phvul.002G30
0	CW-type Zinc Finger	Phvul.003G10
0	CW-type Zinc Finger	Phvul.003G10
0	disease resistance family protein / LRR family protein	Phvul.004G04
emb1417	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.004G10
ATCLC-C,CLC-C	chloride channel C	Phvul.004G13
ATCLC-C,CLC-C	chloride channel C	Phvul.004G13
ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
ACHT2	atypical CYS HIS rich thioredoxin 2	Phvul.004G17
0	Wound-responsive family protein	Phvul.005G08
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	0	Phvul.005G18
0	0	Phvul.005G18
0	Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
0	Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
0	Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
0	Glutathione S-transferase, C-terminal-like;Translation	Phvul.006G01
ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
ATPDR3,PDR3	pleiotropic drug resistance 3	Phvul.006G06
0	Protein of Unknown Function (DUF239)	Phvul.006G10
0	Protein of Unknown Function (DUF239)	Phvul.006G10
0	Sec14p-like phosphatidylinositol transfer family prote	Phvul.006G13
0	Sec14p-like phosphatidylinositol transfer family prote	Phvul.006G13
0	alpha/beta-Hydrolases superfamily protein	Phvul.007G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.007G11
0	Pectin lyase-like superfamily protein	Phvul.007G21
0	Pectin lyase-like superfamily protein	Phvul.007G21
0	SAUR-like auxin-responsive protein family	Phvul.007G21
0	SAUR-like auxin-responsive protein family	Phvul.007G21
0	LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
0	LRR and NB-ARC domains-containing disease resistan	Phvul.008G07
0	0	0
0	0	0
0	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G11
0	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G11
0	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25

	0	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25
	0	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25
	0	NAD(P)-binding Rossmann-fold superfamily protein	Phvul.008G25
COX15		cytochrome c oxidase 15	Phvul.008G28
	0	Endomembrane protein 70 protein family	Phvul.008G28
ATFBP7,FBP7		F-box protein 7	Phvul.009G12
ATFBP7,FBP7		F-box protein 7	Phvul.009G12
ATFBP7,FBP7		F-box protein 7	Phvul.009G12
ATFBP7,FBP7		F-box protein 7	Phvul.009G12
GUT1		Exostosin family protein	Phvul.009G16
GUT1		Exostosin family protein	Phvul.009G16
GUT1		Exostosin family protein	Phvul.009G16
GUT1		Exostosin family protein	Phvul.009G16
	0	NB-ARC domain-containing disease resistance protei	Phvul.010G06
	0	NB-ARC domain-containing disease resistance protei	Phvul.010G06
	0	NB-ARC domain-containing disease resistance protei	Phvul.010G06
	0	NB-ARC domain-containing disease resistance protei	Phvul.010G06
GBF1		G-box binding factor 1	Phvul.011G04
GBF1		G-box binding factor 1	Phvul.011G04
TOR		target of rapamycin	Phvul.011G05
TOR		target of rapamycin	Phvul.011G05
TOR		target of rapamycin	Phvul.011G05
TOR		target of rapamycin	Phvul.011G05
ATLAC2,LAC2		laccase 2	Phvul.L00734
ATLAC2,LAC2		laccase 2	Phvul.L00734
	0	Remorin family protein	Phvul.001G02
	0	Remorin family protein	Phvul.001G02
ATBFRUCT1,ATCWINV1		Glycosyl hydrolases family 32 protein	Phvul.001G03
	0	RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.001G10
	0	RNA-binding (RRM/RBD/RNP motifs) family protein	Phvul.001G10
EDA4		Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
EDA4		Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
EDA4		Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
EDA4		Bifunctional inhibitor/lipid-transfer protein/seed stor	Phvul.001G15
	0	biotin/lipoyl attachment domain-containing protein	Phvul.001G24
AT-EXPR,ATEXLB1,ATEXPR1,		expansin-like B1	Phvul.002G00
SRFR1		Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1		Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
	0	Haloacid dehalogenase-like hydrolase (HAD) superfa	Phvul.002G21
	0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
	0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
PDF1,PP2AA2,PR 65		protein phosphatase 2A subunit A2	Phvul.003G02
PDF1,PP2AA2,PR 65		protein phosphatase 2A subunit A2	Phvul.003G02

0	Thiolase family protein	Phvul.003G08
0	Thiolase family protein	Phvul.003G08
0	Thiolase family protein	Phvul.003G08
0	Thiolase family protein	Phvul.003G08
0	Thiolase family protein	Phvul.003G08
0	Thiolase family protein	Phvul.003G08
0	Thiolase family protein	Phvul.003G08
0	Thiolase family protein	Phvul.003G08
0	Mitochondrial substrate carrier family protein	Phvul.003G10
0	Mitochondrial substrate carrier family protein	Phvul.003G10
0	Ypt/Rab-GAP domain of gyp1p superfamily protein	Phvul.003G14
0	Ypt/Rab-GAP domain of gyp1p superfamily protein	Phvul.003G14
TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
TOR2,TUA4	tubulin alpha-4 chain	Phvul.003G23
ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
0	FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
0	FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
0	FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
0	FBD, F-box and Leucine Rich Repeat domains containi	Phvul.004G01
0	0	0
0	disease resistance family protein / LRR family protein	Phvul.004G04
0	disease resistance family protein / LRR family protein	Phvul.004G04
0	ATP binding microtubule motor family protein	Phvul.004G16
HAM1	histone acetyltransferase of the MYST family 1	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
CYP72A8	cytochrome P450, family 72, subfamily A, polypeptid	Phvul.005G01
0	UDP-Glycosyltransferase superfamily protein	Phvul.005G08
0	UDP-Glycosyltransferase superfamily protein	Phvul.005G08
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09

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

0	RING/U-box superfamily protein	Phvul.008G10
0	RING/U-box superfamily protein	Phvul.008G10
0	RING/U-box superfamily protein	Phvul.008G10
0	Protein of unknown function (DUF674)	Phvul.008G11
0	Protein of unknown function (DUF674)	Phvul.008G11
0	Protein of unknown function (DUF674)	Phvul.008G11
0	Protein of unknown function (DUF674)	Phvul.008G11
0	Protein of unknown function (DUF674)	Phvul.008G11
0	Protein of unknown function (DUF674)	Phvul.008G11
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.008G19
UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
UGT71B6	UDP-glucosyl transferase 71B6	Phvul.008G29
ARF17	auxin response factor 17	Phvul.009G02
ARF17	auxin response factor 17	Phvul.009G02
0	vacuolar iron transporter (VIT) family protein	Phvul.009G04
0	vacuolar iron transporter (VIT) family protein	Phvul.009G04
0	vacuolar iron transporter (VIT) family protein	Phvul.009G04
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
ORP1C	OSBP(oxysterol binding protein)-related protein 1C	Phvul.009G12
0	Mitochondrial substrate carrier family protein	Phvul.009G24
0	Mitochondrial substrate carrier family protein	Phvul.009G24
0	Mitochondrial substrate carrier family protein	Phvul.009G24
0	Mitochondrial substrate carrier family protein	Phvul.009G24
0	Mitochondrial substrate carrier family protein	Phvul.009G24
0	Mitochondrial substrate carrier family protein	Phvul.009G24
0	Mitochondrial substrate carrier family protein	Phvul.009G24
0	Mitochondrial substrate carrier family protein	Phvul.009G24
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04

AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
AtGRF2,GRF2	growth-regulating factor 2	Phvul.010G04
0	ARM repeat superfamily protein	Phvul.010G11
0	ARM repeat superfamily protein	Phvul.010G11
0	ARM repeat superfamily protein	Phvul.010G11
0	ARM repeat superfamily protein	Phvul.010G11
0	Zinc finger (CCCH-type) family protein / RNA recognit	Phvul.011G01
0	Zinc finger (CCCH-type) family protein / RNA recognit	Phvul.011G01
0	Zinc finger (CCCH-type) family protein / RNA recognit	Phvul.011G01
0	Zinc finger (CCCH-type) family protein / RNA recognit	Phvul.011G01
LCR44	low-molecular-weight cysteine-rich 44	0
LCR44	low-molecular-weight cysteine-rich 44	0
LCR44	low-molecular-weight cysteine-rich 44	0
LCR44	low-molecular-weight cysteine-rich 44	0
0	N-terminal nucleophile aminohydrolases (Ntn hydrola	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrola	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrola	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrola	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrola	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrola	Phvul.011G16
ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
ATMSRB1,MSRB1	methionine sulfoxide reductase B 1	Phvul.011G17
SUVH1	SU(VAR)3-9 homolog 1	Phvul.011G19
SUVH1	SU(VAR)3-9 homolog 1	Phvul.011G19
0	0	Phvul.001G09
0	0	Phvul.001G09
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10

0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	ENTH/VHS family protein	Phvul.001G10
0	oxidoreductase, 2OG-Fe(II) oxygenase family protein	Phvul.001G14
0	Thioredoxin superfamily protein	Phvul.001G17
0	Thioredoxin superfamily protein	Phvul.001G17
0	Thioredoxin superfamily protein	Phvul.001G17
0	Thioredoxin superfamily protein	Phvul.001G17
0	phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
0	phosphoadenosine phosphosulfate (PAPS) reductase	Phvul.001G17
0	DNAse I-like superfamily protein	Phvul.001G20
0	DNAse I-like superfamily protein	Phvul.001G20
0	DNAse I-like superfamily protein	Phvul.001G20
0	DNAse I-like superfamily protein	Phvul.001G20
0	DNAse I-like superfamily protein	Phvul.001G20
0	DNAse I-like superfamily protein	Phvul.001G20
0	DNAse I-like superfamily protein	Phvul.001G20
0	DNAse I-like superfamily protein	Phvul.001G20
0	ARM repeat superfamily protein	Phvul.001G26
0	O-methyltransferase family protein	Phvul.001G26
0	O-methyltransferase family protein	Phvul.001G26
0	C2H2-like zinc finger protein	Phvul.002G05
0	C2H2-like zinc finger protein	Phvul.002G05
ATH2,ATTRX2,ATTRXH2,TRX	thioredoxin 2	Phvul.002G06
ATH2,ATTRX2,ATTRXH2,TRX	thioredoxin 2	Phvul.002G06
ATH2,ATTRX2,ATTRXH2,TRX	thioredoxin 2	Phvul.002G06
ATH2,ATTRX2,ATTRXH2,TRX	thioredoxin 2	Phvul.002G06
AtWRKY41,WRKY41	WRKY family transcription factor	Phvul.002G16
AtWRKY41,WRKY41	WRKY family transcription factor	Phvul.002G16
0	Galactose-binding protein	Phvul.002G16
0	Galactose-binding protein	Phvul.002G16
0	Galactose-binding protein	Phvul.002G16
0	Galactose-binding protein	Phvul.002G16
0	basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G21
0	basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G21
0	basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G21
0	basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G21
0	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
0	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24

0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
0	Nodulin MtN3 family protein	Phvul.002G28
0	Nodulin MtN3 family protein	Phvul.002G28
0	Nodulin MtN3 family protein	Phvul.002G28
0	Nodulin MtN3 family protein	Phvul.002G28
0	Peptidase M1 family protein	Phvul.002G29
0	Peptidase M1 family protein	Phvul.002G29
ABI1,AtABI1	Protein phosphatase 2C family protein	Phvul.002G30
ABI1,AtABI1	Protein phosphatase 2C family protein	Phvul.002G30
UFD1	ubiquitin fusion degradation 1	Phvul.002G32
UFD1	ubiquitin fusion degradation 1	Phvul.002G32
UFD1	ubiquitin fusion degradation 1	Phvul.002G32
UFD1	ubiquitin fusion degradation 1	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
ER-ANT1	endoplasmic reticulum-adenine nucleotide transport	Phvul.002G32
DME	HhH-GPD base excision DNA repair family protein	Phvul.003G03
DME	HhH-GPD base excision DNA repair family protein	Phvul.003G03
0	Nucleotide-diphospho-sugar transferases superfamily	Phvul.003G05
0	Nucleotide-diphospho-sugar transferases superfamily	Phvul.003G05
0	0	0
0	0	0
0	0	0
0	0	0
BGAL1	beta galactosidase 1	Phvul.003G13
BGAL1	beta galactosidase 1	Phvul.003G13
BGAL1	beta galactosidase 1	Phvul.003G13
BGAL1	beta galactosidase 1	Phvul.003G13
0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24

0	Disease resistance protein (CC-NBS-LRR class) family	Phvul.003G24
0	S-adenosyl-L-methionine-dependent methyltransfera	Phvul.003G28
0	S-adenosyl-L-methionine-dependent methyltransfera	Phvul.003G28
ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
ATRBP47A,RBP47A	RNA-binding protein 47A	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
ATRBP47B,RBP47B	RNA-binding protein 47B	Phvul.003G29
0	0	0
0	0	0
0	0	0
0	0	0
0	disease resistance family protein / LRR family protein	Phvul.004G04
0	disease resistance family protein / LRR family protein	Phvul.004G04
0	Eukaryotic aspartyl protease family protein	Phvul.004G05
0	Eukaryotic aspartyl protease family protein	Phvul.004G05
0	Eukaryotic aspartyl protease family protein	Phvul.004G05
0	Eukaryotic aspartyl protease family protein	Phvul.004G05
AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
AGP20,AtAGP20	arabinogalactan protein 20	Phvul.004G17
AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
AKR2B	ankyrin repeat-containing 2B	Phvul.005G00
NF-YC11	nuclear factor Y, subunit C11	Phvul.005G01
0	BTB/POZ domain-containing protein	Phvul.005G05
ATPPC2,PPC2	phosphoenolpyruvate carboxylase 2	Phvul.005G09
0	MuDR family transposase	Phvul.005G10
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11

0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	alpha/beta-Hydrolases superfamily protein	Phvul.005G11
0	C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
0	C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
0	Calcium-binding EF-hand family protein	Phvul.006G10
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	zinc knuckle (CCHC-type) family protein	Phvul.006G11
0	HCO3- transporter family	Phvul.006G12
0	HCO3- transporter family	Phvul.006G12
0	HCO3- transporter family	Phvul.006G12
0	HCO3- transporter family	Phvul.006G12
0	HCO3- transporter family	Phvul.006G12
0	HCO3- transporter family	Phvul.006G12
0	HCO3- transporter family	Phvul.006G12
0	HCO3- transporter family	Phvul.006G12
0	0	Phvul.006G15
SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
SCPL19,SNG2	serine carboxypeptidase-like 19	Phvul.006G16
0	phosphoinositide binding	Phvul.006G19
0	phosphoinositide binding	Phvul.006G19
0	Prolyl oligopeptidase family protein	Phvul.007G01
0	Prolyl oligopeptidase family protein	Phvul.007G01
0	Prolyl oligopeptidase family protein	Phvul.007G01
0	Prolyl oligopeptidase family protein	Phvul.007G01
0	TCP family transcription factor	Phvul.007G01
0	TCP family transcription factor	Phvul.007G01
0	phosphatidyl serine synthase family protein	Phvul.007G03
CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
CRK25	cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.007G05
AO1,ATAO1	amine oxidase 1	Phvul.007G05
AO1,ATAO1	amine oxidase 1	Phvul.007G05
AO1,ATAO1	amine oxidase 1	Phvul.007G05
AO1,ATAO1	amine oxidase 1	Phvul.007G05

	0	Protein of unknown function (DUF581)		Phvul.007G05
	0	Protein of unknown function (DUF581)		Phvul.007G05
	0	Protein of unknown function (DUF581)		Phvul.007G05
	0	Protein of unknown function (DUF581)		Phvul.007G05
	0	Protein of unknown function (DUF581)		Phvul.007G05
	0	Protein of unknown function (DUF581)		Phvul.007G05
	0	Protein of unknown function (DUF581)		Phvul.007G05
	0	Protein of unknown function (DUF581)		Phvul.007G05
AtCXE20,CXE20		carboxyesterase 20		Phvul.007G06
AtCXE20,CXE20		carboxyesterase 20		Phvul.007G06
AtCXE20,CXE20		carboxyesterase 20		Phvul.007G06
AtCXE20,CXE20		carboxyesterase 20		Phvul.007G06
AtCXE20,CXE20		carboxyesterase 20		Phvul.007G06
ATFRO2,FRD1,FRO2		ferric reduction oxidase 2		Phvul.007G07
ATFRO2,FRD1,FRO2		ferric reduction oxidase 2		Phvul.007G07
ATFRO2,FRD1,FRO2		ferric reduction oxidase 2		Phvul.007G07
ATFRO2,FRD1,FRO2		ferric reduction oxidase 2		Phvul.007G07
	0		0	Phvul.007G09
	0		0	Phvul.007G09
	0		0	Phvul.007G09
	0		0	Phvul.007G09
ATGST11,ATGSTF7,ATGSTF8		glutathione S-transferase 7		Phvul.007G10
ATGST11,ATGSTF7,ATGSTF8		glutathione S-transferase 7		Phvul.007G10
ATGST11,ATGSTF7,ATGSTF8		glutathione S-transferase 7		Phvul.007G10
ATGST11,ATGSTF7,ATGSTF8		glutathione S-transferase 7		Phvul.007G10
	0	Mog1/PsbP/DUF1795-like photosystem II reaction ce		Phvul.007G18
	0	Mog1/PsbP/DUF1795-like photosystem II reaction ce		Phvul.007G18
	0	Mog1/PsbP/DUF1795-like photosystem II reaction ce		Phvul.007G18
	0	Mog1/PsbP/DUF1795-like photosystem II reaction ce		Phvul.007G18
	0		0	0
	0		0	0
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Protein kinase superfamily protein		Phvul.007G20
	0	Plant invertase/pectin methylesterase inhibitor super		Phvul.007G21
	0		0	Phvul.007G27
	0		0	Phvul.007G27
	0		0	Phvul.007G27

	0		0	Phvul.007G27
	0		0	Phvul.007G27
	0		0	Phvul.007G27
NEF1		no exine formation 1		Phvul.008G00
NEF1		no exine formation 1		Phvul.008G00
NEF1		no exine formation 1		Phvul.008G00
NEF1		no exine formation 1		Phvul.008G00
	0	HEAT repeat-containing protein		Phvul.008G00
	0	HEAT repeat-containing protein		Phvul.008G00
	0	HEAT repeat-containing protein		Phvul.008G00
	0	HEAT repeat-containing protein		Phvul.008G00
	0	HEAT repeat-containing protein		Phvul.008G00
ATTAF6,TAF6,TAFII59		TATA BOX ASSOCIATED FACTOR II 59		Phvul.008G01
ATTAF6,TAF6,TAFII59		TATA BOX ASSOCIATED FACTOR II 59		Phvul.008G01
	0	Mitochondrial transcription termination factor family		Phvul.008G04
	0		0	0
	0		0	0
	0		0	0
	0		0	0
	0	LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
	0	LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
	0	LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
	0	LRR and NB-ARC domains-containing disease resistan		Phvul.008G07
	0	Leucine-rich repeat protein kinase family protein		Phvul.008G09
	0	Leucine-rich repeat protein kinase family protein		Phvul.008G09
	0	Leucine-rich repeat protein kinase family protein		Phvul.008G09
	0	Leucine-rich repeat protein kinase family protein		Phvul.008G09
	0	Leucine-rich repeat protein kinase family protein		Phvul.008G09
	0	Leucine-rich repeat protein kinase family protein		Phvul.008G09
	0	Protein of unknown function (DUF674)		Phvul.008G11
	0	Protein of unknown function (DUF674)		Phvul.008G11
	0	Protein of unknown function (DUF674)		Phvul.008G11
	0	Protein of unknown function (DUF674)		Phvul.008G11
	0	Protein of unknown function (DUF674)		Phvul.008G11
ATASP38,EMB24,PCS1		Eukaryotic aspartyl protease family protein		Phvul.008G11
ATASP38,EMB24,PCS1		Eukaryotic aspartyl protease family protein		Phvul.008G11
	0		0	0
	0		0	0
	0		0	0
	0		0	0
	0	Thioesterase superfamily protein		Phvul.008G20
	0	Thioesterase superfamily protein		Phvul.008G20
	0	Thioesterase superfamily protein		Phvul.008G20

	0	Thioesterase superfamily protein		Phvul.008G20
	0		0	0
	0		0	0
	0		0	0
	0		0	0
ATPROT1,PROT1		proline transporter 1		Phvul.008G22
ATPROT1,PROT1		proline transporter 1		Phvul.008G22
ATPROT1,PROT1		proline transporter 1		Phvul.008G22
ATPROT1,PROT1		proline transporter 1		Phvul.008G22
	0	RNA-binding (RRM/RBD/RNP motifs) family protein		Phvul.008G27
	0	RNA-binding (RRM/RBD/RNP motifs) family protein		Phvul.008G27
	0	RNA-binding (RRM/RBD/RNP motifs) family protein		Phvul.008G27
COX15		cytochrome c oxidase 15		Phvul.008G28
COX15		cytochrome c oxidase 15		Phvul.008G28
ATMYB3R-1,ATMYB3R1,MY		Homeodomain-like protein		Phvul.009G10
ORP1C		OSBP(oxysterol binding protein)-related protein 1C		Phvul.009G12
ORP1C		OSBP(oxysterol binding protein)-related protein 1C		Phvul.009G12
ORP1C		OSBP(oxysterol binding protein)-related protein 1C		Phvul.009G12
ORP1C		OSBP(oxysterol binding protein)-related protein 1C		Phvul.009G12
WNK3		with no lysine (K) kinase 3		Phvul.009G17
WNK3		with no lysine (K) kinase 3		Phvul.009G17
WNK3		with no lysine (K) kinase 3		Phvul.009G17
WNK3		with no lysine (K) kinase 3		Phvul.009G17
BGAL12		beta-galactosidase 12		Phvul.009G23
BGAL12		beta-galactosidase 12		Phvul.009G23
ATOMT1,OMT1		O-methyltransferase 1		Phvul.009G25
ATOMT1,OMT1		O-methyltransferase 1		Phvul.009G25
ATOMT1,OMT1		O-methyltransferase 1		Phvul.009G25
ATOMT1,OMT1		O-methyltransferase 1		Phvul.009G25
	0	DNA binding;ATP binding		Phvul.010G03
	0	DNA binding;ATP binding		Phvul.010G03
	0	DNA binding;ATP binding		Phvul.010G03
	0	DNA binding;ATP binding		Phvul.010G03
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04
CUM2,EIF4G		eukaryotic translation initiation factor 4G		Phvul.010G04

CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
CUM2,EIF4G	eukaryotic translation initiation factor 4G	Phvul.010G04
UNE10	basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.010G07
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
ATLOX1,LOX1	lipoxygenase 1	Phvul.010G13
ACA11	autoinhibited Ca2+-ATPase 11	Phvul.011G01
ACA11	autoinhibited Ca2+-ATPase 11	Phvul.011G01
ACA11	autoinhibited Ca2+-ATPase 11	Phvul.011G01
ACA11	autoinhibited Ca2+-ATPase 11	Phvul.011G01
TOR	target of rapamycin	Phvul.011G05
TOR	target of rapamycin	Phvul.011G05
TOR	target of rapamycin	Phvul.011G05
TOR	target of rapamycin	Phvul.011G05
PTAC16	plastid transcriptionally active 16	Phvul.011G06
PTAC16	plastid transcriptionally active 16	Phvul.011G06
0	Plant self-incompatibility protein S1 family	Phvul.011G11
0	Plant self-incompatibility protein S1 family	Phvul.011G12
LCR44	low-molecular-weight cysteine-rich 44	0
LCR44	low-molecular-weight cysteine-rich 44	0
0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16

	0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
	0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
	0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
	0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
	0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
	0	N-terminal nucleophile aminohydrolases (Ntn hydrol	Phvul.011G16
	0	0	0
	0	0	0
	0	0	0
	0	0	0
emb2458		FtsH extracellular protease family	Phvul.L00205
emb2458		FtsH extracellular protease family	Phvul.L00205
emb2458		FtsH extracellular protease family	Phvul.L00205
emb2458		FtsH extracellular protease family	Phvul.L00205
emb2458		FtsH extracellular protease family	Phvul.L00205
emb2458		FtsH extracellular protease family	Phvul.L00205
emb2458		FtsH extracellular protease family	Phvul.L00205
emb2458		FtsH extracellular protease family	Phvul.L00205
	0	CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L00253
	0	CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L00253
	0	CCCH-type zinc fingerfamily protein with RNA-binding	Phvul.L00253
ATLAC2,LAC2		laccase 2	Phvul.L00734
	0	Zinc-binding dehydrogenase family protein	Phvul.008G00
	0	Zinc-binding dehydrogenase family protein	Phvul.008G00
PLA IIA,PLA2A,PLP2		phospholipase A 2A	Phvul.001G02
PLA IIA,PLA2A,PLP2		phospholipase A 2A	Phvul.001G02
	0	Remorin family protein	Phvul.001G02
	0	Remorin family protein	Phvul.001G02
	0	Remorin family protein	Phvul.001G02
	0	Remorin family protein	Phvul.001G02
ATBFRUCT1,ATCWINV1		Glycosyl hydrolases family 32 protein	Phvul.001G03
	0	Protein of unknown function (DUF2296)	Phvul.001G05
	0	Protein of unknown function (DUF2296)	Phvul.001G05
ARA1,ATISA1,ISA1		arabinose kinase	Phvul.001G07
ARA1,ATISA1,ISA1		arabinose kinase	Phvul.001G07
ACS		acetyl-CoA synthetase	Phvul.001G09
ACS		acetyl-CoA synthetase	Phvul.001G09
	0	transcription regulator NOT2/NOT3/NOT5 family pro	Phvul.001G10
	0	transcription regulator NOT2/NOT3/NOT5 family pro	Phvul.001G10
	0	transcription regulator NOT2/NOT3/NOT5 family pro	Phvul.001G10
	0	transcription regulator NOT2/NOT3/NOT5 family pro	Phvul.001G10
	0	endoribonucleases	Phvul.001G11
	0	endoribonucleases	Phvul.001G11

PSL5,RSW3	Glycosyl hydrolases family 31 protein	Phvul.001G12
PSL5,RSW3	Glycosyl hydrolases family 31 protein	Phvul.001G12
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
0	NB-ARC domain-containing disease resistance proteir	Phvul.001G13
ASL18,LBD16	lateral organ boundaries-domain 16	Phvul.001G15
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtPHR1,PHR1	phosphate starvation response 1	Phvul.001G16
AtSTS,STS	stachyose synthase	Phvul.001G21
AtSTS,STS	stachyose synthase	Phvul.001G21
0	Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
0	Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
0	Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
0	Translation initiation factor 2, small GTP-binding prot	Phvul.001G22
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
SRFR1	Tetratricopeptide repeat (TPR)-like superfamily prote	Phvul.002G01
0	0	Phvul.002G04
0	0	Phvul.002G04
0	0	Phvul.002G04
0	0	Phvul.002G04
0	C2H2-like zinc finger protein	Phvul.002G05
0	C2H2-like zinc finger protein	Phvul.002G05
ATEXP7,ATEXPA7,ATHEXP A	expansin A7	Phvul.002G15
ATEXP7,ATEXPA7,ATHEXP A	expansin A7	Phvul.002G15
ATEXP7,ATEXPA7,ATHEXP A	expansin A7	Phvul.002G15
ATEXP7,ATEXPA7,ATHEXP A	expansin A7	Phvul.002G15
NRS/ER,UER1	nucleotide-rhamnose synthase/epimerase-reductase	Phvul.002G15
0	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
0	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
0	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24

	0	GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.002G24
	0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
	0	Regulator of chromosome condensation (RCC1) famil	Phvul.002G25
CSI1		binding	Phvul.002G26
GL3,MYC6.2		basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G29
GL3,MYC6.2		basic helix-loop-helix (bHLH) DNA-binding superfamil	Phvul.002G29
	0	ARM repeat superfamily protein	Phvul.003G02
	0	ARM repeat superfamily protein	Phvul.003G02
ATXYL1,TRG1,XYL1		alpha-xylosidase 1	Phvul.003G03
ATXYL1,TRG1,XYL1		alpha-xylosidase 1	Phvul.003G03
ATXYL1,TRG1,XYL1		alpha-xylosidase 1	Phvul.003G03
ATXYL1,TRG1,XYL1		alpha-xylosidase 1	Phvul.003G03
	0	HXXXD-type acyl-transferase family protein	Phvul.003G05
	0	HXXXD-type acyl-transferase family protein	Phvul.003G05
	0	HXXXD-type acyl-transferase family protein	Phvul.003G05
	0	HXXXD-type acyl-transferase family protein	Phvul.003G05
	0	C2 calcium/lipid-binding and GRAM domain containin	Phvul.003G08
	0	C2 calcium/lipid-binding and GRAM domain containin	Phvul.003G08
	0	Mitochondrial substrate carrier family protein	Phvul.003G10
	0	Mitochondrial substrate carrier family protein	Phvul.003G10
	0	Mitochondrial substrate carrier family protein	Phvul.003G10
	0	Mitochondrial substrate carrier family protein	Phvul.003G10
	0	calcium-dependent lipid-binding family protein	Phvul.003G11
	0	calcium-dependent lipid-binding family protein	Phvul.003G11
	0	calcium-dependent lipid-binding family protein	Phvul.003G11
XGD1		xylogalacturonan deficient 1	Phvul.003G16
ATFUT11,FUCT1,FUCTA,FUT		fucosyltransferase 11	Phvul.003G29
	0	PQ-loop repeat family protein / transmembrane fami	Phvul.004G05
	0	ATP synthase subunit beta	Phvul.004G12
	0	ATP synthase subunit beta	Phvul.004G12
	0	ATP synthase subunit beta	Phvul.004G12
	0	ATP synthase subunit beta	Phvul.004G12
	0	SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
	0	SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
	0	SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
	0	SWIB/MDM2 domain;Plus-3;GYF	Phvul.004G13
ACHT2		atypical CYS HIS rich thioredoxin 2	Phvul.004G17
ACHT2		atypical CYS HIS rich thioredoxin 2	Phvul.004G17
	0	BTB/POZ domain-containing protein	Phvul.005G05
	0	BTB/POZ domain-containing protein	Phvul.005G05
ARK3,RK3		receptor kinase 3	Phvul.005G08
ATFMN/FHY,FMN/FHY		riboflavin kinase/FMN hydrolase	Phvul.005G09
MEE35,TCP4		TCP family transcription factor 4	Phvul.005G09

MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
MEE35,TCP4	TCP family transcription factor 4	Phvul.005G09
ALA2	aminophospholipid ATPase 2	Phvul.005G10
ALA2	aminophospholipid ATPase 2	Phvul.005G10
ALA2	aminophospholipid ATPase 2	Phvul.005G10
ALA2	aminophospholipid ATPase 2	Phvul.005G10
ALA2	aminophospholipid ATPase 2	Phvul.005G10
ALA2	aminophospholipid ATPase 2	Phvul.005G10
0	C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
0	C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
0	C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
0	C2H2 and C2HC zinc fingers superfamily protein	Phvul.005G13
0	P-loop containing nucleoside triphosphate hydrolases	Phvul.005G17
0	P-loop containing nucleoside triphosphate hydrolases	Phvul.005G17
0	P-loop containing nucleoside triphosphate hydrolases	Phvul.005G17
0	P-loop containing nucleoside triphosphate hydrolases	Phvul.005G17
0	0	0
0	0	0
0	0	0
0	0	0
scpl2	serine carboxypeptidase-like 2	Phvul.006G16
scpl2	serine carboxypeptidase-like 2	Phvul.006G16
ATQSOX1,QSO2,QSOX1	quiescin-sulfhydryl oxidase 1	Phvul.007G03
ATQSOX1,QSO2,QSOX1	quiescin-sulfhydryl oxidase 1	Phvul.007G03
ATQSOX1,QSO2,QSOX1	quiescin-sulfhydryl oxidase 1	Phvul.007G03
ATQSOX1,QSO2,QSOX1	quiescin-sulfhydryl oxidase 1	Phvul.007G03
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06

	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G06
	0	0	Phvul.007G09
	0	RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
	0	RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
	0	RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
	0	RING/FYVE/PHD zinc finger superfamily protein	Phvul.007G11
ATEDR1,EDR1		Protein kinase superfamily protein	Phvul.007G18
ATEDR1,EDR1		Protein kinase superfamily protein	Phvul.007G18
	0	ARM repeat superfamily protein	Phvul.007G19
	0	Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
	0	Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
	0	Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
	0	Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
	0	Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
	0	Plant invertase/pectin methylesterase inhibitor super	Phvul.007G21
	0	transcription coactivators	Phvul.007G21
	0	transcription coactivators	Phvul.007G21
	0	transcription coactivators	Phvul.007G21
	0	transcription coactivators	Phvul.007G21
NTRC		NADPH-dependent thioredoxin reductase C	Phvul.007G25
AtRLP7,RLP7		receptor like protein 7	Phvul.008G04
AtRLP7,RLP7		receptor like protein 7	Phvul.008G04
AtMYB17,MYB17		myb domain protein 17	Phvul.008G06
AtMYB17,MYB17		myb domain protein 17	Phvul.008G06
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11
	0	Protein of unknown function (DUF674)	Phvul.008G11

LUH	LEUNIG_homolog	Phvul.008G12
LUH	LEUNIG_homolog	Phvul.008G12
LUH	LEUNIG_homolog	Phvul.008G12
LUH	LEUNIG_homolog	Phvul.008G12
0	Subtilisin-like serine endopeptidase family protein	Phvul.008G22
ATCSLE1,CSLE1	cellulose synthase like E1	Phvul.008G27
ATCSLE1,CSLE1	cellulose synthase like E1	Phvul.008G27
0	Zn-dependent exopeptidases superfamily protein	Phvul.009G01
0	Zn-dependent exopeptidases superfamily protein	Phvul.009G01
0	Target SNARE coiled-coil domain protein	Phvul.009G03
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
ATCKX5,ATCKX6,CKX5	cytokinin oxidase 5	Phvul.009G06
TMT2	tonoplast monosaccharide transporter2	Phvul.009G11
TMT2	tonoplast monosaccharide transporter2	Phvul.009G11
0	transferases, transferring glycosyl groups	0
0	transferases, transferring glycosyl groups	0
0	transferases, transferring glycosyl groups	0
0	transferases, transferring glycosyl groups	0
COB	COBRA-like extracellular glycosyl-phosphatidyl inosit	Phvul.009G20
BGAL12	beta-galactosidase 12	Phvul.009G23
BGAL12	beta-galactosidase 12	Phvul.009G23
BGAL12	beta-galactosidase 12	Phvul.009G23
BGAL12	beta-galactosidase 12	Phvul.009G23
ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase s	Phvul.009G25
ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase s	Phvul.009G25
ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase s	Phvul.009G25
ATOEP16-2,ATOEP16-S	Mitochondrial import inner membrane translocase s	Phvul.009G25
0	0	0
0	0	0
0	0	0
0	0	0
0	Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
0	Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
0	Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
0	Disease resistance protein (TIR-NBS-LRR class) family	Phvul.010G02
ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06
ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06

ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06
ATWNK5,WNK5,ZIK1	with no lysine (K) kinase 5	Phvul.010G06
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
ATPEX16,PEX16,SSE,SSE1	shrunken seed protein (SSE1)	Phvul.010G08
OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
OLD5,QS,SUFE3	quinolinate synthase	Phvul.010G09
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
ATSAC1	Phosphoinositide phosphatase family protein	Phvul.011G00
0	0	Phvul.011G00
SIB1	sigma factor binding protein 1	Phvul.011G20
SIB1	sigma factor binding protein 1	Phvul.011G20
SIB1	sigma factor binding protein 1	Phvul.011G20
SIB1	sigma factor binding protein 1	Phvul.011G20
0	C2 calcium/lipid-binding and GRAM domain containin	Phvul.L00167
0	C2 calcium/lipid-binding and GRAM domain containin	Phvul.L00167
0	CCCH-type zinc fingerfamily protein with RNA-bindin	Phvul.L00253
0	CCCH-type zinc fingerfamily protein with RNA-bindin	Phvul.L00253
AAC2	ADP/ATP carrier 2	Phvul.L00984
AAC2	ADP/ATP carrier 2	Phvul.L00984
AAC2	ADP/ATP carrier 2	Phvul.L00984
AAC2	ADP/ATP carrier 2	Phvul.L00984

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

PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR12663:SI	Phvul.008G16	Cell cycle orga	cohesin cofactor (PDS5) (original description: pacid=371
PTHR13600:SI	Phvul.009G05	not assigned.n	no hits & (original description: pacid=37148617 transcri
PTHR13600:SI	Phvul.009G05	not assigned.n	no hits & (original description: pacid=37148617 transcri
PTHR13600:SI	Phvul.009G05	not assigned.n	no hits & (original description: pacid=37148617 transcri
PTHR13600:SI	Phvul.009G05	not assigned.n	no hits & (original description: pacid=37148617 transcri
0	Phvul.010G05	not assigned.n	no hits & (original description: pacid=37142098 transcri
0	Phvul.010G05	not assigned.n	no hits & (original description: pacid=37142098 transcri
PF01094 - Rec	Phvul.001G02	Solute transpo	ligand-gated cation channel (GLR) (original description: p
PF01094 - Rec	Phvul.001G02	Solute transpo	ligand-gated cation channel (GLR) (original description: p
PTHR22952//I	Phvul.001G07	RNA biosynth	transcription factor (bZIP9/10/25) (original description: p
PTHR22952//I	Phvul.001G07	RNA biosynth	transcription factor (bZIP9/10/25) (original description: p
K12446 - L-ara	Phvul.001G07	Carbohydrate	L-arabinose kinase (original description: pacid=3716845
K12446 - L-ara	Phvul.001G07	Carbohydrate	L-arabinose kinase (original description: pacid=3716845
PTHR11937:SI	Phvul.001G08	not assigned.a	(original description: pacid=37168999 transcript=Phvul.0
PTHR11937:SI	Phvul.001G08	not assigned.a	(original description: pacid=37168999 transcript=Phvul.0
PTHR11937:SI	Phvul.001G08	not assigned.a	(original description: pacid=37168999 transcript=Phvul.0
PTHR11937:SI	Phvul.001G08	not assigned.a	(original description: pacid=37168999 transcript=Phvul.0
K17260 - actir	Phvul.001G08	not assigned.a	(original description: pacid=37170199 transcript=Phvul.0
K17260 - actir	Phvul.001G08	not assigned.a	(original description: pacid=37170199 transcript=Phvul.0
K17260 - actir	Phvul.001G08	not assigned.a	(original description: pacid=37170199 transcript=Phvul.0
K17260 - actir	Phvul.001G08	not assigned.a	(original description: pacid=37170199 transcript=Phvul.0
PTHR31719:SI	Phvul.001G09	RNA biosynth	transcription factor (NAC) (original description: pacid=37
PTHR31719:SI	Phvul.001G09	RNA biosynth	transcription factor (NAC) (original description: pacid=37
PTHR31719:SI	Phvul.001G09	RNA biosynth	transcription factor (NAC) (original description: pacid=37
PTHR31719:SI	Phvul.001G09	RNA biosynth	transcription factor (NAC) (original description: pacid=37
PTHR10277//I	Phvul.001G12	Amino acid m	hydroxymethylglutaryl-CoA lyase (original description: pa
PTHR10277//I	Phvul.001G12	Amino acid m	hydroxymethylglutaryl-CoA lyase (original description: pa
K05643 - ATP-	Phvul.001G13	Solute transpo	subfamily ABCA transporter (original description: pacid=

K05643 - ATP-	Phvul.001G13	Solute transp	subfamily ABCA transporter (original description: pacid=
K05643 - ATP-	Phvul.001G13	Solute transp	subfamily ABCA transporter (original description: pacid=
K05643 - ATP-	Phvul.001G13	Solute transp	subfamily ABCA transporter (original description: pacid=
K05643 - ATP-	Phvul.001G13	Solute transp	subfamily ABCA transporter (original description: pacid=
K05643 - ATP-	Phvul.001G13	Solute transp	subfamily ABCA transporter (original description: pacid=
K05643 - ATP-	Phvul.001G13	Solute transp	subfamily ABCA transporter (original description: pacid=
K05643 - ATP-	Phvul.001G13	Solute transp	subfamily ABCA transporter (original description: pacid=
PF03110 - SB	Phvul.001G14	RNA biosynth	transcription factor (SBP) (original description: pacid=37
PF03110 - SB	Phvul.001G14	RNA biosynth	transcription factor (SBP) (original description: pacid=37
PF03110 - SB	Phvul.001G14	RNA biosynth	transcription factor (SBP) (original description: pacid=37
PF03110 - SB	Phvul.001G14	RNA biosynth	transcription factor (SBP) (original description: pacid=37
2.7.7.2 - FAD	Phvul.001G17	not assigned.	no hits & (original description: pacid=37168919 transcri
2.7.7.2 - FAD	Phvul.001G17	not assigned.	no hits & (original description: pacid=37168919 transcri
2.7.7.2 - FAD	Phvul.001G17	not assigned.	no hits & (original description: pacid=37168919 transcri
2.7.7.2 - FAD	Phvul.001G17	not assigned.	no hits & (original description: pacid=37168919 transcri
2.7.7.2 - FAD	Phvul.001G17	not assigned.	no hits & (original description: pacid=37168919 transcri
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PF03126 - Plu	Phvul.002G04	Multi-process	TZP circadian clock repression factor (original descriptio
PTHR10438:S	Phvul.002G06	Redox homeo	H-type thioredoxin (original description: pacid=3717719
PTHR10438:S	Phvul.002G06	Redox homeo	H-type thioredoxin (original description: pacid=3717719
PF06075 - Pla	Phvul.002G07	Cytoskeleton	regulatory protein (CORD) of cortical microtubule organi
PF06075 - Pla	Phvul.002G07	Cytoskeleton	regulatory protein (CORD) of cortical microtubule organi
3.4.24.23 - M	Phvul.002G07	Protein home	Matrixin-type metalloprotease (original description: paci
3.4.24.23 - M	Phvul.002G07	Protein home	Matrixin-type metalloprotease (original description: paci
3.4.24.23 - M	Phvul.002G07	Protein home	Matrixin-type metalloprotease (original description: paci
3.4.24.23 - M	Phvul.002G07	Protein home	Matrixin-type metalloprotease (original description: paci
PTHR10110:S	Phvul.002G18	External stim	sodium:proton antiporter (SOS1) (original description: p
PTHR10110:S	Phvul.002G18	External stim	sodium:proton antiporter (SOS1) (original description: p
PTHR10110:S	Phvul.002G18	External stim	sodium:proton antiporter (SOS1) (original description: p

2.7.11.1 - Non	Phvul.002G30	Protein modif	protein kinase (PERK-related) (original description: pacid
PTHR23336:SI	Phvul.003G10	not assigned.r	no hits & (original description: pacid=37147291 transcri
PTHR23336:SI	Phvul.003G10	not assigned.r	no hits & (original description: pacid=37147291 transcri
PF00560//PFC	Phvul.004G04	not assigned.a	(original description: pacid=37161823 transcript=Phvul.(
PF01535 - PPF	Phvul.004G10	not assigned.a	(original description: pacid=37161859 transcript=Phvul.(
PTHR11689:SI	Phvul.004G13	Solute transpc	anion channel / anion:proton antiporter (CLC) (original d
PTHR11689:SI	Phvul.004G13	Solute transpc	anion channel / anion:proton antiporter (CLC) (original d
PTHR10438:SI	Phvul.004G17	Redox homeo	atypical thioredoxin (ACHT) (original description: pacid=3
PTHR10438:SI	Phvul.004G17	Redox homeo	atypical thioredoxin (ACHT) (original description: pacid=3
PTHR10438:SI	Phvul.004G17	Redox homeo	atypical thioredoxin (ACHT) (original description: pacid=3
PTHR10438:SI	Phvul.004G17	Redox homeo	atypical thioredoxin (ACHT) (original description: pacid=3
PF12609 - Wo	Phvul.005G08	not assigned.r	no hits & (original description: pacid=37154279 transcri
K01061 - carb	Phvul.005G11	not assigned.r	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.r	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.r	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.r	no hits & (original description: pacid=37152909 transcri
K14972 - PAX-	Phvul.005G18	RNA biosynth	component MED15 of tail module of MEDIATOR transcri
K14972 - PAX-	Phvul.005G18	RNA biosynth	component MED15 of tail module of MEDIATOR transcri
PTHR11595:SI	Phvul.006G01	Protein biosyr	component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
PTHR11595:SI	Phvul.006G01	Protein biosyr	component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
PTHR11595:SI	Phvul.006G01	Protein biosyr	component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
PTHR11595:SI	Phvul.006G01	Protein biosyr	component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recy
PTHR19241:SI	Phvul.006G06	Solute transpc	subfamily ABCG transporter (original description: pacid=
PTHR19241:SI	Phvul.006G06	Solute transpc	subfamily ABCG transporter (original description: pacid=
PTHR19241:SI	Phvul.006G06	Solute transpc	subfamily ABCG transporter (original description: pacid=
PTHR19241:SI	Phvul.006G06	Solute transpc	subfamily ABCG transporter (original description: pacid=
PF14365 - Dor	Phvul.006G10	not assigned.r	no hits & (original description: pacid=37172094 transcri
PF14365 - Dor	Phvul.006G10	not assigned.r	no hits & (original description: pacid=37172094 transcri
PTHR23324//I	Phvul.006G13	not assigned.r	no hits & (original description: pacid=37171658 transcri
PTHR23324//I	Phvul.006G13	not assigned.r	no hits & (original description: pacid=37171658 transcri
PTHR10992:SI	Phvul.007G11	Coenzyme me	chlorophyll dephytylase (CLD) (original description: pacic
PTHR10992:SI	Phvul.007G11	Coenzyme me	chlorophyll dephytylase (CLD) (original description: pacic
PTHR31375:SI	Phvul.007G21	Enzyme classi	Polygalacturonase At1g48100 OS=Arabidopsis thaliana (
PTHR31375:SI	Phvul.007G21	Enzyme classi	Polygalacturonase At1g48100 OS=Arabidopsis thaliana (
K14488 - SAU	Phvul.007G21	not assigned.r	no hits & (original description: pacid=37166206 transcri
K14488 - SAU	Phvul.007G21	not assigned.r	no hits & (original description: pacid=37166206 transcri
KOG1947 - Le	Phvul.008G07	not assigned.r	no hits & (original description: pacid=37157631 transcri
KOG1947 - Le	Phvul.008G07	not assigned.r	no hits & (original description: pacid=37157631 transcri
0	Phvul.008G10	not assigned.r	no hits & (original description: pacid=37160112 transcri
0	Phvul.008G10	not assigned.r	no hits & (original description: pacid=37160112 transcri
K08081 - Trop	Phvul.008G11	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxid
K08081 - Trop	Phvul.008G11	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxid
PTHR10366:SI	Phvul.008G25	not assigned.a	(original description: pacid=37158298 transcript=Phvul.(

PTHR10366:SI	Phvul.008G25	not assigned.a	(original description: pacid=37158298 transcript=Phvul.
PTHR10366:SI	Phvul.008G25	not assigned.a	(original description: pacid=37158298 transcript=Phvul.
PTHR10366:SI	Phvul.008G25	not assigned.a	(original description: pacid=37158298 transcript=Phvul.
K02259 - cyto	Phvul.008G28	Cellular respir	component COX15 of cytochrome c oxidase assembly (o
PTHR10766:SI	Phvul.008G28	not assigned.a	(original description: pacid=37158021 transcript=Phvul.
K10295 - F-bo	Phvul.009G12	Protein home	component FBX of SCF E3 ubiquitin ligase complex (origi
K10295 - F-bo	Phvul.009G12	Protein home	component FBX of SCF E3 ubiquitin ligase complex (origi
K10295 - F-bo	Phvul.009G12	Protein home	component FBX of SCF E3 ubiquitin ligase complex (origi
K10295 - F-bo	Phvul.009G12	Protein home	component FBX of SCF E3 ubiquitin ligase complex (origi
PTHR11062:SI	Phvul.009G16	Cell wall orgar	xylosyltransferase (IRX10) (original description: pacid=37
PTHR11062:SI	Phvul.009G16	Cell wall orgar	xylosyltransferase (IRX10) (original description: pacid=37
PTHR11062:SI	Phvul.009G16	Cell wall orgar	xylosyltransferase (IRX10) (original description: pacid=37
PTHR11062:SI	Phvul.009G16	Cell wall orgar	xylosyltransferase (IRX10) (original description: pacid=37
PTHR23155//I	Phvul.010G06	not assigned.a	(original description: pacid=37142899 transcript=Phvul.
PTHR23155//I	Phvul.010G06	not assigned.a	(original description: pacid=37142899 transcript=Phvul.
PTHR23155//I	Phvul.010G06	not assigned.a	(original description: pacid=37142899 transcript=Phvul.
PTHR23155//I	Phvul.010G06	not assigned.a	(original description: pacid=37142899 transcript=Phvul.
PF00170 - bZI	Phvul.011G04	not assigned.r	no hits & (original description: pacid=37157418 transcri
PF00170 - bZI	Phvul.011G04	not assigned.r	no hits & (original description: pacid=37157418 transcri
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
PTHR11709//I	Phvul.L00734	Cell wall orgar	lignin laccase (original description: pacid=37178902 tran
PTHR11709//I	Phvul.L00734	Cell wall orgar	lignin laccase (original description: pacid=37178902 tran
PTHR31471:SI	Phvul.001G02	not assigned.r	no hits & (original description: pacid=37167696 transcri
PTHR31471:SI	Phvul.001G02	not assigned.r	no hits & (original description: pacid=37167696 transcri
3.2.1.153 - Fru	Phvul.001G03	Carbohydrate	acid beta-fructofuranosidase (CWIN) (original descriptio
K13157 - U11/	Phvul.001G10	RNA processir	protein factor U11/U12-65K of U11/U12 small nuclear ri
K13157 - U11/	Phvul.001G10	RNA processir	protein factor U11/U12-65K of U11/U12 small nuclear ri
PF14368 - Pro	Phvul.001G15	not assigned.r	no hits & (original description: pacid=37169901 transcri
PF14368 - Pro	Phvul.001G15	not assigned.r	no hits & (original description: pacid=37169901 transcri
PF14368 - Pro	Phvul.001G15	not assigned.r	no hits & (original description: pacid=37169901 transcri
PF14368 - Pro	Phvul.001G15	not assigned.r	no hits & (original description: pacid=37169901 transcri
PTHR18866//I	Phvul.001G24	Lipid metaboli	acetyl-CoA carboxylase regulator (BADC) (original descri
PF01357//PFC	Phvul.002G00	Cell wall orgar	beta-like-class expansin (original description: pacid=3717
PTHR23083//I	Phvul.002G01	not assigned.a	(original description: pacid=37176692 transcript=Phvul.
PTHR23083//I	Phvul.002G01	not assigned.a	(original description: pacid=37176692 transcript=Phvul.
K17619 - mag	Phvul.002G21	not assigned.r	no hits & (original description: pacid=37177891 transcri
PTHR22870:SI	Phvul.002G25	not assigned.a	(original description: pacid=37175448 transcript=Phvul.
PTHR22870:SI	Phvul.002G25	not assigned.a	(original description: pacid=37175448 transcript=Phvul.
K03456 - serir	Phvul.003G02	Protein modif	scaffold component A of PP2A phosphatase complexes (
K03456 - serir	Phvul.003G02	Protein modif	scaffold component A of PP2A phosphatase complexes (

K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K00626 - acet	Phvul.003G08	Secondary me	acetyl-CoA C-acyltransferase (original description: pacid
K15108 - solu	Phvul.003G10	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.003G10	Solute transp	solute transporter (MTCC) (original description: pacid=3
PTHR22957:S	Phvul.003G14	Vesicle traffic	RAB-GTPase-activating protein (RAB-GAP) (original desc
PTHR22957:S	Phvul.003G14	Vesicle traffic	RAB-GTPase-activating protein (RAB-GAP) (original desc
K07374 - tubu	Phvul.003G23	Cytoskeleton	component alpha-Tubulin of alpha-beta-Tubulin heteroc
K07374 - tubu	Phvul.003G23	Cytoskeleton	component alpha-Tubulin of alpha-beta-Tubulin heteroc
K07374 - tubu	Phvul.003G23	Cytoskeleton	component alpha-Tubulin of alpha-beta-Tubulin heteroc
K07374 - tubu	Phvul.003G23	Cytoskeleton	component alpha-Tubulin of alpha-beta-Tubulin heteroc
PTHR24012:S	Phvul.003G29	not assigned.	(original description: pacid=37147487 transcript=Phvul.
PTHR24012:S	Phvul.003G29	RNA processi	mRNA-binding regulatory factor (RBP45/47) (original de
PTHR24012:S	Phvul.003G29	RNA processi	mRNA-binding regulatory factor (RBP45/47) (original de
PTHR32212:S	Phvul.004G01	not assigned.	no hits & (original description: pacid=37163167 transcri
PTHR32212:S	Phvul.004G01	not assigned.	no hits & (original description: pacid=37163167 transcri
PTHR32212:S	Phvul.004G01	not assigned.	no hits & (original description: pacid=37163167 transcri
PTHR32212:S	Phvul.004G01	not assigned.	no hits & (original description: pacid=37163167 transcri
0	Phvul.004G03	not assigned.	no hits & (original description: pacid=37163425 transcri
PF00560//PF	Phvul.004G04	not assigned.	(original description: pacid=37161946 transcript=Phvul.
PF00560//PF	Phvul.004G04	not assigned.	(original description: pacid=37161946 transcript=Phvul.
K10393 - kine	Phvul.004G16	Cytoskeleton	motor protein (Kinesin-13) (original description: pacid=3
K11308 - hist	Phvul.005G01	Chromatin or	acetyltransferase component HAM of NuA4 histone acet
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
1.14.13.37 -	Phvul.005G01	Enzyme classi	Cytochrome P450 714B2 OS=Oryza sativa subsp. japonic
2.4.1.132 - G	Phvul.005G08	Protein modif	alpha-1,3/1,6-mannosyltransferase (ALG2) (original desc
2.4.1.132 - G	Phvul.005G08	Protein modif	alpha-1,3/1,6-mannosyltransferase (ALG2) (original desc
PTHR31072:S	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:S	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:S	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:S	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:S	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37

PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
0	Phvul.006G06	not assigned.r	no hits & (original description: pacid=37172254 transcri
0	Phvul.006G06	not assigned.r	no hits & (original description: pacid=37172254 transcri
4.1.1.28 - Aro	Phvul.006G13	Secondary me	aromatic L-amino acid decarboxylase (original descriptio
4.1.1.28 - Aro	Phvul.006G13	Secondary me	aromatic L-amino acid decarboxylase (original descriptio
K15047 - hete	Phvul.006G19	not assigned.r	no hits & (original description: pacid=37171957 transcri
K15047 - hete	Phvul.006G19	not assigned.r	no hits & (original description: pacid=37171957 transcri
K15047 - hete	Phvul.006G19	not assigned.r	no hits & (original description: pacid=37171957 transcri
K15047 - hete	Phvul.006G19	not assigned.r	no hits & (original description: pacid=37171957 transcri
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PTHR23024:SI	Phvul.007G06	not assigned.a	(original description: pacid=37166219 transcript=Phvul.
PTHR23024:SI	Phvul.007G06	not assigned.a	(original description: pacid=37166219 transcript=Phvul.
PTHR37764:SI	Phvul.007G18	not assigned.r	no hits & (original description: pacid=37166249 transcri
PF13414 - TPF	Phvul.007G19	not assigned.r	no hits & (original description: pacid=37165459 transcri
PF13414 - TPF	Phvul.007G19	not assigned.r	no hits & (original description: pacid=37165459 transcri
0	Phvul.007G23	Protein transl	NUP1/NUP136 nucleoporin of nuclear pore complex (ori
0	Phvul.007G23	Protein transl	NUP1/NUP136 nucleoporin of nuclear pore complex (ori
0	Phvul.007G23	Protein transl	NUP1/NUP136 nucleoporin of nuclear pore complex (ori
0	Phvul.007G23	Protein transl	NUP1/NUP136 nucleoporin of nuclear pore complex (ori
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
PTHR23240//I	Phvul.008G00	DNA damage	DNA ligase (LIG6) (original description: pacid=37159578
PTHR23240//I	Phvul.008G00	DNA damage	DNA ligase (LIG6) (original description: pacid=37159578
PTHR23240//I	Phvul.008G00	DNA damage	DNA ligase (LIG6) (original description: pacid=37159578
PTHR23240//I	Phvul.008G00	DNA damage	DNA ligase (LIG6) (original description: pacid=37159578
PTHR10783:SI	Phvul.008G03	Nutrient uptal	phosphate transporter (PHO1) (original description: paci
PTHR10783:SI	Phvul.008G03	Nutrient uptal	phosphate transporter (PHO1) (original description: paci
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
K15685 - E3 u	Phvul.008G10	RNA processir	E3 ubiquitin ligase (HAKAI) (original description: pacid=3

K15685 - E3 u	Phvul.008G10	RNA processir	E3 ubiquitin ligase (HAKAI) (original description: pacid=3
K15685 - E3 u	Phvul.008G10	RNA processir	E3 ubiquitin ligase (HAKAI) (original description: pacid=3
K15685 - E3 u	Phvul.008G10	RNA processir	E3 ubiquitin ligase (HAKAI) (original description: pacid=3
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37158099 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161406 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161406 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161383 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37160139 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37160139 transcri
PTHR13343:SI	Phvul.008G19	not assigned.a	(original description: pacid=37158415 transcript=Phvul.
PTHR11926:SI	Phvul.008G29	Enzyme classi	UDP-glycosyltransferase 71A16 OS=Pyrus communis (sp
PTHR11926:SI	Phvul.008G29	Enzyme classi	UDP-glycosyltransferase 71A16 OS=Pyrus communis (sp
PTHR11926:SI	Phvul.008G29	Enzyme classi	UDP-glycosyltransferase 71A16 OS=Pyrus communis (sp
PTHR11926:SI	Phvul.008G29	Enzyme classi	UDP-glycosyltransferase 71A16 OS=Pyrus communis (sp
PTHR31384:SI	Phvul.009G02	RNA biosynth	transcription factor (ARF) (original description: pacid=37
PTHR31384:SI	Phvul.009G02	RNA biosynth	transcription factor (ARF) (original description: pacid=37
PTHR31851:SI	Phvul.009G04	Solute transp	metal cation transporter (MEB) (original description: pac
PTHR31851:SI	Phvul.009G04	Solute transp	metal cation transporter (MEB) (original description: pac
PTHR31851:SI	Phvul.009G04	Solute transp	metal cation transporter (MEB) (original description: pac
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:SI	Phvul.009G12	not assigned.a	(original description: pacid=37148875 transcript=Phvul.
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.009G24	Solute transp	solute transporter (MTCC) (original description: pacid=3
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig
PTHR31602:SI	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (orig

PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR31602:S	Phvul.010G04	RNA biosynth	component GRF of GRF-GIF transcriptional complex (ori
PTHR22849//	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
PTHR22849//	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
PTHR22849//	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
PTHR22849//	Phvul.010G11	Protein home	E3 ubiquitin ligase (PUB) (original description: pacid=371
PTHR24009:S	Phvul.011G01	RNA biosynth	C3H zinc finger transcription factor (original description:
PTHR24009:S	Phvul.011G01	RNA biosynth	C3H zinc finger transcription factor (original description:
PTHR24009:S	Phvul.011G01	RNA biosynth	C3H zinc finger transcription factor (original description:
PTHR24009:S	Phvul.011G01	RNA biosynth	C3H zinc finger transcription factor (original description:
0	Phvul.011G12	not assigned.r	no hits & (original description: pacid=37155251 transcri
0	Phvul.011G12	not assigned.r	no hits & (original description: pacid=37155251 transcri
0	Phvul.011G12	not assigned.r	no hits & (original description: pacid=37155251 transcri
0	Phvul.011G12	not assigned.r	no hits & (original description: pacid=37155251 transcri
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
PTHR10173:S	Phvul.011G17	not assigned.	(original description: pacid=37157390 transcript=Phvul.
PTHR10173:S	Phvul.011G17	not assigned.	(original description: pacid=37157390 transcript=Phvul.
PTHR10173:S	Phvul.011G17	not assigned.	(original description: pacid=37157390 transcript=Phvul.
PTHR10173:S	Phvul.011G17	not assigned.	(original description: pacid=37157390 transcript=Phvul.
PTHR22884:S	Phvul.011G19	Chromatin or	methylated DNA binding component SUVH1/3 of SUVH-
PTHR22884:S	Phvul.011G19	Chromatin or	methylated DNA binding component SUVH1/3 of SUVH-
PF05553 - Cot	Phvul.001G09	not assigned.r	no hits & (original description: pacid=37170071 transcri
PF05553 - Cot	Phvul.001G09	not assigned.r	no hits & (original description: pacid=37170071 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri

K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
K15559 - regu	Phvul.001G10	not assigned.r	no hits & (original description: pacid=37170360 transcri
PTHR31447:S	Phvul.001G14	RNA processir	N6-methyladenosine demethylase (ALKBH10) (original d
PTHR28630:S	Phvul.001G17	not assigned.a	(original description: pacid=37168987 transcript=Phvul.
PTHR28630:S	Phvul.001G17	not assigned.a	(original description: pacid=37168987 transcript=Phvul.
PTHR28630:S	Phvul.001G17	not assigned.a	(original description: pacid=37168987 transcript=Phvul.
PTHR28630:S	Phvul.001G17	not assigned.a	(original description: pacid=37168987 transcript=Phvul.
2.7.7.2 - FAD s	Phvul.001G17	not assigned.r	no hits & (original description: pacid=37168919 transcri
2.7.7.2 - FAD s	Phvul.001G17	not assigned.r	no hits & (original description: pacid=37168919 transcri
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
K12603 - CCR	Phvul.001G20	RNA processir	deadenylase component CCR4 of CCR4-NOT complex (or
PTHR22849:S	Phvul.001G26	not assigned.a	(original description: pacid=37168993 transcript=Phvul.
PTHR11746:S	Phvul.001G26	Enzyme classi	Acetylserotonin O-methyltransferase OS=Arabidopsis th
PTHR11746:S	Phvul.001G26	Enzyme classi	Acetylserotonin O-methyltransferase OS=Arabidopsis th
PF13912 - C2H	Phvul.002G05	RNA biosynth	C2H2 zinc finger transcription factor (original descriptio
PF13912 - C2H	Phvul.002G05	RNA biosynth	C2H2 zinc finger transcription factor (original descriptio
PTHR10438:S	Phvul.002G06	Redox homeo	H-type thioredoxin (original description: pacid=3717719
PTHR10438:S	Phvul.002G06	Redox homeo	H-type thioredoxin (original description: pacid=3717719
PTHR10438:S	Phvul.002G06	Redox homeo	H-type thioredoxin (original description: pacid=3717719
PTHR10438:S	Phvul.002G06	Redox homeo	H-type thioredoxin (original description: pacid=3717719
PF03106 - WR	Phvul.002G16	RNA biosynth	transcription factor (WRKY) (original description: pacid=
PF03106 - WR	Phvul.002G16	RNA biosynth	transcription factor (WRKY) (original description: pacid=
PTHR12953 - I	Phvul.002G16	Cytoskeleton	regulatory factor (SUN3/4/5) nuclear shape determinati
PTHR12953 - I	Phvul.002G16	Cytoskeleton	regulatory factor (SUN3/4/5) nuclear shape determinati
PTHR12953 - I	Phvul.002G16	Cytoskeleton	regulatory factor (SUN3/4/5) nuclear shape determinati
PTHR12953 - I	Phvul.002G16	Cytoskeleton	regulatory factor (SUN3/4/5) nuclear shape determinati
PTHR23042:S	Phvul.002G21	Nutrient upta	bHLH-IVa-class iron homeostasis regulator (original desc
PTHR23042:S	Phvul.002G21	Nutrient upta	bHLH-IVa-class iron homeostasis regulator (original desc
PTHR23042:S	Phvul.002G21	Nutrient upta	bHLH-IVa-class iron homeostasis regulator (original desc
PTHR23042:S	Phvul.002G21	Nutrient upta	bHLH-IVa-class iron homeostasis regulator (original desc
PTHR22835//I	Phvul.002G24	not assigned.a	(original description: pacid=37176697 transcript=Phvul.
PTHR22835//I	Phvul.002G24	not assigned.a	(original description: pacid=37176697 transcript=Phvul.

PTHR22870:S	Phvul.002G25	not assigned.	(original description: pacid=37175448 transcript=Phvul.
PTHR22870:S	Phvul.002G25	not assigned.	(original description: pacid=37175448 transcript=Phvul.
PTHR22870:S	Phvul.002G25	not assigned.	(original description: pacid=37175448 transcript=Phvul.
PTHR22870:S	Phvul.002G25	not assigned.	(original description: pacid=37175448 transcript=Phvul.
PTHR10791:S	Phvul.002G28	Solute transp	sugar efflux transporter (SWEET) (original description: p
PTHR10791:S	Phvul.002G28	Solute transp	sugar efflux transporter (SWEET) (original description: p
PTHR10791:S	Phvul.002G28	Solute transp	sugar efflux transporter (SWEET) (original description: p
PTHR10791:S	Phvul.002G28	Solute transp	sugar efflux transporter (SWEET) (original description: p
3.4.11.14 - Cy	Phvul.002G29	not assigned.	(original description: pacid=37176433 transcript=Phvul.
3.4.11.14 - Cy	Phvul.002G29	not assigned.	(original description: pacid=37176433 transcript=Phvul.
PTHR13832//	Phvul.002G30	Protein modif	clade A phosphatase (original description: pacid=371752
PTHR13832//	Phvul.002G30	Protein modif	clade A phosphatase (original description: pacid=371752
K14016 - ubiq	Phvul.002G32	Protein home	component UFD1 of ER-associated protein degradation (
K14016 - ubiq	Phvul.002G32	Protein home	component UFD1 of ER-associated protein degradation (
K14016 - ubiq	Phvul.002G32	Protein home	component UFD1 of ER-associated protein degradation (
K14016 - ubiq	Phvul.002G32	Protein home	component UFD1 of ER-associated protein degradation (
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
K05863 - solu	Phvul.002G32	Solute transp	solute transporter (MTCC) (original description: pacid=3
PTHR10359:S	Phvul.003G03	Chromatin or	methylcytosine-specific DNA glycosylase (ROS1) (original
PTHR10359:S	Phvul.003G03	Chromatin or	methylcytosine-specific DNA glycosylase (ROS1) (original
K00721 - dolic	Phvul.003G05	Protein modif	catalytic component DPMS1 of DPMS dolichol-phosphat
K00721 - dolic	Phvul.003G05	Protein modif	catalytic component DPMS1 of DPMS dolichol-phosphat
0	Phvul.003G07	not assigned.	no hits & (original description: pacid=37147041 transcri
0	Phvul.003G07	not assigned.	no hits & (original description: pacid=37147041 transcri
0	Phvul.003G07	not assigned.	no hits & (original description: pacid=37147041 transcri
0	Phvul.003G07	not assigned.	no hits & (original description: pacid=37147041 transcri
PTHR23421:S	Phvul.003G13	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=3
PTHR23421:S	Phvul.003G13	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=3
PTHR23421:S	Phvul.003G13	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=3
PTHR23421:S	Phvul.003G13	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=3
PTHR23155//	Phvul.003G24	not assigned.	(original description: pacid=37146857 transcript=Phvul.
PTHR23155//	Phvul.003G24	not assigned.	(original description: pacid=37146857 transcript=Phvul.
PTHR23155//	Phvul.003G24	not assigned.	(original description: pacid=37146857 transcript=Phvul.
PTHR23155//	Phvul.003G24	not assigned.	(original description: pacid=37146857 transcript=Phvul.
PTHR23155//	Phvul.003G24	not assigned.	(original description: pacid=37146857 transcript=Phvul.
PTHR23155//	Phvul.003G24	not assigned.	(original description: pacid=37146857 transcript=Phvul.
PTHR23155//	Phvul.003G24	not assigned.	(original description: pacid=37146857 transcript=Phvul.

PTHR23155//I	Phvul.003G24	not assigned.a	(original description: pacid=37146857 transcript=Phvul.0
PTHR10108:SI	Phvul.003G28	not assigned.a	(original description: pacid=37146681 transcript=Phvul.0
PTHR10108:SI	Phvul.003G28	not assigned.a	(original description: pacid=37146681 transcript=Phvul.0
PTHR24012:SI	Phvul.003G29	not assigned.a	(original description: pacid=37147487 transcript=Phvul.0
PTHR24012:SI	Phvul.003G29	not assigned.a	(original description: pacid=37147487 transcript=Phvul.0
PTHR24012:SI	Phvul.003G29	not assigned.a	(original description: pacid=37147487 transcript=Phvul.0
PTHR24012:SI	Phvul.003G29	not assigned.a	(original description: pacid=37147487 transcript=Phvul.0
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
PTHR24012:SI	Phvul.003G29	RNA processin	mRNA-binding regulatory factor (RBP45/47) (original des
0	Phvul.004G03	not assigned.n	no hits & (original description: pacid=37163425 transcri
0	Phvul.004G03	not assigned.n	no hits & (original description: pacid=37163425 transcri
0	Phvul.004G03	not assigned.n	no hits & (original description: pacid=37163425 transcri
0	Phvul.004G03	not assigned.n	no hits & (original description: pacid=37163425 transcri
PF00560//PFC	Phvul.004G04	not assigned.a	(original description: pacid=37161823 transcript=Phvul.0
PF00560//PFC	Phvul.004G04	not assigned.a	(original description: pacid=37161823 transcript=Phvul.0
PF13650 - Asp	Phvul.004G05	not assigned.n	no hits & (original description: pacid=37163227 transcri
PF13650 - Asp	Phvul.004G05	not assigned.n	no hits & (original description: pacid=37163227 transcri
PF13650 - Asp	Phvul.004G05	not assigned.n	no hits & (original description: pacid=37163227 transcri
PF13650 - Asp	Phvul.004G05	not assigned.n	no hits & (original description: pacid=37163227 transcri
PF06376 - Pro	Phvul.004G17	not assigned.n	no hits & (original description: pacid=37162464 transcri
PF06376 - Pro	Phvul.004G17	not assigned.n	no hits & (original description: pacid=37162464 transcri
PF06376 - Pro	Phvul.004G17	not assigned.n	no hits & (original description: pacid=37162464 transcri
PF06376 - Pro	Phvul.004G17	not assigned.n	no hits & (original description: pacid=37162464 transcri
PTHR24193//I	Phvul.005G00	Protein transl	chaperone (AKR2) (original description: pacid=37154384
PTHR24193//I	Phvul.005G00	Protein transl	chaperone (AKR2) (original description: pacid=37154384
PTHR24193//I	Phvul.005G00	Protein transl	chaperone (AKR2) (original description: pacid=37154384
PTHR24193//I	Phvul.005G00	Protein transl	chaperone (AKR2) (original description: pacid=37154384
PTHR10252//I	Phvul.005G01	RNA biosynth	component alpha of TATA box-binding protein NC2 regu
PF00651 - BTE	Phvul.005G05	not assigned.a	(original description: pacid=37154040 transcript=Phvul.0
K01595 - phos	Phvul.005G09	Photosynthesi	PEP carboxylase (original description: pacid=37154500 tr
PTHR31973:SI	Phvul.005G10	not assigned.n	no hits & (original description: pacid=37152872 transcri
K01061 - carb	Phvul.005G11	not assigned.n	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.n	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.n	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.n	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.n	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.n	no hits & (original description: pacid=37152909 transcri

K01061 - carb	Phvul.005G11	not assigned.	no hits & (original description: pacid=37152909 transcri
K01061 - carb	Phvul.005G11	not assigned.	no hits & (original description: pacid=37152909 transcri
PTHR10593//I	Phvul.005G13	RNA biosynth	C2H2 zinc finger transcription factor (original descriptio
PTHR10593//I	Phvul.005G13	RNA biosynth	C2H2 zinc finger transcription factor (original descriptio
K11583 - seri	Phvul.006G10	Protein modif	regulatory component B2 of PP2A phosphatase complex
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR13215:SI	Phvul.006G11	not assigned.	(original description: pacid=37173654 transcript=Phvul.
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PTHR11453:SI	Phvul.006G12	Solute transp	borate transporter (BOR) (original description: pacid=37
PF15365 - Pro	Phvul.006G15	not assigned.	no hits & (original description: pacid=37174157 transcri
PTHR11802:SI	Phvul.006G16	Protein home	serine carboxypeptidase (original description: pacid=371
PTHR11802:SI	Phvul.006G16	Protein home	serine carboxypeptidase (original description: pacid=371
PTHR11802:SI	Phvul.006G16	Protein home	serine carboxypeptidase (original description: pacid=371
PTHR11802:SI	Phvul.006G16	Protein home	serine carboxypeptidase (original description: pacid=371
K13125 - nitri	Phvul.006G19	not assigned.	(original description: pacid=37172724 transcript=Phvul.
K13125 - nitri	Phvul.006G19	not assigned.	(original description: pacid=37172724 transcript=Phvul.
K01354 - olig	Phvul.007G01	not assigned.	no hits & (original description: pacid=37164997 transcri
K01354 - olig	Phvul.007G01	not assigned.	no hits & (original description: pacid=37164997 transcri
K01354 - olig	Phvul.007G01	not assigned.	no hits & (original description: pacid=37164997 transcri
K01354 - olig	Phvul.007G01	not assigned.	no hits & (original description: pacid=37164997 transcri
PTHR31072:SI	Phvul.007G01	Multi-process	CHE circadian clock repression factor (original descriptio
PTHR31072:SI	Phvul.007G01	Multi-process	CHE circadian clock repression factor (original descriptio
2.7.8.8 - CDP-	Phvul.007G03	Lipid metaboli	base-exchange-type phosphatidylserine synthase (origin
2.7.10.2 - Non	Phvul.007G05	Protein modif	protein kinase (SD-1) (original description: pacid=37166
2.7.10.2 - Non	Phvul.007G05	Protein modif	protein kinase (SD-1) (original description: pacid=37166
2.7.10.2 - Non	Phvul.007G05	Protein modif	protein kinase (SD-1) (original description: pacid=37166
2.7.10.2 - Non	Phvul.007G05	Protein modif	protein kinase (SD-1) (original description: pacid=37166
PTHR10638:SI	Phvul.007G05	Polyamine me	copper-containing amine oxidase (CuAO) (original descri
PTHR10638:SI	Phvul.007G05	Polyamine me	copper-containing amine oxidase (CuAO) (original descri
PTHR10638:SI	Phvul.007G05	Polyamine me	copper-containing amine oxidase (CuAO) (original descri
PTHR10638:SI	Phvul.007G05	Polyamine me	copper-containing amine oxidase (CuAO) (original descri

PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PF04570 - zin	Phvul.007G05	Multi-process	SnRK1-interacting factor (FLZ) (original description: paci
PTHR23024:S	Phvul.007G06	not assigned.	(original description: pacid=37166219 transcript=Phvul.
PTHR23024:S	Phvul.007G06	not assigned.	(original description: pacid=37166219 transcript=Phvul.
PTHR23024:S	Phvul.007G06	not assigned.	(original description: pacid=37166219 transcript=Phvul.
PTHR23024:S	Phvul.007G06	not assigned.	(original description: pacid=37166219 transcript=Phvul.
PTHR23024:S	Phvul.007G06	not assigned.	(original description: pacid=37166219 transcript=Phvul.
PTHR11972//	Phvul.007G07	Nutrient upta	metal ion-chelate reductase (FRO) (original description:
PTHR11972//	Phvul.007G07	Nutrient upta	metal ion-chelate reductase (FRO) (original description:
PTHR11972//	Phvul.007G07	Nutrient upta	metal ion-chelate reductase (FRO) (original description:
PTHR11972//	Phvul.007G07	Nutrient upta	metal ion-chelate reductase (FRO) (original description:
PF12646 - Do	Phvul.007G09	not assigned.	no hits & (original description: pacid=37167603 transcri
PF12646 - Do	Phvul.007G09	not assigned.	no hits & (original description: pacid=37167603 transcri
PF12646 - Do	Phvul.007G09	not assigned.	no hits & (original description: pacid=37167603 transcri
PF12646 - Do	Phvul.007G09	not assigned.	no hits & (original description: pacid=37167603 transcri
PTHR11260:S	Phvul.007G10	Protein modif	class phi glutathione S-transferase (original description:
PTHR11260:S	Phvul.007G10	Protein modif	class phi glutathione S-transferase (original description:
PTHR11260:S	Phvul.007G10	Protein modif	class phi glutathione S-transferase (original description:
PTHR11260:S	Phvul.007G10	Protein modif	class phi glutathione S-transferase (original description:
PTHR37764:S	Phvul.007G18	not assigned.	no hits & (original description: pacid=37166249 transcri
PTHR37764:S	Phvul.007G18	not assigned.	no hits & (original description: pacid=37166249 transcri
PTHR37764:S	Phvul.007G18	not assigned.	no hits & (original description: pacid=37166249 transcri
PTHR37764:S	Phvul.007G18	not assigned.	no hits & (original description: pacid=37166249 transcri
0	Phvul.007G18	not assigned.	no hits & (original description: pacid=37164309 transcri
0	Phvul.007G18	not assigned.	no hits & (original description: pacid=37164309 transcri
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
2.7.11.1 - Non	Phvul.007G20	Protein modif	receptor-like protein kinase (RLCK-V) (original descriptio
PTHR31707:S	Phvul.007G21	Cell wall orga	pectin methylesterase (original description: pacid=3716
PF00045 - He	Phvul.007G27	not assigned.	(original description: pacid=37164350 transcript=Phvul.
PF00045 - He	Phvul.007G27	not assigned.	(original description: pacid=37164350 transcript=Phvul.
PF00045 - He	Phvul.007G27	not assigned.	(original description: pacid=37166099 transcript=Phvul.

PF00045 - Her	Phvul.007G27	not assigned.a	(original description: pacid=37166099 transcript=Phvul.0
PF00045 - Her	Phvul.007G27	not assigned.a	(original description: pacid=37164734 transcript=Phvul.0
PF00045 - Her	Phvul.007G27	not assigned.a	(original description: pacid=37164734 transcript=Phvul.0
PTHR35313:SI	Phvul.008G00	Cell wall orga	exine patterning factor (NEF1) (original description: paci
PTHR35313:SI	Phvul.008G00	Cell wall orga	exine patterning factor (NEF1) (original description: paci
PTHR35313:SI	Phvul.008G00	Cell wall orga	exine patterning factor (NEF1) (original description: paci
PTHR35313:SI	Phvul.008G00	Cell wall orga	exine patterning factor (NEF1) (original description: paci
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
KOG0211 - Pr	Phvul.008G00	not assigned.r	no hits & (original description: pacid=37158928 transcri
K03131 - tran	Phvul.008G01	RNA biosynth	component TAF6 of TFIId basal transcription regulation c
K03131 - tran	Phvul.008G01	RNA biosynth	component TAF6 of TFIId basal transcription regulation c
PTHR13068//I	Phvul.008G04	RNA biosynth	transcription factor (mTERF) (original description: pacid=
0	Phvul.008G06	not assigned.r	no hits & (original description: pacid=37159335 transcri
0	Phvul.008G06	not assigned.r	no hits & (original description: pacid=37159335 transcri
0	Phvul.008G06	not assigned.r	no hits & (original description: pacid=37159335 transcri
0	Phvul.008G06	not assigned.r	no hits & (original description: pacid=37159335 transcri
KOG1947 - Le	Phvul.008G07	not assigned.r	no hits & (original description: pacid=37157631 transcri
KOG1947 - Le	Phvul.008G07	not assigned.r	no hits & (original description: pacid=37157631 transcri
KOG1947 - Le	Phvul.008G07	not assigned.r	no hits & (original description: pacid=37157631 transcri
KOG1947 - Le	Phvul.008G07	not assigned.r	no hits & (original description: pacid=37157631 transcri
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PF00069//PFC	Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=3715
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37158099 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37158099 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37159657 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161383 transcri
PTHR33103:SI	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161383 transcri
PTHR13683:SI	Phvul.008G11	Protein home	pepsin-type protease (original description: pacid=37158
PTHR13683:SI	Phvul.008G11	Protein home	pepsin-type protease (original description: pacid=37158
0	Phvul.008G15	not assigned.r	no hits & (original description: pacid=37160418 transcri
0	Phvul.008G15	not assigned.r	no hits & (original description: pacid=37160418 transcri
0	Phvul.008G15	not assigned.r	no hits & (original description: pacid=37160418 transcri
0	Phvul.008G15	not assigned.r	no hits & (original description: pacid=37160418 transcri
4.2.1.119 - En	Phvul.008G20	Lipid metaboli	hydroxyacyl-ACP dehydratase (mtHD) (original descriptic
4.2.1.119 - En	Phvul.008G20	Lipid metaboli	hydroxyacyl-ACP dehydratase (mtHD) (original descriptic
4.2.1.119 - En	Phvul.008G20	Lipid metaboli	hydroxyacyl-ACP dehydratase (mtHD) (original descriptic

4.2.1.119 - En	Phvul.008G20	Lipid metaboli	hydroxyacyl-ACP dehydratase (mtHD) (original descripti
0	Phvul.008G22	not assigned.	no hits & (original description: pacid=37161082 transcri
0	Phvul.008G22	not assigned.	no hits & (original description: pacid=37161082 transcri
0	Phvul.008G22	not assigned.	no hits & (original description: pacid=37161082 transcri
0	Phvul.008G22	not assigned.	no hits & (original description: pacid=37161082 transcri
PTHR22950:S	Phvul.008G22	Solute transp	proline transporter (ProT) (original description: pacid=37
PTHR22950:S	Phvul.008G22	Solute transp	proline transporter (ProT) (original description: pacid=37
PTHR22950:S	Phvul.008G22	Solute transp	proline transporter (ProT) (original description: pacid=37
PTHR22950:S	Phvul.008G22	Solute transp	proline transporter (ProT) (original description: pacid=37
PTHR24012:S	Phvul.008G27	not assigned.	(original description: pacid=37160931 transcript=Phvul.
PTHR24012:S	Phvul.008G27	not assigned.	(original description: pacid=37160931 transcript=Phvul.
PTHR24012:S	Phvul.008G27	not assigned.	(original description: pacid=37160931 transcript=Phvul.
K02259 - cyto	Phvul.008G28	Cellular respir	component COX15 of cytochrome c oxidase assembly (o
K02259 - cyto	Phvul.008G28	Cellular respir	component COX15 of cytochrome c oxidase assembly (o
PTHR10641:S	Phvul.009G10	RNA biosynth	transcription factor (MYB) (original description: pacid=3
PTHR10972:S	Phvul.009G12	not assigned.	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:S	Phvul.009G12	not assigned.	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:S	Phvul.009G12	not assigned.	(original description: pacid=37148875 transcript=Phvul.
PTHR10972:S	Phvul.009G12	not assigned.	(original description: pacid=37148875 transcript=Phvul.
K08867 - WN	Phvul.009G17	Protein modif	protein kinase (MAP3K-WNK) (original description: pacid
K08867 - WN	Phvul.009G17	Protein modif	protein kinase (MAP3K-WNK) (original description: pacid
K08867 - WN	Phvul.009G17	Protein modif	protein kinase (MAP3K-WNK) (original description: pacid
K08867 - WN	Phvul.009G17	Protein modif	protein kinase (MAP3K-WNK) (original description: pacid
PTHR23421:S	Phvul.009G23	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=3
PTHR23421:S	Phvul.009G23	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=3
K13066 - caffe	Phvul.009G25	Enzyme classi	Enzyme classification.EC_2 transferases.EC_2.1 transfer
K13066 - caffe	Phvul.009G25	Enzyme classi	Enzyme classification.EC_2 transferases.EC_2.1 transfer
K13066 - caffe	Phvul.009G25	Enzyme classi	Enzyme classification.EC_2 transferases.EC_2.1 transfer
K13066 - caffe	Phvul.009G25	Enzyme classi	Enzyme classification.EC_2 transferases.EC_2.1 transfer
K17592 - sacsi	Phvul.010G03	not assigned.	(original description: pacid=37143296 transcript=Phvul.
K17592 - sacsi	Phvul.010G03	not assigned.	(original description: pacid=37143296 transcript=Phvul.
K17592 - sacsi	Phvul.010G03	not assigned.	(original description: pacid=37143296 transcript=Phvul.
K17592 - sacsi	Phvul.010G03	not assigned.	(original description: pacid=37143296 transcript=Phvul.
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o

PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR23253:S	Phvul.010G04	Protein biosy	component eIF4G of eIF4F mRNA unwinding complex (o
PTHR12565:S	Phvul.010G07	RNA biosynth	transcription factor (bHLH) (original description: pacid=3
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
1.13.11.58 - Li	Phvul.010G13	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
1.13.11.58 - Li	Phvul.010G13	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
1.13.11.58 - Li	Phvul.010G13	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
1.13.11.58 - Li	Phvul.010G13	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxi
K01537 - Ca2	Phvul.011G01	Solute transp	P2B-type calcium cation-transporting ATPase (ACA) (orig
K01537 - Ca2	Phvul.011G01	Solute transp	P2B-type calcium cation-transporting ATPase (ACA) (orig
K01537 - Ca2	Phvul.011G01	Solute transp	P2B-type calcium cation-transporting ATPase (ACA) (orig
K01537 - Ca2	Phvul.011G01	Solute transp	P2B-type calcium cation-transporting ATPase (ACA) (orig
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
K08873 - PI-3-	Phvul.011G05	Protein modif	protein kinase (PIKK) (original description: pacid=37154
PTHR14194:S	Phvul.011G06	RNA biosynth	TAC16 cofactor of plastid-encoded RNA polymerase (ori
PTHR14194:S	Phvul.011G06	RNA biosynth	TAC16 cofactor of plastid-encoded RNA polymerase (ori
PF05938 - Pla	Phvul.011G11	not assigned.	(original description: pacid=37156233 transcript=Phvul.
PF05938 - Pla	Phvul.011G12	not assigned.	(original description: pacid=37155659 transcript=Phvul.
0	Phvul.011G12	not assigned.	no hits & (original description: pacid=37155251 transcri
0	Phvul.011G12	not assigned.	no hits & (original description: pacid=37155251 transcri
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s

3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
3.4.19.5//3.5.	Phvul.011G16	Enzyme classi	Putative threonine aspartase OS=Arabidopsis thaliana (s
0	Phvul.011G20	not assigned.	no hits & (original description: pacid=37156963 transcri
0	Phvul.011G20	not assigned.	no hits & (original description: pacid=37156963 transcri
0	Phvul.011G20	not assigned.	no hits & (original description: pacid=37156963 transcri
0	Phvul.011G20	not assigned.	no hits & (original description: pacid=37156963 transcri
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
PTHR23076:S	Phvul.L00205	not assigned.	(original description: pacid=37144324 transcript=Phvul.
K12872 - pre-	Phvul.L00253	RNA processi	component MAC5 of non-snRNP MOS4-associated comp
K12872 - pre-	Phvul.L00253	RNA processi	component MAC5 of non-snRNP MOS4-associated comp
K12872 - pre-	Phvul.L00253	RNA processi	component MAC5 of non-snRNP MOS4-associated comp
PTHR11709//	Phvul.L00734	Cell wall orga	lignin laccase (original description: pacid=37178902 tran
PTHR11695//	Phvul.008G00	Enzyme classi	2-alkenal reductase (NADP(+)-dependent) OS=Nicotiana
PTHR11695//	Phvul.008G00	Enzyme classi	2-alkenal reductase (NADP(+)-dependent) OS=Nicotiana
KOG0513 - Ca	Phvul.001G02	Lipid metaboli	phospholipase A2 (pPLA2-II) (original description: pacid=
KOG0513 - Ca	Phvul.001G02	Lipid metaboli	phospholipase A2 (pPLA2-II) (original description: pacid=
PTHR31471:S	Phvul.001G02	not assigned.	no hits & (original description: pacid=37167696 transcri
PTHR31471:S	Phvul.001G02	not assigned.	no hits & (original description: pacid=37167696 transcri
PTHR31471:S	Phvul.001G02	not assigned.	no hits & (original description: pacid=37167696 transcri
PTHR31471:S	Phvul.001G02	not assigned.	no hits & (original description: pacid=37167696 transcri
3.2.1.153 - Fr	Phvul.001G03	Carbohydrate	acid beta-fructofuranosidase (CWIN) (original descriptio
PTHR22166:S	Phvul.001G05	Cell cycle orga	ER cisternae formation factor (LUNAPARK) (original desc
PTHR22166:S	Phvul.001G05	Cell cycle orga	ER cisternae formation factor (LUNAPARK) (original desc
K12446 - L-ar	Phvul.001G07	Carbohydrate	L-arabinose kinase (original description: pacid=3716845
K12446 - L-ar	Phvul.001G07	Carbohydrate	L-arabinose kinase (original description: pacid=3716845
K01895 - acet	Phvul.001G09	Lipid metaboli	acetyl-CoA synthetase (original description: pacid=3717
K01895 - acet	Phvul.001G09	Lipid metaboli	acetyl-CoA synthetase (original description: pacid=3717
K12580 - CCR	Phvul.001G10	RNA processi	component NOT3/5 of mRNA deadenylation CCR4-NOT
K12580 - CCR	Phvul.001G10	RNA processi	component NOT3/5 of mRNA deadenylation CCR4-NOT
K12580 - CCR	Phvul.001G10	RNA processi	component NOT3/5 of mRNA deadenylation CCR4-NOT
K12580 - CCR	Phvul.001G10	RNA processi	component NOT3/5 of mRNA deadenylation CCR4-NOT
6.3.1.14 - Dip	Phvul.001G11	Protein biosy	diphthamide synthetase (DPH6) (original description: pa
6.3.1.14 - Dip	Phvul.001G11	Protein biosy	diphthamide synthetase (DPH6) (original description: pa

PTHR22762//I	Phvul.001G12	not assigned.	(original description: pacid=37171176 transcript=Phvul.
PTHR22762//I	Phvul.001G12	not assigned.	(original description: pacid=37171176 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR23155//I	Phvul.001G13	not assigned.	(original description: pacid=37169278 transcript=Phvul.
PTHR31529:SI	Phvul.001G15	RNA biosynth	transcription factor (AS2/LOB) (original description: paci
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
PF14379 - MY	Phvul.001G16	Nutrient uptal	transcription factor (PHR1) (original description: pacid=3
2.4.1.67 - Gal	Phvul.001G21	Carbohydrate	stachyose synthase (original description: pacid=3717114
2.4.1.67 - Gal	Phvul.001G21	Carbohydrate	stachyose synthase (original description: pacid=3717114
PTHR23115:SI	Phvul.001G22	Protein biosyr	IF-2 translation initiation factor (original description: pac
PTHR23115:SI	Phvul.001G22	Protein biosyr	IF-2 translation initiation factor (original description: pac
PTHR23115:SI	Phvul.001G22	Protein biosyr	IF-2 translation initiation factor (original description: pac
PTHR23115:SI	Phvul.001G22	Protein biosyr	IF-2 translation initiation factor (original description: pac
PTHR23083//I	Phvul.002G01	not assigned.	(original description: pacid=37176692 transcript=Phvul.
PTHR23083//I	Phvul.002G01	not assigned.	(original description: pacid=37176692 transcript=Phvul.
PTHR23083//I	Phvul.002G01	not assigned.	(original description: pacid=37176692 transcript=Phvul.
PTHR23083//I	Phvul.002G01	not assigned.	(original description: pacid=37176692 transcript=Phvul.
PF01535//PF1	Phvul.002G04	RNA processir	RNA editing factor (YS1) (original description: pacid=371
PF01535//PF1	Phvul.002G04	RNA processir	RNA editing factor (YS1) (original description: pacid=371
PF01535//PF1	Phvul.002G04	RNA processir	RNA editing factor (YS1) (original description: pacid=371
PF01535//PF1	Phvul.002G04	RNA processir	RNA editing factor (YS1) (original description: pacid=371
PF13912 - C2I	Phvul.002G05	RNA biosynth	C2H2 zinc finger transcription factor (original descriptior
PF13912 - C2I	Phvul.002G05	RNA biosynth	C2H2 zinc finger transcription factor (original descriptior
PTHR31867:SI	Phvul.002G15	Cell wall orgar	alpha-class expansin (original description: pacid=371767
PTHR31867:SI	Phvul.002G15	Cell wall orgar	alpha-class expansin (original description: pacid=371767
PTHR31867:SI	Phvul.002G15	Cell wall orgar	alpha-class expansin (original description: pacid=371767
PTHR31867:SI	Phvul.002G15	Cell wall orgar	alpha-class expansin (original description: pacid=371767
1.1.1.133 - dT	Phvul.002G15	Carbohydrate	UDP-L-rhamnose synthase (original description: pacid=3
PTHR22835//I	Phvul.002G24	not assigned.	(original description: pacid=37176697 transcript=Phvul.
PTHR22835//I	Phvul.002G24	not assigned.	(original description: pacid=37176697 transcript=Phvul.
PTHR22835//I	Phvul.002G24	not assigned.	(original description: pacid=37176697 transcript=Phvul.

PTHR22835//	Phvul.002G24	not assigned.a	(original description: pacid=37176697 transcript=Phvul.
PTHR22870:S	Phvul.002G25	not assigned.a	(original description: pacid=37177422 transcript=Phvul.
PTHR22870:S	Phvul.002G25	not assigned.a	(original description: pacid=37177422 transcript=Phvul.
PTHR23315:S	Phvul.002G26	Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (origi
PTHR11514:S	Phvul.002G29	RNA biosynth	transcription factor (bHLH) (original description: pacid=3
PTHR11514:S	Phvul.002G29	RNA biosynth	transcription factor (bHLH) (original description: pacid=3
PTHR23315:S	Phvul.003G02	not assigned.r	no hits & (original description: pacid=37144503 transcri
PTHR23315:S	Phvul.003G02	not assigned.r	no hits & (original description: pacid=37144503 transcri
3.2.1.177 - Al	Phvul.003G03	Cell wall orga	1,6-alpha-xylosidase (original description: pacid=371470
3.2.1.177 - Al	Phvul.003G03	Cell wall orga	1,6-alpha-xylosidase (original description: pacid=371470
3.2.1.177 - Al	Phvul.003G03	Cell wall orga	1,6-alpha-xylosidase (original description: pacid=371470
3.2.1.177 - Al	Phvul.003G03	Cell wall orga	1,6-alpha-xylosidase (original description: pacid=371470
PTHR31642:S	Phvul.003G05	Lipid metaboli	catalytic protein (CER2) (original description: pacid=371
PTHR31642:S	Phvul.003G05	Lipid metaboli	catalytic protein (CER2) (original description: pacid=371
PTHR31642:S	Phvul.003G05	Lipid metaboli	catalytic protein (CER2) (original description: pacid=371
PTHR31642:S	Phvul.003G05	Lipid metaboli	catalytic protein (CER2) (original description: pacid=371
PTHR10774//	Phvul.003G08	not assigned.a	(original description: pacid=37146764 transcript=Phvul.
PTHR10774//	Phvul.003G08	not assigned.a	(original description: pacid=37146764 transcript=Phvul.
K15108 - solu	Phvul.003G10	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.003G10	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.003G10	Solute transp	solute transporter (MTCC) (original description: pacid=3
K15108 - solu	Phvul.003G10	Solute transp	solute transporter (MTCC) (original description: pacid=3
PTHR16166:S	Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcri
PTHR16166:S	Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcri
PTHR16166:S	Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcri
K18789 - xylo	Phvul.003G16	Cell wall orga	xylogalacturonan xylosyltransferase (original description
K00753 - glyc	Phvul.003G29	Protein modif	alpha-1,3-fucosyltransferase (original description: pacid=
K12386 - cysti	Phvul.004G05	not assigned.a	(original description: pacid=37163777 transcript=Phvul.
K02112 - F-ty	Phvul.004G12	Photosynthesi	subunit beta of peripheral CF1 subcomplex of ATP synth
K02112 - F-ty	Phvul.004G12	Photosynthesi	subunit beta of peripheral CF1 subcomplex of ATP synth
K02112 - F-ty	Phvul.004G12	Photosynthesi	subunit beta of peripheral CF1 subcomplex of ATP synth
K02112 - F-ty	Phvul.004G12	Photosynthesi	subunit beta of peripheral CF1 subcomplex of ATP synth
PTHR14445:S	Phvul.004G13	not assigned.a	(original description: pacid=37163533 transcript=Phvul.
PTHR14445:S	Phvul.004G13	not assigned.a	(original description: pacid=37163533 transcript=Phvul.
PTHR14445:S	Phvul.004G13	not assigned.a	(original description: pacid=37163533 transcript=Phvul.
PTHR14445:S	Phvul.004G13	not assigned.a	(original description: pacid=37163533 transcript=Phvul.
PTHR10438:S	Phvul.004G17	Redox homeo	atypical thioredoxin (ACHT) (original description: pacid=
PTHR10438:S	Phvul.004G17	Redox homeo	atypical thioredoxin (ACHT) (original description: pacid=
PF00651 - BT	Phvul.005G05	not assigned.a	(original description: pacid=37154040 transcript=Phvul.
PF00651 - BT	Phvul.005G05	not assigned.a	(original description: pacid=37154040 transcript=Phvul.
PF00954//PF	Phvul.005G08	Protein modif	protein kinase (SD-1) (original description: pacid=37153
2.7.1.26 - Rib	Phvul.005G09	not assigned.a	(original description: pacid=37154603 transcript=Phvul.
PTHR31072:S	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37

PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
PTHR31072:SI	Phvul.005G09	RNA biosynth	transcription factor (TCP) (original description: pacid=37
K01530 - phos	Phvul.005G10	Solute transp	P4-type ATPase component ALA of phospholipid flippase
K01530 - phos	Phvul.005G10	Solute transp	P4-type ATPase component ALA of phospholipid flippase
K01530 - phos	Phvul.005G10	Solute transp	P4-type ATPase component ALA of phospholipid flippase
K01530 - phos	Phvul.005G10	Solute transp	P4-type ATPase component ALA of phospholipid flippase
K01530 - phos	Phvul.005G10	Solute transp	P4-type ATPase component ALA of phospholipid flippase
K01530 - phos	Phvul.005G10	Solute transp	P4-type ATPase component ALA of phospholipid flippase
PTHR10593//I	Phvul.005G13	RNA biosynth	C2H2 zinc finger transcription factor (original description
PTHR10593//I	Phvul.005G13	RNA biosynth	C2H2 zinc finger transcription factor (original description
PTHR10593//I	Phvul.005G13	RNA biosynth	C2H2 zinc finger transcription factor (original description
PTHR10593//I	Phvul.005G13	RNA biosynth	C2H2 zinc finger transcription factor (original description
K15918 - D-gly	Phvul.005G17	Photosynthesi	glycerate kinase (original description: pacid=37152247 tr
K15918 - D-gly	Phvul.005G17	Photosynthesi	glycerate kinase (original description: pacid=37152247 tr
K15918 - D-gly	Phvul.005G17	Photosynthesi	glycerate kinase (original description: pacid=37152247 tr
K15918 - D-gly	Phvul.005G17	Photosynthesi	glycerate kinase (original description: pacid=37152247 tr
0	Phvul.006G14	not assigned.n	no hits & (original description: pacid=37171334 transcri
0	Phvul.006G14	not assigned.n	no hits & (original description: pacid=37171334 transcri
0	Phvul.006G14	not assigned.n	no hits & (original description: pacid=37171334 transcri
0	Phvul.006G14	not assigned.n	no hits & (original description: pacid=37171334 transcri
K16296 - serin	Phvul.006G16	Protein home	serine carboxypeptidase (original description: pacid=371
K16296 - serin	Phvul.006G16	Protein home	serine carboxypeptidase (original description: pacid=371
K10758 - thiol	Phvul.007G03	Protein modif	atypical quiescin sulfhydryl oxidase (QSOX) (original desc
K10758 - thiol	Phvul.007G03	Protein modif	atypical quiescin sulfhydryl oxidase (QSOX) (original desc
K10758 - thiol	Phvul.007G03	Protein modif	atypical quiescin sulfhydryl oxidase (QSOX) (original desc
K10758 - thiol	Phvul.007G03	Protein modif	atypical quiescin sulfhydryl oxidase (QSOX) (original desc
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0
PF13041 - PPF	Phvul.007G06	not assigned.a	(original description: pacid=37164814 transcript=Phvul.0

PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF13041 - PP	Phvul.007G06	not assigned.	(original description: pacid=37164814 transcript=Phvul.
PF12646 - Do	Phvul.007G09	not assigned.r	no hits & (original description: pacid=37167603 transcri
PTHR15856//	Phvul.007G11	RNA biosynth	PHD finger transcription factor (original description: paci
PTHR15856//	Phvul.007G11	RNA biosynth	PHD finger transcription factor (original description: paci
PTHR15856//	Phvul.007G11	RNA biosynth	PHD finger transcription factor (original description: paci
PTHR15856//	Phvul.007G11	RNA biosynth	PHD finger transcription factor (original description: paci
PTHR23257//	Phvul.007G18	Protein modif	protein kinase (MAP3K-RAF) (original description: pacid=
PTHR23257//	Phvul.007G18	Protein modif	protein kinase (MAP3K-RAF) (original description: pacid=
PTHR23315:S	Phvul.007G19	not assigned.	(original description: pacid=37164330 transcript=Phvul.
PTHR31707:S	Phvul.007G21	Cell wall orga	pectin methylesterase (original description: pacid=37165
PTHR31707:S	Phvul.007G21	Cell wall orga	pectin methylesterase (original description: pacid=37165
PTHR31707:S	Phvul.007G21	Cell wall orga	pectin methylesterase (original description: pacid=37165
PTHR31707:S	Phvul.007G21	Cell wall orga	pectin methylesterase (original description: pacid=37165
PTHR31707:S	Phvul.007G21	Cell wall orga	pectin methylesterase (original description: pacid=37165
PTHR31707:S	Phvul.007G21	Cell wall orga	pectin methylesterase (original description: pacid=37165
K10728 - topo	Phvul.007G21	Cell cycle orga	cell cycle replicated DNA checkpoint protein (TopBP1) (o
K10728 - topo	Phvul.007G21	Cell cycle orga	cell cycle replicated DNA checkpoint protein (TopBP1) (o
K10728 - topo	Phvul.007G21	Cell cycle orga	cell cycle replicated DNA checkpoint protein (TopBP1) (o
K10728 - topo	Phvul.007G21	Cell cycle orga	cell cycle replicated DNA checkpoint protein (TopBP1) (o
PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-dependent thioredoxin reductase (original descr
PTHR27004:S	Phvul.008G04	not assigned.	(original description: pacid=37160665 transcript=Phvul.
PTHR27004:S	Phvul.008G04	not assigned.	(original description: pacid=37160665 transcript=Phvul.
PTHR10641//	Phvul.008G06	RNA biosynth	transcription factor (MYB) (original description: pacid=3
PTHR10641//	Phvul.008G06	RNA biosynth	transcription factor (MYB) (original description: pacid=3
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37159657 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37159657 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37159657 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37159657 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161406 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161406 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161406 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37161406 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37160139 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37160139 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37160139 transcri
PTHR33103:S	Phvul.008G11	not assigned.r	no hits & (original description: pacid=37160139 transcri

PTHR22847//I	Phvul.008G12	RNA biosynth	transcriptional co-repressor (LUG) (original description:
PTHR22847//I	Phvul.008G12	RNA biosynth	transcriptional co-repressor (LUG) (original description:
PTHR22847//I	Phvul.008G12	RNA biosynth	transcriptional co-repressor (LUG) (original description:
PTHR22847//I	Phvul.008G12	RNA biosynth	transcriptional co-repressor (LUG) (original description:
PTHR10795//I	Phvul.008G22	Protein home	protease (SBT4) (original description: pacid=37158609 tr
PTHR13301//I	Phvul.008G27	not assigned.	(original description: pacid=37161159 transcript=Phvul.
PTHR13301//I	Phvul.008G27	not assigned.	(original description: pacid=37161159 transcript=Phvul.
3.4.17.1 - Car	Phvul.009G01	Protein home	M14 carboxypeptidase (original description: pacid=3715
3.4.17.1 - Car	Phvul.009G01	Protein home	M14 carboxypeptidase (original description: pacid=3715
K08505 - prot	Phvul.009G03	Vesicle traffic	SFT12 group Qc-type SNARE protein (original description
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR13878:S	Phvul.009G06	Phytohormon	cytokinin dehydrogenase (original description: pacid=37
PTHR23500:S	Phvul.009G11	Solute transp	monosaccharide transporter (AZT) (original description:
PTHR23500:S	Phvul.009G11	Solute transp	monosaccharide transporter (AZT) (original description:
0	Phvul.009G15	not assigned.	(original description: pacid=37149132 transcript=Phvul.
0	Phvul.009G15	not assigned.	(original description: pacid=37149132 transcript=Phvul.
0	Phvul.009G15	not assigned.	(original description: pacid=37149132 transcript=Phvul.
0	Phvul.009G15	not assigned.	(original description: pacid=37149132 transcript=Phvul.
PTHR31673:S	Phvul.009G20	Cell wall orga	COB cellulose microfibrils and hemicellulose interaction
PTHR23421:S	Phvul.009G23	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=37
PTHR23421:S	Phvul.009G23	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=37
PTHR23421:S	Phvul.009G23	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=37
PTHR23421:S	Phvul.009G23	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=37
PTHR15371:S	Phvul.009G25	not assigned.	(original description: pacid=37151366 transcript=Phvul.
PTHR15371:S	Phvul.009G25	not assigned.	(original description: pacid=37151366 transcript=Phvul.
PTHR15371:S	Phvul.009G25	not assigned.	(original description: pacid=37151366 transcript=Phvul.
PTHR15371:S	Phvul.009G25	not assigned.	(original description: pacid=37151366 transcript=Phvul.
0	Phvul.010G02	not assigned.	no hits & (original description: pacid=37143141 transcri
0	Phvul.010G02	not assigned.	no hits & (original description: pacid=37143141 transcri
0	Phvul.010G02	not assigned.	no hits & (original description: pacid=37143141 transcri
0	Phvul.010G02	not assigned.	no hits & (original description: pacid=37143141 transcri
PF00931//PF	Phvul.010G02	External stim	effector receptor (NLR) (original description: pacid=3714
PF00931//PF	Phvul.010G02	External stim	effector receptor (NLR) (original description: pacid=3714
PF00931//PF	Phvul.010G02	External stim	effector receptor (NLR) (original description: pacid=3714
PF00931//PF	Phvul.010G02	External stim	effector receptor (NLR) (original description: pacid=3714
PTHR13902//I	Phvul.010G06	Protein modif	protein kinase (MAP3K-WNK) (original description: pacid
PTHR13902//I	Phvul.010G06	Protein modif	protein kinase (MAP3K-WNK) (original description: pacid

PTHR13902//I	Phvul.010G06	Protein modif	protein kinase (MAP3K-WNK) (original description: paci
PTHR13902//I	Phvul.010G06	Protein modif	protein kinase (MAP3K-WNK) (original description: paci
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
K13335 - pero	Phvul.010G08	not assigned.	(original description: pacid=37142487 transcript=Phvul.
2.5.1.72 - Qui	Phvul.010G09	not assigned.	(original description: pacid=37143242 transcript=Phvul.
2.5.1.72 - Qui	Phvul.010G09	not assigned.	(original description: pacid=37143242 transcript=Phvul.
2.5.1.72 - Qui	Phvul.010G09	not assigned.	(original description: pacid=37143242 transcript=Phvul.
2.5.1.72 - Qui	Phvul.010G09	not assigned.	(original description: pacid=37143242 transcript=Phvul.
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
PTHR11200:S	Phvul.011G00	Multi-process	SAC-group-I inositol-polyphosphate 3,5-phosphatase (or
5.3.4.1 - Prote	Phvul.011G00	not assigned.	(original description: pacid=37156678 transcript=Phvul.
PF05678 - VQ	Phvul.011G20	External stim	WRKY33-activating protein (SIB) (original description: pa
PF05678 - VQ	Phvul.011G20	External stim	WRKY33-activating protein (SIB) (original description: pa
PF05678 - VQ	Phvul.011G20	External stim	WRKY33-activating protein (SIB) (original description: pa
PF05678 - VQ	Phvul.011G20	External stim	WRKY33-activating protein (SIB) (original description: pa
PTHR10774//I	Phvul.L00167	not assigned.	(original description: pacid=37157494 transcript=Phvul.
PTHR10774//I	Phvul.L00167	not assigned.	(original description: pacid=37157494 transcript=Phvul.
K12872 - pre-	Phvul.L00253	RNA processin	component MAC5 of non-snRNP MOS4-associated comp
K12872 - pre-	Phvul.L00253	RNA processin	component MAC5 of non-snRNP MOS4-associated comp
PTHR24089:S	Phvul.L00984	Solute transp	solute transporter (MTCC) (original description: pacid=3
PTHR24089:S	Phvul.L00984	Solute transp	solute transporter (MTCC) (original description: pacid=3
PTHR24089:S	Phvul.L00984	Solute transp	solute transporter (MTCC) (original description: pacid=3
PTHR24089:S	Phvul.L00984	Solute transp	solute transporter (MTCC) (original description: pacid=3

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avage heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
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isation (original description: pacid=37176892 transcript=Phvul.002G071800.1 locus=Phvul.002G071
isation (original description: pacid=37176892 transcript=Phvul.002G071800.1 locus=Phvul.002G071
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178944 transcript=Phvul.L009543.1 locus=Phvul.L009543 ID=Phvul.L009543.1.v2.1 annot-version=v
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avage heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
avage heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
avage heterodimer (original description: pacid=37176220 transcript=Phvul.002G267400.1 locus=Ph
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010G094450.1 locus=Phvul.010G094450 ID=Phvul.010G094450.1.v2.1 annot-version=v2.1) & Quinc
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iginal description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
iginal description: pacid=37156003 transcript=Phvul.011G001200.2 locus=Phvul.011G001200 ID=Ph
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011G004200.1 locus=Phvul.011G004200 ID=Phvul.011G004200.1.v2.1 annot-version=v2.1) & Prote
icid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
icid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
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icid=37155891 transcript=Phvul.011G203450.1 locus=Phvul.011G203450 ID=Phvul.011G203450.1.v
L001679.1 locus=Phvul.L001679 ID=Phvul.L001679.1.v2.1 annot-version=v2.1) & C2 and GRAM dom
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plex (original description: pacid=37157526 transcript=Phvul.L002537.1 locus=Phvul.L002537 ID=Phv
7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
7179027 transcript=Phvul.L009843.2 locus=Phvul.L009843 ID=Phvul.L009843.2.v2.1 annot-version=
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vul.002G267400 ID=Phvul.002G267400.1.v2.1 annot-version=v2.1) &
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ein EXECUTER 1, chloroplastic OS=Arabidopsis thaliana (sp|q93yw0|exec1_arath : 424.0)
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smembrane 9 superfamily member 9 OS=Arabidopsis thaliana (sp|q9c5n2|tmn9_arath : 972.0)
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ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 499.0)
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ɔt-version=v2.1) &
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sion=v2.1) &
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-related protein 2 OS=Oryza sativa subsp. japonica (sp|q6z256|arp2_orysj : 226.0)
-related protein 2 OS=Oryza sativa subsp. japonica (sp|q6z256|arp2_orysj : 226.0)
-related protein 2 OS=Oryza sativa subsp. japonica (sp|q6z256|arp2_orysj : 226.0)
-related protein 2 OS=Oryza sativa subsp. japonica (sp|q6z256|arp2_orysj : 226.0)
-related protein 2 OS=Arabidopsis thaliana (sp|q9lsd6|arp2_arath : 174.0)
-related protein 2 OS=Arabidopsis thaliana (sp|q9lsd6|arp2_arath : 174.0)
-related protein 2 OS=Arabidopsis thaliana (sp|q9lsd6|arp2_arath : 174.0)
-related protein 2 OS=Arabidopsis thaliana (sp|q9lsd6|arp2_arath : 174.0)
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1800 ID=Phvul.002G071800.1.v2.1 annot-version=v2.1) &
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ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 539.0)

atricopeptide repeat-containing protein At4g21190 OS=Arabidopsis thaliana (sp|q8lg95|pp332_ara

4G133400.1.v2.1 annot-version=v2.1) &

4G133400.1.v2.1 annot-version=v2.1) &

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ocus=Phvul.005G180200 ID=Phvul.005G180200.1.v2.1 annot-version=v2.1) &

ocus=Phvul.005G180200 ID=Phvul.005G180200.1.v2.1 annot-version=v2.1) &

06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &

06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &

06G019800 ID=Phvul.006G019800.1.v2.1 annot-version=v2.1) &

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tura stramonium (sp|p50165|trnh_datst : 311.0) (original description: pacid=37158053 transcript=

tura stramonium (sp|p50165|trnh_datst : 311.0) (original description: pacid=37158053 transcript=

moyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1_arath : 214.0)

amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1_arath : 214.0)
amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1_arath : 214.0)
amoyl-CoA reductase 1 OS=Arabidopsis thaliana (sp|q9s9n9|ccr1_arath : 214.0)
Phvul.008G282700.1.v2.1 annot-version=v2.1) &
smembrane 9 superfamily member 12 OS=Arabidopsis thaliana (sp|f4jre0|tmn12_arath : 1080.0)
ul.009G127300.1.v2.1 annot-version=v2.1) &
ul.009G127300.1.v2.1 annot-version=v2.1) &
ul.009G127300.1.v2.1 annot-version=v2.1) &
ul.009G127300.1.v2.1 annot-version=v2.1) &
nnot-version=v2.1) &
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tive disease resistance RPP13-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 265.0)
tive disease resistance RPP13-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 265.0)
tive disease resistance RPP13-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 265.0)
tive disease resistance RPP13-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 265.0)
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700.2 locus=Phvul.001G100700 ID=Phvul.001G100700.2.v2.1 annot-version=v2.1) &
700.2 locus=Phvul.001G100700 ID=Phvul.001G100700.2.v2.1 annot-version=v2.1) &
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7000.1.v2.1 annot-version=v2.1) &
ot-version=v2.1) &
ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
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violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
=Phvul.003G029000.2.v2.1 annot-version=v2.1) &
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41700.1.v2.1 annot-version=v2.1) &
00 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
00 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
00 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
00 ID=Phvul.003G231500.1.v2.1 annot-version=v2.1) &
denylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
294800.4.v2.1 annot-version=v2.1) &
294800.4.v2.1 annot-version=v2.1) &
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ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 499.0)
ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 499.0)
nnot-version=v2.1) &
=Phvul.005G010700 ID=Phvul.005G010700.2.v2.1 annot-version=v2.1) &
ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (
ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (
ctase acting on paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 68.0) (
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081600.1.v2.1 annot-version=v2.1) &
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xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
xylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
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vul.007G233800.2.v2.1 annot-version=v2.1) &
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e(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
e(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
e(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
e(50.2.4 : 244.3) (original description: pacid=37159277 transcript=Phvul.008G290300.1 locus=Phvu
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terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
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vul.010G048400.4.v2.1 annot-version=v2.1) &
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n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
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n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
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n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01
de methionine sulfoxide reductase B1, chloroplastic OS=Oryza sativa subsp. japonica (sp|q0dc89|m
de methionine sulfoxide reductase B1, chloroplastic OS=Oryza sativa subsp. japonica (sp|q0dc89|m
de methionine sulfoxide reductase B1, chloroplastic OS=Oryza sativa subsp. japonica (sp|q0dc89|m
de methionine sulfoxide reductase B1, chloroplastic OS=Oryza sativa subsp. japonica (sp|q0dc89|m
)200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
)200.3 locus=Phvul.011G190200 ID=Phvul.011G190200.3.v2.1 annot-version=v2.1) &
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hvul.001G200700.5.v2.1 annot-version=v2.1) &
hvul.001G200700.5.v2.1 annot-version=v2.1) &
hvul.001G200700.5.v2.1 annot-version=v2.1) &
hvul.001G200700.5.v2.1 annot-version=v2.1) &
hvul.001G200700.5.v2.1 annot-version=v2.1) &
hvul.001G200700.5.v2.1 annot-version=v2.1) &
hvul.001G200700.5.v2.1 annot-version=v2.1) &
x domain-containing protein 6 OS=Arabidopsis thaliana (sp|o48700|pub6_arath : 901.0)
se transferring one-carbon group(50.2.1 : 212.4) (original description: pacid=37169062 transcript=Pl
se transferring one-carbon group(50.2.1 : 212.4) (original description: pacid=37169062 transcript=Pl
).1.v2.1 annot-version=v2.1) &
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rsion=v2.1) &
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ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
ID=Phvul.002G165300.1.v2.1 annot-version=v2.1) &
216700.3.v2.1 annot-version=v2.1) &
216700.3.v2.1 annot-version=v2.1) &
216700.3.v2.1 annot-version=v2.1) &
216700.3.v2.1 annot-version=v2.1) &
esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)

violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 108.0)
v2.1 annot-version=v2.1) &
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mycin-sensitive aminopeptidase OS=Arabidopsis thaliana (sp|q8h0s9|psa_arath : 805.0)
mycin-sensitive aminopeptidase OS=Arabidopsis thaliana (sp|q8h0s9|psa_arath : 805.0)
ersion=v2.1) &
ersion=v2.1) &
ul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
ul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
ul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
ul.002G320900 ID=Phvul.002G320900.1.v2.1 annot-version=v2.1) &
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03G032300.1.v2.1 annot-version=v2.1) &
03G032300.1.v2.1 annot-version=v2.1) &
.1 locus=Phvul.003G057700 ID=Phvul.003G057700.1.v2.1 annot-version=v2.1) &
.1 locus=Phvul.003G057700 ID=Phvul.003G057700.1.v2.1 annot-version=v2.1) &
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not-version=v2.1) &
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able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)

able disease resistance protein At5g66900 OS=Arabidopsis thaliana (sp|q9fkz1|drl42_arath : 431.0)
able methyltransferase PMT20 OS=Arabidopsis thaliana (sp|q9c6s7|pmtk_arath : 983.0)
able methyltransferase PMT20 OS=Arabidopsis thaliana (sp|q9c6s7|pmtk_arath : 983.0)
ıdenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
ıdenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
ıdenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
ıdenylate-binding protein RBP47B OS=Arabidopsis thaliana (sp|q0ww84|rb47b_arath : 97.4)
G294800.4.v2.1 annot-version=v2.1) &
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G294800.4.v2.1 annot-version=v2.1) &
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ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 539.0)
ptor-like protein EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 539.0)
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)05G014300 ID=Phvul.005G014300.2.v2.1 annot-version=v2.1) &
POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439_arath : 760
on=v2.1) &
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.1.v2.1 annot-version=v2.1) &

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

ID=Phvul.006G105800.1.v2.1 annot-version=v2.1) &

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

polymerase II transcriptional coactivator KELP OS=Arabidopsis thaliana (sp|o65155|kelp_arath : 80

ot-version=v2.1) &

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iquitin-protein ligase CSU1 OS=Arabidopsis thaliana (sp|q9sy88|csu1_arath : 419.0)

iquitin-protein ligase CSU1 OS=Arabidopsis thaliana (sp|q9sy88|csu1_arath : 419.0)

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

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l.007G034000.2.v2.1 annot-version=v2.1) &

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6600.1.v2.1 annot-version=v2.1) &

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1 annot-version=v2.1) &
oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
oxylesterase 1 OS=Actinidia eriantha (sp|q0zpv7|cxe1_acter : 319.0)
1.v2.1 annot-version=v2.1) &
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-version=v2.1) &
min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 223.0)
min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 223.0)
min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 253.0)

min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 253.0)
min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 222.0)
min-2 OS=Pisum sativum (sp|p08688|alb2_pea : 222.0)
.1 annot-version=v2.1) &
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.1 annot-version=v2.1) &
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12100 ID=Phvul.008G012100.2.v2.1 annot-version=v2.1) &
12100 ID=Phvul.008G012100.2.v2.1 annot-version=v2.1) &
annot-version=v2.1) &
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00.6.v2.1 annot-version=v2.1) &
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nnot-version=v2.1) &
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nnot-version=v2.1) &
rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1_arath : 211.0)
rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1_arath : 211.0)
rogeneous nuclear ribonucleoprotein 1 OS=Arabidopsis thaliana (sp|q8w034|rnp1_arath : 211.0)
Phvul.008G282700.1.v2.1 annot-version=v2.1) &
Phvul.008G282700.1.v2.1 annot-version=v2.1) &
nnot-version=v2.1) &
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
terol-binding protein-related protein 1C OS=Arabidopsis thaliana (sp|q8l751|orp1c_arath : 1134.0)
1 annot-version=v2.1) &
1 annot-version=v2.1) &
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1 annot-version=v2.1) &
nnot-version=v2.1) &
nnot-version=v2.1) &
um basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Ph
um basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Ph
um basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Ph
um basilicum (sp|q9xgw0|comt1_ociba : 362.0) (original description: pacid=37151728 transcript=Ph
escription available(sp|f4jts8|nov_arath : 150.0)
escription available(sp|f4jts8|nov_arath : 150.0)
escription available(sp|f4jts8|nov_arath : 150.0)
escription available(sp|f4jts8|nov_arath : 150.0)
Phvul.010G043700.9.v2.1 annot-version=v2.1) &
Phvul.010G043700.9.v2.1 annot-version=v2.1) &
Phvul.010G043700.9.v2.1 annot-version=v2.1) &
Phvul.010G043700.9.v2.1 annot-version=v2.1) &
Phvul.010G043700.9.v2.1 annot-version=v2.1) &
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Phvul.010G043700.9.v2.1 annot-version=v2.1) &
Phvul.010G043700.9.v2.1 annot-version=v2.1) &
Phvul.010G043700.9.v2.1 annot-version=v2.1) &
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hvul.010G043700.9.v2.1 annot-version=v2.1) &

hvul.010G043700.9.v2.1 annot-version=v2.1) &

hvul.010G043700.9.v2.1 annot-version=v2.1) &

hvul.010G043700.9.v2.1 annot-version=v2.1) &

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hvul.010G043700.9.v2.1 annot-version=v2.1) &

hvul.010G043700.9.v2.1 annot-version=v2.1) &

hvul.010G043700.9.v2.1 annot-version=v2.1) &

nnot-version=v2.1) &

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

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

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

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

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

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

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

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

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

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

33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d

33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d

33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d

33.8) & Seed linoleate 9S-lipoxygenase OS=Glycine max (sp|p24095|loxx_soybn : 884.0) (original d

ul.011G013900.1.v2.1 annot-version=v2.1) &

ul.011G013900.1.v2.1 annot-version=v2.1) &

ul.011G013900.1.v2.1 annot-version=v2.1) &

ul.011G013900.1.v2.1 annot-version=v2.1) &

ersion=v2.1) &

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vul.011G061600.1.v2.1 annot-version=v2.1) &

vul.011G061600.1.v2.1 annot-version=v2.1) &

tein homolog 5 OS=Arabidopsis thaliana (sp|o23020|sph5_arath : 90.5)

tein homolog 5 OS=Arabidopsis thaliana (sp|o23020|sph5_arath : 90.9)

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n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01

n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01

n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01

n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01

n peptide bond (peptidase)(50.3.4 : 50.1) (original description: pacid=37155970 transcript=Phvul.01

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ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ATP-dependent zinc metalloprotease FTSHI 5, chloroplastic OS=Arabidopsis thaliana (sp|f4j3n2|ftsi
ul.L002537.1.v2.1 annot-version=v2.1) &
ul.L002537.1.v2.1 annot-version=v2.1) &
ul.L002537.1.v2.1 annot-version=v2.1) &

oreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tı
oreductase acting on CH-CH group of donor(50.1.3 : 281.4) (original description: pacid=37157789 tı
annot-version=v2.1) &
annot-version=v2.1) &
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0.1.v2.1 annot-version=v2.1) &
57800.1.v2.1 annot-version=v2.1) &
57800.1.v2.1 annot-version=v2.1) &
sion=v2.1) &
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-version=v2.1) &
-version=v2.1) &
09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
09300 ID=Phvul.001G109300.2.v2.1 annot-version=v2.1) &
2.1 annot-version=v2.1) &
2.1 annot-version=v2.1) &

-glucosidase OS=Spinacia oleracea (sp|o04893|aglu_spiol : 80.9)
-glucosidase OS=Spinacia oleracea (sp|o04893|aglu_spiol : 80.9)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
ive disease resistance protein RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 339.0)
.1 annot-version=v2.1) &
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.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
.1 annot-version=v2.1) &
ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
ressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|srfr1_arath : 275.0)
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.1.v2.1 annot-version=v2.1) &
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not-version=v2.1) &
esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)

esterase/lipase At1g29670 OS=Arabidopsis thaliana (sp|q9c7n4|gdl15_arath : 284.0)
violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 98.6)
violet-B receptor UVR8 OS=Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 98.6)
ul.002G262600.2.v2.1 annot-version=v2.1) &
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d GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath :
d GRAM domain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath :
not-version=v2.1) &
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.1.v2.1 annot-version=v2.1) &
annot-version=v2.1) &
nosin homolog OS=Arabidopsis thaliana (sp|p57758|ctns_arath : 317.0)
4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &
4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &
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4G121666 ID=Phvul.004G121666.1.v2.1 annot-version=v2.1) &
aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
aracterized protein At5g08430 OS=Arabidopsis thaliana (sp|q9ft92|y5843_arath : 311.0)
nnot-version=v2.1) &
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POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439_arath : 760
POZ domain-containing protein At1g04390 OS=Arabidopsis thaliana (sp|p93820|y1439_arath : 760
ersion=v2.1) &
ctional riboflavin kinase/FMN phosphatase OS=Arabidopsis thaliana (sp|q84md8|fhyrk_arath : 248
ot-version=v2.1) &

not-version=v2.1) &
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atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
atricopeptide repeat-containing protein At1g55630 OS=Arabidopsis thaliana (sp|q7x6a5|ppr81_ara
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x domain-containing protein 3 OS=Arabidopsis thaliana (sp|q8gwv5|pub3_arath : 647.0)
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hvul.007G215300.1.v2.1 annot-version=v2.1) &
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51800.1.v2.1 annot-version=v2.1) &
ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6_arath : 408.0)
ptor-like protein 6 OS=Arabidopsis thaliana (sp|q9c637|rlp6_arath : 408.0)
nnot-version=v2.1) &
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n=v2.1) &
lose synthase-like protein E6 OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)
lose synthase-like protein E6 OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)
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1.v2.1 annot-version=v2.1) &
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aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
aracterized protein At4g14100 OS=Arabidopsis thaliana (sp|q67yc9|y4141_arath : 263.0)
3100 ID=Phvul.009G203100.1.v2.1 annot-version=v2.1) &
not-version=v2.1) &
not-version=v2.1) &
not-version=v2.1) &
not-version=v2.1) &
r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
r envelope pore protein 16-2, chloroplastic OS=Arabidopsis thaliana (sp|q0wmz5|op162_arath : 18
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‹isome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
‹isome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
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‹isome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
‹isome biogenesis protein 16 OS=Arabidopsis thaliana (sp|q8s8s1|pex16_arath : 380.0)
olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada_arath : 152.0)
olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada_arath : 152.0)
olinate synthase, chloroplastic OS=Arabidopsis thaliana (sp|q9fgs4|nada_arath : 152.0)
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hvul.011G001200.2.v2.1 annot-version=v2.1) &
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hvul.011G001200.2.v2.1 annot-version=v2.1) &
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hvul.011G001200.2.v2.1 annot-version=v2.1) &
hvul.011G001200.2.v2.1 annot-version=v2.1) &
hvul.011G001200.2.v2.1 annot-version=v2.1) &
hvul.011G001200.2.v2.1 annot-version=v2.1) &
ein ORANGE, chloroplastic OS=Arabidopsis thaliana (sp|q9fkf4|orang_arath : 453.0)
/2.1 annot-version=v2.1) &
/2.1 annot-version=v2.1) &
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nain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath : 135.0)
nain-containing protein At1g03370 OS=Arabidopsis thaliana (sp|q9zvt9|c2gr1_arath : 135.0)
/ul.L002537.1.v2.1 annot-version=v2.1) &
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ı1400 ID=Phvul.007G211400.1.v2.1 annot-version=v2.1) &

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1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
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hvul.001G268700.1 locus=Phvul.001G268700 ID=Phvul.001G268700.1.v2.1 annot-version=v2.1) &

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l1G160800.3 locus=Phvul.011G160800 ID=Phvul.011G160800.3.v2.1 annot-version=v2.1) &
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miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
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uagcuuaucaga	Phvul.004G023066.1	3	-1	1	22
uagcuuaucaga	Phvul.004G023066.1	3	-1	1	23
uagcuuaucaga	Phvul.002G097400.1	3.5	-1	1	22
uagcuuaucaga	Phvul.002G097400.1	3.5	-1	1	22
uagcuuaucaga	Phvul.002G097400.1	3.5	-1	1	23
uagcuuaucaga	Phvul.006G008480.2	3.5	-1	1	22
uagcuuaucaga	Phvul.006G008480.1	3.5	-1	1	22
uagcuuaucaga	Phvul.006G008480.2	3.5	-1	1	22
uagcuuaucaga	Phvul.006G008480.1	3.5	-1	1	22
uagcuuaucaga	Phvul.006G008480.2	3.5	-1	1	23
uagcuuaucaga	Phvul.006G008480.1	3.5	-1	1	23
uagcuuaucaga	Phvul.006G029000.1	3.5	-1	1	22
uagcuuaucaga	Phvul.006G029000.1	3.5	-1	1	22
uagcuuaucaga	Phvul.006G029000.1	3.5	-1	1	23
uagcuuaucaga	Phvul.006G110300.1	3.5	-1	1	22
uagcuuaucaga	Phvul.006G110300.1	3.5	-1	1	22
uagcuuaucaga	Phvul.006G110300.1	3.5	-1	1	23
uagcuuaucaga	Phvul.007G191600.1	3.5	-1	1	22
uagcuuaucaga	Phvul.007G191600.1	3.5	-1	1	22
uagcuuaucaga	Phvul.007G191600.1	3.5	-1	1	23
uagcuuaucaga	Phvul.001G070000.1	4	-1	1	22
uagcuuaucaga	Phvul.001G070000.1	4	-1	1	22
uagcuuaucaga	Phvul.001G070000.1	4	-1	1	23
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uagcuuaucaga	Phvul.010G021700.1	5	-1	1	22
uagcuuaucaga	Phvul.010G021700.1	5	-1	1	23
uagcuuaucaga	Phvul.010G104900.2	5	-1	1	22
uagcuuaucaga	Phvul.010G104900.2	5	-1	1	22
uagcuuaucaga	Phvul.010G104900.2	5	-1	1	23
uagcuuaucaga	Phvul.010G129400.1	5	-1	1	22
uagcuuaucaga	Phvul.010G129400.1	5	-1	1	22
uagcuuaucaga	Phvul.010G129400.1	5	-1	1	23
uagcuuaucaga	Phvul.010G157900.4	5	-1	1	22
uagcuuaucaga	Phvul.010G157900.3	5	-1	1	22
uagcuuaucaga	Phvul.010G157900.2	5	-1	1	22
uagcuuaucaga	Phvul.010G157900.4	5	-1	1	22
uagcuuaucaga	Phvul.010G157900.3	5	-1	1	22
uagcuuaucaga	Phvul.010G157900.2	5	-1	1	22
uagcuuaucaga	Phvul.010G157900.4	5	-1	1	23
uagcuuaucaga	Phvul.010G157900.3	5	-1	1	23
uagcuuaucaga	Phvul.010G157900.2	5	-1	1	23
uagcuuaucaga	Phvul.011G006200.1	5	-1	1	22
uagcuuaucaga	Phvul.011G006200.1	5	-1	1	22
uagcuuaucaga	Phvul.011G006200.1	5	-1	1	23

uagcuuaucaga	Phvul.011G161100.1	5	-1	1	22
uagcuuaucaga	Phvul.011G161100.1	5	-1	1	22
uagcuuaucaga	Phvul.011G161100.1	5	-1	1	23
uagcuuaucaga	Phvul.011G161900.1	5	-1	1	22
uagcuuaucaga	Phvul.011G161900.1	5	-1	1	22

Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
1193	1214	UAGCUUAUCA	:::..:::::.::::: :	AGCACAUUG	Cleavage	pacid=371638
1193	1214	UAGCUUAUCA	:::..:::::.::::: :	AGCACAUUG	Cleavage	pacid=371638
1192	1214	UAGCUUAUCA	:::..:::::.:::::	AAGCACAUU	Cleavage	pacid=371638
1039	1060	UAGCUUAUCA	::::::.::.:.::::	UGAUGAUCA	Cleavage	pacid=371751
1039	1060	UAGCUUAUCA	::::::.::.:.::::	UGAUGAUCA	Cleavage	pacid=371751
1038	1060	UAGCUUAUCA	::::::.::.:.::::	CUGAUGAUCA	Cleavage	pacid=371751
2781	2802	UAGCUUAUCA	:::::. :::::::: :.::	AGAACAUUU	Cleavage	pacid=371720
2784	2805	UAGCUUAUCA	:::::. :::::::: :.::	AGAACAUUU	Cleavage	pacid=371720
2781	2802	UAGCUUAUCA	:::::. :::::::: :.::	AGAACAUUU	Cleavage	pacid=371720
2784	2805	UAGCUUAUCA	:::::. :::::::: :.::	AGAACAUUU	Cleavage	pacid=371720
2780	2802	UAGCUUAUCA	:::::. :::::::: :.:	UAGAACAUUU	Cleavage	pacid=371720
2783	2805	UAGCUUAUCA	:::::. :::::::: :.:	UAGAACAUUU	Cleavage	pacid=371720
811	832	UAGCUUAUCA	: :::::.::.::::::.	CCCUCCUCAG	Cleavage	pacid=371735
811	832	UAGCUUAUCA	: :::::.::.::::::.	CCCUCCUCAG	Cleavage	pacid=371735
810	832	UAGCUUAUCA	: :::::.::.::::::	UCCCUCCUCA	Cleavage	pacid=371735
1572	1594	UAGCUUAUCA	:..::: ::::::::: :::	UUGACAGUCA	Cleavage	pacid=371722
1572	1594	UAGCUUAUCA	:..::: ::::::::: :::	UUGACAGUCA	Cleavage	pacid=371722
1571	1594	UAGCUUAUCA	:..::: ::::::::: :::	UUUGACAGU	Cleavage	pacid=371722
3701	3722	UAGCUUAUCA	: :::::::::::.:: :.:	UGAACAUCAG	Cleavage	pacid=371651
3701	3722	UAGCUUAUCA	: :::::::::::.:: :.:	UGAACAUCAG	Cleavage	pacid=371651
3700	3722	UAGCUUAUCA	: :::::::::::.:: :.:	UUGAACAUCA	Cleavage	pacid=371651
263	284	UAGCUUAUCA	.:::::: :::::::::	UCCUAGUCA	Translation	pacid=371681
263	284	UAGCUUAUCA	.:::::: :::::::::	UCCUAGUCA	Translation	pacid=371681
262	284	UAGCUUAUCA	.:::::: ::::::::	CUCCUAGUCA	Translation	pacid=371681
835	856	UAGCUUAUCA	:::: : :::::::::::::	UCAAACUGU	Cleavage	pacid=371688
871	892	UAGCUUAUCA	:::: : :::::::::::::	UCAAACUGU	Cleavage	pacid=371688
835	856	UAGCUUAUCA	:::: : :::::::::::::	UCAAACUGU	Cleavage	pacid=371688
871	892	UAGCUUAUCA	:::: : :::::::::::::	UCAAACUGU	Cleavage	pacid=371688
834	856	UAGCUUAUCA	:::: : ::::::::::::	UUCAAACUGU	Cleavage	pacid=371688
870	892	UAGCUUAUCA	:::: : ::::::::::::	UUCAAACUGU	Cleavage	pacid=371688
483	504	UAGCUUAUCA	:::: ::: :::::::: :::	ACAACCUCAU	Cleavage	pacid=371764
483	504	UAGCUUAUCA	:::: ::: :::::::: :::	ACAACCUCAU	Cleavage	pacid=371764
482	504	UAGCUUAUCA	:::: ::: :::::::: ::	AACAACCUCA	Cleavage	pacid=371764
2079	2100	UAGCUUAUCA	:::::::::.: :::: .::	UGCACAUCAG	Cleavage	pacid=371447
2079	2100	UAGCUUAUCA	:::::::::.: :::: .::	UGCACAUCAG	Cleavage	pacid=371447
1281	1302	UAGCUUAUCA	::::::::.:::::: ::	AGUUCAUCA	Cleavage	pacid=371616
1281	1302	UAGCUUAUCA	::::::::.:::::: ::	AGUUCAUCA	Cleavage	pacid=371616
1280	1302	UAGCUUAUCA	::::::::.:::::: ::	CAGUUCAUCA	Cleavage	pacid=371616
3452	3473	UAGCUUAUCA	.::: :::: :::::::: ::	AUAACUUCAG	Cleavage	pacid=371630
3452	3473	UAGCUUAUCA	.::: :::: :::::::: ::	AUAACUUCAG	Cleavage	pacid=371630
3451	3473	UAGCUUAUCA	: .::: :::: :::::::: :	GAUAACUUCA	Cleavage	pacid=371630
1823	1846	UAGCUUAUCA	.:::::: :::.:::::::::	AUAACAUCCA	Cleavage	pacid=371529
1823	1846	UAGCUUAUCA	.:::::: :::.:::::::::	AUAACAUCCA	Cleavage	pacid=371529
1823	1846	UAGCUUAUCA	.:::::: :::.:::::::::	AUAACAUCCA	Cleavage	pacid=371529
1823	1846	UAGCUUAUCA	.:::::: :::.:::::::::	AUAACAUCCA	Cleavage	pacid=371529

1822	1846	UAGCUUAUC	.:::::: :::.:::::::	AAUAACAUC	Cleavage	pacid=371529
1822	1846	UAGCUUAUC	.:::::: :::.:::::::	AAUAACAUC	Cleavage	pacid=371529
287	308	UAGCUUAUC	: :: .: :::::: ::::::	UGAAGGUGA	Cleavage	pacid=371660
287	308	UAGCUUAUC	: :: .: :::::: ::::::	UGAAGGUGA	Cleavage	pacid=371660
95	116	UAGCUUAUC	: :: .: :::::: ::::::	UGAAGGUGA	Cleavage	pacid=371642
95	116	UAGCUUAUC	: :: .: :::::: ::::::	UGAAGGUGA	Cleavage	pacid=371642
2187	2208	UAGCUUAUC	::.:::: : :::::.::.:.	UCGACAUCU	Cleavage	pacid=371676
2187	2208	UAGCUUAUC	::.:::: : :::::.::.:.	UCGACAUCU	Cleavage	pacid=371676
2186	2208	UAGCUUAUC	::.:::: : :::::.::.:	AUCGACAUC	Cleavage	pacid=371676
948	969	UAGCUUAUC	: .: :::.:::::. :::::.	UGGAGAUCG	Cleavage	pacid=371669
1098	1119	UAGCUUAUC	: .: :::.:::::. :::::.	UGGAGAUCG	Cleavage	pacid=371669
948	969	UAGCUUAUC	: .: :::.:::::. :::::.	UGGAGAUCG	Cleavage	pacid=371669
1098	1119	UAGCUUAUC	: .: :::.:::::. :::::.	UGGAGAUCG	Cleavage	pacid=371669
947	969	UAGCUUAUC	:: .: :::.:::::. :::::	GUGGAGAUC	Cleavage	pacid=371669
1097	1119	UAGCUUAUC	:: .: :::.:::::. :::::	GUGGAGAUC	Cleavage	pacid=371669
2222	2243	UAGCUUAUC	:... ::: ::::::::.::::	UUGGGAUCC	Cleavage	pacid=371590
2222	2243	UAGCUUAUC	:... ::: ::::::::.::::	UUGGGAUCC	Cleavage	pacid=371590
2221	2243	UAGCUUAUC	:... ::: ::::::::.::::	AUUGGGAUC	Cleavage	pacid=371590
1470	1491	UAGCUUAUC	:::.::: ::::::.::: .::	UCAGCAUAA	Cleavage	pacid=371582
1470	1491	UAGCUUAUC	:::.::: ::::::.::: .::	UCAGCAUAA	Cleavage	pacid=371582
1469	1491	UAGCUUAUC	::::::: ::::::.::: .:	AUCAGCAUA	Cleavage	pacid=371582
1096	1117	UAGCUUAUC	::.:::..:: .:::::::	ACAGCAUUG	Translation	pacid=371550
1096	1117	UAGCUUAUC	::.:::..:: .:::::::	ACAGCAUUG	Translation	pacid=371550
1095	1117	UAGCUUAUC	::.:::..:: .::::::	AACAGCAUU	Translation	pacid=371550
852	873	UAGCUUAUC	:.:.:::::::::::...: :	UUAGCAUCA	Cleavage	pacid=371556
852	873	UAGCUUAUC	:.:.:::::::::::...: :	UUAGCAUCA	Cleavage	pacid=371556
851	873	UAGCUUAUC	:.:.:::::::::::...: :	AUUAGCAUC	Cleavage	pacid=371556
99	120	UAGCUUAUC	:::.::.:::.:::: :.:.	GCAAUAUUA	Cleavage	pacid=371484
99	120	UAGCUUAUC	:::.::.:::.:::: :.:.	GCAAUAUUA	Cleavage	pacid=371484
99	120	UAGCUUAUC	:::.::.:::.:::: :.:.	GCAAUAUUA	Cleavage	pacid=371484
99	120	UAGCUUAUC	:::.::.:::.:::: :.:.	GCAAUAUUA	Cleavage	pacid=371484
98	120	UAGCUUAUC	:::.::.:::.:::: :.:	AGCAAUAUU	Cleavage	pacid=371484
98	120	UAGCUUAUC	:::.::.:::.:::: :.:	AGCAAUAUU	Cleavage	pacid=371484
459	480	UAGCUUAUC	::::: :: .::::::::.:	AGAACAUGA	Cleavage	pacid=371702
459	480	UAGCUUAUC	::::: :: .::::::::.:	AGAACAUGA	Cleavage	pacid=371702
458	480	UAGCUUAUC	::::: :: .::::::::.:	UAGAACAUG	Cleavage	pacid=371702
780	801	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371690
780	801	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371690
661	682	UAGCUUAUC	: ...::.: ::::::.::::	UGGGUAUUA	Cleavage	pacid=371769
661	682	UAGCUUAUC	: ...::.: ::::::.::::	UGGGUAUUA	Cleavage	pacid=371769
660	682	UAGCUUAUC	: ...::.: ::::::.::::	UUGGGUAUU	Cleavage	pacid=371769
768	789	UAGCUUAUC	::::::: ::::.:.::	UACUGAUCA	Translation	pacid=371744
768	789	UAGCUUAUC	::::::: ::::.:.::	UACUGAUCA	Translation	pacid=371744
1209	1230	UAGCUUAUC	:::. .:::.::.:.::.:.	AGAACGCUA	Cleavage	pacid=371745
1209	1230	UAGCUUAUC	:::. .:::.::.:.::.:.	AGAACGCUA	Cleavage	pacid=371745
2296	2317	UAGCUUAUC	::. : ::::.:::::.:.:.	GCAGAAACA	Cleavage	pacid=371754

2296	2317	UAGCUUAUC	::. : ::::.:::::.:.:.	GCAGAAACA	Cleavage	pacid=371754
2295	2317	UAGCUUAUC	::. : ::::.:::::.:.:	UGCAGAAAC	Cleavage	pacid=371754
831	852	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371478
831	852	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371478
294	315	UAGCUUAUC	: .::::.. ::: .::::::	UGGACAUUG	Cleavage	pacid=371458
294	315	UAGCUUAUC	: .::::.. ::: .::::::	UGGACAUUG	Cleavage	pacid=371458
293	315	UAGCUUAUC	:: .::::.. ::: .:::::	GUGGACAUU	Cleavage	pacid=371458
125	146	UAGCUUAUC	: :.:: ..:::::::..:::	UGAGCACUG	Cleavage	pacid=371449
125	146	UAGCUUAUC	: :.:: ..:::::::..:::	UGAGCACUG	Cleavage	pacid=371449
124	146	UAGCUUAUC	: :.:: ..:::::::..:::	AUGAGCACU	Cleavage	pacid=371449
780	801	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371620
780	801	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371620
714	734	UAGCUUAUC	::.:: ::::.:::: :::::	ACAGCA-CAG	Cleavage	pacid=371638
714	734	UAGCUUAUC	::.:: ::::.:::: :::::	ACAGCA-CAG	Cleavage	pacid=371638
713	734	UAGCUUAUC	::.:: ::::.:::: ::::	CACAGCA-CA	Cleavage	pacid=371638
1341	1362	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1258	1279	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1418	1439	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1414	1435	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1341	1362	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1258	1279	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1418	1439	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1414	1435	UAGCUUAUC	::.::: ..::.: .::::::	UCGACACUG	Cleavage	pacid=371615
1340	1362	UAGCUUAUC	::.::: ..::.: .:::::	AUCGACACU	Cleavage	pacid=371615
1257	1279	UAGCUUAUC	::.::: ..::.: .:::::	AUCGACACU	Cleavage	pacid=371615
1417	1439	UAGCUUAUC	::.::: ..::.: .:::::	AUCGACACU	Cleavage	pacid=371615
1413	1435	UAGCUUAUC	::.::: ..::.: .:::::	AUCGACACU	Cleavage	pacid=371615
1969	1990	UAGCUUAUC	:: .:::::::::: :::.:	GCACUAUCA	Cleavage	pacid=371732
1969	1990	UAGCUUAUC	:: .:::::::::: :::.:	GCACUAUCA	Cleavage	pacid=371732
1968	1990	UAGCUUAUC	:: .:::::::::: :::.:	UGCACUAUC	Cleavage	pacid=371732
441	462	UAGCUUAUC	::: :::: ::::::..:.:.	CCAAGAUCA	Cleavage	pacid=371725
671	692	UAGCUUAUC	::: :::: ::::::..:.:.	CCAAGAUCA	Cleavage	pacid=371725
441	462	UAGCUUAUC	::: :::: ::::::..:.:.	CCAAGAUCA	Cleavage	pacid=371725
671	692	UAGCUUAUC	::: :::: ::::::..:.:.	CCAAGAUCA	Cleavage	pacid=371725
440	462	UAGCUUAUC	::: :::: ::::::..:.:	ACCAAGAUC	Cleavage	pacid=371725
670	692	UAGCUUAUC	::: :::: ::::::..:.:	ACCAAGAUC	Cleavage	pacid=371725
454	475	UAGCUUAUC	:::.::::.::. :::.::::	UCAGCAUCG	Translation	pacid=371642
454	475	UAGCUUAUC	:::.::::.::. :::.::::	UCAGCAUCG	Translation	pacid=371642
453	475	UAGCUUAUC	:::.::::.::. :::.::::	UUCAGCAUC	Translation	pacid=371642
1920	1941	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1924	1945	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1993	2014	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2005	2026	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2005	2026	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2009	2030	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2009	2030	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663

2097	2118	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2101	2122	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1920	1941	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1924	1945	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1993	2014	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2005	2026	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2005	2026	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2009	2030	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2009	2030	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2097	2118	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
2101	2122	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1629	1650	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1827	1848	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1831	1852	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1828	1849	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1832	1853	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1997	2018	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1629	1650	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1827	1848	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1831	1852	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1828	1849	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1832	1853	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1997	2018	UAGCUUAUC	: :.::: .:::::.:.: :::	UGAGCAUAG	Cleavage	pacid=371663
1728	1749	UAGCUUAUC	:: :.:: :::.::.:: .::	UCCAUAUGA	Cleavage	pacid=371580
1728	1749	UAGCUUAUC	:: :.:: :::.::.::: .::	UCCAUAUGA	Cleavage	pacid=371580
1146	1167	UAGCUUAUC	::. ::::.::.::: :::::	UCGUCAUCG	Cleavage	pacid=371506
1146	1167	UAGCUUAUC	::. ::::.::.::: :::::	UCGUCAUCG	Cleavage	pacid=371506
1145	1167	UAGCUUAUC	::. ::::.::.::: :::::	UUCGUCAUC	Cleavage	pacid=371506
750	771	UAGCUUAUC	.::.:::: .::::.: :::	AAGACGUCA	Cleavage	pacid=371507
751	772	UAGCUUAUC	.::.:::: .::::.: :::	AAGACGUCA	Cleavage	pacid=371507
750	771	UAGCUUAUC	.::.:::: .::::.: :::	AAGACGUCA	Cleavage	pacid=371507
751	772	UAGCUUAUC	.::.:::: .::::.: :::	AAGACGUCA	Cleavage	pacid=371507
786	807	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371493
786	807	UAGCUUAUC	::::::: ::::.:.::	UAGUGAUCA	Translation	pacid=371493
2152	2173	UAGCUUAUC	:: .:::::::.: :: ::.::	UCUGCAUCA	Cleavage	pacid=371502
2237	2258	UAGCUUAUC	:: .:::::::.: :: ::.::	UCUGCAUCA	Cleavage	pacid=371502
2326	2347	UAGCUUAUC	:: .:::::::.: :: ::.::	UCUGCAUCA	Cleavage	pacid=371502
2152	2173	UAGCUUAUC	:: .:::::::.: :: ::.::	UCUGCAUCA	Cleavage	pacid=371502
2237	2258	UAGCUUAUC	:: .:::::::.: :: ::.::	UCUGCAUCA	Cleavage	pacid=371502
2326	2347	UAGCUUAUC	:: .:::::::.: :: ::.::	UCUGCAUCA	Cleavage	pacid=371502
2151	2173	UAGCUUAUC	:: .:::::::.: :: ::.:	AUCUGCAUC	Cleavage	pacid=371502
2236	2258	UAGCUUAUC	:: .:::::::.: :: ::.:	AUCUGCAUC	Cleavage	pacid=371502
2325	2347	UAGCUUAUC	:: .:::::::.: :: ::.:	AUCUGCAUC	Cleavage	pacid=371502
908	929	UAGCUUAUC	:: ::.: ::::::::: :	GGAAAAUUA	Cleavage	pacid=371432
908	929	UAGCUUAUC	:: ::.: ::::::::: :	GGAAAAUUA	Cleavage	pacid=371432
1518	1539	UAGCUUAUC	::.:::: : :::: ::::::	CCAGCAUCU	Cleavage	pacid=371552

1518	1539	UAGCUUAUC	::.:::: : :::: ::::::	CCAGCAUCU	Cleavage	pacid=371552
1517	1539	UAGCUUAUC	::.:::: : :::: :::::	ACCAGCAUCU	Cleavage	pacid=371552
752	773	UAGCUUAUC	:::. : :::: :::::::.::	UCAGGAGCA	Translation	pacid=371566
752	773	UAGCUUAUC	:::. : :::: :::::::.::	UCAGGAGCA	Translation	pacid=371566
751	773	UAGCUUAUC	:::. : :::: :::::::.:	CUCAGGAGC	Translation	pacid=371566
3	24	UAGCUUAUC	:::::: ::::::::.	CACACAUCAU	Cleavage	pacid=371555
3	24	UAGCUUAUC	:::::: ::::::::.	CACACAUCAU	Cleavage	pacid=371555
2	24	UAGCUUAUC	:::::: ::::::::.	ACACACAUCA	Cleavage	pacid=371555
2751	2772	UAGCUUAUC	:: :::: ::: ::. ::::::	UCUACAUGA	Translation	pacid=371559
2751	2772	UAGCUUAUC	:: :::: ::: ::. ::::::	UCUACAUGA	Translation	pacid=371559
2750	2772	UAGCUUAUC	::: :::: ::: ::. :::::	GUCUACAUG	Translation	pacid=371559
1565	1586	UAGCUUAUC	::... ::: ::::::.:.::	GCAGUGGCA	Cleavage	pacid=371701
1565	1586	UAGCUUAUC	::... ::: ::::::.:.::	GCAGUGGCA	Cleavage	pacid=371701
1564	1586	UAGCUUAUC	::... ::: ::::::.:.:	AGCAGUGGC	Cleavage	pacid=371701
1691	1712	UAGCUUAUC	:... ::..:::: ::..::::	UUGGAAUUG	Cleavage	pacid=371762
1829	1850	UAGCUUAUC	:... ::..:::: ::..::::	UUGGAAUUG	Cleavage	pacid=371762
1691	1712	UAGCUUAUC	:... ::..:::: ::..::::	UUGGAAUUG	Cleavage	pacid=371762
1829	1850	UAGCUUAUC	:... ::..:::: ::..::::	UUGGAAUUG	Cleavage	pacid=371762
1690	1712	UAGCUUAUC	::... ::..:::: ::..:::	GUUGGAAUU	Cleavage	pacid=371762
1828	1850	UAGCUUAUC	::... ::..:::: ::..:::	GUUGGAAUU	Cleavage	pacid=371762
133	154	UAGCUUAUC	:::::: :::: ::.::.::	ACAACAUGA	Translation	pacid=371760
133	154	UAGCUUAUC	:::::: :::: ::.::.::	ACAACAUGA	Translation	pacid=371760
132	154	UAGCUUAUC	:::::: :::: ::.::.:	UACAACAUG	Translation	pacid=371760
863	884	UAGCUUAUC	:...: :::::.::::: ::	UUGGCUUCA	Cleavage	pacid=371776
863	884	UAGCUUAUC	:...: :::::.::::: ::	UUGGCUUCA	Cleavage	pacid=371776
862	884	UAGCUUAUC	:...: :::::.::::: :	UUUGGCUUC	Cleavage	pacid=371776
685	707	UAGCUUAUC	::::::: .::::::::.:	AUUUCAUCA	Translation	pacid=371755
726	748	UAGCUUAUC	::::::: .::::::::.:	AUUUCAUCA	Translation	pacid=371755
685	707	UAGCUUAUC	::::::: .::::::::.:	AUUUCAUCA	Translation	pacid=371755
726	748	UAGCUUAUC	::::::: .::::::::.:	AUUUCAUCA	Translation	pacid=371755
1047	1068	UAGCUUAUC	:..::::..: .: :::::.::	UUGACAUUG	Cleavage	pacid=371444
1047	1068	UAGCUUAUC	:..::::..: .: :::::.::	UUGACAUUG	Cleavage	pacid=371444
1046	1068	UAGCUUAUC	:..::::..: .: :::::.:	UUUGACAUU	Cleavage	pacid=371444
768	790	UAGCUUAUC	::: :: :::::. :::.:::	GUCUACUUC	Translation	pacid=371478
630	651	UAGCUUAUC	:: .:::::::::: :.: .:.	UCUGCAUCA	Cleavage	pacid=371479
630	651	UAGCUUAUC	:: .:::::::::: :.: .:.	UCUGCAUCA	Cleavage	pacid=371479
845	866	UAGCUUAUC	:::::: :: :::: :::::	ACAACAUGA	Cleavage	pacid=371457
845	866	UAGCUUAUC	:::::: :: :::: :::::	ACAACAUGA	Cleavage	pacid=371457
844	866	UAGCUUAUC	:::::: :: :::: :::::	UACAACAUG	Cleavage	pacid=371457
1335	1356	UAGCUUAUC	:.:::::: ::.:: :::.::	UUAACAUCC	Cleavage	pacid=371619
1438	1459	UAGCUUAUC	:.:::::: ::.:: :::.::	UUAACAUCC	Cleavage	pacid=371619
1523	1544	UAGCUUAUC	:.:::::: ::.:: :::.::	UUAACAUCC	Cleavage	pacid=371619
1335	1356	UAGCUUAUC	:.:::::: ::.:: :::.::	UUAACAUCC	Cleavage	pacid=371619
1438	1459	UAGCUUAUC	:.:::::: ::.:: :::.::	UUAACAUCC	Cleavage	pacid=371619
1523	1544	UAGCUUAUC	:.:::::: ::.:: :::.::	UUAACAUCC	Cleavage	pacid=371619
1334	1356	UAGCUUAUC	::.:::::: ::.:: :::.:	GUUAACAUC	Cleavage	pacid=371619

1437	1459	UAGCUUAUCA	::.:::::: ::.:: :::.:	GUUAACAUC	Cleavage	pacid=371619
1522	1544	UAGCUUAUCA	::.:::::: ::.:: :::.:	GUUAACAUC	Cleavage	pacid=371619
1415	1436	UAGCUUAUCA	:.....:..::: ::..:::	UUGGUGUUG	Cleavage	pacid=371625
1415	1436	UAGCUUAUCA	:.....:..::: ::..:::	UUGGUGUUG	Cleavage	pacid=371625
1415	1436	UAGCUUAUCA	:.....:..::: ::..:::	UUGGUGUUG	Cleavage	pacid=371625
1415	1436	UAGCUUAUCA	:.....:..::: ::..:::	UUGGUGUUG	Cleavage	pacid=371625
1414	1436	UAGCUUAUCA	::.....:..::: ::..:::	GUUGGUGUU	Cleavage	pacid=371625
1414	1436	UAGCUUAUCA	::.....:..::: ::..:::	GUUGGUGUU	Cleavage	pacid=371625
1345	1366	UAGCUUAUCA	::.:: :: :.:::: ::::	GCAGCAACAC	Cleavage	pacid=371625
1345	1366	UAGCUUAUCA	::.:: :: :.:::: ::::	GCAGCAACAC	Cleavage	pacid=371625
1344	1366	UAGCUUAUCA	::.:: :: :.:::: :::	AGCAGCAACA	Cleavage	pacid=371625
636	657	UAGCUUAUCA	:: :::::::.::.:. :. :	UCCACAUCAG	Cleavage	pacid=371531
636	657	UAGCUUAUCA	:: :::::::.::.:. :. :	UCCACAUCAG	Cleavage	pacid=371531
167	188	UAGCUUAUCA	:::: ::. : .:::::::::.	UCAAGAUUC	Cleavage	pacid=371718
167	188	UAGCUUAUCA	:::: ::. : .:::::::::.	UCAAGAUUC	Cleavage	pacid=371718
166	188	UAGCUUAUCA	:::: ::. : .::::::::	UUCAAGAUU	Cleavage	pacid=371718
606	627	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
709	730	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
721	742	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
736	757	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
741	762	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
849	870	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
895	916	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
606	627	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
709	730	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
721	742	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
736	757	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
741	762	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
849	870	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
895	916	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
471	492	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
652	673	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
744	765	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
1237	1258	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
471	492	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
652	673	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
744	765	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
1237	1258	UAGCUUAUCA	:::.::. :.::: .:::::	GAAACGUCG	Cleavage	pacid=371640
327	348	UAGCUUAUCA	:..:::::::.::. :: ::.	GCGGCAUCA	Cleavage	pacid=371657
327	348	UAGCUUAUCA	:..:::::::.::. :: ::.	GCGGCAUCA	Cleavage	pacid=371657
326	348	UAGCUUAUCA	:..:::::::.::. :: ::	CGCGGCAUCA	Cleavage	pacid=371657
1317	1338	UAGCUUAUCA	:..:.::. ::.::.:.::.:	UUGAUAUUU	Cleavage	pacid=371655
1317	1338	UAGCUUAUCA	:..:.::. ::.::.:.::.:	UUGAUAUUU	Cleavage	pacid=371655
1316	1338	UAGCUUAUCA	:..:.::. ::.::.:.::.:	AUUGAUAUU	Cleavage	pacid=371655
463	484	UAGCUUAUCA	.:. : ::::::::::::	AUAGAAGCA	Cleavage	pacid=371610
1712	1733	UAGCUUAUCA	.:. : ::::::::::::	AUAGAAGCA	Cleavage	pacid=371610

3970	3991	UAGCUUAUC	.:. : :::::::::::::	AUAGAAGCA	Cleavage	pacid=371610
4017	4038	UAGCUUAUC	.:. : :::::::::::::	AUAGAAGCA	Cleavage	pacid=371610
463	484	UAGCUUAUC	.:. : :::::::::::::	AUAGAAGCA	Cleavage	pacid=371610
1712	1733	UAGCUUAUC	.:. : :::::::::::::	AUAGAAGCA	Cleavage	pacid=371610
3970	3991	UAGCUUAUC	.:. : :::::::::::::	AUAGAAGCA	Cleavage	pacid=371610
4017	4038	UAGCUUAUC	.:. : :::::::::::::	AUAGAAGCA	Cleavage	pacid=371610
1321	1342	UAGCUUAUC	::.:::::::.::: .: .::	AAAAUAUCA	Cleavage	pacid=371593
1321	1342	UAGCUUAUC	::.:::::::.::: .: .::	AAAAUAUCA	Cleavage	pacid=371593
1781	1802	UAGCUUAUC	.:.:::::::.:::: ::	CUAGCAUCA	Cleavage	pacid=371590
1781	1802	UAGCUUAUC	.:.:::::::.:::: ::	CUAGCAUCA	Cleavage	pacid=371590
1780	1802	UAGCUUAUC	.:.:::::::.:::: ::	UCUAGCAUC	Cleavage	pacid=371590
1544	1565	UAGCUUAUC	:....::: ::: ::::.:::	UUGGUAUCU	Translation	pacid=371606
1544	1565	UAGCUUAUC	:....::: ::: ::::.:::	UUGGUAUCU	Translation	pacid=371606
1543	1565	UAGCUUAUC	:....::: ::: ::::.:::	AUUGGUAUC	Translation	pacid=371606
955	979	UAGCUUAUC	::. :::: :::::::: :::	GUUCACAUU	Cleavage	pacid=371603
500	522	UAGCUUAUC	::: ::::: :::::::::.	GUCCUAAUC	Cleavage	pacid=371593
382	403	UAGCUUAUC	::::::: ::::::::.:.	GAAACAUCA	Cleavage	pacid=371512
382	403	UAGCUUAUC	::::::: ::::::::.:.	GAAACAUCA	Cleavage	pacid=371512
381	403	UAGCUUAUC	::::::: ::::::::.:.	AGAAACAUC	Cleavage	pacid=371512
5344	5365	UAGCUUAUC	::::.::.:::: :::.:	UGUUCAUCG	Cleavage	pacid=371485
5344	5365	UAGCUUAUC	::::.::.:::: :::.:	UGUUCAUCG	Cleavage	pacid=371485
5343	5365	UAGCUUAUC	::::.::.:::: :::.:	CUGUUCAUC	Cleavage	pacid=371485
926	947	UAGCUUAUC	..::::::::::. ::: :	AUGACAUCA	Cleavage	pacid=371519
926	947	UAGCUUAUC	..::::::::::. ::: :	AUGACAUCA	Cleavage	pacid=371519
925	947	UAGCUUAUC	: ..::::::::.:: ::: :	GAUGACAUC	Cleavage	pacid=371519
1319	1340	UAGCUUAUC	:::.: .:::.: ::.::.::	ACAAUAAUA	Cleavage	pacid=371431
1319	1340	UAGCUUAUC	:::.: .:::.: ::.::.::	ACAAUAAUA	Cleavage	pacid=371431
1318	1340	UAGCUUAUC	:::.: .:::.: ::.::.:	AACAAUAAU	Cleavage	pacid=371431
142	163	UAGCUUAUC	::.::::: :::: .::.:: :	UCGACAUCU	Cleavage	pacid=371436
142	163	UAGCUUAUC	::.::::: :::: .::.:: :	UCGACAUCU	Cleavage	pacid=371436
141	163	UAGCUUAUC	:::.::::: :::: .::.::	GUCGACAUC	Cleavage	pacid=371436
532	553	UAGCUUAUC	::::: ::::. :: :::::.	ACAACAACAG	Translation	pacid=371440
532	553	UAGCUUAUC	::::: ::::. :: :::::.	ACAACAACAG	Translation	pacid=371440
531	553	UAGCUUAUC	: ::::: ::::. :: :::::	GACAACAACA	Translation	pacid=371440
1994	2014	UAGCUUAUC	:::. ::::: .:::::::::.	UCAG-AUCAG	Cleavage	pacid=371441
2056	2076	UAGCUUAUC	:::. ::::: .:::::::::.	UCAG-AUCAG	Cleavage	pacid=371441
2070	2090	UAGCUUAUC	:::. ::::: .:::::::::.	UCAG-AUCAG	Cleavage	pacid=371441
1994	2014	UAGCUUAUC	:::. ::::: .:::::::::.	UCAG-AUCAG	Cleavage	pacid=371441
2056	2076	UAGCUUAUC	:::. ::::: .:::::::::.	UCAG-AUCAG	Cleavage	pacid=371441
2070	2090	UAGCUUAUC	:::. ::::: .:::::::::.	UCAG-AUCAG	Cleavage	pacid=371441
1993	2014	UAGCUUAUC	:::. ::::: .:::::::::	AUCAG-AUCA	Cleavage	pacid=371441
2055	2076	UAGCUUAUC	:::. ::::: .:::::::::	AUCAG-AUCA	Cleavage	pacid=371441
2069	2090	UAGCUUAUC	:::. ::::: .:::::::::	AUCAG-AUCA	Cleavage	pacid=371441
1207	1229	UAGCUUAUC	.::.::::: :.::.:.::::	CUAAUAUCA	Cleavage	pacid=371561
1207	1229	UAGCUUAUC	.::.::::: :.::.:.::::	CUAAUAUCA	Cleavage	pacid=371561
1206	1229	UAGCUUAUC	.::.::::: :.::.:.:::	ACUAAUAUC	Cleavage	pacid=371561

470	491	UAGCUUAUC	::: :: ..: ::::::::.::	UCACCAAUG	Cleavage	pacid=371556
470	491	UAGCUUAUC	::: :: ..: ::::::::.::	UCACCAAUG	Cleavage	pacid=371556
469	491	UAGCUUAUC	::: :: ..: ::::::::.:	UUCACCAAU	Cleavage	pacid=371556
413	434	UAGCUUAUC	::: : ..:::::.::::.::	UCAUCUGUG	Cleavage	pacid=371568
413	434	UAGCUUAUC	::: : ..:::::.::::.::	UCAUCUGUG	Cleavage	pacid=371568

Multiplicity	Target_Acc.	ID	locusName	Pfam
1	Phvul.004G023066.1	Phvul.004G023066	Phvul.004G023066	PF00005,PF00
1	Phvul.004G023066.1	Phvul.004G023066	Phvul.004G023066	PF00005,PF00
1	Phvul.004G023066.1	Phvul.004G023066	Phvul.004G023066	PF00005,PF00
1	Phvul.002G097400.1	Phvul.002G097400	Phvul.002G097400	PF01193,PF01
1	Phvul.002G097400.1	Phvul.002G097400	Phvul.002G097400	PF01193,PF01
1	Phvul.002G097400.1	Phvul.002G097400	Phvul.002G097400	PF01193,PF01
1	Phvul.006G008480.2	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.1	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.2	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.1	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.2	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G008480.1	Phvul.006G008480	Phvul.006G008480	PF00917,PF13
1	Phvul.006G029000.1	Phvul.006G029000	Phvul.006G029000	PF08263,PF00
1	Phvul.006G029000.1	Phvul.006G029000	Phvul.006G029000	PF08263,PF00
1	Phvul.006G029000.1	Phvul.006G029000	Phvul.006G029000	PF08263,PF00
1	Phvul.006G110300.1	Phvul.006G110300	Phvul.006G110300	PF00153
1	Phvul.006G110300.1	Phvul.006G110300	Phvul.006G110300	PF00153
1	Phvul.006G110300.1	Phvul.006G110300	Phvul.006G110300	PF00153
1	Phvul.007G191600.1	Phvul.007G191600	Phvul.007G191600	PF00271,PF00
1	Phvul.007G191600.1	Phvul.007G191600	Phvul.007G191600	PF00271,PF00
1	Phvul.007G191600.1	Phvul.007G191600	Phvul.007G191600	PF00271,PF00
1	Phvul.001G070000.1	Phvul.001G070000	Phvul.001G070000	PF07714
1	Phvul.001G070000.1	Phvul.001G070000	Phvul.001G070000	PF07714
1	Phvul.001G070000.1	Phvul.001G070000	Phvul.001G070000	PF07714
1	Phvul.001G264600.2	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.1	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.2	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.1	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.2	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.001G264600.1	Phvul.001G264600	Phvul.001G264600	PF01936
1	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
1	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
1	Phvul.002G153500.1	Phvul.002G153500	Phvul.002G153500	PF04321
1	Phvul.003G092500.1	Phvul.003G092500	Phvul.003G092500	PF00403
1	Phvul.003G092500.1	Phvul.003G092500	Phvul.003G092500	PF00403
1	Phvul.004G000300.1	Phvul.004G000300	Phvul.004G000300	PF13180,PF13
1	Phvul.004G000300.1	Phvul.004G000300	Phvul.004G000300	PF13180,PF13
1	Phvul.004G000300.1	Phvul.004G000300	Phvul.004G000300	PF13180,PF13
1	Phvul.004G126100.1	Phvul.004G126100	Phvul.004G126100	PF08263,PF00
1	Phvul.004G126100.1	Phvul.004G126100	Phvul.004G126100	PF08263,PF00
1	Phvul.004G126100.1	Phvul.004G126100	Phvul.004G126100	PF08263,PF00
1	Phvul.005G063700.2	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.005G063700.1	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.005G063700.2	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.005G063700.1	Phvul.005G063700	Phvul.005G063700	PF07714

1	Phvul.005G063700.2	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.005G063700.1	Phvul.005G063700	Phvul.005G063700	PF07714
1	Phvul.007G020600.1	Phvul.007G020600	Phvul.007G020600	PF00201
1	Phvul.007G020600.1	Phvul.007G020600	Phvul.007G020600	PF00201
1	Phvul.007G020700.1	Phvul.007G020700	Phvul.007G020700	PF00201
1	Phvul.007G020700.1	Phvul.007G020700	Phvul.007G020700	PF00201
1	Phvul.007G080800.1	Phvul.007G080800	Phvul.007G080800	PF03033
1	Phvul.007G080800.1	Phvul.007G080800	Phvul.007G080800	PF03033
1	Phvul.007G080800.1	Phvul.007G080800	Phvul.007G080800	PF03033
1	Phvul.007G254000.2	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
1	Phvul.007G254000.1	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
1	Phvul.007G254000.2	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
1	Phvul.007G254000.1	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
1	Phvul.007G254000.2	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
1	Phvul.007G254000.1	Phvul.007G254000	Phvul.007G254000	PF00954,PF07
1	Phvul.008G212500.1	Phvul.008G212500	Phvul.008G212500	PF01476,PF00
1	Phvul.008G212500.1	Phvul.008G212500	Phvul.008G212500	PF01476,PF00
1	Phvul.008G212500.1	Phvul.008G212500	Phvul.008G212500	PF01476,PF00
1	Phvul.008G266300.1	Phvul.008G266300	Phvul.008G266300	PF16656,PF14
1	Phvul.008G266300.1	Phvul.008G266300	Phvul.008G266300	PF16656,PF14
1	Phvul.008G266300.1	Phvul.008G266300	Phvul.008G266300	PF16656,PF14
1	Phvul.011G002600.1	Phvul.011G002600	Phvul.011G002600	0
1	Phvul.011G002600.1	Phvul.011G002600	Phvul.011G002600	0
1	Phvul.011G002600.1	Phvul.011G002600	Phvul.011G002600	0
1	Phvul.011G194501.1	Phvul.011G194501	Phvul.011G194501	PF01657
1	Phvul.011G194501.1	Phvul.011G194501	Phvul.011G194501	PF01657
1	Phvul.011G194501.1	Phvul.011G194501	Phvul.011G194501	PF01657
1	Phvul.L000308.2	Phvul.L000308	Phvul.L000308	PF00847
1	Phvul.L000308.1	Phvul.L000308	Phvul.L000308	PF00847
1	Phvul.L000308.2	Phvul.L000308	Phvul.L000308	PF00847
1	Phvul.L000308.1	Phvul.L000308	Phvul.L000308	PF00847
1	Phvul.L000308.2	Phvul.L000308	Phvul.L000308	PF00847
1	Phvul.L000308.1	Phvul.L000308	Phvul.L000308	PF00847
1	Phvul.001G021750.1	Phvul.001G021750	Phvul.001G021750	PF00036
1	Phvul.001G021750.1	Phvul.001G021750	Phvul.001G021750	PF00036
1	Phvul.001G021750.1	Phvul.001G021750	Phvul.001G021750	PF00036
1	Phvul.001G168600.1	Phvul.001G168600	Phvul.001G168600	PF12776
1	Phvul.001G168600.1	Phvul.001G168600	Phvul.001G168600	PF12776
1	Phvul.002G010100.1	Phvul.002G010100	Phvul.002G010100	PF10225
1	Phvul.002G010100.1	Phvul.002G010100	Phvul.002G010100	PF10225
1	Phvul.002G010100.1	Phvul.002G010100	Phvul.002G010100	PF10225
1	Phvul.002G149100.1	Phvul.002G149100	Phvul.002G149100	PF12776
1	Phvul.002G149100.1	Phvul.002G149100	Phvul.002G149100	PF12776
1	Phvul.002G155200.1	Phvul.002G155200	Phvul.002G155200	PF02214
1	Phvul.002G155200.1	Phvul.002G155200	Phvul.002G155200	PF02214
1	Phvul.002G211400.1	Phvul.002G211400	Phvul.002G211400	PF03000

1	Phvul.002G211400.1	Phvul.002G211400	Phvul.002G211400	PF03000
1	Phvul.002G211400.1	Phvul.002G211400	Phvul.002G211400	PF03000
1	Phvul.003G069400.1	Phvul.003G069400	Phvul.003G069400	PF12776
1	Phvul.003G069400.1	Phvul.003G069400	Phvul.003G069400	PF12776
1	Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
1	Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
1	Phvul.003G141800.1	Phvul.003G141800	Phvul.003G141800	PF02225,PF06
1	Phvul.003G239800.1	Phvul.003G239800	Phvul.003G239800	0
1	Phvul.003G239800.1	Phvul.003G239800	Phvul.003G239800	0
1	Phvul.003G239800.1	Phvul.003G239800	Phvul.003G239800	0
1	Phvul.004G053900.1	Phvul.004G053900	Phvul.004G053900	PF12776
1	Phvul.004G053900.1	Phvul.004G053900	Phvul.004G053900	PF12776
1	Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
1	Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
1	Phvul.004G157700.1	Phvul.004G157700	Phvul.004G157700	PF10496
1	Phvul.004G177000.3	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.2	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.4	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.1	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.3	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.2	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.4	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.1	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.3	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.2	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.4	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.004G177000.1	Phvul.004G177000	Phvul.004G177000	0
1	Phvul.006G103900.1	Phvul.006G103900	Phvul.006G103900	PF02736,PF00
1	Phvul.006G103900.1	Phvul.006G103900	Phvul.006G103900	PF02736,PF00
1	Phvul.006G103900.1	Phvul.006G103900	Phvul.006G103900	PF02736,PF00
1	Phvul.006G158500.2	Phvul.006G158500	Phvul.006G158500	PF13920
1	Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
1	Phvul.006G158500.2	Phvul.006G158500	Phvul.006G158500	PF13920
1	Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
1	Phvul.006G158500.2	Phvul.006G158500	Phvul.006G158500	PF13920
1	Phvul.006G158500.1	Phvul.006G158500	Phvul.006G158500	PF13920
1	Phvul.007G054000.2	Phvul.007G054000	Phvul.007G054000	PF04851,PF14
1	Phvul.007G054000.2	Phvul.007G054000	Phvul.007G054000	PF04851,PF14
1	Phvul.007G054000.2	Phvul.007G054000	Phvul.007G054000	PF04851,PF14
1	Phvul.007G154900.2	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.3	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.9	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.7	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.6	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.5	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.8	Phvul.007G154900	Phvul.007G154900	PF13921

1	Phvul.007G154900.4	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.1	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.2	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.3	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.9	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.7	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.6	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.5	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.8	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.4	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.1	Phvul.007G154900	Phvul.007G154900	PF13921
1	Phvul.007G154900.15	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.13	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.14	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.11	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.12	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.10	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.15	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.13	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.14	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.11	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.12	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.007G154900.10	Phvul.007G154900.	Phvul.007G154900	PF13921
1	Phvul.008G106500.1	Phvul.008G106500	Phvul.008G106500	PF08263,PF13
1	Phvul.008G106500.1	Phvul.008G106500	Phvul.008G106500	PF08263,PF13
1	Phvul.009G021300.1	Phvul.009G021300	Phvul.009G021300	PF01490
1	Phvul.009G021300.1	Phvul.009G021300	Phvul.009G021300	PF01490
1	Phvul.009G021300.1	Phvul.009G021300	Phvul.009G021300	PF01490
1	Phvul.009G097000.1	Phvul.009G097000	Phvul.009G097000	PF09762
1	Phvul.009G097000.2	Phvul.009G097000	Phvul.009G097000	PF09762
1	Phvul.009G097000.1	Phvul.009G097000	Phvul.009G097000	PF09762
1	Phvul.009G097000.2	Phvul.009G097000	Phvul.009G097000	PF09762
1	Phvul.009G122000.1	Phvul.009G122000	Phvul.009G122000	PF12776
1	Phvul.009G122000.1	Phvul.009G122000	Phvul.009G122000	PF12776
1	Phvul.009G227900.2	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.3	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.1	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.2	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.3	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.1	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.2	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.3	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.009G227900.1	Phvul.009G227900	Phvul.009G227900	PF03456,PF02
1	Phvul.010G159600.1	Phvul.010G159600	Phvul.010G159600	PF03556
1	Phvul.010G159600.1	Phvul.010G159600	Phvul.010G159600	PF03556
1	Phvul.011G084000.1	Phvul.011G084000	Phvul.011G084000	PF12848,PF00

1	Phvul.011G084000.1	Phvul.011G084000	Phvul.011G084000	PF12848,PF00
1	Phvul.011G084000.1	Phvul.011G084000	Phvul.011G084000	PF12848,PF00
1	Phvul.011G130500.1	Phvul.011G130500	Phvul.011G130500	0
1	Phvul.011G130500.1	Phvul.011G130500	Phvul.011G130500	0
1	Phvul.011G130500.1	Phvul.011G130500	Phvul.011G130500	0
1	Phvul.011G158500.1	Phvul.011G158500	Phvul.011G158500	PF00201
1	Phvul.011G158500.1	Phvul.011G158500	Phvul.011G158500	PF00201
1	Phvul.011G158500.1	Phvul.011G158500	Phvul.011G158500	PF00201
1	Phvul.011G198100.1	Phvul.011G198100	Phvul.011G198100	PF00931
1	Phvul.011G198100.1	Phvul.011G198100	Phvul.011G198100	PF00931
1	Phvul.011G198100.1	Phvul.011G198100	Phvul.011G198100	PF00931
1	Phvul.001G199500.1	Phvul.001G199500	Phvul.001G199500	PF01805,PF04
1	Phvul.001G199500.1	Phvul.001G199500	Phvul.001G199500	PF01805,PF04
1	Phvul.001G199500.1	Phvul.001G199500	Phvul.001G199500	PF01805,PF04
1	Phvul.002G005300.2	Phvul.002G005300	Phvul.002G005300	PF03372
1	Phvul.002G005300.1	Phvul.002G005300	Phvul.002G005300	PF03372
1	Phvul.002G005300.2	Phvul.002G005300	Phvul.002G005300	PF03372
1	Phvul.002G005300.1	Phvul.002G005300	Phvul.002G005300	PF03372
1	Phvul.002G005300.2	Phvul.002G005300	Phvul.002G005300	PF03372
1	Phvul.002G005300.1	Phvul.002G005300	Phvul.002G005300	PF03372
1	Phvul.002G119100.1	Phvul.002G119100	Phvul.002G119100	0
1	Phvul.002G119100.1	Phvul.002G119100	Phvul.002G119100	0
1	Phvul.002G119100.1	Phvul.002G119100	Phvul.002G119100	0
1	Phvul.002G132700.1	Phvul.002G132700	Phvul.002G132700	PF01632
1	Phvul.002G132700.1	Phvul.002G132700	Phvul.002G132700	PF01632
1	Phvul.002G132700.1	Phvul.002G132700	Phvul.002G132700	PF01632
1	Phvul.002G141000.2	Phvul.002G141000	Phvul.002G141000	0
1	Phvul.002G141000.1	Phvul.002G141000	Phvul.002G141000	0
1	Phvul.002G141000.2	Phvul.002G141000	Phvul.002G141000	0
1	Phvul.002G141000.1	Phvul.002G141000	Phvul.002G141000	0
1	Phvul.003G131900.1	Phvul.003G131900	Phvul.003G131900	PF08612
1	Phvul.003G131900.1	Phvul.003G131900	Phvul.003G131900	PF08612
1	Phvul.003G131900.1	Phvul.003G131900	Phvul.003G131900	PF08612
1	Phvul.003G225700.1	Phvul.003G225700	Phvul.003G225700	PF00324
1	Phvul.003G238000.1	Phvul.003G238000	Phvul.003G238000	PF13371,PF13
1	Phvul.003G238000.1	Phvul.003G238000	Phvul.003G238000	PF13371,PF13
1	Phvul.003G259300.1	Phvul.003G259300	Phvul.003G259300	PF07798
1	Phvul.003G259300.1	Phvul.003G259300	Phvul.003G259300	PF07798
1	Phvul.003G259300.1	Phvul.003G259300	Phvul.003G259300	PF07798
1	Phvul.004G037700.1	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G037700.3	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G037700.2	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G037700.1	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G037700.3	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G037700.2	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G037700.1	Phvul.004G037700	Phvul.004G037700	PF03634

1	Phvul.004G037700.3	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G037700.2	Phvul.004G037700	Phvul.004G037700	PF03634
1	Phvul.004G089300.2	Phvul.004G089300	Phvul.004G089300	PF03372
1	Phvul.004G089300.4	Phvul.004G089300	Phvul.004G089300	PF03372
1	Phvul.004G089300.2	Phvul.004G089300	Phvul.004G089300	PF03372
1	Phvul.004G089300.4	Phvul.004G089300	Phvul.004G089300	PF03372
1	Phvul.004G089300.2	Phvul.004G089300	Phvul.004G089300	PF03372
1	Phvul.004G089300.4	Phvul.004G089300	Phvul.004G089300	PF03372
1	Phvul.004G174700.1	Phvul.004G174700	Phvul.004G174700	PF03485,PF05
1	Phvul.004G174700.1	Phvul.004G174700	Phvul.004G174700	PF03485,PF05
1	Phvul.004G174700.1	Phvul.004G174700	Phvul.004G174700	PF03485,PF05
1	Phvul.005G125500.1	Phvul.005G125500	Phvul.005G125500	PF03015,PF07
1	Phvul.005G125500.1	Phvul.005G125500	Phvul.005G125500	PF03015,PF07
1	Phvul.006G044400.1	Phvul.006G044400	Phvul.006G044400	PF05739,PF09
1	Phvul.006G044400.1	Phvul.006G044400	Phvul.006G044400	PF05739,PF09
1	Phvul.006G044400.1	Phvul.006G044400	Phvul.006G044400	PF05739,PF09
1	Phvul.007G072700.3	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.9	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.8	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.6	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.7	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.2	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.5	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.3	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.9	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.8	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.6	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.7	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.2	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.5	Phvul.007G072700	Phvul.007G072700	PF02902
1	Phvul.007G072700.12	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G072700.13	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G072700.10	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G072700.11	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G072700.12	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G072700.13	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G072700.10	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G072700.11	Phvul.007G072700.	Phvul.007G072700	PF02902
1	Phvul.007G215400.1	Phvul.007G215400	Phvul.007G215400	PF13664
1	Phvul.007G215400.1	Phvul.007G215400	Phvul.007G215400	PF13664
1	Phvul.007G215400.1	Phvul.007G215400	Phvul.007G215400	PF13664
1	Phvul.007G249800.1	Phvul.007G249800	Phvul.007G249800	PF00149
1	Phvul.007G249800.1	Phvul.007G249800	Phvul.007G249800	PF00149
1	Phvul.007G249800.1	Phvul.007G249800	Phvul.007G249800	PF00149
1	Phvul.008G074600.3	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
1	Phvul.008G074600.2	Phvul.008G074600	Phvul.008G074600	PF00400,PF14

1	Phvul.008G074600.4	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
1	Phvul.008G074600.1	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
1	Phvul.008G074600.3	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
1	Phvul.008G074600.2	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
1	Phvul.008G074600.4	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
1	Phvul.008G074600.1	Phvul.008G074600	Phvul.008G074600	PF00400,PF14
1	Phvul.008G123400.1	Phvul.008G123400	Phvul.008G123400	PF00646
1	Phvul.008G123400.1	Phvul.008G123400	Phvul.008G123400	PF00646
1	Phvul.008G129500.1	Phvul.008G129500	Phvul.008G129500	PF04851,PF02
1	Phvul.008G129500.1	Phvul.008G129500	Phvul.008G129500	PF04851,PF02
1	Phvul.008G129500.1	Phvul.008G129500	Phvul.008G129500	PF04851,PF02
1	Phvul.008G164600.1	Phvul.008G164600	Phvul.008G164600	PF13855,PF12
1	Phvul.008G164600.1	Phvul.008G164600	Phvul.008G164600	PF13855,PF12
1	Phvul.008G164600.1	Phvul.008G164600	Phvul.008G164600	PF13855,PF12
1	Phvul.008G225300.1	Phvul.008G225300	Phvul.008G225300	PF01490
1	Phvul.008G230200.1	Phvul.008G230200	Phvul.008G230200	PF04893
1	Phvul.009G030500.1	Phvul.009G030500	Phvul.009G030500	PF07690
1	Phvul.009G030500.1	Phvul.009G030500	Phvul.009G030500	PF07690
1	Phvul.009G030500.1	Phvul.009G030500	Phvul.009G030500	PF07690
1	Phvul.009G099700.1	Phvul.009G099700	Phvul.009G099700	0
1	Phvul.009G099700.1	Phvul.009G099700	Phvul.009G099700	0
1	Phvul.009G099700.1	Phvul.009G099700	Phvul.009G099700	0
1	Phvul.009G233000.1	Phvul.009G233000	Phvul.009G233000	PF04178
1	Phvul.009G233000.1	Phvul.009G233000	Phvul.009G233000	PF04178
1	Phvul.009G233000.1	Phvul.009G233000	Phvul.009G233000	PF04178
1	Phvul.010G021700.1	Phvul.010G021700	Phvul.010G021700	0
1	Phvul.010G021700.1	Phvul.010G021700	Phvul.010G021700	0
1	Phvul.010G021700.1	Phvul.010G021700	Phvul.010G021700	0
1	Phvul.010G104900.2	Phvul.010G104900	Phvul.010G104900	PF02548
1	Phvul.010G104900.2	Phvul.010G104900	Phvul.010G104900	PF02548
1	Phvul.010G104900.2	Phvul.010G104900	Phvul.010G104900	PF02548
1	Phvul.010G129400.1	Phvul.010G129400	Phvul.010G129400	PF03514
1	Phvul.010G129400.1	Phvul.010G129400	Phvul.010G129400	PF03514
1	Phvul.010G129400.1	Phvul.010G129400	Phvul.010G129400	PF03514
1	Phvul.010G157900.4	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.3	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.2	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.4	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.3	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.2	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.4	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.3	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.010G157900.2	Phvul.010G157900	Phvul.010G157900	PF16987
1	Phvul.011G006200.1	Phvul.011G006200	Phvul.011G006200	PF01399
1	Phvul.011G006200.1	Phvul.011G006200	Phvul.011G006200	PF01399
1	Phvul.011G006200.1	Phvul.011G006200	Phvul.011G006200	PF01399

1	Phvul.011G161100.1	Phvul.011G161100	Phvul.011G161100	PF00067
1	Phvul.011G161100.1	Phvul.011G161100	Phvul.011G161100	PF00067
1	Phvul.011G161100.1	Phvul.011G161100	Phvul.011G161100	PF00067
1	Phvul.011G161900.1	Phvul.011G161900	Phvul.011G161900	PF00067
1	Phvul.011G161900.1	Phvul.011G161900	Phvul.011G161900	PF00067

Panther	KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
PTHR24221,P	KOG0058	3.6.3.44	0	GO:0016887,(	AT3G28345.1	0
PTHR24221,P	KOG0058	3.6.3.44	0	GO:0016887,(	AT3G28345.1	0
PTHR24221,P	KOG0058	3.6.3.44	0	GO:0016887,(	AT3G28345.1	0
PTHR11800	KOG1522	2.7.7.6	K03011	GO:0046983,(	AT2G15430.1	NRPB3,NRPD3
PTHR11800	KOG1522	2.7.7.6	K03011	GO:0046983,(	AT2G15430.1	NRPB3,NRPD3
PTHR11800	KOG1522	2.7.7.6	K03011	GO:0046983,(	AT2G15430.1	NRPB3,NRPD3
PTHR24006,P	0	3.4.19.12	K11838	GO:0005515	AT5G06600.2	UBP12
PTHR24006,P	0	3.4.19.12	K11838	GO:0005515	AT5G06600.2	UBP12
PTHR24006,P	0	3.4.19.12	K11838	GO:0005515	AT5G06600.2	UBP12
PTHR24006,P	0	3.4.19.12	K11838	GO:0005515	AT5G06600.2	UBP12
PTHR24006,P	0	3.4.19.12	K11838	GO:0005515	AT5G06600.2	UBP12
PTHR24006,P	0	3.4.19.12	K11838	GO:0005515	AT5G06600.2	UBP12
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT4G20270.1	BAM3
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT4G20270.1	BAM3
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT4G20270.1	BAM3
PTHR24089,P	KOG0761	0	K15119	0	AT2G46320.1	0
PTHR24089,P	KOG0761	0	K15119	0	AT2G46320.1	0
PTHR24089,P	KOG0761	0	K15119	0	AT2G46320.1	0
PTHR10799,P	0	3.6.4.12	K10841	GO:0005524	AT2G18760.1	CHR8
PTHR10799,P	0	3.6.4.12	K10841	GO:0005524	AT2G18760.1	CHR8
PTHR10799,P	0	3.6.4.12	K10841	GO:0005524	AT2G18760.1	CHR8
PTHR27009,P	KOG1187	3.1.4.46	0	GO:0006468,(	AT5G38260.1	0
PTHR27009,P	KOG1187	3.1.4.46	0	GO:0006468,(	AT5G38260.1	0
PTHR27009,P	KOG1187	3.1.4.46	0	GO:0006468,(	AT5G38260.1	0
PTHR35744,P	0	0	0	0	AT4G12240.1	0
PTHR35744,P	0	0	0	0	AT4G12240.1	0
PTHR35744,P	0	0	0	0	AT4G12240.1	0
PTHR35744,P	0	0	0	0	AT4G12240.1	0
PTHR35744,P	0	0	0	0	AT4G12240.1	0
PTHR35744,P	0	0	0	0	AT4G12240.1	0
PTHR10366,P	0	1.1.1.133	K12451	0	AT1G63000.1	NRS/ER,UER1
PTHR10366,P	0	1.1.1.133	K12451	0	AT1G63000.1	NRS/ER,UER1
PTHR10366,P	0	1.1.1.133	K12451	0	AT1G63000.1	NRS/ER,UER1
PTHR22814,P	KOG1603	0	0	GO:0046872,(	AT5G19090.2	0
PTHR22814,P	KOG1603	0	0	GO:0046872,(	AT5G19090.2	0
PTHR22939,P	KOG1320	3.4.21.107	0	GO:0005515	AT5G36950.1	DegP10
PTHR22939,P	KOG1320	3.4.21.107	0	GO:0005515	AT5G36950.1	DegP10
PTHR22939,P	KOG1320	3.4.21.107	0	GO:0005515	AT5G36950.1	DegP10
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT5G62230.1	ERL1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT5G62230.1	ERL1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT5G62230.1	ERL1
PTHR22967,P	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2	0
PTHR22967,P	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2	0
PTHR22967,P	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2	0
PTHR22967,P	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2	0

PTHR22967,P	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2	0
PTHR22967,P	KOG1989	2.7.11.1	K08853	GO:0006468,(	AT2G32850.2	0
PTHR11926,P	KOG1192	2.4.1.272	0	GO:0016758,(	AT2G15480.2	UGT73B5
PTHR11926,P	KOG1192	2.4.1.272	0	GO:0016758,(	AT2G15480.2	UGT73B5
PTHR11926,P	KOG1192	2.4.1.272	0	GO:0016758,(	AT2G15480.2	UGT73B5
PTHR11926,P	KOG1192	2.4.1.272	0	GO:0016758,(	AT2G15480.2	UGT73B5
PTHR11926,P	0	2.4.1.173	0	GO:0030259,(	AT1G43620.2	TT15,UGT80B
PTHR11926,P	0	2.4.1.173	0	GO:0030259,(	AT1G43620.2	TT15,UGT80B
PTHR11926,P	0	2.4.1.173	0	GO:0030259,(	AT1G43620.2	TT15,UGT80B
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0048544,(	AT2G41890.1	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0048544,(	AT2G41890.1	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0048544,(	AT2G41890.1	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0048544,(	AT2G41890.1	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0048544,(	AT2G41890.1	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0048544,(	AT2G41890.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G33580.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G33580.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G33580.1	0
PTHR22953,P	KOG1378	3.1.3.2	0	GO:0016787	AT3G20500.1	ATPAP18,PAP
PTHR22953,P	KOG1378	3.1.3.2	0	GO:0016787	AT3G20500.1	ATPAP18,PAP
PTHR22953,P	KOG1378	3.1.3.2	0	GO:0016787	AT3G20500.1	ATPAP18,PAP
PTHR36356,P	0	0	0	0	AT2G44870.1	0
PTHR36356,P	0	0	0	0	AT2G44870.1	0
PTHR36356,P	0	0	0	0	AT2G44870.1	0
PTHR32411	0	0	0	0	AT4G05200.1	CRK25
PTHR32411	0	0	0	0	AT4G05200.1	CRK25
PTHR32411	0	0	0	0	AT4G05200.1	CRK25
PTHR32467,P	0	0	K09284	GO:0006355,(	AT2G28550.1	RAP2.7,TOE1
PTHR32467,P	0	0	K09284	GO:0006355,(	AT2G28550.1	RAP2.7,TOE1
PTHR32467,P	0	0	K09284	GO:0006355,(	AT2G28550.1	RAP2.7,TOE1
PTHR32467,P	0	0	K09284	GO:0006355,(	AT2G28550.1	RAP2.7,TOE1
PTHR32467,P	0	0	K09284	GO:0006355,(	AT2G28550.1	RAP2.7,TOE1
PTHR32467,P	0	0	K09284	GO:0006355,(	AT2G28550.1	RAP2.7,TOE1
0	0	0	0	GO:0005509	0	0
0	0	0	0	GO:0005509	0	0
0	0	0	0	GO:0005509	0	0
PTHR31704,P	0	0	0	0	AT4G02550.1	0
PTHR31704,P	0	0	0	0	AT4G02550.1	0
PTHR31587,P	0	0	0	0	AT5G67610.1	0
PTHR31587,P	0	0	0	0	AT5G67610.1	0
PTHR31587,P	0	0	0	0	AT5G67610.1	0
PTHR31704,P	0	0	0	0	AT4G02210.2	0
PTHR31704,P	0	0	0	0	AT4G02210.2	0
PTHR11145	KOG2714	0	0	GO:0051260	AT3G09030.1	0
PTHR11145	KOG2714	0	0	GO:0051260	AT3G09030.1	0
PTHR32370,P	0	0	0	GO:0016567	AT5G64330.1	JK218,NPH3,R

PTHR32370,P		0		0		0	GO:0016567		AT5G64330.1	JK218,NPH3,R
PTHR32370,P		0		0		0	GO:0016567		AT5G64330.1	JK218,NPH3,R
PTHR31704,P		0		0		0		0	AT4G02550.1	0
PTHR31704,P		0		0		0		0	AT4G02550.1	0
PTHR10795,P		0	3.4.21.25			0	GO:0016020,(		AT2G19170.1	SLP3
PTHR10795,P		0	3.4.21.25			0	GO:0016020,(		AT2G19170.1	SLP3
PTHR10795,P		0	3.4.21.25			0	GO:0016020,(		AT2G19170.1	SLP3
PTHR34663,P		0		0		0		0	AT2G23270.1	0
PTHR34663,P		0		0		0		0	AT2G23270.1	0
PTHR34663,P		0		0		0		0	AT2G23270.1	0
PTHR31704,P		0		0		0		0	AT4G02550.1	0
PTHR31704,P		0		0		0		0	AT4G02550.1	0
PTHR15959,P	KOG3894			0	K08492			0	AT1G51740.1	ATSYP81,ATU
PTHR15959,P	KOG3894			0	K08492			0	AT1G51740.1	ATSYP81,ATU
PTHR15959,P	KOG3894			0	K08492			0	AT1G51740.1	ATSYP81,ATU
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR10302,P		0		0		0	GO:0006260,(		AT4G20010.1	OSB2,PTAC9
PTHR13140,P		0	3.6.4.1		K10357		GO:0016459,(		AT1G54560.1	ATXIE,XIE
PTHR13140,P		0	3.6.4.1		K10357		GO:0016459,(		AT1G54560.1	ATXIE,XIE
PTHR13140,P		0	3.6.4.1		K10357		GO:0016459,(		AT1G54560.1	ATXIE,XIE
PTHR10044,P	KOG4172			0		0		0	AT4G03000.2	0
PTHR10044,P	KOG4172			0		0		0	AT4G03000.2	0
PTHR10044,P	KOG4172			0		0		0	AT4G03000.2	0
PTHR10044,P	KOG4172			0		0		0	AT4G03000.2	0
PTHR10044,P	KOG4172			0		0		0	AT4G03000.2	0
PTHR10044,P	KOG4172			0		0		0	AT4G03000.2	0
PTHR10799,P		0	3.6.4.12		K11647		GO:0016787,(		AT3G06010.1	ATCHR12
PTHR10799,P		0	3.6.4.12		K11647		GO:0016787,(		AT3G06010.1	ATCHR12
PTHR10799,P		0	3.6.4.12		K11647		GO:0016787,(		AT3G06010.1	ATCHR12
PTHR10641,P		0		0		0		0	AT5G41020.1	0
PTHR10641,P		0		0		0		0	AT5G41020.1	0
PTHR10641,P		0		0		0		0	AT5G41020.1	0
PTHR10641,P		0		0		0		0	AT5G41020.1	0
PTHR10641,P		0		0		0		0	AT5G41020.1	0
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PTHR10641,P		0		0		0		0	AT5G41020.1	0

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PTHR10641,P	0	0	0	0	AT5G41020.1	0
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PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR10641,P	0	0	0	0	AT5G41020.1	0
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT4G08850.1	0
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT4G08850.1	0
PTHR22950,P	KOG1303	0	0	0	AT1G47670.1	0
PTHR22950,P	KOG1303	0	0	0	AT1G47670.1	0
PTHR22950,P	KOG1303	0	0	0	AT1G47670.1	0
PTHR16441	0	0	0	0	AT4G32560.1	0
PTHR16441	0	0	0	0	AT4G32560.1	0
PTHR16441	0	0	0	0	AT4G32560.1	0
PTHR16441	0	0	0	0	AT4G32560.1	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR15288,P	0	0	0	0	AT5G35560.1	0
PTHR12281,P	0	0	K17824	0	AT1G15860.2	0
PTHR12281,P	0	0	K17824	0	AT1G15860.2	0
PTHR19211,P	0	3.6.1.3	K06185	GO:0016887,(	AT5G60790.1	ATGCN1,GCN

PTHR19211,P	0	3.6.1.3	K06185	GO:0016887,(	AT5G60790.1	ATGCN1,GCN
PTHR19211,P	0	3.6.1.3	K06185	GO:0016887,(	AT5G60790.1	ATGCN1,GCN
PTHR34118,P	0	0	K02116	0	AT2G31040.1	0
PTHR34118,P	0	0	K02116	0	AT2G31040.1	0
PTHR34118,P	0	0	K02116	0	AT2G31040.1	0
PTHR11926,P	0	2.4.1.324	0	GO:0016758,(	AT1G22380.1	AtUGT85A3,U
PTHR11926,P	0	2.4.1.324	0	GO:0016758,(	AT1G22380.1	AtUGT85A3,U
PTHR11926,P	0	2.4.1.324	0	GO:0016758,(	AT1G22380.1	AtUGT85A3,U
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR12323	KOG0007	0	0	GO:0006396,(	AT4G31200.3	0
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PTHR12323	KOG0007	0	0	GO:0006396,(	AT4G31200.3	0
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT4G18010.2	5PTASE2,AT5
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT4G18010.2	5PTASE2,AT5
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT4G18010.2	5PTASE2,AT5
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT4G18010.2	5PTASE2,AT5
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT4G18010.2	5PTASE2,AT5
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT4G18010.2	5PTASE2,AT5
PTHR34996,P	0	0	0	0	0	0
PTHR34996,P	0	0	0	0	0	0
PTHR34996,P	0	0	0	0	0	0
PTHR36400	0	0	0	GO:0006412,(	AT5G45590.1	0
PTHR36400	0	0	0	GO:0006412,(	AT5G45590.1	0
PTHR36400	0	0	0	GO:0006412,(	AT5G45590.1	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
PTHR12465	0	0	K13528	GO:0016592,(	AT2G28230.1	0
PTHR12465	0	0	K13528	GO:0016592,(	AT2G28230.1	0
PTHR12465	0	0	K13528	GO:0016592,(	AT2G28230.1	0
PTHR11785,P	KOG1286	0	0	GO:0055085,(	AT5G04770.1	ATCAT6,CAT6
PTHR23083,P	KOG0548	0	0	0	AT4G37460.1	SRFR1
PTHR23083,P	KOG0548	0	0	0	AT4G37460.1	SRFR1
PTHR14360,P	KOG3156	0	0	0	AT2G16460.1	0
PTHR14360,P	KOG3156	0	0	0	AT2G16460.1	0
PTHR14360,P	KOG3156	0	0	0	AT2G16460.1	0
PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,T
PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,T
PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,T
PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,T
PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,T
PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,T
PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,T

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PTHR31072,P	0	0	0	0	AT3G02150.2	PTF1,TCP13,TI
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT1G71710.1	0
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT1G71710.1	0
PTHR11200,P	KOG0565	3.1.3.56	0	0	AT1G71710.1	0
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PTHR11956,P	0	6.1.1.19	K01887	GO:0006420,(	AT4G26300.1	emb1027
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PTHR11956,P	0	6.1.1.19	K01887	GO:0006420,(	AT4G26300.1	emb1027
PTHR11011,P	KOG1221	1.2.1.50,1.2.1	K13356	GO:0080019	AT4G33790.1	CER4,FAR3,G7
PTHR11011,P	KOG1221	1.2.1.50,1.2.1	K13356	GO:0080019	AT4G33790.1	CER4,FAR3,G7
PTHR19957,P	KOG3202	0	K08498	GO:0005515,(	AT1G28490.1	ATSYP61,OSM
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PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
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PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
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PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
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PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
PTHR12606,P	KOG3246	3.4.22.68	0	GO:0008234,(	AT4G00690.1	ULP1B
PTHR23241,P	KOG2886	0	0	0	AT3G62580.1	0
PTHR23241,P	KOG2886	0	0	0	AT3G62580.1	0
PTHR23241,P	KOG2886	0	0	0	AT3G62580.1	0
PTHR32440,P	KOG1432	0	0	GO:0016787	AT3G10150.1	ATPAP16,PAP
PTHR32440,P	KOG1432	0	0	GO:0016787	AT3G10150.1	ATPAP16,PAP
PTHR32440,P	KOG1432	0	0	GO:0016787	AT3G10150.1	ATPAP16,PAP
PTHR13743,P	0	0	0	GO:0005515	AT2G45540.1	0
PTHR13743,P	0	0	0	GO:0005515	AT2G45540.1	0

PTHR13743,P	0	0	0	GO:0005515	AT2G45540.1	0
PTHR13743,P	0	0	0	GO:0005515	AT2G45540.1	0
PTHR13743,P	0	0	0	GO:0005515	AT2G45540.1	0
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PTHR13743,P	0	0	0	GO:0005515	AT2G45540.1	0
PTHR32133,P	0	0	0	GO:0005515	AT3G24760.1	0
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PTHR14950,P	KOG0701	3.1.26.3	K11592	GO:0016787,	AT3G03300.3	ATDCL2,DCL2
PTHR14950,P	KOG0701	3.1.26.3	K11592	GO:0016787,	AT3G03300.3	ATDCL2,DCL2
PTHR14950,P	KOG0701	3.1.26.3	K11592	GO:0016787,	AT3G03300.3	ATDCL2,DCL2
PTHR27003,P	0	2.7.11.1	0	GO:0005515	AT1G05700.1	0
PTHR27003,P	0	2.7.11.1	0	GO:0005515	AT1G05700.1	0
PTHR27003,P	0	2.7.11.1	0	GO:0005515	AT1G05700.1	0
PTHR22950,P	KOG1303	0	K13946	0	AT2G38120.1	AUX1,MAP1,P
PTHR12822,P	KOG3114	0	0	GO:0016020	AT2G39805.1	0
PTHR23500,P	KOG0254	0	0	GO:0055085,	AT1G34580.1	0
PTHR23500,P	KOG0254	0	0	GO:0055085,	AT1G34580.1	0
PTHR23500,P	KOG0254	0	0	GO:0055085,	AT1G34580.1	0
PTHR13129,P	0	0	K11789	0	AT4G31160.1	DCAF1
PTHR13129,P	0	0	K11789	0	AT4G31160.1	DCAF1
PTHR13129,P	0	0	K11789	0	AT4G31160.1	DCAF1
PTHR21493,P	KOG1743	0	0	GO:0016192	AT3G49420.1	0
PTHR21493,P	KOG1743	0	0	GO:0016192	AT3G49420.1	0
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PTHR31851,P	0	0	0	0	AT4G27860.1	0
PTHR31851,P	0	0	0	0	AT4G27860.1	0
PTHR31851,P	0	0	0	0	AT4G27860.1	0
PTHR20881	KOG2949	2.1.2.11	K00606	GO:0015940,	AT3G61530.1	PANB2
PTHR20881	KOG2949	2.1.2.11	K00606	GO:0015940,	AT3G61530.1	PANB2
PTHR20881	KOG2949	2.1.2.11	K00606	GO:0015940,	AT3G61530.1	PANB2
PTHR31636,P	0	0	0	0	AT3G13840.1	0
PTHR31636,P	0	0	0	0	AT3G13840.1	0
PTHR31636,P	0	0	0	0	AT3G13840.1	0
PTHR33137,P	0	0	K14972	0	AT1G15780.1	0
PTHR33137,P	0	0	K14972	0	AT1G15780.1	0
PTHR33137,P	0	0	K14972	0	AT1G15780.1	0
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PTHR33137,P	0	0	K14972	0	AT1G15780.1	0
PTHR33137,P	0	0	K14972	0	AT1G15780.1	0
PTHR33137,P	0	0	K14972	0	AT1G15780.1	0
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PTHR33137,P	0	0	K14972	0	AT1G15780.1	0
PTHR10855	KOG1497	0	K12178	GO:0005515	AT5G42970.1	ATS4,COP14,
PTHR10855	KOG1497	0	K12178	GO:0005515	AT5G42970.1	ATS4,COP14,
PTHR10855	KOG1497	0	K12178	GO:0005515	AT5G42970.1	ATS4,COP14,

PTHR24282,P	KOG0157	1.14.13.173	0	GO:0055114,(	AT3G14690.1	CYP72A15
PTHR24282,P	KOG0157	1.14.13.173	0	GO:0055114,(	AT3G14690.1	CYP72A15
PTHR24282,P	KOG0157	1.14.13.173	0	GO:0055114,(	AT3G14690.1	CYP72A15
PTHR24282,P	KOG0159	1.14.13.173	0	GO:0055114,(	AT3G14690.1	CYP72A15
PTHR24282,P	KOG0159	1.14.13.173	0	GO:0055114,(	AT3G14690.1	CYP72A15

arabi-defline	ID	Annot_define	IDENTIFIER	NAME	DESCRIPTION
ABC transporter family protei	Phvul.004G02	PTHR24221:S	Phvul.004G02	Solute transp	subfamily ABC
ABC transporter family protei	Phvul.004G02	PTHR24221:S	Phvul.004G02	Solute transp	subfamily ABC
ABC transporter family protei	Phvul.004G02	PTHR24221:S	Phvul.004G02	Solute transp	subfamily ABC
DNA-directed RNA polymeras	Phvul.002G09	K03011 - DNA	Phvul.002G09	RNA biosynth	subunit 3 of R
DNA-directed RNA polymeras	Phvul.002G09	K03011 - DNA	Phvul.002G09	RNA biosynth	subunit 3 of R
DNA-directed RNA polymeras	Phvul.002G09	K03011 - DNA	Phvul.002G09	RNA biosynth	subunit 3 of R
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
ubiquitin-specific protease 12	Phvul.006G00	K11838 - ubiq	Phvul.006G00	Protein home	deubiquitinas
Leucine-rich receptor-like pro	Phvul.006G02	PTHR27000:S	Phvul.006G02	Protein modif	protein kinase
Leucine-rich receptor-like pro	Phvul.006G02	PTHR27000:S	Phvul.006G02	Protein modif	protein kinase
Leucine-rich receptor-like pro	Phvul.006G02	PTHR27000:S	Phvul.006G02	Protein modif	protein kinase
Mitochondrial substrate carri	Phvul.006G11	K15119 - solu	Phvul.006G11	Solute transp	solute transp
Mitochondrial substrate carri	Phvul.006G11	K15119 - solu	Phvul.006G11	Solute transp	solute transp
Mitochondrial substrate carri	Phvul.006G11	K15119 - solu	Phvul.006G11	Solute transp	solute transp
chromatin remodeling 8	Phvul.007G19	K10841 - DNA	Phvul.007G19	DNA damage	DNA repair pr
chromatin remodeling 8	Phvul.007G19	K10841 - DNA	Phvul.007G19	DNA damage	DNA repair pr
chromatin remodeling 8	Phvul.007G19	K10841 - DNA	Phvul.007G19	DNA damage	DNA repair pr
Protein kinase superfamily pr	Phvul.001G07	PTHR27009:S	Phvul.001G07	Enzyme classi	Rust resistanc
Protein kinase superfamily pr	Phvul.001G07	PTHR27009:S	Phvul.001G07	Enzyme classi	Rust resistanc
Protein kinase superfamily pr	Phvul.001G07	PTHR27009:S	Phvul.001G07	Enzyme classi	Rust resistanc
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:S	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:S	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:S	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:S	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:S	Phvul.001G26	RNA biosynth	C2H2 zinc fing
zinc finger (C2H2 type) family	Phvul.001G26	PTHR35744:S	Phvul.001G26	RNA biosynth	C2H2 zinc fing
nucleotide-rhamnose synthas	Phvul.002G15	1.1.1.133 - dT	Phvul.002G15	Carbohydrate	UDP-L-rhamn
nucleotide-rhamnose synthas	Phvul.002G15	1.1.1.133 - dT	Phvul.002G15	Carbohydrate	UDP-L-rhamn
nucleotide-rhamnose synthas	Phvul.002G15	1.1.1.133 - dT	Phvul.002G15	Carbohydrate	UDP-L-rhamn
Heavy metal transport/detoxi	Phvul.003G09	PTHR22814:S	Phvul.003G09	not assigned.	(original desc
Heavy metal transport/detoxi	Phvul.003G09	PTHR22814:S	Phvul.003G09	not assigned.	(original desc
DegP protease 10	Phvul.004G00	PTHR22939:S	Phvul.004G00	Protein home	protease (Deg
DegP protease 10	Phvul.004G00	PTHR22939:S	Phvul.004G00	Protein home	protease (Deg
DegP protease 10	Phvul.004G00	PTHR22939:S	Phvul.004G00	Protein home	protease (Deg
ERECTA-like 1	Phvul.004G12	PTHR27000:S	Phvul.004G12	Protein modif	protein kinase
ERECTA-like 1	Phvul.004G12	PTHR27000:S	Phvul.004G12	Protein modif	protein kinase
ERECTA-like 1	Phvul.004G12	PTHR27000:S	Phvul.004G12	Protein modif	protein kinase
Protein kinase superfamily pr	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
Protein kinase superfamily pr	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
Protein kinase superfamily pr	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
Protein kinase superfamily pr	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase

Protein kinase superfamily pr	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
Protein kinase superfamily pr	Phvul.005G06	K08853 - AP2-	Phvul.005G06	Protein modif	protein kinase
UDP-glucosyl transferase 73B	Phvul.007G02	PTHR11926//I	Phvul.007G02	Enzyme classi	Soyasapogen
UDP-glucosyl transferase 73B	Phvul.007G02	PTHR11926//I	Phvul.007G02	Enzyme classi	Soyasapogen
UDP-glucosyl transferase 73B	Phvul.007G02	PTHR11926//I	Phvul.007G02	Enzyme classi	Soyasapogen
UDP-glucosyl transferase 73B	Phvul.007G02	PTHR11926//I	Phvul.007G02	Enzyme classi	Soyasapogen
UDP-Glycosyltransferase supe	Phvul.007G08	PTHR11926:S	Phvul.007G08	Lipid metabol	UDP-glucose:
UDP-Glycosyltransferase supe	Phvul.007G08	PTHR11926:S	Phvul.007G08	Lipid metabol	UDP-glucose:
UDP-Glycosyltransferase supe	Phvul.007G08	PTHR11926:S	Phvul.007G08	Lipid metabol	UDP-glucose:
curculin-like (mannose-bindin	Phvul.007G25	PTHR27002:S	Phvul.007G25	Protein modif	protein kinase
curculin-like (mannose-bindin	Phvul.007G25	PTHR27002:S	Phvul.007G25	Protein modif	protein kinase
curculin-like (mannose-bindin	Phvul.007G25	PTHR27002:S	Phvul.007G25	Protein modif	protein kinase
curculin-like (mannose-bindin	Phvul.007G25	PTHR27002:S	Phvul.007G25	Protein modif	protein kinase
curculin-like (mannose-bindin	Phvul.007G25	PTHR27002:S	Phvul.007G25	Protein modif	protein kinase
curculin-like (mannose-bindin	Phvul.007G25	PTHR27002:S	Phvul.007G25	Protein modif	protein kinase
Protein kinase superfamily pr	Phvul.008G21	PTHR27001:S	Phvul.008G21	External stimu	LysM receptor
Protein kinase superfamily pr	Phvul.008G21	PTHR27001:S	Phvul.008G21	External stimu	LysM receptor
Protein kinase superfamily pr	Phvul.008G21	PTHR27001:S	Phvul.008G21	External stimu	LysM receptor
purple acid phosphatase 18	Phvul.008G26	PTHR22953:S	Phvul.008G26	not assigned.	(original desc
purple acid phosphatase 18	Phvul.008G26	PTHR22953:S	Phvul.008G26	not assigned.	(original desc
purple acid phosphatase 18	Phvul.008G26	PTHR22953:S	Phvul.008G26	not assigned.	(original desc
0	Phvul.011G00	PTHR36356:S	Phvul.011G00	not assigned.	no hits & (ori
0	Phvul.011G00	PTHR36356:S	Phvul.011G00	not assigned.	no hits & (ori
0	Phvul.011G00	PTHR36356:S	Phvul.011G00	not assigned.	no hits & (ori
cysteine-rich RLK (RECEPTOR-	Phvul.011G19	PF01657 - Salt	Phvul.011G19	not assigned.	(original desc
cysteine-rich RLK (RECEPTOR-	Phvul.011G19	PF01657 - Salt	Phvul.011G19	not assigned.	(original desc
cysteine-rich RLK (RECEPTOR-	Phvul.011G19	PF01657 - Salt	Phvul.011G19	not assigned.	(original desc
related to AP2.7	Phvul.L00030	PTHR32467:S	Phvul.L00030	RNA biosynth	transcription
related to AP2.7	Phvul.L00030	PTHR32467:S	Phvul.L00030	RNA biosynth	transcription
related to AP2.7	Phvul.L00030	PTHR32467:S	Phvul.L00030	RNA biosynth	transcription
related to AP2.7	Phvul.L00030	PTHR32467:S	Phvul.L00030	RNA biosynth	transcription
related to AP2.7	Phvul.L00030	PTHR32467:S	Phvul.L00030	RNA biosynth	transcription
related to AP2.7	Phvul.L00030	PTHR32467:S	Phvul.L00030	RNA biosynth	transcription
0	Phvul.001G02	PF00036 - EF	Phvul.001G02	not assigned.	no hits & (ori
0	Phvul.001G02	PF00036 - EF	Phvul.001G02	not assigned.	no hits & (ori
0	Phvul.001G02	PF00036 - EF	Phvul.001G02	not assigned.	no hits & (ori
0	Phvul.001G16	PF12776 - My	Phvul.001G16	not assigned.	no hits & (ori
0	Phvul.001G16	PF12776 - My	Phvul.001G16	not assigned.	no hits & (ori
Uncharacterized conserved pr	Phvul.002G01	PF10225 - Un	Phvul.002G01	not assigned.	no hits & (ori
Uncharacterized conserved pr	Phvul.002G01	PF10225 - Un	Phvul.002G01	not assigned.	no hits & (ori
Uncharacterized conserved pr	Phvul.002G01	PF10225 - Un	Phvul.002G01	not assigned.	no hits & (ori
0	Phvul.002G14	PF12776 - My	Phvul.002G14	not assigned.	no hits & (ori
0	Phvul.002G14	PF12776 - My	Phvul.002G14	not assigned.	no hits & (ori
BTB/POZ domain-containing p	Phvul.002G15	PTHR11145 -	Phvul.002G15	not assigned.	(original desc
BTB/POZ domain-containing p	Phvul.002G15	PTHR11145 -	Phvul.002G15	not assigned.	(original desc
Phototropic-responsive NPH3	Phvul.002G21	PTHR32370:S	Phvul.002G21	Protein home	component N

Phototropic-responsive NPH3	Phvul.002G21	PTHR32370:S	Phvul.002G21	Protein home	component N
Phototropic-responsive NPH3	Phvul.002G21	PTHR32370:S	Phvul.002G21	Protein home	component N
0	Phvul.003G06	PF12776 - My	Phvul.003G06	not assigned.	no hits & (ori
0	Phvul.003G06	PF12776 - My	Phvul.003G06	not assigned.	no hits & (ori
subtilisin-like serine protease	Phvul.003G14	PTHR10795:S	Phvul.003G14	Protein home	protease (SBT
subtilisin-like serine protease	Phvul.003G14	PTHR10795:S	Phvul.003G14	Protein home	protease (SBT
subtilisin-like serine protease	Phvul.003G14	PTHR10795:S	Phvul.003G14	Protein home	protease (SBT
0	0	0	Phvul.003G23	Phytohormon	PIP/PIPL prec
0	0	0	Phvul.003G23	Phytohormon	PIP/PIPL prec
0	0	0	Phvul.003G23	Phytohormon	PIP/PIPL prec
0	Phvul.004G05	PF12776 - My	Phvul.004G05	not assigned.	no hits & (ori
0	Phvul.004G05	PF12776 - My	Phvul.004G05	not assigned.	no hits & (ori
syntaxin of plants 81	Phvul.004G15	K08492 - synt	Phvul.004G15	Vesicle traffic	SYP8-group Q
syntaxin of plants 81	Phvul.004G15	K08492 - synt	Phvul.004G15	Vesicle traffic	SYP8-group Q
syntaxin of plants 81	Phvul.004G15	K08492 - synt	Phvul.004G15	Vesicle traffic	SYP8-group Q
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
plastid transcriptionally active	Phvul.004G17	PTHR10302:S	Phvul.004G17	RNA biosynth	TAC9 cofactor
Myosin family protein with Dil	Phvul.006G10	PTHR13140:S	Phvul.006G10	Cytoskeleton	class XI myosi
Myosin family protein with Dil	Phvul.006G10	PTHR13140:S	Phvul.006G10	Cytoskeleton	class XI myosi
Myosin family protein with Dil	Phvul.006G10	PTHR13140:S	Phvul.006G10	Cytoskeleton	class XI myosi
RING/U-box superfamily prot	Phvul.006G15	PTHR10044:S	Phvul.006G15	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.006G15	PTHR10044:S	Phvul.006G15	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.006G15	PTHR10044:S	Phvul.006G15	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.006G15	PTHR10044:S	Phvul.006G15	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.006G15	PTHR10044:S	Phvul.006G15	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.006G15	PTHR10044:S	Phvul.006G15	not assigned.	(original desc
Homeotic gene regulator	Phvul.007G05	PTHR10799:S	Phvul.007G05	Chromatin or	chromatin re
Homeotic gene regulator	Phvul.007G05	PTHR10799:S	Phvul.007G05	Chromatin or	chromatin re
Homeotic gene regulator	Phvul.007G05	PTHR10799:S	Phvul.007G05	Chromatin or	chromatin re
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription

myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
myb family transcription facto	Phvul.007G15	PTHR10641:S	Phvul.007G15	RNA biosynth	transcription f
Leucine-rich repeat receptor-l	Phvul.008G10	PF00069//PF	Phvul.008G10	Protein modif	protein kinase
Leucine-rich repeat receptor-l	Phvul.008G10	PF00069//PF	Phvul.008G10	Protein modif	protein kinase
Transmembrane amino acid tr	Phvul.009G02	PTHR22950//	Phvul.009G02	Solute transp	amino acid tra
Transmembrane amino acid tr	Phvul.009G02	PTHR22950//	Phvul.009G02	Solute transp	amino acid tra
Transmembrane amino acid tr	Phvul.009G02	PTHR22950//	Phvul.009G02	Solute transp	amino acid tra
paramyosin-related	Phvul.009G09	PTHR16441 -	Phvul.009G09	not assigned.	no hits & (ori
paramyosin-related	Phvul.009G09	PTHR16441 -	Phvul.009G09	not assigned.	no hits & (ori
paramyosin-related	Phvul.009G09	PTHR16441 -	Phvul.009G09	not assigned.	no hits & (ori
paramyosin-related	Phvul.009G09	PTHR16441 -	Phvul.009G09	not assigned.	no hits & (ori
0	Phvul.009G12	PF12776 - My	Phvul.009G12	not assigned.	no hits & (ori
0	Phvul.009G12	PF12776 - My	Phvul.009G12	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
DENN (AEX-3) domain-contain	Phvul.009G22	PTHR15288:S	Phvul.009G22	not assigned.	no hits & (ori
Domain of unknown function	Phvul.010G15	PTHR12281:S	Phvul.010G15	not assigned.	no hits & (ori
Domain of unknown function	Phvul.010G15	PTHR12281:S	Phvul.010G15	not assigned.	no hits & (ori
ABC transporter family protei	Phvul.011G08	K06185 - ATP-	Phvul.011G08	not assigned.	(original desc

ABC transporter family protei	Phvul.011G08	K06185 - ATP-	Phvul.011G08	not assigned.	(original desc
ABC transporter family protei	Phvul.011G08	K06185 - ATP-	Phvul.011G08	not assigned.	(original desc
ATP synthase protein I -relate	Phvul.011G13	K02116 - ATP	Phvul.011G13	Photosynthes	CGL160 factor
ATP synthase protein I -relate	Phvul.011G13	K02116 - ATP	Phvul.011G13	Photosynthes	CGL160 factor
ATP synthase protein I -relate	Phvul.011G13	K02116 - ATP	Phvul.011G13	Photosynthes	CGL160 factor
UDP-glucosyl transferase 85A	Phvul.011G15	PTHR11926:S	Phvul.011G15	Enzyme classi	Linamarin syn
UDP-glucosyl transferase 85A	Phvul.011G15	PTHR11926:S	Phvul.011G15	Enzyme classi	Linamarin syn
UDP-glucosyl transferase 85A	Phvul.011G15	PTHR11926:S	Phvul.011G15	Enzyme classi	Linamarin syn
LRR and NB-ARC domains-con	Phvul.011G19	PTHR23155//I	Phvul.011G19	not assigned.	(original desc
LRR and NB-ARC domains-con	Phvul.011G19	PTHR23155//I	Phvul.011G19	not assigned.	(original desc
LRR and NB-ARC domains-con	Phvul.011G19	PTHR23155//I	Phvul.011G19	not assigned.	(original desc
SWAP (Suppressor-of-White-A	Phvul.001G19	PTHR12323 -	Phvul.001G19	not assigned.	no hits & (ori
SWAP (Suppressor-of-White-A	Phvul.001G19	PTHR12323 -	Phvul.001G19	not assigned.	no hits & (ori
SWAP (Suppressor-of-White-A	Phvul.001G19	PTHR12323 -	Phvul.001G19	not assigned.	no hits & (ori
myo-inositol polyphosphate 5	Phvul.002G00	PTHR11200:S	Phvul.002G00	Multi-process	type-I inositol
myo-inositol polyphosphate 5	Phvul.002G00	PTHR11200:S	Phvul.002G00	Multi-process	type-I inositol
myo-inositol polyphosphate 5	Phvul.002G00	PTHR11200:S	Phvul.002G00	Multi-process	type-I inositol
myo-inositol polyphosphate 5	Phvul.002G00	PTHR11200:S	Phvul.002G00	Multi-process	type-I inositol
myo-inositol polyphosphate 5	Phvul.002G00	PTHR11200:S	Phvul.002G00	Multi-process	type-I inositol
myo-inositol polyphosphate 5	Phvul.002G00	PTHR11200:S	Phvul.002G00	Multi-process	type-I inositol
0	0	0	Phvul.002G11	not assigned.	no hits & (ori
0	0	0	Phvul.002G11	not assigned.	no hits & (ori
0	0	0	Phvul.002G11	not assigned.	no hits & (ori
Ribosomal protein L35	Phvul.002G13	PF01632 - Rib	Phvul.002G13	not assigned.	no hits & (ori
Ribosomal protein L35	Phvul.002G13	PF01632 - Rib	Phvul.002G13	not assigned.	no hits & (ori
Ribosomal protein L35	Phvul.002G13	PF01632 - Rib	Phvul.002G13	not assigned.	no hits & (ori
0	0	0	Phvul.002G14	not assigned.	no hits & (ori
0	0	0	Phvul.002G14	not assigned.	no hits & (ori
0	0	0	Phvul.002G14	not assigned.	no hits & (ori
0	0	0	Phvul.002G14	not assigned.	no hits & (ori
TATA-binding related factor (T	Phvul.003G13	K13528 - med	Phvul.003G13	RNA biosynth	component M
TATA-binding related factor (T	Phvul.003G13	K13528 - med	Phvul.003G13	RNA biosynth	component M
TATA-binding related factor (T	Phvul.003G13	K13528 - med	Phvul.003G13	RNA biosynth	component M
cationic amino acid transporte	Phvul.003G22	PTHR11785//I	Phvul.003G22	Solute transp	cationic amin
Tetratricopeptide repeat (TPR	Phvul.003G23	PF13371//PF1	Phvul.003G23	not assigned.	(original desc
Tetratricopeptide repeat (TPR	Phvul.003G23	PF13371//PF1	Phvul.003G23	not assigned.	(original desc
Protein of unknown function (	Phvul.003G25	PTHR14360:S	Phvul.003G25	not assigned.	no hits & (ori
Protein of unknown function (	Phvul.003G25	PTHR14360:S	Phvul.003G25	not assigned.	no hits & (ori
Protein of unknown function (	Phvul.003G25	PTHR14360:S	Phvul.003G25	not assigned.	no hits & (ori
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription

plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription f
plastid transcription factor 1	Phvul.004G03	PTHR31072:S	Phvul.004G03	RNA biosynth	transcription f
DNAse I-like superfamily prote	Phvul.004G08	PTHR11200:S	Phvul.004G08	Multi-process	type-I inositol
DNAse I-like superfamily prote	Phvul.004G08	PTHR11200:S	Phvul.004G08	Multi-process	type-I inositol
DNAse I-like superfamily prote	Phvul.004G08	PTHR11200:S	Phvul.004G08	Multi-process	type-I inositol
DNAse I-like superfamily prote	Phvul.004G08	PTHR11200:S	Phvul.004G08	Multi-process	type-I inositol
DNAse I-like superfamily prote	Phvul.004G08	PTHR11200:S	Phvul.004G08	Multi-process	type-I inositol
DNAse I-like superfamily prote	Phvul.004G08	PTHR11200:S	Phvul.004G08	Multi-process	type-I inositol
Arginyl-tRNA synthetase, class	Phvul.004G17	K01887 - argi	Phvul.004G17	Protein biosy	arginine-tRNA
Arginyl-tRNA synthetase, class	Phvul.004G17	K01887 - argi	Phvul.004G17	Protein biosy	arginine-tRNA
Arginyl-tRNA synthetase, class	Phvul.004G17	K01887 - argi	Phvul.004G17	Protein biosy	arginine-tRNA
Jojoba acyl CoA reductase-rel	Phvul.005G12	1.2.1.50//1.2.	Phvul.005G12	Cell wall orga	acyl CoA redu
Jojoba acyl CoA reductase-rel	Phvul.005G12	1.2.1.50//1.2.	Phvul.005G12	Cell wall orga	acyl CoA redu
syntaxin of plants 61	Phvul.006G04	K08498 - synt	Phvul.006G04	Vesicle traffic	SYP6 group Q
syntaxin of plants 61	Phvul.006G04	K08498 - synt	Phvul.006G04	Vesicle traffic	SYP6 group Q
syntaxin of plants 61	Phvul.006G04	K08498 - synt	Phvul.006G04	Vesicle traffic	SYP6 group Q
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
UB-like protease 1B	Phvul.007G07	PTHR12606:S	Phvul.007G07	not assigned.	no hits & (ori
Late embryogenesis abundant	Phvul.007G21	PTHR23241//	Phvul.007G21	not assigned.	no hits & (ori
Late embryogenesis abundant	Phvul.007G21	PTHR23241//	Phvul.007G21	not assigned.	no hits & (ori
Late embryogenesis abundant	Phvul.007G21	PTHR23241//	Phvul.007G21	not assigned.	no hits & (ori
purple acid phosphatase 16	Phvul.007G24	PTHR32440:S	Phvul.007G24	not assigned.	(original desc
purple acid phosphatase 16	Phvul.007G24	PTHR32440:S	Phvul.007G24	not assigned.	(original desc
purple acid phosphatase 16	Phvul.007G24	PTHR32440:S	Phvul.007G24	not assigned.	(original desc
WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc
WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc

WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc
WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc
WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc
WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc
WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc
WD-40 repeat family protein /	Phvul.008G07	PF00400//PF	Phvul.008G07	not assigned.	(original desc
Galactose oxidase/kelch repea	Phvul.008G12	PF00646 - F-b	Phvul.008G12	Protein home	component F
Galactose oxidase/kelch repea	Phvul.008G12	PF00646 - F-b	Phvul.008G12	Protein home	component F
dicer-like 2	Phvul.008G12	K11592 - end	Phvul.008G12	not assigned.	(original desc
dicer-like 2	Phvul.008G12	K11592 - end	Phvul.008G12	not assigned.	(original desc
dicer-like 2	Phvul.008G12	K11592 - end	Phvul.008G12	not assigned.	(original desc
Leucine-rich repeat transmem	Phvul.008G16	PF12819//PF1	Phvul.008G16	not assigned.	(original desc
Leucine-rich repeat transmem	Phvul.008G16	PF12819//PF1	Phvul.008G16	not assigned.	(original desc
Leucine-rich repeat transmem	Phvul.008G16	PF12819//PF1	Phvul.008G16	not assigned.	(original desc
Transmembrane amino acid tr	Phvul.008G22	PTHR22950//I	Phvul.008G22	Solute transp	auxin transpo
Integral membrane Yip1 famil	Phvul.008G23	PTHR12822:S	Phvul.008G23	not assigned.	no hits & (ori
Major facilitator superfamily	Phvul.009G03	PTHR23500:S	Phvul.009G03	Solute transp	monosacchari
Major facilitator superfamily	Phvul.009G03	PTHR23500:S	Phvul.009G03	Solute transp	monosacchari
Major facilitator superfamily	Phvul.009G03	PTHR23500:S	Phvul.009G03	Solute transp	monosacchari
DDB1-CUL4 associated factor	Phvul.009G09	K11789 - HIV-	Phvul.009G09	not assigned.	(original desc
DDB1-CUL4 associated factor	Phvul.009G09	K11789 - HIV-	Phvul.009G09	not assigned.	(original desc
DDB1-CUL4 associated factor	Phvul.009G09	K11789 - HIV-	Phvul.009G09	not assigned.	(original desc
Got1/Sft2-like vescicle transp	Phvul.009G23	PTHR21493:S	Phvul.009G23	not assigned.	(original desc
Got1/Sft2-like vescicle transp	Phvul.009G23	PTHR21493:S	Phvul.009G23	not assigned.	(original desc
Got1/Sft2-like vescicle transp	Phvul.009G23	PTHR21493:S	Phvul.009G23	not assigned.	(original desc
vacuolar iron transporter (VIT	Phvul.010G02	PTHR31851:S	Phvul.010G02	Solute transp	metal cation t
vacuolar iron transporter (VIT	Phvul.010G02	PTHR31851:S	Phvul.010G02	Solute transp	metal cation t
vacuolar iron transporter (VIT	Phvul.010G02	PTHR31851:S	Phvul.010G02	Solute transp	metal cation t
Phosphoenolpyruvate carbox	Phvul.010G10	2.1.2.11 - 3-m	Phvul.010G10	Coenzyme me	ketopantoate
Phosphoenolpyruvate carbox	Phvul.010G10	2.1.2.11 - 3-m	Phvul.010G10	Coenzyme me	ketopantoate
Phosphoenolpyruvate carbox	Phvul.010G10	2.1.2.11 - 3-m	Phvul.010G10	Coenzyme me	ketopantoate
GRAS family transcription fact	Phvul.010G12	PTHR31636:S	Phvul.010G12	External stim	component N
GRAS family transcription fact	Phvul.010G12	PTHR31636:S	Phvul.010G12	External stim	component N
GRAS family transcription fact	Phvul.010G12	PTHR31636:S	Phvul.010G12	External stim	component N
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
0	Phvul.010G15	K14972 - PAX-	Phvul.010G15	RNA biosynth	component M
Proteasome component (PCI)	Phvul.011G00	K12178 - COP	Phvul.011G00	Protein home	component C
Proteasome component (PCI)	Phvul.011G00	K12178 - COP	Phvul.011G00	Protein home	component C
Proteasome component (PCI)	Phvul.011G00	K12178 - COP	Phvul.011G00	Protein home	component C

cytochrome P450, family 72, s	Phvul.011G16	1.14.13.173 -	Phvul.011G16	Enzyme classi	11-oxo-beta-a
cytochrome P450, family 72, s	Phvul.011G16	1.14.13.173 -	Phvul.011G16	Enzyme classi	11-oxo-beta-a
cytochrome P450, family 72, s	Phvul.011G16	1.14.13.173 -	Phvul.011G16	Enzyme classi	11-oxo-beta-a
cytochrome P450, family 72, s	Phvul.011G16	KOG0159 - Cy	Phvul.011G16	Enzyme classi	11-oxo-beta-a
cytochrome P450, family 72, s	Phvul.011G16	KOG0159 - Cy	Phvul.011G16	Enzyme classi	11-oxo-beta-a

B transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0

B transporter (original description: pacid=37163835 transcript=Phvul.004G023066.1 locus=Phvul.0

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NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.

NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.

NA polymerase (original description: pacid=37175101 transcript=Phvul.002G097400.1 locus=Phvul.

e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0

e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0

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e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0

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e (UBP12-13) (original description: pacid=37172071 transcript=Phvul.006G008480.2 locus=Phvul.0

(LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G

(LRR-XI) (original description: pacid=37173573 transcript=Phvul.006G029000.1 locus=Phvul.006G

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rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00

rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00

rter (MTCC) (original description: pacid=37172256 transcript=Phvul.006G110300.1 locus=Phvul.00

otein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007

otein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007

otein (CSB) (original description: pacid=37165162 transcript=Phvul.007G191600.1 locus=Phvul.007

e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10_wheat : 383.0) & Enzyme classification.EC_

e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10_wheat : 383.0) & Enzyme classification.EC_

e kinase Lr10 OS=Triticum aestivum (sp|p93604|lrk10_wheat : 383.0) & Enzyme classification.EC_

ger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus

ger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus

ger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus

ger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus

ger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus

ger transcription factor (original description: pacid=37168889 transcript=Phvul.001G264600.2 locus

ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00

ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00

ose synthase (original description: pacid=37176460 transcript=Phvul.002G153500.1 locus=Phvul.00

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(LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004

(LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004

(LRR-XIIIb) (original description: pacid=37163092 transcript=Phvul.004G126100.1 locus=Phvul.004

(NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G06

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(NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G06 e (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063

e (NAK) (original description: pacid=37152911 transcript=Phvul.005G063700.2 locus=Phvul.005G063

ol B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 540.0) & Enzyme c

ol B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 540.0) & Enzyme c

ol B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 554.0) & Enzyme c

ol B glucuronide galactosyltransferase OS=Glycine max (sp|d4q9z4|sgt2_soybn : 554.0) & Enzyme c

sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 loc

sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 loc

sterol glucosyltransferase (original description: pacid=37167623 transcript=Phvul.007G080800.2 loc

e (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254

e (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254

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e (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254

e (SD-2) (original description: pacid=37166958 transcript=Phvul.007G254000.2 locus=Phvul.007G254

r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=P

r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=P

r kinase (NFR1/LYK3) (original description: pacid=37159081 transcript=Phvul.008G212500.1 locus=P

cription: pacid=37158281 transcript=Phvul.008G266300.1 locus=Phvul.008G266300 ID=Phvul.008G2

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ginal description: pacid=37155004 transcript=Phvul.011G002600.1 locus=Phvul.011G002600 ID=Ph

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cription: pacid=37155693 transcript=Phvul.011G194501.1 locus=Phvul.011G194501 ID=Phvul.011G1

cription: pacid=37155693 transcript=Phvul.011G194501.1 locus=Phvul.011G194501 ID=Phvul.011G1

cription: pacid=37155693 transcript=Phvul.011G194501.1 locus=Phvul.011G194501 ID=Phvul.011G1

factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308

factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308

factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308

factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308

factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308

factor (AP2) (original description: pacid=37148483 transcript=Phvul.L000308.2 locus=Phvul.L000308

ginal description: pacid=37170232 transcript=Phvul.001G021750.1 locus=Phvul.001G021750 ID=Ph

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cription: pacid=37174540 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G1

cription: pacid=37174540 transcript=Phvul.002G155200.1 locus=Phvul.002G155200 ID=Phvul.002G1

PH3 of CUL3-BTB E3 ubiquitin ligase complex (original description: pacid=37175454 transcript=Phvu

PH3 of CUL3-BTB E3 ubiquitin ligase complex (original description: pacid=37175454 transcript=Phvu
PH3 of CUL3-BTB E3 ubiquitin ligase complex (original description: pacid=37175454 transcript=Phvu
ginal description: pacid=37147834 transcript=Phvul.003G069400.1 locus=Phvul.003G069400 ID=Ph
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ursor polypeptide (original description: pacid=37144932 transcript=Phvul.003G239800.1 locus=Phvu
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ginal description: pacid=37162038 transcript=Phvul.004G053900.1 locus=Phvul.004G053900 ID=Ph
a-type SNARE component (original description: pacid=37163883 transcript=Phvul.004G157700.1 lo
a-type SNARE component (original description: pacid=37163883 transcript=Phvul.004G157700.1 lo
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of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
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of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
of plastid-encoded RNA polymerase (original description: pacid=37161586 transcript=Phvul.004G1
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266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju
266300.1.v2.1 annot-version=v2.1) & Purple acid phosphatase 18 OS=Arabidopsis thaliana (sp|q9lju
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194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t
194501.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protein kinase 25 OS=Arabidopsis t
8 ID=Phvul.L000308.2.v2.1 annot-version=v2.1) &
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vul.002G149100.1.v2.1 annot-version=v2.1)
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155200.1.v2.1 annot-version=v2.1) & BTB/POZ domain-containing protein At3g09030 OS=Arabidops
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vul.010G159600.1.v2.1 annot-version=v2.1)
vul.010G159600.1.v2.1 annot-version=v2.1)
84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (

84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (
84000.1.v2.1 annot-version=v2.1) & ABC transporter F family member 1 OS=Arabidopsis thaliana (
l.011G130500.1 locus=Phvul.011G130500 ID=Phvul.011G130500.1.v2.1 annot-version=v2.1) &
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sferases.EC_2.4 glycosyltransferase(50.2.4 : 237.6) (original description: pacid=37155521 transcript
sferases.EC_2.4 glycosyltransferase(50.2.4 : 237.6) (original description: pacid=37155521 transcript
98100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidops
98100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidops
98100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13-like protein 1 OS=Arabidops
vul.001G199500.1.v2.1 annot-version=v2.1)
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238000.1.v2.1 annot-version=v2.1) & Suppressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|
238000.1.v2.1 annot-version=v2.1) & Suppressor of RPS4-RLD 1 OS=Arabidopsis thaliana (sp|f4js25|
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Phvul.006G044400 ID=Phvul.006G044400.1.v2.1 annot-version=v2.1) &
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vul.007G215400.1.v2.1 annot-version=v2.1)
49800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis
49800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis
49800.1.v2.1 annot-version=v2.1) & Probable inactive purple acid phosphatase 16 OS=Arabidopsis
74600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana
74600.4.v2.1 annot-version=v2.1) & BEACH domain-containing protein C2 OS=Arabidopsis thaliana

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129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s
129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s
129500.1.v2.1 annot-version=v2.1) & Endoribonuclease Dicer homolog 2 OS=Arabidopsis thaliana (s
164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At
164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At
164600.1.v2.1 annot-version=v2.1) & Probable LRR receptor-like serine/threonine-protein kinase At
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hvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &
hvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &
hvul.009G030500 ID=Phvul.009G030500.1.v2.1 annot-version=v2.1) &
99700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis
99700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis
99700.1.v2.1 annot-version=v2.1) & DDB1- and CUL4-associated factor homolog 1 OS=Arabidopsis
233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q
233000.1.v2.1 annot-version=v2.1) & Vesicle transport protein GOT1 OS=Arabidopsis thaliana (sp|q
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7144174 transcript=Phvul.010G157900.4 locus=Phvul.010G157900 ID=Phvul.010G157900.4.v2.1 ar
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n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu

n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu

n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu

n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu

n.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with incorporation or redu

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haliana (sp|q9m0x5|crk25_arath : 142.0)

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sis thaliana (sp|q9s7r7|y3903_arath : 505.0)

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liana (sp|q0wpj7|rf298_arath : 405.0)
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sp|q9fjh6|ab1f_arath : 941.0)

sp|q9fjh6|ab1f_arath : 941.0)

sp|q9fjh6|ab1f_arath : 941.0)

:=Phvul.011G158500.1 locus=Phvul.011G158500 ID=Phvul.011G158500.1.v2.1 annot-version=v2.1)

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(sp|f4ig73|bchc2_arath : 2405.0)

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ı (sp|f4ig73|bchc2_arath : 2405.0)

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t1g05700 OS=Arabidopsis thaliana (sp|c0lgd6|y1570_arath : 285.0)
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thaliana (sp|q9m086|dcaf1_arath : 1457.0)
thaliana (sp|q9m086|dcaf1_arath : 1457.0)
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ɿ6nmm1|got1_arath : 139.0)
ɿ6nmm1|got1_arath : 139.0)
ɿ6nmm1|got1_arath : 139.0)

nnot-version=v2.1) &
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ıction of molecular oxygen(50.1.13 : 91.0) (original description: pacid=37156825 transcript=Phvul.0
ıction of molecular oxygen(50.1.13 : 91.0) (original description: pacid=37156825 transcript=Phvul.0

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&
&
&

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miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
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uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
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uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.2	5	-1	1	21
uaaucugcaucc	Phvul.009G207500.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21

uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
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uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
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uaaucugcaucc	Phvul.009G219300.1	5	-1	1	21
uaaucugcaucc	Phvul.010G125200.1	5	-1	1	21
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uaaucugcaucc	Phvul.010G125200.1	5	-1	1	21
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uaaucugcaucc	Phvul.010G125200.1	5	-1	1	21
uaaucugcaucc	Phvul.010G125200.1	5	-1	1	21
uaaucugcaucc	Phvul.010G125200.1	5	-1	1	21
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uaaucugcaucc	Phvul.010G125200.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
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uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21

uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
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uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
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uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.011G091400.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21

uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21
uaaucugcaucc	Phvul.L002060.3	5	-1	1	21
uaaucugcaucc	Phvul.L002060.2	5	-1	1	21
uaaucugcaucc	Phvul.L002060.1	5	-1	1	21

Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
326	346	UAAUCUGCAU	::::::::::::::::::	UUUACCUCAC	Cleavage	pacid=371679
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
1206	1226	UAAUCUGCAU	:::.:.::: :::::::::	GCAACUUUAC	Translation	pacid=371687
435	455	UAAUCUGCAU	::::::: :::::::::: :.	UAAACCUAAG	Cleavage	pacid=371629
435	455	UAAUCUGCAU	::::::: :::::::::: :.	UAAACCUAAG	Cleavage	pacid=371629
435	455	UAAUCUGCAU	::::::: :::::::::: :.	UAAACCUAAG	Cleavage	pacid=371629

435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
435	455	UAAUCUGCA	::::::: :::::::::: :.	UAAACCUAA	Cleavage	pacid=371629
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
895	915	UAAUCUGCA	::::.: :::::: ::::::	AAAACUUGA	Cleavage	pacid=371733
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515

1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
1082	1102	UAAUCUGCA	: :...:::::::: ::::::	UUAGUUUCA	Cleavage	pacid=371515
777	797	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
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793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
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793	813	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.:::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693

777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
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777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
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853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
828	848	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
853	873	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
777	797	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693
793	813	UAAUCUGCA	.:.::: :.::::::::.	AUGAUCUCA	Cleavage	pacid=371693

828	848	UAAUCUGCAU	.:.:::: :.::::::::.	AUGAUCUCAU	Cleavage	pacid=371693
853	873	UAAUCUGCAU	.:.:::: :.::::::::.	AUGAUCUCAU	Cleavage	pacid=371693
777	797	UAAUCUGCAU	.:.:::: :.::::::::.	AUGAUCUCAU	Cleavage	pacid=371693
793	813	UAAUCUGCAU	.:.:::: :.::::::::.	AUGAUCUCAU	Cleavage	pacid=371693
828	848	UAAUCUGCAU	.:.:::: :.::::::::.	AUGAUCUCAU	Cleavage	pacid=371693
853	873	UAAUCUGCAU	.:.:::: :.::::::::.	AUGAUCUCAU	Cleavage	pacid=371693
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
237	257	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
292	312	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
475	495	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709
530	550	UAAUCUGCAU	.: ::::.::::::.::: :	CGAUCCUCGG	Cleavage	pacid=371709

237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
237	257	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
292	312	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
475	495	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
530	550	UAAUCUGCA	.: ::::.::::::.::: :	CGAUCCUCG	Cleavage	pacid=371709
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765

1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
1483	1503	UAAUCUGCA	:..::.::::::::..: :::	UGGACUUCA	Cleavage	pacid=371765
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786

669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
669	689	UAAUCUGCA	.::::::::::::::.:	GUGACCUCA	Cleavage	pacid=371786
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .:::::::::::.	UGAAAUUAG	Cleavage	pacid=371452

427	447	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
352	372	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
427	447	UAAUCUGCA	:.:: .: .::::::::::.	UGAAAUUAG	Cleavage	pacid=371452
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
26	46	UAAUCUGCA	::: :.. ::::::::::	GUAACGUUG	Cleavage	pacid=371445
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCA	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534

222	242	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
222	242	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371534
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
1413	1433	UAAUCUGCAU	:::.:: .:::::::::: :	AAAAUCUGG	Cleavage	pacid=371739
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCAU	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674

2259	2279	UAAUCUGCA	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCA	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
2259	2279	UAAUCUGCA	.:::: :::: ::::::::	AGAACCCCAG	Translation	pacid=371674
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
658	678	UAAUCUGCA	:::.: .::.::::::::	GCAACUUGG	Cleavage	pacid=371653
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658

742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658

575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
575	595	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658
742	762	UAAUCUGCAU	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371658

575	595 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
575	595 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
575	595 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
575	595 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
742	762 UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA(	Cleavage	pacid=371658
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
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3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
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3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
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3824	3844 UAAUCUGCAU	.::: ::::::. :::::	ACGACCCCAG	Cleavage	pacid=371664
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21 UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608

1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
1	21	UAAUCUGCAU	::::.::: ::::.::.::.	CAAACUUCAA	Cleavage	pacid=371608
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCAU	.:.::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589

773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
565	585	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
624	644	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
773	793	UAAUCUGCA	.:.:::::::::::.::	GUUGCUUCA	Cleavage	pacid=371589
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610
849	869	UAAUCUGCA	:::. ::::.:::::.::	GUAACUACA	Cleavage	pacid=371610

868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
868	888	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
901	921	UAAUCUGCA	:.:. : :::.::::::::::	AAGAUGUAA	Cleavage	pacid=371430
1557	1577	UAAUCUGCA	:: :.:::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442
1557	1577	UAAUCUGCA	:: :.:::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442
1557	1577	UAAUCUGCA	:: :.:::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442
1557	1577	UAAUCUGCA	:: :.:::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442

1557	1577	UAAUCUGCA	:: :.::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442
1557	1577	UAAUCUGCA	:: :.::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442
1557	1577	UAAUCUGCA	:: :.::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442
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1557	1577	UAAUCUGCA	:: :.::::::::..::::	CAAUCUUCA	Cleavage	pacid=371442
897	917	UAAUCUGCA	::: :: :::::::: :::.	GAAAGCUGA	Cleavage	pacid=371766
897	917	UAAUCUGCA	::: :: :::::::: :::.	GAAAGCUGA	Cleavage	pacid=371766
897	917	UAAUCUGCA	::: :: :::::::: :::.	GAAAGCUGA	Cleavage	pacid=371766
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897	917	UAAUCUGCA	::: :: :::::::: :::.	GAAAGCUGA	Cleavage	pacid=371766
897	917	UAAUCUGCA	::: :: :::::::: :::.	GAAAGCUGA	Cleavage	pacid=371766
897	917	UAAUCUGCA	::: :: :::::::: :::.	GAAAGCUGA	Cleavage	pacid=371766
811	831	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744
939	959	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744
811	831	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744
939	959	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744
811	831	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744
939	959	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744
811	831	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744
939	959	UAAUCUGCA	..:.:::: :::: ::::::	AGGAUCUCA	Cleavage	pacid=371744

811	831	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
939	959	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
811	831	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
939	959	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
811	831	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
939	959	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
811	831	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
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811	831	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
939	959	UAAUCUGCAU	..:.:::: :::: ::::::	AGGAUCUCAU	Cleavage	pacid=371744
665	685	UAAUCUGCAU	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746
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665	685	UAAUCUGCAU	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746
665	685	UAAUCUGCAU	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746

665	685	UAAUCUGCA	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746
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665	685	UAAUCUGCA	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746
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665	685	UAAUCUGCA	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746
665	685	UAAUCUGCA	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746
665	685	UAAUCUGCA	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746

665	685	UAAUCUGCAU	:::.::..:::::..: :::	AAAAUCUUG	Cleavage	pacid=371746
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
171	192	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371757
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCAU	: ::::::: ::.::.:::::	UUAACCUCAA	Cleavage	pacid=371772
121	141	UAAUCUGCAU	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772

145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
145	166	UAAUCUGCA	: ::::::: ::.::.:::::	UUAACCUCA	Cleavage	pacid=371772
121	141	UAAUCUGCA	.::.:::.::::::::.	UUGCUCUUA	Cleavage	pacid=371772
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
1522	1542	UAAUCUGCA	:::.:::::: ::::::.	CAAACUUCA	Cleavage	pacid=371769
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786

341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
341	361	UAAUCUGCA	:.:::::: ::::::: :.	GUAGCCUCA	Translation	pacid=371786
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460
544	563	UAAUCUGCA	::.::::::: ::::::::.	GAAGCCUCA	Translation	pacid=371460

544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
544	563	UAAUCUGCAU	::.:::::: ::::::::.	GAAGCCUCAG	Translation	pacid=371460
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
2076	2095	UAAUCUGCAU	:::::: :::::::.:.::	CAAACCU-AG	Cleavage	pacid=371624
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCAU	:::.::..::.::::: ::.	AAAAUCUUG	Cleavage	pacid=371662

689	709	UAAUCUGCA	:::.::..::.:::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCA	:::.::..::.:::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCA	:::.::..::.:::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCA	:::.::..::.:::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCA	:::.::..::.:::: ::.	AAAAUCUUG	Cleavage	pacid=371662
689	709	UAAUCUGCA	:::.::..::.:::: ::.	AAAAUCUUG	Cleavage	pacid=371662
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
455	475	UAAUCUGCA	:: :::.::::::::::	CCAAGCUCG	Cleavage	pacid=371671
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599

2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2491	2511	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
2500	2520	UAAUCUGCA	: :::::.:::: : .:::::	UCAACCUUA	Cleavage	pacid=371599
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
76	96	UAAUCUGCA	::: .::: ::::..:::::	GAAAGUUCA	Cleavage	pacid=371591
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489

515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
515	535	UAAUCUGCA	:.::.:: :::::::::. :.	UGAAUCUGA	Cleavage	pacid=371489
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
1083	1103	UAAUCUGCA	:::::: :::::::..:::	UAAACCACAG	Cleavage	pacid=371685
3558	3578	UAAUCUGCA	:.:::.: :: :::.:::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.:::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.:::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.:::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.:::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.:::::	UGAACUUAA	Translation	pacid=371712

3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
3558	3578	UAAUCUGCA	:.:::.: :: :::.::::	UGAACUUAA	Translation	pacid=371712
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
1853	1873	UAAUCUGCA	::::. ..:::::::: :.	CAAACUGUG	Cleavage	pacid=371695
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688

2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
2660	2680	UAAUCUGCA	::.:.:: : .::::::::	CAAGCUUCC	Translation	pacid=371688
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
1326	1345	UAAUCUGCA	:.:::.:::::: :::::::	UGAACUUCA	Cleavage	pacid=371760
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCA	::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747

398	418	UAAUCUGCAU	:::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCAU	:::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCAU	:::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCAU	:::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCAU	:::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCAU	:::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
398	418	UAAUCUGCAU	:::::.:::::::: ::	CCAACCUUAG	Cleavage	pacid=371747
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
276	296	UAAUCUGCAU	:.::::::::.:::: :	GGUUCUUCA	Cleavage	pacid=371483
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
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386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
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386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478

386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
386	406	UAAUCUGCAU	.::.::: :::: ::::::	AGAAUCUCCG	Cleavage	pacid=371478
2591	2611	UAAUCUGCAU	:.:::. ..:::: ::.:::	UGAACUAUGC	Cleavage	pacid=371477
2591	2611	UAAUCUGCAU	:.:::. ..:::: ::.:::	UGAACUAUGC	Cleavage	pacid=371477
2591	2611	UAAUCUGCAU	:.:::. ..:::: ::.:::	UGAACUAUGC	Cleavage	pacid=371477
2591	2611	UAAUCUGCAU	:.:::. ..:::: ::.:::	UGAACUAUGC	Cleavage	pacid=371477
2591	2611	UAAUCUGCAU	:.:::. ..:::: ::.:::	UGAACUAUGC	Cleavage	pacid=371477
2591	2611	UAAUCUGCAU	:.:::. ..:::: ::.:::	UGAACUAUGC	Cleavage	pacid=371477
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2591	2611	UAAUCUGCAU	:.:::. ..:::: ::.:::	UGAACUAUGC	Cleavage	pacid=371477
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5280	5300	UAAUCUGCAU	:..:..::: :::::::::	UGGAUUUCA	Cleavage	pacid=371475
5280	5300	UAAUCUGCAU	:..:..::: ::::.::::	UGGAUUUCA	Cleavage	pacid=371475
5280	5300	UAAUCUGCAU	:..:..::: ::::.::::	UGGAUUUCA	Cleavage	pacid=371475
5280	5300	UAAUCUGCAU	:..:..::: ::::.::::	UGGAUUUCA	Cleavage	pacid=371475
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5280	5300	UAAUCUGCAU	:..:..::: ::::.::::	UGGAUUUCA	Cleavage	pacid=371475
691	711	UAAUCUGCAU	::. .::::::::.. ::::	CAAGAUUCAG	Cleavage	pacid=371453

691	711	UAAUCUGCA	::. .::::::::.. ::::	CAAGAUUCA	Cleavage	pacid=371453
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1169	1189	UAAUCUGCA	::::.: : ::::: :::::	CAAACUUGA	Cleavage	pacid=371457
1246	1266	UAAUCUGCA	::::.: : ::::: :::::	CAAACUUGA	Cleavage	pacid=371457
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1169	1189	UAAUCUGCA	::::.: : :::: ::::	CAAACUUGA	Cleavage	pacid=371457
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1169	1189	UAAUCUGCA	::::.: : :::: ::::	CAAACUUGA	Cleavage	pacid=371457
1246	1266	UAAUCUGCA	::::.: : :::: ::::	CAAACUUGA	Cleavage	pacid=371457
188	208	UAAUCUGCA	:.:::::.::: ::::	GCCAUCUCA	Cleavage	pacid=371545
188	208	UAAUCUGCA	:.:::::.::: ::::	GCCAUCUCA	Cleavage	pacid=371545
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617	637	UAAUCUGCA	:: :.. .:::::.:::::.	UAUAUUGUA	Cleavage	pacid=371524
617	637	UAAUCUGCA	:: :.. .:::::.:::::.	UAUAUUGUA	Cleavage	pacid=371524
617	637	UAAUCUGCA	:: :.. .:::::.:::::.	UAUAUUGUA	Cleavage	pacid=371524
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617	637	UAAUCUGCA	:: :.. .:::::.:::::.	UAUAUUGUA	Cleavage	pacid=371524

617	637 UAAUCUGCA	:: :.. .:::::::.:::::.	UAUAUUGUA	Cleavage	pacid=371524
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617	637 UAAUCUGCA	:: :.. .:::::::.:::::.	UAUAUUGUA	Cleavage	pacid=371524
617	637 UAAUCUGCA	:: :.. .:::::::.:::::.	UAUAUUGUA	Cleavage	pacid=371524
821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
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821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
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834	854 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844 UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536

834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536

821	841	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
824	844	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
834	854	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
837	857	UAAUCUGCA	:.: ::.::::::.:: ::.	AAGAGCUUA	Cleavage	pacid=371536
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
1011	1031	UAAUCUGCA	::..::::::: .: ::::	AAAGUCUCA	Cleavage	pacid=371717
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720
2004	2024	UAAUCUGCA	:::...::::::: ::: ::	UAAGUUUCA	Cleavage	pacid=371720

1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651

1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1214	1234	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1684	1704	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1681	1701	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
1868	1888	UAAUCUGCA	:...:.: . ::::::::::	UGGGCUUGG	Cleavage	pacid=371651
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.::: :::.: :::.	GAAACUUCA	Translation	pacid=371594

259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
259	279	UAAUCUGCA	::::.:::: :::.: :::.	GAAACUUCA	Translation	pacid=371594
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
1169	1189	UAAUCUGCA	:::::: :::. ::::.::	AAAACCUGA	Cleavage	pacid=371597
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587

505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
505	525	UAAUCUGCA	..:..:::::: :::: :::	AGGAUUUCA	Cleavage	pacid=371587
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
490	510	UAAUCUGCA	::.:.: :::.::..:.::.	GAAGCUUAA	Cleavage	pacid=371576
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	:::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586

544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCA	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586

652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
544	564	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
652	672	UAAUCUGCAU	::::::::: :: :::.::	AAAACCUCAG	Translation	pacid=371586
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516
643	663	UAAUCUGCAU	:.:: :: : ::::::::::	UGAAACUGAU	Cleavage	pacid=371516
667	687	UAAUCUGCAU	.::..::.::.:::::	UGCCUCUUGC	Cleavage	pacid=371516

643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
643	663	UAAUCUGCA	:.:: :: : :::::::::	UGAAACUGA	Cleavage	pacid=371516
667	687	UAAUCUGCA	.::..::.::.::::::	UGCCUCUUG	Cleavage	pacid=371516
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCA	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490

571	591	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
571	591	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
606	626	UAAUCUGCAU	:.:..:::::::::: : :	GAGAUUUCA	Cleavage	pacid=371490
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
2290	2310	UAAUCUGCAU	::.:. :.::: ::.:::::	UAGAUGUUA	Translation	pacid=371493
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCAU	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434

834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
834	854	UAAUCUGCA	:::...::: ::::.::::	UAAGUUUCA	Cleavage	pacid=371434
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1591	1612	UAAUCUGCA	:...:.: : :::.::::::::	UGGAUCAUG	Cleavage	pacid=371436
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .::::::::::::::	UGGAUAUUC	Cleavage	pacid=371554

1284	1305	UAAUCUGCA	:...:. .:::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .:::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .:::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .:::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .:::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1284	1305	UAAUCUGCA	:...:. .:::::::::::::	UGGAUAUUC	Cleavage	pacid=371554
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
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1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
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1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742

1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1473	1493	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
1476	1496	UAAUCUGCA	:::: ::::::::::	AGCUCCUCU	Cleavage	pacid=371742
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
284	306	UAAUCU--GC	: .::.::::::::: ::::::	UUGACUUCA	Cleavage	pacid=371772
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691

1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
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1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1551	1571	UAAUCUGCA	::.:.:::: :: .::::.	AAAGCUUCA	Translation	pacid=371691
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776

1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1624	1644	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371777
1837	1857	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1804	1824	UAAUCUGCA	:::.::: : :::: :::::.	UAAGCCUGA	Cleavage	pacid=371776
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777

1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1456	1476	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371777
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
1340	1360	UAAUCUGCA	::::::::::: ..:::	CAAACCUCAG	Cleavage	pacid=371776
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .::: :::	UGAGCCUCA	Translation	pacid=371756

737	757	UAAUCUGCA	:.:.:::::: .:::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .:::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .:::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .:::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .:::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .:::: :::	UGAGCCUCA	Translation	pacid=371756
737	757	UAAUCUGCA	:.:.:::::: .:::: :::	UGAGCCUCA	Translation	pacid=371756
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744

970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
970	990	UAAUCUGCA	::::. :..::.::.::.::	UAAAUAUUG	Cleavage	pacid=371744
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2673	2697	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
2728	2752	UAAUCUGCA	:::.:.: :.:::::::::	UAAGCUUUG	Cleavage	pacid=371756
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772

377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
377	397	UAAUCUGCA	:::::: :::: :::::: :	UAAACCAGA	Cleavage	pacid=371772
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
81	101	UAAUCUGCA	::: ::::: :::::::::	UAAUCCUCA	Cleavage	pacid=371464
1399	1419	UAAUCUGCA	::.:.:: ::::: :::::	GAAGCUUCC	Cleavage	pacid=371462
1399	1419	UAAUCUGCA	::.:.:: ::::: :::::	GAAGCUUCC	Cleavage	pacid=371462
1399	1419	UAAUCUGCA	::.:.:: ::::: :::::	GAAGCUUCC	Cleavage	pacid=371462
1399	1419	UAAUCUGCA	::.:.:: ::::: :::::	GAAGCUUCC	Cleavage	pacid=371462
1399	1419	UAAUCUGCA	::.:.:: ::::: :::::	GAAGCUUCC	Cleavage	pacid=371462

1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1399	1419	UAAUCUGCAU	::.:.:: ::::: :::::	GAAGCUUCCG	Cleavage	pacid=371462
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1361	1381	UAAUCUGCAU	::: :.::::: :: .:::::	UAACCUUCAG	Translation	pacid=371460
1590	1610	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCAU	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452

1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1590	1610	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1690	1710	UAAUCUGCA	::::::::::.: :. .::.	CAAACCUCAG	Cleavage	pacid=371452
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448

1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1095	1115	UAAUCUGCA	:.::..:::::: :::: :	UGAAUUUCA	Cleavage	pacid=371448
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.:::::::::.:::	AUAACUUCA	Cleavage	pacid=371479

1309	1329	UAAUCUGCA	:::.::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1309	1329	UAAUCUGCA	:::.::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
1363	1383	UAAUCUGCA	:::.::::::::.:::	AUAACUUCA	Cleavage	pacid=371479
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
2848	2868	UAAUCUGCA	:::: ::::: . :::::::.	UAAAGCUCA	Translation	pacid=371460
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628
554	574	UAAUCUGCA	::...:::: :::: :.:::	CAAGUUUCA	Translation	pacid=371628

453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
453	473	UAAUCUGCA	:.:::::: :.:: ::.::.	AAGACCUCAA	Cleavage	pacid=371623
284	304	UAAUCUGCA	:.::..:::::.:: : .:::	UGAAUUUCA	Cleavage	pacid=371527
284	304	UAAUCUGCA	:.::..:::::.:: : .:::	UGAAUUUCA	Cleavage	pacid=371527
284	304	UAAUCUGCA	:.::..:::::.:: : .:::	UGAAUUUCA	Cleavage	pacid=371527
284	304	UAAUCUGCA	:.::..:::::.:: : .:::	UGAAUUUCA	Cleavage	pacid=371527
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284	304	UAAUCUGCA	:.::..:::::.:: : .:::	UGAAUUUCA	Cleavage	pacid=371527
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414	434	UAAUCUGCA	:: ::::::::::::::	CAAUCCUCAG	Cleavage	pacid=371537
414	434	UAAUCUGCA	:: ::::::::::::::	CAAUCCUCAG	Cleavage	pacid=371537
414	434	UAAUCUGCA	:: ::::::::::::::	CAAUCCUCAG	Cleavage	pacid=371537
414	434	UAAUCUGCA	:: ::::::::::::::	CAAUCCUCAG	Cleavage	pacid=371537

414	434	UAAUCUGCA	:: ::::::::::::::	CAAUCCUCAG	Cleavage	pacid=371537
414	434	UAAUCUGCA	:: ::::::::::::::	CAAUCCUCAG	Cleavage	pacid=371537
414	434	UAAUCUGCA	:: ::::::::::::::	CAAUCCUCAG	Cleavage	pacid=371537
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71	91	UAAUCUGCA	:.:..:: :: :::::::: :	UGAGUCUGA	Translation	pacid=371739
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71	91	UAAUCUGCA	:.:..:: :: :::::::: :	UGAGUCUGA	Translation	pacid=371739
71	91	UAAUCUGCA	:.:..:: :: :::::::: :	UGAGUCUGA	Translation	pacid=371739
530	550	UAAUCUGCA	:::::: ::::: ::::::	UAAACCACAG	Cleavage	pacid=371734
530	550	UAAUCUGCA	:::::: ::::: ::::::	UAAACCACAG	Cleavage	pacid=371734
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530	550	UAAUCUGCA	:::::: ::::: ::::::	UAAACCACAG	Cleavage	pacid=371734

530	550	UAAUCUGCA	:::::: ::::: ::::::	UAAACCACAG	Cleavage	pacid=371734
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530	550	UAAUCUGCA	:::::: ::::: ::::::	UAAACCACAG	Cleavage	pacid=371734
530	550	UAAUCUGCA	:::::: ::::: ::::::	UAAACCACAG	Cleavage	pacid=371734
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
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610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
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610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
610	630	UAAUCUGCA	:.::: :..::.::::: :	UGAACGUUG	Cleavage	pacid=371654
332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
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332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598

332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
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332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
332	351	UAAUCUGCA	:.:::::::: :::: :::.	UGAACCUCA	Translation	pacid=371598
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: ::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513

1425	1445	UAAUCUGCA	:.. .:: :::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: :::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
2061	2081	UAAUCUGCA	:::.::::::.:::: ::	CAAAUCUCA	Cleavage	pacid=371513
1425	1445	UAAUCUGCA	:.. .:: :::::::: .:::	UGGUUCUGA	Cleavage	pacid=371513
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
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323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
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323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
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323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
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323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
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323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509

323	343	UAAUCUGCA	:::: .::::: ::: ::::.	UAAAGUUCA	Translation	pacid=371509
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
857	877	UAAUCUGCA	:::.::: : :.:::: ::::	UAAGCCUGA	Cleavage	pacid=371503
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493

1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1275	1295	UAAUCUGCA	..: .:::::.:: ::.::.	AGGAAUUCA	Cleavage	pacid=371493
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
1096	1116	UAAUCUGCA	:::::.: .::: :::: :	UAAACUUGG	Cleavage	pacid=371442
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553

485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
485	505	UAAUCUGCA	:.:.: :::: ::::::: :.	UGAGCAUCA	Translation	pacid=371553
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574

861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
754	774	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
798	818	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574
861	881	UAAUCUGCA	::::::.:::: :..:: :.	AAAACCUUA	Cleavage	pacid=371574

Multiplicity	Target_Acc.	ID	locusName	Pfam	Panther
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G094400.1	Phvul.001G094400	Phvul.001G09	PF01344	PTHR24413,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
1	Phvul.001G035800.1	Phvul.001G035800	Phvul.001G03	PF02535	PTHR11040,P
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1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.1	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.1	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147
1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF00	PTHR23147

1	Phvul.001G172700.1	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.1	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.1	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
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1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
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1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
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1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.1	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
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1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.1	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.2	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.3	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
1	Phvul.001G172700.4	Phvul.001G172700	Phvul.001G17	PF00076,PF0	PTHR23147
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1	Phvul.002G150900.1	Phvul.002G150900	Phvul.002G15	PF13793,PF0C	PTHR10210,P
1	Phvul.002G150900.1	Phvul.002G150900	Phvul.002G15	PF13793,PF0C	PTHR10210,P
1	Phvul.002G150900.1	Phvul.002G150900	Phvul.002G15	PF13793,PF0C	PTHR10210,P
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1	Phvul.005G045433.1	Phvul.005G045433	Phvul.005G04	PF00134		PTHR10026,P
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1	Phvul.007G143100.4	Phvul.007G143100	Phvul.007G14	PF00134	PTHR10026,P
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1	Phvul.007G143100.7	Phvul.007G143100	Phvul.007G14	PF00134	PTHR10026,P
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1	Phvul.007G143100.4	Phvul.007G143100	Phvul.007G14	PF00134	PTHR10026,P
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1	Phvul.010G014800.1	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
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1	Phvul.010G014800.2	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.1	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.2	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.1	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.2	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.1	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.2	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.1	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.2	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G014800.1	Phvul.010G014800	Phvul.010G01	PF13419	PTHR12725,P
1	Phvul.010G070400.1	Phvul.010G070400	Phvul.010G07	PF08263,PF0	PTHR27000,P
1	Phvul.010G070400.1	Phvul.010G070400	Phvul.010G07	PF08263,PF0	PTHR27000,P
1	Phvul.010G070400.1	Phvul.010G070400	Phvul.010G07	PF08263,PF0	PTHR27000,P
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1	Phvul.010G070400.1	Phvul.010G070400	Phvul.010G07	PF08263,PF0	PTHR27000,P
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1	Phvul.010G070400.1	Phvul.010G070400	Phvul.010G07	PF08263,PF0	PTHR27000,P
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1	Phvul.002G032300.2	Phvul.002G032300	Phvul.002G03	PF05705	PTHR12265,P
1	Phvul.002G032300.1	Phvul.002G032300	Phvul.002G03	PF05705	PTHR12265,P
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1	Phvul.002G032300.2	Phvul.002G032300	Phvul.002G03	PF05705	PTHR12265,P
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1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P

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1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.1	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.1	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.1	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.1	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.1	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
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1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.2	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.4	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.5	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.1	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P
1	Phvul.002G047100.3	Phvul.002G047100	Phvul.002G04	PF00134	PTHR10026,P

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1	Phvul.002G080100.1	Phvul.002G080100	Phvul.002G08	PF00043,PF02	PTHR11260,P
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1	Phvul.002G080100.1	Phvul.002G080100	Phvul.002G08	PF00043,PF02	PTHR11260,P
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1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
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1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
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1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
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1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF0	PTHR24326,P
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1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G19	PF02183,PF00	PTHR24326,P
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1	Phvul.006G186500.1	Phvul.006G186500	Phvul.006G18	PF08590	PTHR13308,P
1	Phvul.006G186500.1	Phvul.006G186500	Phvul.006G18	PF08590	PTHR13308,P
1	Phvul.006G186500.1	Phvul.006G186500	Phvul.006G18	PF08590	PTHR13308,P
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1	Phvul.006G186500.1	Phvul.006G186500	Phvul.006G18	PF08590	PTHR13308,P
1	Phvul.006G186500.1	Phvul.006G186500	Phvul.006G18	PF08590	PTHR13308,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
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1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
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1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
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1	Phvul.006G211900.1	Phvul.006G211900	Phvul.006G21	PF03801	PTHR10643,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.4	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.4	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.007G243700.3	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.2	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
1	Phvul.007G243700.1	Phvul.007G243700	Phvul.007G24	PF00397	PTHR21737,P
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1	Phvul.008G119600.1	Phvul.008G119600	Phvul.008G11	PF13460	PTHR14194,P
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1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G274500.1	Phvul.008G274500	Phvul.008G27	PF02970	PTHR21500,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P

1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
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1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
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1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
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1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
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1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28	0	PTHR31110,P
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1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
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1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.3	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.2	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.1	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
1	Phvul.008G289400.4	Phvul.008G289400	Phvul.008G28		0	PTHR31110,P
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2	Phvul.009G142100.1	Phvul.009G142100	Phvul.009G14	PF16499		PTHR11452,P
2	Phvul.009G142100.1	Phvul.009G142100	Phvul.009G14	PF16499		PTHR11452,P
2	Phvul.009G142100.1	Phvul.009G142100	Phvul.009G14	PF16499		PTHR11452,P
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2	Phvul.009G142100.1	Phvul.009G142100	Phvul.009G14	PF16499	PTHR11452,P
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1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P

1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.2	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
1	Phvul.009G177500.1	Phvul.009G177500	Phvul.009G17	PF02151,PF04	PTHR14289,P
2	Phvul.009G219300.1	Phvul.009G219300	Phvul.009G21	PF00069	PTHR27001,P
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1	Phvul.002G006400.2	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.3	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.1	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.2	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.3	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
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1	Phvul.002G006400.1	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.2	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.3	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.1	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.2	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.3	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.1	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.2	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
1	Phvul.002G006400.3	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
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1	Phvul.002G006400.3	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
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1	Phvul.002G006400.3	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
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1	Phvul.002G006400.2	Phvul.002G006400	Phvul.002G00	PF13920	PTHR10044,P
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1	Phvul.002G162800.2	Phvul.002G162800	Phvul.002G16	PF00400	PTHR22847,P
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1	Phvul.007G251800.1	Phvul.007G251800	Phvul.007G25	PF00085,PF0	PTHR22912,P
1	Phvul.008G181800.1	Phvul.008G181800	Phvul.008G18	PF00225	PTHR24115,P
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1	Phvul.008G181800.1	Phvul.008G181800	Phvul.008G18	PF00225	PTHR24115,P
1	Phvul.008G181800.1	Phvul.008G181800	Phvul.008G18	PF00225	PTHR24115,P
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1	Phvul.008G181800.1	Phvul.008G181800	Phvul.008G18	PF00225	PTHR24115,P
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1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
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1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
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1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
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1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
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1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G12	PF03914	PTHR12048
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1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206(	PF00155	PTHR10289,P

1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
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1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.3	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
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1	Phvul.L002060.2	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P
1	Phvul.L002060.1	Phvul.L002060	Phvul.L00206	PF00155	PTHR10289,P

KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
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0	0	0	GO:0005515	AT3G27150.1	0
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0	0	0	GO:0005515	AT3G27150.1	0
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KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
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KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
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KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
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KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
KOG1558	0	K14709	GO:0055085,	AT1G10970.1	ATZIP4,ZIP4
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0	2.7.11.1	0	GO:0005515	AT3G28890.1	AtRLP43,RLP43
0	2.7.11.1	0	GO:0005515	AT3G28890.1	AtRLP43,RLP43

	0	2.7.11.1	0	GO:0005515	AT3G28890.1	AtRLP43,RLP43
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	0	2.7.11.1	0	GO:0005515	AT3G28890.1	AtRLP43,RLP43
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	0	0	0	GO:0005515	AT5G12300.1	0
	0	0	0	GO:0005515	AT5G12300.1	0
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	0	0	0	GO:0005515	AT5G12300.1	0
	0	0	0	GO:0005515	AT5G12300.1	0
	0	0	0	GO:0005515	AT5G12300.1	0
KOG0907		3.5.1.52	0	GO:0045454,	AT1G08570.1	ACHT4
KOG0907		3.5.1.52	0	GO:0045454,	AT1G08570.1	ACHT4
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KOG0907		3.5.1.52	0	GO:0045454,	AT1G08570.1	ACHT4
KOG0907		3.5.1.52	0	GO:0045454,	AT1G08570.1	ACHT4

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0	3.2.1.39	0	GO:0005975,(	AT4G31140.1		0
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0	3.2.1.39	0	GO:0005975,(	AT4G31140.1		0
0	3.2.1.39	0	GO:0005975,(	AT4G31140.1		0
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KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10370.1	ATGSTU17,ERD9,GST3
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10370.1	ATGSTU17,ERD9,GST3
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10370.1	ATGSTU17,ERD9,GST3
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10370.1	ATGSTU17,ERD9,GST3
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KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10370.1	ATGSTU17,ERD9,GST3
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KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10370.1	ATGSTU17,ERD9,GST3
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KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10370.1	ATGSTU17,ERD9,GST3
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST
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KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST
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KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST

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KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG0406	2.5.1.18	K00799	GO:0005515	AT1G10360.1	ATGSTU18,GST29,GST	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
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KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
KOG1650	0	0	GO:0006813,	AT4G04850.2	ATKEA3,KEA3	
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0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0

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0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
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0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	0	0	0	AT5G42655.1		0
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
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0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	
0	3.6.4.4	K10395	GO:0008017,(	AT5G47820.2	FRA1	

	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
	0	3.6.4.4	K10395	GO:0008017,	AT5G47820.2	FRA1
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
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KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
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KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
KOG4529		0	0	0	AT1G73380.1	0
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
	0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA

0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
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0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
0	0	0	0	AT1G65680.1	ATEXPB2,ATHEXP BETA
KOG4495	0	0	GO:0005515	AT5G57860.3	0
KOG4495	0	0	GO:0005515	AT5G57860.3	0
KOG4495	0	0	GO:0005515	AT5G57860.3	0
KOG4495	0	0	GO:0005515	AT5G57860.3	0
KOG4495	0	0	GO:0005515	AT5G57860.3	0
KOG4495	0	0	GO:0005515	AT5G57860.3	0
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KOG4495	0	0	GO:0005515	AT5G57860.3	0
KOG4495	0	0	GO:0005515	AT5G57860.3	0
KOG4495	0	0	GO:0005515	AT5G57860.3	0
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0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
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0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
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0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt

0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
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0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
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0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	2.7.11.22,2.7.	0	GO:0006468,(	AT5G39420.1	cdc2cAt	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
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0	1.10.3.2	K05909	GO:0005507,(	AT2G38080.1	ATLMCO4,IRX12,LAC4,I	
KOG4696	0	0	0	AT5G24680.1		0
KOG4696	0	0	0	AT5G24680.1		0

KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
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KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
KOG4696	0	0	0	AT5G24680.1	0
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0	0	0	0	AT2G40820.1	0
0	0	0	0	AT2G40820.1	0
0	0	0	0	AT2G40820.1	0
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0	0	0	0	AT2G40820.1	0
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KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
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KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
KOG0257	2.6.1.78,2.6.1	K15849	GO:0030170,(	AT2G22250.3	AAT,ATAAT,MEE17
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0	0	K15164	GO:0016592,(	AT1G55325.2	GCT
0	0	K15164	GO:0016592,(	AT1G55325.2	GCT
0	0	K15164	GO:0016592,(	AT1G55325.2	GCT
0	0	K15164	GO:0016592,(	AT1G55325.2	GCT
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0	0	K15164	GO:0016592,(	AT1G55325.2	GCT

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0	0	K15164	GO:0016592,(	AT1G55325.2	GCT	
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0	0	0	0	0		0
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0	0	0	GO:0043565,(	AT3G01470.1	ATHB-1,ATHB1,HAT5,H	
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KOG4208	0	K14838	GO:0003676	AT5G04600.1		0
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KOG0806	3.5.1.53	K12251	GO:0016810,(	AT2G27450.1	ATNLP1,CPA,NLP1	
KOG0806	3.5.1.53	K12251	GO:0016810,(	AT2G27450.1	ATNLP1,CPA,NLP1	
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0	0	0	0	AT5G45480.1		0
0	0	0	0	AT5G45480.1		0
0	0	0	0	AT5G45480.1		0
0	0	0	0	AT5G45480.1		0
0	0	0	0	AT5G45480.1		0
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0	0	0	0	AT5G45480.1		0
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0	0	0	0	AT5G45480.1		0
KOG2915	2.1.1.220	K07442	GO:0031515,(	AT5G14600.1		0
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0	1.8.1.9	K00384	GO:0045454,(	AT2G41680.1	NTRC	
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0	1.8.1.9	K00384	GO:0045454,(	AT2G41680.1	NTRC	
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KOG2131		0	0	0	AT5G63080.1		0
KOG3882		0	0	GO:0016021	AT4G28050.1	TET7	
KOG3882		0	0	GO:0016021	AT4G28050.1	TET7	
KOG3882		0	0	GO:0016021	AT4G28050.1	TET7	
KOG3882		0	0	GO:0016021	AT4G28050.1	TET7	
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KOG1187	2.7.11.1		0	GO:0006468,	AT1G56720.3		0
KOG1187	2.7.11.1		0	GO:0006468,	AT1G56720.3		0
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KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
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KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
KOG1187	2.7.11.1	0	GO:0006468,	AT1G56720.3	0
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0	0	K14832	0	AT1G72440.1	EDA25,SWA2
0	0	K14832	0	AT1G72440.1	EDA25,SWA2
0	0	K14832	0	AT1G72440.1	EDA25,SWA2
0	0	K14832	0	AT1G72440.1	EDA25,SWA2
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0	0	K14832	0	AT1G72440.1	EDA25,SWA2
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0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,

0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
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0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
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0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
0	0	0	GO:0006355,	AT4G25470.1	ATCBF2,CBF2,DREB1C,
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1

KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1
KOG1368	4.1.2.5,4.1.2.4	0	GO:0030170,	AT1G08630.4	THA1

arabi-defline	ID	Annot_defline	IDENTIFIER	NAME	DESCRIPTION
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
Galactose oxidase/kelch repe	Phvul.001G09	PF01344 - Kel	Phvul.001G09	not assigned.a	(original desc
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
zinc transporter 4 precursor	Phvul.001G03	PTHR11040//I	Phvul.001G03	Solute transp	metal cation t
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig

receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
receptor like protein 43	Phvul.004G09	2.7.11.1 - Non	Phvul.004G09	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
Calcium-dependent lipid-bin	Phvul.006G03	PF00168 - C2	Phvul.006G03	not assigned.r	no hits & (orig
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore

atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
atypical CYS HIS rich thiored	Phvul.009G18	PTHR10438:S	Phvul.009G18	Redox homeo	atypical thiore
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G053	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-

O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-

O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
O-Glycosyl hydrolases family	Phvul.001G05	3.2.1.39 - Glu	Phvul.001G05	Enzyme classi	Glucan endo-
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processi	RSZ32/33 RN

RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
RNA-binding (RRM/RBD/RNP	Phvul.001G17	K12896 - splic	Phvul.001G17	RNA processir	RSZ32/33 RNA
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:SI	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:SI	Phvul.002G15	Amino acid m	ribose-phosph

phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
phosphoribosyl pyrophospha	Phvul.002G15	PTHR10210:S	Phvul.002G15	Amino acid m	ribose-phosph
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymer

Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
Y-family DNA polymerase H	Phvul.002G18	K03509 - DNA	Phvul.002G18	DNA damage	DNA polymera
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc

RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.003G09	KOG1003//KC	Phvul.003G09	not assigned.	(original desc
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
0	0	0	Phvul.003G22	not assigned.	no hits & (ori
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C

Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Cyclin family protein	Phvul.005G04	PTHR10026:S	Phvul.005G04	RNA biosynth	component C
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.	no hits & (ori

P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.r	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.r	no hits & (ori
P-loop containing nucleoside	Phvul.007G02	PTHR20953:S	Phvul.007G02	not assigned.r	no hits & (ori
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
myb-like transcription factor	Phvul.007G10	PTHR31003:S	Phvul.007G10	RNA biosynth	G2-like GARP
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C

Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy

Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component Cy

Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
Cyclin family protein	Phvul.007G14	K15161 - cycli	Phvul.007G14	RNA biosynth	component C
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
0	Phvul.007G16	KOG1893 - Un	Phvul.007G16	Solute transp	mechanosens
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.	(original desc

NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G07	PTHR10366:SI	Phvul.008G07	not assigned.a	(original desc
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein	Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy

Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
Cyclin family protein		Phvul.008G13	K15161 - cycli	Phvul.008G13	RNA biosynth	component Cy
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori
	0	0	0	Phvul.008G14	not assigned.r	no hits & (ori

Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Haloacid dehalogenase-like h	Phvul.010G01	PTHR12725:SI	Phvul.010G01	not assigned.r	no hits & (orig
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase

Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Leucine-rich repeat protein ki	Phvul.010G07	PF00069//PFC	Phvul.010G07	Protein modif	protein kinase
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
Tetratricopeptide repeat (TPF	Phvul.002G01	PTHR23083//I	Phvul.002G01	not assigned.a	(original desc
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (ori

alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
alpha/beta-Hydrolases super	Phvul.002G03	KOG2521 - Un	Phvul.002G03	not assigned.r	no hits & (orig
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (

Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (

Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Cyclin family protein	Phvul.002G04	PTHR10026//I	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (

Cyclin family protein	Phvul.002G04	PTHR10026//	Phvul.002G04	Cell cycle orga	cyclin (CYCT) (
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
Glutathione S-transferase fan	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta

glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
glutathione S-transferase TA	Phvul.002G08	PTHR11260:S	Phvul.002G08	Protein modif	class tau gluta
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
K+ efflux antiporter 3	Phvul.002G21	PTHR16254:S	Phvul.002G21	Solute transp	proton:potass
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori

Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
Disease resistance-responsiv	Phvul.002G32	PTHR21495:S	Phvul.002G32	not assigned.	no hits & (ori
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein

P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.003G24	K10395 - kine	Phvul.003G24	Cytoskeleton	motor protein
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
0	Phvul.004G13	PTHR13379 -	Phvul.004G13	not assigned.	no hits & (ori
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.	(original desc

expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.a	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.a	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.a	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.a	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.a	(original desc
expansin B2	Phvul.007G23	PTHR31692:S	Phvul.007G23	not assigned.a	(original desc
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
Ubiquitin-like superfamily pro	Phvul.007G24	KOG4495 - RN	Phvul.007G24	not assigned.n	no hits & (ori
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase

CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
CDC2C	Phvul.008G03	PTHR24056//I	Phvul.008G03	Protein modif	protein kinase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Laccase/Diphenol oxidase fan	Phvul.008G26	PTHR11709:SI	Phvul.008G26	Cell wall orgar	lignin laccase
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.r	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.r	no hits & (ori

Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
Peptidase C78, ubiquitin fold	Phvul.009G04	KOG4696 - Un	Phvul.009G04	not assigned.	no hits & (ori
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
0	Phvul.001G11	PF16709 - Fus	Phvul.001G11	Cytoskeleton	SCAB actin org
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB

ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
ATP binding cassette subfami	Phvul.001G17	PTHR24221:S	Phvul.001G17	Solute transp	subfamily AB
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
aspartate aminotransferase	Phvul.001G25	2.6.1.78 - Asp	Phvul.001G25	Amino acid m	prephenate a
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M

RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
RNA polymerase II transcripti	Phvul.001G26	K15164 - med	Phvul.001G26	RNA biosynth	component M
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
Kinase interacting (KIP1-like)	Phvul.002G14	PTHR31631:SI	Phvul.002G14	Cytoskeleton	actin-binding
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing

C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
C2H2 and C2HC zinc fingers s	Phvul.002G25	PTHR10593//I	Phvul.002G25	RNA biosynth	C2H2 zinc fing
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
2-oxoacid dehydrogenases ac	Phvul.003G03	2.3.1.12 - Dih	Phvul.003G03	not assigned.	(original desc
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori

0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
0	0	0	Phvul.003G06	not assigned.	no hits & (ori
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
aldehyde dehydrogenase 22A	Phvul.003G11	PTHR11699:S	Phvul.003G11	Enzyme classi	Aldehyde deh
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
HOPM interactor 7	Phvul.003G12	K13462 - guar	Phvul.003G12	Vesicle traffic	BIG-type ARF-
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.	(original desc

Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
Endomembrane protein 70 p	Phvul.003G17	PTHR10766:S	Phvul.003G17	not assigned.a	(original desc
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f

homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
homeobox 1	Phvul.003G19	KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription f
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
RNA-binding (RRM/RBD/RNP	Phvul.005G08	K14838 - nucl	Phvul.005G08	Protein biosyn	pre-60S riboso
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig
0	0	0	Phvul.005G11	not assigned.n	no hits & (orig

	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
	0	0	0	Phvul.005G11	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.r	no hits & (ori

IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6	Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori

IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
IQ-domain 6		Phvul.005G15	PF00612 - IQ	Phvul.005G15	not assigned.	no hits & (ori
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
silencing defective 5		Phvul.006G18	PTHR13308:S	Phvul.006G18	not assigned.	(original desc
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N
	0	Phvul.006G21	K11547 - kine	Phvul.006G21	Cell cycle org	component N

WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prote	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori

WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
WW domain-containing prot	Phvul.007G24	K12865 - poly	Phvul.007G24	not assigned.	no hits & (ori
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein hom	ATG4 autopha

Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
Peptidase family C54 protein	Phvul.008G04	K08342 - cyst	Phvul.008G04	Protein home	ATG4 autopha
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
NAD(P)-binding Rossmann-fo	Phvul.008G11	PTHR14194//I	Phvul.008G11	not assigned.	(original desc
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca

delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
delta 1-pyrroline-5-carboxyla	Phvul.008G23	1.2.1.41//2.7.	Phvul.008G23	Amino acid m	pyrroline-5-ca
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
tubulin folding cofactor A (KI	Phvul.008G27	K17292 - tubu	Phvul.008G27	Cytoskeleton	TFC-A cofacto
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori

0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori

0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
0	0	0	Phvul.008G28	not assigned.r	no hits & (ori
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto

Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
Melibiase family protein	Phvul.009G14	K07407 - alph	Phvul.009G14	Enzyme classi	Alpha-galacto
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa	Phvul.009G17	not assigned.	no hits & (ori

SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
SKP1/ASK-interacting protein	Phvul.009G17	K06195 - Apa(	Phvul.009G17	not assigned.r	no hits & (ori
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori

0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
0	0	0	Phvul.010G11	not assigned.r	no hits & (ori
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
protein kinase family protein	Phvul.010G14	PTHR27001:SI	Phvul.010G14	Protein modif	protein kinase
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription f

basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription
basic helix-loop-helix (bHLH)	Phvul.011G21	PF00010 - Hel	Phvul.011G21	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription

Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
Calmodulin-binding transcrip	Phvul.L00294	PTHR23335:S	Phvul.L00294	RNA biosynth	transcription
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
VQ motif-containing protein	Phvul.002G14	PF05678 - VQ	Phvul.002G14	not assigned.	no hits & (ori
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:S	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:S	Phvul.001G06	Vesicle traffic	RAB-GTPase-a

Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
Ypt/Rab-GAP domain of gyp1	Phvul.001G06	PTHR22957:SI	Phvul.001G06	Vesicle traffic	RAB-GTPase-a
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.	(original desc

RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
RING/U-box superfamily prot	Phvul.002G00	PTHR10044:SI	Phvul.002G00	not assigned.a	(original desc
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P

cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
cytochrome P450, family 71,	Phvul.002G02	1.14.13.121 -	Phvul.002G02	Enzyme classi	Cytochrome P
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (ori

Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (orig
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (orig
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (orig
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (orig
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (orig
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (orig
Protein of unknown function,	Phvul.002G05	PF04784//PF1	Phvul.002G05	not assigned.r	no hits & (orig
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran

transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
transferases, transferring hex	Phvul.002G09	K07542 - phos	Phvul.002G09	Protein modif	mannosyltran
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
SPA1-related 2	Phvul.002G16	PTHR22847:SI	Phvul.002G16	External stimu	regulator com
0	0	0	Phvul.002G22	not assigned.r	no hits & (orig

0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
0	0	0	Phvul.002G22	not assigned.r	no hits & (ori
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
polyubiquitin 10	Phvul.003G12	K08770 - ubiq	Phvul.003G12	Protein home	ubiquitin-fold
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.r	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.r	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.r	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.r	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.r	no hits & (ori

ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
ARM repeat superfamily prot	Phvul.003G12	PTHR21576:S	Phvul.003G12	not assigned.	no hits & (ori
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
basic helix-loop-helix (bHLH)	Phvul.003G13	PTHR12565//	Phvul.003G13	RNA biosynth	transcription f
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen

Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Fatty acid hydroxylase superf	Phvul.003G15	PTHR11863:S	Phvul.003G15	Cell wall orga	aldehyde-gen
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prot	Phvul.003G21	PTHR11709:S	Phvul.003G21	Enzyme classi	Monocopper

Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
Cupredoxin superfamily prote	Phvul.003G21	PTHR11709:SI	Phvul.003G21	Enzyme classi	Monocopper
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (

EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
EYES ABSENT homolog	Phvul.003G23	PTHR10190 - I	Phvul.003G23	Protein modif	phosphatase (
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
Transcription factor jumonji (	Phvul.003G28	PTHR10694:S	Phvul.003G28	RNA biosynth	transcription f
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti
cyclic nucleotide-binding tran	Phvul.004G14	PTHR10217:S	Phvul.004G14	Solute transp	cyclic nucleoti

thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
thioredoxin-dependent perox	Phvul.004G16	PTHR10430 - I	Phvul.004G16	Redox homeo	type-2 peroxi
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
0	0	0	Phvul.005G01	not assigned.	no hits & (ori
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp

nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
nitrilase-like protein 1	Phvul.005G12	K12251 - N-ca	Phvul.005G12	Polyamine me	N-carbamoylp
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
Protein of unknown function	Phvul.006G04	PF04578 - Pro	Phvul.006G04	not assigned.	no hits & (ori
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processi	component T

S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
S-adenosyl-L-methionine-dep	Phvul.006G18	2.1.1.220 - tR	Phvul.006G18	RNA processir	component T
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
NADPH-dependent thioredox	Phvul.007G25	PTHR22912:S	Phvul.007G25	Redox homeo	NADPH-deper
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein

P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
P-loop containing nucleoside	Phvul.008G18	K10395 - kine	Phvul.008G18	Cytoskeleton	motor protein
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori

Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
Putative endonuclease or gly	Phvul.009G14	PTHR14379:S	Phvul.009G14	not assigned.	no hits & (ori
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription
2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:S	Phvul.009G17	RNA biosynth	transcription

2-oxoglutarate (2OG) and Fe(	Phvul.009G17	PTHR12480:SI	Phvul.009G17	RNA biosynth	transcription f
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
tetraspanin7	Phvul.009G20	PTHR32191:SI	Phvul.009G20	not assigned.a	(original desc
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:SI	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:SI	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:SI	Phvul.009G21	Protein modif	receptor-like

Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
Protein kinase superfamily pr	Phvul.009G21	PTHR27001:S	Phvul.009G21	Protein modif	receptor-like
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
CCAAT-binding factor	Phvul.010G12	K14832 - ribo	Phvul.010G12	Protein biosy	component N
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f

C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
C-repeat/DRE binding factor	Phvul.011G09	PF00847 - AP	Phvul.011G09	RNA biosynth	transcription f
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
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threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
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threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald

threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
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threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
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threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
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threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
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threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald
threonine aldolase 1	Phvul.L00206	4.1.2.5 - L-thr	Phvul.L00206	Amino acid m	threonine ald

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miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
ggaaugggcuga	Phvul.008G004800.1	2.5	-1	1	22
ggaaugggcuga	Phvul.009G006000.1	2.5	-1	1	22
ggaaugggcuga	Phvul.009G006000.2	2.5	-1	1	22
ggaaugggcuga	Phvul.002G315000.1	3	-1	1	22
ggaaugggcuga	Phvul.002G315000.2	3	-1	1	22
ggaaugggcuga	Phvul.004G164800.1	3	-1	1	22
ggaaugggcuga	Phvul.005G049000.1	3	-1	1	22
ggaaugggcuga	Phvul.010G108200.1	3	-1	1	22
ggaaugggcuga	Phvul.L008143.1	3	-1	1	22
ggaaugggcuga	Phvul.002G189700.1	3.5	-1	1	22
ggaaugggcuga	Phvul.002G189700.2	3.5	-1	1	22
ggaaugggcuga	Phvul.002G189700.3	3.5	-1	1	22
ggaaugggcuga	Phvul.002G189700.4	3.5	-1	1	22
ggaaugggcuga	Phvul.002G258800.1	3.5	-1	1	22
ggaaugggcuga	Phvul.003G202100.1	3.5	-1	1	22
ggaaugggcuga	Phvul.003G282800.1	3.5	-1	1	22
ggaaugggcuga	Phvul.004G083900.1	3.5	-1	1	22
ggaaugggcuga	Phvul.006G110000.1	3.5	-1	1	22
ggaaugggcuga	Phvul.007G031800.1	3.5	-1	1	22
ggaaugggcuga	Phvul.007G031800.2	3.5	-1	1	22
ggaaugggcuga	Phvul.007G094100.1	3.5	-1	1	22
ggaaugggcuga	Phvul.008G081700.2	3.5	-1	1	22
ggaaugggcuga	Phvul.009G201900.1	3.5	-1	1	22
ggaaugggcuga	Phvul.009G233100.2	3.5	-1	1	22
ggaaugggcuga	Phvul.009G246200.2	3.5	-1	1	22
ggaaugggcuga	Phvul.010G125200.1	3.5	-1	1	22
ggaaugggcuga	Phvul.011G073400.1	3.5	-1	1	22
ggaaugggcuga	Phvul.001G001700.1	4	-1	1	22
ggaaugggcuga	Phvul.001G160000.1	4	-1	1	22
ggaaugggcuga	Phvul.002G011900.1	4	-1	1	22
ggaaugggcuga	Phvul.002G028700.1	4	-1	1	22
ggaaugggcuga	Phvul.002G185800.1	4	-1	1	22
ggaaugggcuga	Phvul.002G206900.1	4	-1	1	22
ggaaugggcuga	Phvul.002G206900.2	4	-1	1	22
ggaaugggcuga	Phvul.003G078900.1	4	-1	1	22
ggaaugggcuga	Phvul.003G210500.1	4	-1	1	22
ggaaugggcuga	Phvul.003G262300.3	4	-1	1	22
ggaaugggcuga	Phvul.003G262300.1	4	-1	1	22
ggaaugggcuga	Phvul.003G262300.2	4	-1	1	22
ggaaugggcuga	Phvul.003G262300.4	4	-1	1	22
ggaaugggcuga	Phvul.004G093900.4	4	-1	1	22
ggaaugggcuga	Phvul.004G093900.6	4	-1	1	22
ggaaugggcuga	Phvul.004G093900.5	4	-1	1	22
ggaaugggcuga	Phvul.004G093900.3	4	-1	1	22
ggaaugggcuga	Phvul.004G093900.1	4	-1	1	22

ggaaugggcuga	Phvul.004G093900.2	4	-1	1	22
ggaaugggcuga	Phvul.004G093900.7	4	-1	1	22
ggaaugggcuga	Phvul.004G105600.1	4	-1	1	22
ggaaugggcuga	Phvul.004G135400.1	4	-1	1	22
ggaaugggcuga	Phvul.004G159500.1	4	-1	1	22
ggaaugggcuga	Phvul.004G170000.1	4	-1	1	22
ggaaugggcuga	Phvul.005G001000.1	4	-1	1	22
ggaaugggcuga	Phvul.005G022800.1	4	-1	1	22
ggaaugggcuga	Phvul.005G072300.1	4	-1	1	22
ggaaugggcuga	Phvul.007G034000.1	4	-1	1	22
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ggaaugggcuga	Phvul.007G244033.1	4	-1	1	22
ggaaugggcuga	Phvul.007G244033.1	4	-1	1	22
ggaaugggcuga	Phvul.007G244066.1	4	-1	1	22
ggaaugggcuga	Phvul.008G079000.1	4	-1	1	22
ggaaugggcuga	Phvul.008G267400.5	4	-1	1	22
ggaaugggcuga	Phvul.008G267400.2	4	-1	1	22
ggaaugggcuga	Phvul.008G267400.3	4	-1	1	22
ggaaugggcuga	Phvul.008G267400.4	4	-1	1	22
ggaaugggcuga	Phvul.009G053900.2	4	-1	1	22
ggaaugggcuga	Phvul.009G081900.1	4	-1	1	22
ggaaugggcuga	Phvul.009G213000.1	4	-1	1	22
ggaaugggcuga	Phvul.011G065200.2	4	-1	1	22
ggaaugggcuga	Phvul.001G079400.1	4.5	-1	1	22
ggaaugggcuga	Phvul.001G087700.1	4.5	-1	1	22
ggaaugggcuga	Phvul.001G117500.1	4.5	-1	1	22
ggaaugggcuga	Phvul.002G007100.1	4.5	-1	1	22
ggaaugggcuga	Phvul.002G115800.1	4.5	-1	1	22
ggaaugggcuga	Phvul.002G115800.3	4.5	-1	1	22
ggaaugggcuga	Phvul.002G163600.1	4.5	-1	1	22
ggaaugggcuga	Phvul.002G168500.1	4.5	-1	1	22
ggaaugggcuga	Phvul.002G168500.2	4.5	-1	1	22
ggaaugggcuga	Phvul.002G177500.1	4.5	-1	1	22
ggaaugggcuga	Phvul.002G315000.1	4.5	-1	1	22
ggaaugggcuga	Phvul.002G315000.2	4.5	-1	1	22
ggaaugggcuga	Phvul.003G185300.1	4.5	-1	1	22
ggaaugggcuga	Phvul.003G212800.2	4.5	-1	1	22
ggaaugggcuga	Phvul.004G121900.1	4.5	-1	1	22
ggaaugggcuga	Phvul.006G033600.1	4.5	-1	1	22
ggaaugggcuga	Phvul.006G033600.2	4.5	-1	1	22
ggaaugggcuga	Phvul.006G219000.1	4.5	-1	1	22
ggaaugggcuga	Phvul.007G008100.2	4.5	-1	1	22
ggaaugggcuga	Phvul.007G086600.1	4.5	-1	1	22
ggaaugggcuga	Phvul.007G168600.1	4.5	-1	1	22
ggaaugggcuga	Phvul.008G002700.1	4.5	-1	1	22
ggaaugggcuga	Phvul.009G062500.1	4.5	-1	1	22

ggaaugggcuga	Phvul.001G186500.1	5	-1	1	22
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ggaaugggcuga	Phvul.003G202300.1	5	-1	1	22
ggaaugggcuga	Phvul.003G202300.2	5	-1	1	22
ggaaugggcuga	Phvul.003G248400.1	5	-1	1	22
ggaaugggcuga	Phvul.003G248400.2	5	-1	1	22
ggaaugggcuga	Phvul.003G248400.3	5	-1	1	22
ggaaugggcuga	Phvul.004G024400.1	5	-1	1	22
ggaaugggcuga	Phvul.004G071800.1	5	-1	1	22
ggaaugggcuga	Phvul.004G178500.1	5	-1	1	22
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ggaaugggcuga	Phvul.006G110000.1	5	-1	1	22
ggaaugggcuga	Phvul.007G204100.1	5	-1	1	22
ggaaugggcuga	Phvul.008G006800.1	5	-1	1	22
ggaaugggcuga	Phvul.008G034200.2	5	-1	1	22
ggaaugggcuga	Phvul.009G184400.1	5	-1	1	22
ggaaugggcuga	Phvul.009G184400.2	5	-1	1	22

Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
1335	1356	GGAAUGGGC	: ::::.::::::::.::: ::	UUCUUCUCA	Cleavage	pacid=371611
2	23	GGAAUGGGC	::::.:::::..::.:::::.	CGCUUUCCAA	Cleavage	pacid=371508
2	23	GGAAUGGGC	::::.:::::..::.:::::.	CGCUUUCCAA	Cleavage	pacid=371508
540	561	GGAAUGGGC	: .::.:::::.::...::::.	UCUUUUCCA	Cleavage	pacid=371747
540	561	GGAAUGGGC	: .::.:::::.::...::::.	UCUUUUCCA	Cleavage	pacid=371747
1753	1774	GGAAUGGGC	::::.:::::::.:.:: ::::	GGCUUUCCA	Cleavage	pacid=371625
113	134	GGAAUGGGC	:::::: ::.:::::: :::	ACCUUCCCUA	Cleavage	pacid=371536
1551	1572	GGAAUGGGC	: .::.:: :::::::::: :	UUUUUUCCU	Cleavage	pacid=371423
341	362	GGAAUGGGC	.::.:: :::::::::::.	CAUUUUCCCA	Cleavage	pacid=371789
9591	9612	GGAAUGGGC	.:::: ::::::::.::: :.	GCUUUCCGA	Cleavage	pacid=371766
9591	9612	GGAAUGGGC	.:::: ::::::::.::: :.	GCUUUCCGA	Cleavage	pacid=371766
9588	9609	GGAAUGGGC	.:::: ::::::::.::: :.	GCUUUCCGA	Cleavage	pacid=371766
9588	9609	GGAAUGGGC	.:::: ::::::::.::: :.	GCUUUCCGA	Cleavage	pacid=371766
1145	1166	GGAAUGGGC	::::..:::. :::.:::::	CUCUUCUUA	Translation	pacid=371750
2509	2530	GGAAUGGGC	: :::::: : :::.::::::	GGAUUCCAC	Translation	pacid=371476
3121	3142	GGAAUGGGC	: :::.::::: :::...::::	UUCUUUCCA	Translation	pacid=371474
377	398	GGAAUGGGC	::. :::. :::::::::::..	UGUCUCCUU	Cleavage	pacid=371616
579	600	GGAAUGGGC	:::::: ::: :.::::::	CAAUUCCCAU	Cleavage	pacid=371739
2928	2949	GGAAUGGGC	: ::: ::::: :::::.::.:	UUCUUGCCA	Translation	pacid=371658
2300	2321	GGAAUGGGC	: ::: ::::: :::::.::.:	UUCUUGCCA	Translation	pacid=371658
955	976	GGAAUGGGC	:::::::: :::.::::::	CACUUCCCAA	Translation	pacid=371671
160	181	GGAAUGGGC	: :.:::::: ::::::.:	GCCCUUCCAA	Cleavage	pacid=371591
1187	1208	GGAAUGGGC	::::::::::::.: ::.:	GAUAUCCCA	Cleavage	pacid=371507
3000	3021	GGAAUGGGC	: .::..::::.::..:::::..	UAUUUUUCA	Cleavage	pacid=371497
831	852	GGAAUGGGC	: ::::.: :::::: ::::	GGGUUCCUA	Cleavage	pacid=371514
1552	1573	GGAAUGGGC	.::.:::::..:..:::::	ACUUUUCCA	Cleavage	pacid=371442
594	615	GGAAUGGGC	: : ::.. ::::::::.:::::	UUCCUCUUC	Cleavage	pacid=371549
2062	2083	GGAAUGGGC	:: :::::::::::.: ::::	AGCAUCCCAA	Cleavage	pacid=371695
812	833	GGAAUGGGC	:.::.:.: :::::::.::::	AGUUUUCUA	Cleavage	pacid=371680
964	985	GGAAUGGGC	:::::: .::::::::::	UUUAGCCCA	Translation	pacid=371755
22	43	GGAAUGGGC	:: ..:::::: ::.:::::	ACCUCUUCAA	Cleavage	pacid=371746
1652	1673	GGAAUGGGC	: :: ::::::.::...:::..	UACUACCCAA	Cleavage	pacid=371744
480	501	GGAAUGGGC	:::.: ..::::::...::::	ACCUUUCGG	Cleavage	pacid=371768
407	428	GGAAUGGGC	:::.: ..::::::...::::	ACCUUUCGG	Cleavage	pacid=371768
2529	2550	GGAAUGGGC	::::.. ::::: :.:::::	CUCUUCUUC	Cleavage	pacid=371470
606	627	GGAAUGGGC	.::::::.: :::.::::::	GCUUUCCCG	Translation	pacid=371444
644	665	GGAAUGGGC	.::::::..::::::::.	UAAACUCCAA	Cleavage	pacid=371454
500	521	GGAAUGGGC	.::::::..::::::::.	UAAACUCCAA	Cleavage	pacid=371453
500	521	GGAAUGGGC	.::::::..::::::::.	UAAACUCCAA	Cleavage	pacid=371454
472	493	GGAAUGGGC	.::::::..::::::::.	UAAACUCCAA	Cleavage	pacid=371454
75	96	GGAAUGGGC	.:::.:::::: .:.::::..	CAUUUCUCA	Cleavage	pacid=371627
76	97	GGAAUGGGC	.:::.:::::: .:.::::..	CAUUUCUCA	Cleavage	pacid=371628
96	117	GGAAUGGGC	.:::.:::::: .:.::::..	CAUUUCUCA	Cleavage	pacid=371627
69	90	GGAAUGGGC	.:::.:::::: .:.::::..	CAUUUCUCA	Cleavage	pacid=371628
69	90	GGAAUGGGC	.:::.:::::: .:.::::..	CAUUUCUCA	Cleavage	pacid=371627

96	117	GGAAUGGGC	.:::.::::: .:.:::..	CAUUUCUCA	Cleavage	pacid=371628
69	90	GGAAUGGGC	.:::.::::: .:.:::..	CAUUUCUCA	Cleavage	pacid=371628
212	233	GGAAUGGGC	:::.::.:::: ..:::::.	GCCUUUCCG	Cleavage	pacid=371629
357	378	GGAAUGGGC	:: :::::::: :::::::	AACUCCCCAA	Cleavage	pacid=371629
1475	1496	GGAAUGGGC	: .:::.::::..:..:::: :	UCUUUCUCA	Cleavage	pacid=371632
273	294	GGAAUGGGC	::::.:.::: :.:.::::.	GCCUUCUCG	Translation	pacid=371616
2164	2185	GGAAUGGGC	::::::.::.:..: ::::::..	UGCUUCUCA	Cleavage	pacid=371530
1223	1244	GGAAUGGGC	::::.::: ::::: .::::	AUCUUCUCA	Cleavage	pacid=371540
885	906	GGAAUGGGC	.:::.::::: :::: :::.	AUUUUCUCA	Translation	pacid=371543
1650	1671	GGAAUGGGC	:: ::: .::::::::. :::.	UGAUUCGUA	Cleavage	pacid=371676
1160	1181	GGAAUGGGC	:: ::: .::::::::. :::.	UGAUUCGUA	Cleavage	pacid=371676
311	332	GGAAUGGGC	:::::::: .::::.::::	CUCUUCCCAA	Translation	pacid=371653
497	518	GGAAUGGGC	:::::::: .::::.::::	CUCUUCCCAA	Translation	pacid=371653
497	518	GGAAUGGGC	:::::::: .::::.::::	CUCUUCCCAA	Translation	pacid=371643
1570	1591	GGAAUGGGC	:::.:::: ::: ::::::.:	AUCUUUCCA	Cleavage	pacid=371607
1521	1542	GGAAUGGGC	:::::: ::::...:.:: ::::	UGCUUCACA	Cleavage	pacid=371602
1517	1538	GGAAUGGGC	:::::: ::::...:.:: ::::	UGCUUCACA	Cleavage	pacid=371602
1636	1657	GGAAUGGGC	:::::: ::::...:.:: ::::	UGCUUCACA	Cleavage	pacid=371602
1630	1651	GGAAUGGGC	:::::: ::::...:.:: ::::	UGCUUCACA	Cleavage	pacid=371602
5313	5334	GGAAUGGGC	::::::::::::.:: :	GAAAACCCAA	Cleavage	pacid=371507
3042	3063	GGAAUGGGC	: .::::::.:.::. :::::.:	UUUUUCCUA	Cleavage	pacid=371520
21	42	GGAAUGGGC	:: ::.:.:.::: ::::::	CCCUCCCUAG	Cleavage	pacid=371495
114	135	GGAAUGGGC	::: : ::.::::.:.::::.:	GGCUACGCA	Cleavage	pacid=371555
154	175	GGAAUGGGC	::::::: ..:.::::::	GACUUCCCA	Cleavage	pacid=371688
537	558	GGAAUGGGC	::::::::::...: : :::::	CGCUUCCCAA	Cleavage	pacid=371681
179	200	GGAAUGGGC	: ::::.::::. :: :::::.	UUCUUCUCA	Translation	pacid=371685
9	30	GGAAUGGGC	::: :..:::.: :.::::::	AGCUGCUUA	Cleavage	pacid=371751
39	60	GGAAUGGGC	:.::..::::.: ..:::::.	GGUUUUUCA	Cleavage	pacid=371771
39	60	GGAAUGGGC	:.::..::::.: ..:::::.	GGUUUUUCA	Cleavage	pacid=371771
340	361	GGAAUGGGC	:.::.::..:..: ::::::.	AGUUUUCCG	Cleavage	pacid=371780
745	766	GGAAUGGGC	:::.::::::: ::. :::.:	ACCUUUCCA	Cleavage	pacid=371779
745	766	GGAAUGGGC	:::.::::::: ::. :::.:	ACCUUUCCA	Cleavage	pacid=371779
190	211	GGAAUGGGC	: :::::::::. :.. :::::	UUCUUCCCA	Translation	pacid=371764
296	317	GGAAUGGGC	:..::::::::...::::	CCUCUUUCA	Cleavage	pacid=371747
296	317	GGAAUGGGC	:..::::::::...::::	CCUCUUUCA	Cleavage	pacid=371747
775	796	GGAAUGGGC	:.:::..::::: .:..:::.	AGUUUCUUA	Cleavage	pacid=371444
3	24	GGAAUGGGC	:.:::.:: ::::.: ::::.:	CGUUUCUCA	Cleavage	pacid=371453
938	959	GGAAUGGGC	::::.::::. : :.:::::	CUCUUCUCA	Translation	pacid=371625
2003	2024	GGAAUGGGC	::::::::.: ::: ::..::::	UGCUUCCUA	Cleavage	pacid=371727
1944	1965	GGAAUGGGC	::::::::.: ::: ::..::::	UGCUUCCUA	Cleavage	pacid=371727
2213	2234	GGAAUGGGC	: ::::.:: ::::.:. ::::	UCCUUCUCA	Cleavage	pacid=371737
610	630	GGAAUGGGC	:::: ::. ::::::::.::::.:	UGCU-CCUUA	Cleavage	pacid=371646
72	93	GGAAUGGGC	::::.:::::: :..:::.	CCCUUCUCAA	Cleavage	pacid=371652
428	449	GGAAUGGGC	:::.:::: .::: ::::.:	AUCUUUCCA	Cleavage	pacid=371667
2027	2048	GGAAUGGGC	::.:::..:.:.: :.::::.:	UGUUUCUUA	Cleavage	pacid=371597
431	452	GGAAUGGGC	::::.:::::::...:: :	CUCUUCUCA	Cleavage	pacid=371494

356	377	GGAAUGGGC	:::::. :. :::...:::::	AGCUUCUGA	Cleavage	pacid=371681
369	390	GGAAUGGGC	.:::::.:: .::::::	UCAGGUCCA	Cleavage	pacid=371746
1365	1386	GGAAUGGGC	::::.:::: . .:::::.:	GGCUUUCCA	Translation	pacid=371476
1353	1374	GGAAUGGGC	::::.:::: . .:::::.:	GGCUUUCCA	Translation	pacid=371476
1808	1829	GGAAUGGGC	:::::. .::.: :.::::.:	UGCUUCUAG	Cleavage	pacid=371477
1808	1829	GGAAUGGGC	:::::. .::.: :.::::.:	UGCUUCUAG	Cleavage	pacid=371477
1753	1774	GGAAUGGGC	:::::. .::.: :.::::.:	UGCUUCUAG	Cleavage	pacid=371477
631	652	GGAAUGGGC	::.::.:..::.: :..::::.	UGUUUUCUG	Cleavage	pacid=371627
1160	1181	GGAAUGGGC	::: :..::::.::: ::::..	UGCCUUUCA	Cleavage	pacid=371631
2494	2515	GGAAUGGGC	::::.:::::.: ....::.:	UGCUUUCCA	Cleavage	pacid=371625
1938	1959	GGAAUGGGC	: .:::: :: :: .:::::.:	UAUUUCCAA	Cleavage	pacid=371625
2522	2543	GGAAUGGGC	:::.:::::.: ..::::.	GACUUUCCA	Cleavage	pacid=371531
2522	2543	GGAAUGGGC	:::.:::::.: ..::::.	GACUUUCCA	Cleavage	pacid=371531
562	584	GGAAUGGGC	::::: .::::::::.::: :	UGCUUCAUC	Cleavage	pacid=371714
207	229	GGAAUGGGC	::::: .::::::::.::: :	UGCUUCAUC	Cleavage	pacid=371714
427	448	GGAAUGGGC	::.:. :::: :.:::::	CAAUUUCUC	Cleavage	pacid=371739
2093	2113	GGAAUGGGC	::::.:::::::::.: ::::	AGCUUUCCA	Cleavage	pacid=371675
1852	1873	GGAAUGGGC	::.::::. :..::.:::::.	UGUUUCCUU	Cleavage	pacid=371582
553	574	GGAAUGGGC	: : :.:::::..::::::	UUCCUUCCA	Cleavage	pacid=371600
1626	1646	GGAAUGGGC	:::::.:: ::::.:.::.	UGCUUCUCA-	Cleavage	pacid=371494
1620	1640	GGAAUGGGC	:::::.::: ::::.:.::.	UGCUUCUCA-	Cleavage	pacid=371494

Multiplicity	Target_Acc.	ID	locusName	Pfam
1	Phvul.008G004800.1	Phvul.008G004800	Phvul.008G004800	PF00175,PF00
1	Phvul.009G006000.1	Phvul.009G006000	Phvul.009G006000	PF00650
1	Phvul.009G006000.2	Phvul.009G006000	Phvul.009G006000	PF00650
2	Phvul.002G315000.1	Phvul.002G315000	Phvul.002G315000	0
2	Phvul.002G315000.2	Phvul.002G315000	Phvul.002G315000	0
1	Phvul.004G164800.1	Phvul.004G164800	Phvul.004G164800	PF16113,PF00
1	Phvul.005G049000.1	Phvul.005G049000	Phvul.005G049000	PF10184
1	Phvul.010G108200.1	Phvul.010G108200	Phvul.010G108200	PF07707,PF00
1	Phvul.L008143.1	Phvul.L008143	Phvul.L008143	0
1	Phvul.002G189700.1	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
1	Phvul.002G189700.2	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
1	Phvul.002G189700.3	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
1	Phvul.002G189700.4	Phvul.002G189700	Phvul.002G189700	PF00627,PF14
1	Phvul.002G258800.1	Phvul.002G258800	Phvul.002G258800	0
1	Phvul.003G202100.1	Phvul.003G202100	Phvul.003G202100	PF08263,PF00
1	Phvul.003G282800.1	Phvul.003G282800	Phvul.003G282800	PF05965
1	Phvul.004G083900.1	Phvul.004G083900	Phvul.004G083900	PF00155
2	Phvul.006G110000.1	Phvul.006G110000	Phvul.006G110000	0
1	Phvul.007G031800.1	Phvul.007G031800	Phvul.007G031800	PF02358,PF00
1	Phvul.007G031800.2	Phvul.007G031800	Phvul.007G031800	PF02358,PF00
1	Phvul.007G094100.1	Phvul.007G094100	Phvul.007G094100	PF04715,PF00
1	Phvul.008G081700.2	Phvul.008G081700	Phvul.008G081700	PF00122,PF12
1	Phvul.009G201900.1	Phvul.009G201900	Phvul.009G201900	0
1	Phvul.009G233100.2	Phvul.009G233100	Phvul.009G233100	0
1	Phvul.009G246200.2	Phvul.009G246200	Phvul.009G246200	PF03171,PF14
1	Phvul.010G125200.1	Phvul.010G125200	Phvul.010G125200	PF03914
1	Phvul.011G073400.1	Phvul.011G073400	Phvul.011G073400	PF09786
1	Phvul.001G001700.1	Phvul.001G001700	Phvul.001G001700	PF00326,PF02
1	Phvul.001G160000.1	Phvul.001G160000	Phvul.001G160000	PF13639
1	Phvul.002G011900.1	Phvul.002G011900	Phvul.002G011900	PF00332,PF07
2	Phvul.002G028700.1	Phvul.002G028700	Phvul.002G028700	PF04788
1	Phvul.002G185800.1	Phvul.002G185800	Phvul.002G185800	PF00282
1	Phvul.002G206900.1	Phvul.002G206900	Phvul.002G206900	PF08263,PF00
1	Phvul.002G206900.2	Phvul.002G206900	Phvul.002G206900	PF08263,PF00
1	Phvul.003G078900.1	Phvul.003G078900	Phvul.003G078900	0
1	Phvul.003G210500.1	Phvul.003G210500	Phvul.003G210500	PF02201
1	Phvul.003G262300.3	Phvul.003G262300	Phvul.003G262300	PF00641
1	Phvul.003G262300.1	Phvul.003G262300	Phvul.003G262300	PF00641
1	Phvul.003G262300.2	Phvul.003G262300	Phvul.003G262300	PF00641
1	Phvul.003G262300.4	Phvul.003G262300	Phvul.003G262300	PF00641
1	Phvul.004G093900.4	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
1	Phvul.004G093900.6	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
1	Phvul.004G093900.5	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
1	Phvul.004G093900.3	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
1	Phvul.004G093900.1	Phvul.004G093900	Phvul.004G093900	PF00201,PF03

1	Phvul.004G093900.2	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
1	Phvul.004G093900.7	Phvul.004G093900	Phvul.004G093900	PF00201,PF03
1	Phvul.004G105600.1	Phvul.004G105600	Phvul.004G105600	PF00560
1	Phvul.004G135400.1	Phvul.004G135400	Phvul.004G135400	PF00005,PF01
1	Phvul.004G159500.1	Phvul.004G159500	Phvul.004G159500	PF00067
1	Phvul.004G170000.1	Phvul.004G170000	Phvul.004G170000	PF02516
1	Phvul.005G001000.1	Phvul.005G001000	Phvul.005G001000	PF03552
1	Phvul.005G022800.1	Phvul.005G022800	Phvul.005G022800	PF00022
1	Phvul.005G072300.1	Phvul.005G072300	Phvul.005G072300	PF00179
1	Phvul.007G034000.1	Phvul.007G034000	Phvul.007G034000	PF03034
1	Phvul.007G034000.2	Phvul.007G034000	Phvul.007G034000	PF03034
2	Phvul.007G244033.1	Phvul.007G244033	Phvul.007G244033	0
2	Phvul.007G244033.1	Phvul.007G244033	Phvul.007G244033	0
1	Phvul.007G244066.1	Phvul.007G244066	Phvul.007G244066	0
1	Phvul.008G079000.1	Phvul.008G079000	Phvul.008G079000	PF06697
1	Phvul.008G267400.5	Phvul.008G267400	Phvul.008G267400	PF00012
1	Phvul.008G267400.2	Phvul.008G267400	Phvul.008G267400	PF00012
1	Phvul.008G267400.3	Phvul.008G267400	Phvul.008G267400	PF00012
1	Phvul.008G267400.4	Phvul.008G267400	Phvul.008G267400	PF00012
1	Phvul.009G053900.2	Phvul.009G053900	Phvul.009G053900	PF14691,PF07
1	Phvul.009G081900.1	Phvul.009G081900	Phvul.009G081900	PF12937
1	Phvul.009G213000.1	Phvul.009G213000	Phvul.009G213000	PF14531,PF03
1	Phvul.011G065200.2	Phvul.011G065200	Phvul.011G065200	0
1	Phvul.001G079400.1	Phvul.001G079400	Phvul.001G079400	PF11145
1	Phvul.001G087700.1	Phvul.001G087700	Phvul.001G087700	PF03982,PF00
1	Phvul.001G117500.1	Phvul.001G117500	Phvul.001G117500	PF02446,PF00
1	Phvul.002G007100.1	Phvul.002G007100	Phvul.002G007100	PF13912
1	Phvul.002G115800.1	Phvul.002G115800	Phvul.002G115800	PF07714
1	Phvul.002G115800.3	Phvul.002G115800	Phvul.002G115800	PF07714
1	Phvul.002G163600.1	Phvul.002G163600	Phvul.002G163600	0
1	Phvul.002G168500.1	Phvul.002G168500	Phvul.002G168500	PF13912
1	Phvul.002G168500.2	Phvul.002G168500	Phvul.002G168500	PF13912
1	Phvul.002G177500.1	Phvul.002G177500	Phvul.002G177500	PF01762,PF00
2	Phvul.002G315000.1	Phvul.002G315000	Phvul.002G315000	0
2	Phvul.002G315000.2	Phvul.002G315000	Phvul.002G315000	0
1	Phvul.003G185300.1	Phvul.003G185300	Phvul.003G185300	PF07983
1	Phvul.003G212800.2	Phvul.003G212800	Phvul.003G212800	PF00847
1	Phvul.004G121900.1	Phvul.004G121900	Phvul.004G121900	PF01554
1	Phvul.006G033600.1	Phvul.006G033600	Phvul.006G033600	PF00069
1	Phvul.006G033600.2	Phvul.006G033600	Phvul.006G033600	PF00069
1	Phvul.006G219000.1	Phvul.006G219000	Phvul.006G219000	PF00439
1	Phvul.007G008100.2	Phvul.007G008100	Phvul.007G008100	PF10075
1	Phvul.007G086600.1	Phvul.007G086600	Phvul.007G086600	PF00847
1	Phvul.007G168600.1	Phvul.007G168600	Phvul.007G168600	PF07883
1	Phvul.008G002700.1	Phvul.008G002700	Phvul.008G002700	PF03141
1	Phvul.009G062500.1	Phvul.009G062500	Phvul.009G062500	PF04130

1	Phvul.001G186500.1	Phvul.001G186500	Phvul.001G186500	PF15629,PF15
2	Phvul.002G028700.1	Phvul.002G028700	Phvul.002G028700	PF04788
1	Phvul.003G202300.1	Phvul.003G202300	Phvul.003G202300	0
1	Phvul.003G202300.2	Phvul.003G202300	Phvul.003G202300	0
1	Phvul.003G248400.1	Phvul.003G248400	Phvul.003G248400	PF14694,PF14
1	Phvul.003G248400.2	Phvul.003G248400	Phvul.003G248400	PF14694,PF14
1	Phvul.003G248400.3	Phvul.003G248400	Phvul.003G248400	PF14694,PF14
1	Phvul.004G024400.1	Phvul.004G024400	Phvul.004G024400	0
1	Phvul.004G071800.1	Phvul.004G071800	Phvul.004G071800	PF03094
2	Phvul.004G178500.1	Phvul.004G178500	Phvul.004G178500	PF00432
2	Phvul.004G178500.1	Phvul.004G178500	Phvul.004G178500	PF00432
1	Phvul.005G175600.1	Phvul.005G175600	Phvul.005G175600	PF00005,PF00
1	Phvul.005G175600.2	Phvul.005G175600	Phvul.005G175600	PF00005,PF00
1	Phvul.006G053300.1	Phvul.006G053300	Phvul.006G053300	PF03106
1	Phvul.006G053300.2	Phvul.006G053300	Phvul.006G053300	PF03106
2	Phvul.006G110000.1	Phvul.006G110000	Phvul.006G110000	0
1	Phvul.007G204100.1	Phvul.007G204100	Phvul.007G204100	PF04810,PF08
1	Phvul.008G006800.1	Phvul.008G006800	Phvul.008G006800	PF00400,PF12
1	Phvul.008G034200.2	Phvul.008G034200	Phvul.008G034200	PF00201
1	Phvul.009G184400.1	Phvul.009G184400	Phvul.009G184400	PF05904
1	Phvul.009G184400.2	Phvul.009G184400	Phvul.009G184400	PF05904

Panther	KOG	KEGG	KOG	GO	Best-hit-arabi
PTHR19384,P	0	1.5.1.30	0	GO:0055114,	AT3G02280.1
PTHR23324,P	0	0	0	0	AT4G39170.1
PTHR23324,P	0	0	0	0	AT4G39170.1
PTHR11005,P	KOG2624	3.1.1.3	0	0	AT1G73920.1
PTHR11005,P	KOG2624	3.1.1.3	0	0	AT1G73920.1
PTHR23309,P	KOG1683	5.1.2.3,1.1.1.3	K10527	GO:0055114,	AT4G29010.1
PTHR22750,P	KOG4457	0	0	0	AT1G79510.1
PTHR24412,P	0	0	0	GO:0005515	AT3G61600.1
PTHR33912,P	0	0	0	0	0
PTHR11254,P	0	6.3.2.19	K10592	GO:0004842	AT1G55860.2
PTHR11254,P	0	6.3.2.19	K10592	GO:0004842	AT1G55860.2
PTHR11254,P	0	6.3.2.19	K10592	GO:0004842	AT1G55860.2
PTHR11254,P	0	6.3.2.19	K10592	GO:0004842	AT1G55860.2
PTHR31852,P	0	0	0	0	AT3G26350.1
PTHR27000,P	KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1
PTHR22715,P	0	2.1.1.43	0	GO:0005634	AT1G26330.1
PTHR11751,P	KOG0633	2.6.1.9	K00817	GO:0030170,	AT1G71920.2
PTHR31234,P	0	0	0	0	AT4G01110.1
PTHR10788,P	0	2.4.1.15,3.1.3	K16055	GO:0005992,	AT4G17770.1
PTHR10788,P	0	2.4.1.15,3.1.3	K16055	GO:0005992,	AT4G17770.1
PTHR11236,P	0	2.6.1.85	K13950	GO:0016833,	AT2G28880.1
PTHR24092,P	0	3.6.3.1	K14802	GO:0046872,	AT5G04930.1
PTHR33673,P	0	0	0	0	AT1G74220.1
PTHR33977,P	0	0	0	0	AT4G13970.1
PTHR10209,P	KOG0143	1.14.11.32	0	GO:0055114,	AT3G21420.1
PTHR12048	0	0	K14832	0	AT1G72440.1
PTHR21780,P	KOG4670	0	0	0	AT1G07970.1
PTHR11757,P	0	3.4.21.26	K01322	GO:0008236,	AT1G76140.1
PTHR14155,P	0	0	0	GO:0008270,	AT5G43420.1
PTHR32227,P	0	3.2.1.39	0	GO:0005975,	AT5G67460.1
PTHR31300,P	0	0	0	0	AT5G66740.1
PTHR11999,P	0	4.1.1.15	K01580	GO:0030170,	AT5G17330.1
PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT4G33430.1
PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT4G33430.1
PTHR34775,P	0	0	0	0	AT2G16270.1
PTHR13844,P	KOG2570	0	K11650	GO:0005515	AT5G14170.1
PTHR23111,P	0	0	0	GO:0008270	AT2G17975.1
PTHR23111,P	0	0	0	GO:0008270	AT2G17975.1
PTHR23111,P	0	0	0	GO:0008270	AT2G17975.1
PTHR23111,P	0	0	0	GO:0008270	AT2G17975.1
PTHR11926,P	0	2.4.1.173	0	GO:0016758,	AT1G43620.3
PTHR11926,P	0	2.4.1.173	0	GO:0016758,	AT1G43620.3
PTHR11926,P	0	2.4.1.173	0	GO:0016758,	AT1G43620.3
PTHR11926,P	0	2.4.1.173	0	GO:0016758,	AT1G43620.3
PTHR11926,P	0	2.4.1.173	0	GO:0016758,	AT1G43620.3

PTHR11926,P	0	2.4.1.173	0	GO:0016758,(	AT1G43620.3
PTHR11926,P	0	2.4.1.173	0	GO:0016758,(	AT1G43620.3
PTHR27004,P	KOG0472	2.7.11.1	0	GO:0005515	AT2G34930.1
PTHR19241,P	0	3.6.3.25	0	GO:0016887,(	AT1G17840.1
PTHR24298,P	0	1.14.13.123,1	0	GO:0055114,(	AT3G26300.1
PTHR13872,P	0	2.4.99.18	K07151	GO:0016020,(	AT5G19690.1
PTHR13301,P	0	2.4.1.12	0	GO:0030244,(	AT4G24010.1
PTHR11937,P	KOG0676	0	K16615	0	AT3G60830.1
PTHR24067,P	KOG0417	6.3.2.19	K10581	0	AT3G15355.1
PTHR15362,P	0	2.7.8.8	K08730	GO:0006659	AT1G15110.1
PTHR15362,P	0	2.7.8.8	K08730	GO:0006659	AT1G15110.1
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PTHR33512,P	0	0	0	0	AT3G08600.1
PTHR19375,P	0	0	K09489	0	AT1G11660.1
PTHR19375,P	0	0	K09489	0	AT1G11660.1
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PTHR19375,P	0	0	K09489	0	AT1G11660.1
PTHR11938,P	0	1.4.1.14	K00264	GO:0055114,(	AT5G53460.1
PTHR24006,P	KOG4341	0	0	GO:0005515	AT4G33210.1
PTHR24343,P	KOG0583	2.7.11.1	0	GO:0007165	AT1G30270.1
0	0	0	0	0	AT5G59305.1
PTHR33389,P	0	0	0	0	AT4G21700.1
PTHR22753,P	0	0	0	GO:0016747	AT5G41130.1
PTHR32518,P	0	2.4.1.25	K00705	GO:0005975,(	AT2G40840.1
PTHR26374,P	0	0	0	0	AT4G17810.1
PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,(	AT2G17220.1
PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,(	AT2G17220.1
0	0	0	0	0	0
PTHR26374,P	0	0	0	0	AT1G26610.1
PTHR26374,P	0	0	0	0	AT1G26610.1
PTHR11214,P	KOG2287	2.4.1.134	0	GO:0016020,(	AT4G21060.2
PTHR11005,P	KOG2624	3.1.1.3	0	0	AT1G73920.1
PTHR11005,P	KOG2624	3.1.1.3	0	0	AT1G73920.1
PTHR32227,P	0	0	0	0	AT1G18650.1
PTHR31839,P	0	0	0	GO:0006355,(	AT5G51990.1
PTHR11206,P	KOG1347	0	K03327	GO:0055085,(	AT4G23030.1
PTHR24055,P	KOG0660	2.7.11.24	K04371	GO:0006468,(	AT2G42880.1
PTHR24055,P	KOG0660	2.7.11.24	K04371	GO:0006468,(	AT2G42880.1
PTHR22880,P	0	0	0	GO:0005515	AT1G58025.3
PTHR12436,P	KOG1861	0	0	0	AT2G39340.1
PTHR31677,P	0	0	0	GO:0006355,(	AT1G12890.1
PTHR37236,P	0	0	0	0	AT4G02980.1
PTHR10108,P	0	2.1.1.41	0	GO:0008168	AT2G43200.1
PTHR19302,P	0	0	K16572	GO:0005815,(	AT1G80260.1

PTHR10359,P	0	4.2.99.18	0	0	AT5G04560.2
PTHR31300,P	0	0	0	0	AT5G66740.1
PTHR34805	0	0	0	0	AT4G24680.1
PTHR34805	0	0	0	0	AT4G24680.1
PTHR16057,P	0	0	0	0	AT3G50430.1
PTHR16057,P	0	0	0	0	AT3G50430.1
PTHR16057,P	0	0	0	0	AT3G50430.1
0	0	0	0	0	0
PTHR31942,P	0	0	K08472	GO:0016021,(	AT2G39200.1
PTHR11764,P	0	5.4.99.41	0	GO:0003824	AT2G07050.1
PTHR11764,P	0	5.4.99.41	0	GO:0003824	AT2G07050.1
PTHR24223,P	0	3.6.3.44	K05674	GO:0016887,(	AT2G07680.1
PTHR24223,P	0	3.6.3.44	K05674	GO:0016887,(	AT2G07680.1
PTHR31221,P	0	0	0	GO:0043565,(	AT4G26640.2
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PTHR31234,P	0	0	0	0	AT4G01110.1
PTHR13803,P	0	0	K14007	GO:0030127,(	AT3G07100.1
PTHR22850	0	0	K14848	GO:0005515	AT2G19540.1
PTHR11926,P	0	2.4.1.170	0	GO:0016758,(	AT3G02100.1
PTHR33167,P	0	0	0	0	AT1G13940.1
PTHR33167,P	0	0	0	0	AT1G13940.1

arabi-symbol	arabi-defline	ID	Annot_defline
0	Flavodoxin family protein	Phvul.008G00	1.5.1.30 - Flav
0	Sec14p-like phosphatidylinositol transfer family	Phvul.009G00	PTHR23324:S
0	Sec14p-like phosphatidylinositol transfer family	Phvul.009G00	PTHR23324:S
0	alpha/beta-Hydrolases superfamily protein	Phvul.002G31	PTHR11005:S
0	alpha/beta-Hydrolases superfamily protein	Phvul.002G31	PTHR11005:S
AIM1	Enoyl-CoA hydratase/isomerase family	Phvul.004G16	1.1.1.35//4.2.
0	Uncharacterized conserved protein (DUF2358)	Phvul.005G04	PTHR22750 -
ATPOB1,POB1	POZ/BTB containin G-protein 1	Phvul.010G10	PF00651//PF
0	0	Phvul.L00814	PTHR33912:S
UPL1	ubiquitin-protein ligase 1	Phvul.002G18	PTHR11254:S
UPL1	ubiquitin-protein ligase 1	Phvul.002G18	PTHR11254:S
UPL1	ubiquitin-protein ligase 1	Phvul.002G18	PTHR11254:S
UPL1	ubiquitin-protein ligase 1	Phvul.002G18	PTHR11254:S
0	0	Phvul.002G25	PTHR31852:S
GSO1	Leucine-rich repeat transmembrane protein kin	Phvul.003G20	PF00560//PF
0	DNA binding	Phvul.003G28	PTHR22715 -
HISN6B	HISTIDINE BIOSYNTHESIS 6B	Phvul.004G08	2.6.1.9 - Histi
0	0	Phvul.006G11	PTHR31234:S
ATTPS5,TPS5	trehalose phosphatase/synthase 5	Phvul.007G03	PTHR10788:S
ATTPS5,TPS5	trehalose phosphatase/synthase 5	Phvul.007G03	PTHR10788:S
ADCS,emb1997	para-aminobenzoate (PABA) synthase family pr	Phvul.007G09	2.6.1.85 - Ami
ALA1	aminophospholipid ATPase 1	Phvul.008G08	K14802 - phos
0	0	0	0
0	zinc ion binding	Phvul.009G23	PTHR33977:S
0	2-oxoglutarate (2OG) and Fe(II)-dependent oxy	Phvul.009G24	PTHR10209//
EDA25,SWA2	CCAAT-binding factor	Phvul.010G12	K14832 - ribos
0	0	Phvul.011G07	PTHR21780:S
0	Prolyl oligopeptidase family protein	Phvul.001G00	3.4.21.26 - Pr
0	RING/U-box superfamily protein	Phvul.001G16	PTHR14155//
0	O-Glycosyl hydrolases family 17 protein	Phvul.002G01	PTHR32227:S
0	Protein of unknown function (DUF620)	Phvul.002G02	PF04788 - Pro
GAD,GAD1	glutamate decarboxylase	Phvul.002G18	PTHR11999//
ATBAK1,ATSERK3,BAK	BRI1-associated receptor kinase	Phvul.002G20	K13416 - bras
ATBAK1,ATSERK3,BAK	BRI1-associated receptor kinase	Phvul.002G20	K13416 - bras
0	0	0	0
CHC1	SWIB/MDM2 domain superfamily protein	Phvul.003G21	K11650 - SWI/
0	zinc finger (Ran-binding) family protein	Phvul.003G26	PTHR23111//
0	zinc finger (Ran-binding) family protein	Phvul.003G26	PTHR23111//
0	zinc finger (Ran-binding) family protein	Phvul.003G26	PTHR23111//
0	zinc finger (Ran-binding) family protein	Phvul.003G26	PTHR23111//
TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09	PTHR11926:S
TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09	PTHR11926:S
TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09	PTHR11926:S
TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09	PTHR11926:S
TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09	PTHR11926:S

TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09	PTHR11926:S
TT15,UGT80B1	UDP-Glycosyltransferase superfamily protein	Phvul.004G09	PTHR11926:S
0	disease resistance family protein / LRR family p	Phvul.004G10	KOG0472 - Le
ABCG11,ATWBC11,CO	white-brown complex homolog protein 11	Phvul.004G13	PTHR19241//
CYP71B34	cytochrome P450, family 71, subfamily B, polyp	Phvul.004G15	PF00067 - Cyt
STT3A	staurosporin and temperature sensitive 3-like A	Phvul.004G17	PTHR13872:S
ATCSLG1,CSLG1	cellulose synthase like G1	Phvul.005G00	PTHR13301//
ARP7,ATARP7	actin-related protein 7	Phvul.005G02	K16615 - acti
PFU1,UBC25	ubiquitin-conjugating enzyme 25	Phvul.005G07	PTHR24067:S
0	phosphatidyl serine synthase family protein	Phvul.007G03	2.7.8.8 - CDP-
0	phosphatidyl serine synthase family protein	Phvul.007G03	2.7.8.8 - CDP-
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0	0	0	0
0	Protein of unknown function (DUF1191)	Phvul.008G07	PF06697 - Pro
0	heat shock protein 70 (Hsp 70) family protein	Phvul.008G26	PTHR19375//
0	heat shock protein 70 (Hsp 70) family protein	Phvul.008G26	PTHR19375//
0	heat shock protein 70 (Hsp 70) family protein	Phvul.008G26	PTHR19375//
0	heat shock protein 70 (Hsp 70) family protein	Phvul.008G26	PTHR19375//
GLT1	NADH-dependent glutamate synthase 1	Phvul.009G05	1.4.1.14 - Glu
SLOMO	F-box family protein	Phvul.009G08	PTHR24006:S
ATCIPK23,CIPK23,LKS1	CBL-interacting protein kinase 23	Phvul.009G21	PTHR24343:S
0	0	0	0
0	Protein of unknown function (DUF2921)	Phvul.001G07	PF11145 - Pro
0	Esterase/lipase/thioesterase family protein	Phvul.001G08	PTHR22753:S
DPE2	disproportionating enzyme 2	Phvul.001G11	2.4.1.25 - 4-al
0	C2H2 and C2HC zinc fingers superfamily protein	Phvul.002G00	PF13912 - C2
0	Protein kinase superfamily protein	Phvul.002G11	PTHR27001:S
0	Protein kinase superfamily protein	Phvul.002G11	PTHR27001:S
0	0	0	0
0	C2H2-like zinc finger protein	Phvul.002G16	PTHR26374:S
0	C2H2-like zinc finger protein	Phvul.002G16	PTHR26374:S
0	Galactosyltransferase family protein	Phvul.002G17	PTHR11214:S
0	alpha/beta-Hydrolases superfamily protein	Phvul.002G31	PTHR11005:S
0	alpha/beta-Hydrolases superfamily protein	Phvul.002G31	PTHR11005:S
PDCB3	plasmodesmata callose-binding protein 3	Phvul.003G18	PTHR32227:S
CBF4,DREB1D	C-repeat-binding factor 4	Phvul.003G21	PTHR31839:S
0	MATE efflux family protein	Phvul.004G12	PTHR11206:S
ATMPK20,MPK20	MAP kinase 20	Phvul.006G03	PTHR24055:S
ATMPK20,MPK20	MAP kinase 20	Phvul.006G03	PTHR24055:S
0	DNA-binding bromodomain-containing protein	Phvul.006G21	PTHR22880:S
0	SAC3/GANP/Nin1/mts3/eIF-3 p25 family	Phvul.007G00	PTHR12436:S
0	Integrase-type DNA-binding superfamily protei	Phvul.007G08	PF00847 - AP
ABP,ABP1	endoplasmic reticulum auxin binding protein 1	Phvul.007G16	PTHR37236:S
0	S-adenosyl-L-methionine-dependent methyltra	Phvul.008G00	PTHR10108//
emb1427	Spc97 / Spc98 family of spindle pole body (SBP)	Phvul.009G06	K16572 - gam

DME	HhH-GPD base excision DNA repair family prote	Phvul.001G18	PTHR10359:S
0	Protein of unknown function (DUF620)	Phvul.002G02	PF04788 - Pro
MOS1	modifier of snc1	Phvul.003G20	PF07001 - BAT
MOS1	modifier of snc1	Phvul.003G20	PF07001 - BAT
0	0	Phvul.003G24	PTHR16057 -
0	0	Phvul.003G24	PTHR16057 -
0	0	Phvul.003G24	PTHR16057 -
0	0	0	0
ATMLO12,MLO12	Seven transmembrane MLO family protein	Phvul.004G07	PTHR31942:S
CAS1	cycloartenol synthase 1	Phvul.004G17	PTHR11764//
CAS1	cycloartenol synthase 1	Phvul.004G17	PTHR11764//
ATMRP11,MRP11	multidrug resistance-associated protein 11	Phvul.005G17	K05674 - ATP-
ATMRP11,MRP11	multidrug resistance-associated protein 11	Phvul.005G17	K05674 - ATP-
AtWRKY20,WRKY20	WRKY family transcription factor family protein	Phvul.006G05	PTHR31221:S
AtWRKY20,WRKY20	WRKY family transcription factor family protein	Phvul.006G05	PTHR31221:S
0	0	Phvul.006G11	PTHR31234:S
ERMO2,SEC24A	Sec23/Sec24 protein transport family protein	Phvul.007G20	K14007 - prot
0	Transducin family protein / WD-40 repeat famil	Phvul.008G00	K14848 - ribos
0	UDP-Glycosyltransferase superfamily protein	Phvul.008G03	PTHR11926//
0	Plant protein of unknown function (DUF863)	Phvul.009G18	PTHR33167:S
0	Plant protein of unknown function (DUF863)	Phvul.009G18	PTHR33167:S

IDENTIFIER	NAME	DESCRIPTION
Phvul.008G00	Coenzyme me	component TAH18 of cytosolic CIA system assembly phase (original de
Phvul.009G00	not assigned.a	(original description: pacid=37150821 transcript=Phvul.009G006000.3
Phvul.009G00	not assigned.a	(original description: pacid=37150821 transcript=Phvul.009G006000.3
Phvul.002G31	not assigned.r	no hits & (original description: pacid=37174769 transcript=Phvul.002G
Phvul.002G31	not assigned.r	no hits & (original description: pacid=37174769 transcript=Phvul.002G
Phvul.004G16	Lipid metaboli	multifunctional enzyme (MFP) (original description: pacid=37162576 t
Phvul.005G04	not assigned.r	no hits & (original description: pacid=37153695 transcript=Phvul.005G
Phvul.010G10	Protein home	component LRB of CUL3-BTB E3 ubiquitin ligase complex (original desc
Phvul.L00814	not assigned.r	no hits & (original description: pacid=37178968 transcript=Phvul.L008
Phvul.002G18	Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717
Phvul.002G18	Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717
Phvul.002G18	Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717
Phvul.002G18	Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=3717
Phvul.002G25	not assigned.r	no hits & (original description: pacid=37175064 transcript=Phvul.002G
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G28	not assigned.r	no hits & (original description: pacid=37147414 transcript=Phvul.003G
Phvul.004G08	Amino acid m	histidinol-phosphate aminotransferase (original description: pacid=371
Phvul.006G11	not assigned.r	no hits & (original description: pacid=37173968 transcript=Phvul.006G
Phvul.007G03	Enzyme classi	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabic
Phvul.007G03	Enzyme classi	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 5 OS=Arabic
Phvul.007G09	Coenzyme me	aminodeoxychorismate synthase (original description: pacid=3716718
Phvul.008G08	Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (orig
Phvul.009G20	not assigned.r	no hits & (original description: pacid=37150792 transcript=Phvul.009G
Phvul.009G23	not assigned.r	no hits & (original description: pacid=37149731 transcript=Phvul.009G
Phvul.009G24	Phytohormon	oxidoreductase (LBO) (original description: pacid=37151443 transcript
Phvul.010G12	Protein biosy	component NOC1 of ribosomal subunit nuclear export complex (origin
Phvul.011G07	not assigned.r	no hits & (original description: pacid=37154989 transcript=Phvul.011G
Phvul.001G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.4 hydrolase acting on pept
Phvul.001G16	Protein home	RING-H2-class E3 ligase (original description: pacid=37168057 transcri
Phvul.002G01	Enzyme classi	Glucan endo-1,3-beta-glucosidase 13 OS=Arabidopsis thaliana (sp|q9fj
Phvul.002G02	Multi-process	GTPase effector (BDR) (original description: pacid=37174686 transcript
Phvul.002G18	Amino acid m	glutamate decarboxylase (original description: pacid=37174418 transc
Phvul.002G20	Protein modif	protein kinase (LRR-II) (original description: pacid=37176803 transcript
Phvul.002G20	Protein modif	protein kinase (LRR-II) (original description: pacid=37176803 transcript
Phvul.003G07	not assigned.r	no hits & (original description: pacid=37147041 transcript=Phvul.003G
Phvul.003G21	Chromatin org	component BAF60 of chromatin remodeling complex (original descript
Phvul.003G26	not assigned.r	no hits & (original description: pacid=37145402 transcript=Phvul.003G
Phvul.003G26	not assigned.r	no hits & (original description: pacid=37145402 transcript=Phvul.003G
Phvul.003G26	not assigned.r	no hits & (original description: pacid=37145402 transcript=Phvul.003G
Phvul.003G26	not assigned.r	no hits & (original description: pacid=37145402 transcript=Phvul.003G
Phvul.004G09	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=371
Phvul.004G09	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=371
Phvul.004G09	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=371
Phvul.004G09	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=371
Phvul.004G09	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=371

Phvul.004G09	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=37
Phvul.004G09	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=37
Phvul.004G10	not assigned.	(original description: pacid=37162970 transcript=Phvul.004G105600.1
Phvul.004G13	Solute transp	subfamily ABCG transporter (original description: pacid=37162910 tran
Phvul.004G15	Enzyme classi	Cytochrome P450 CYP736A12 OS=Panax ginseng (sp|h2dh18|c7a12_p
Phvul.004G17	Protein modif	component STT3 of oligosaccharyl transferase (OST) complex (original
Phvul.005G00	not assigned.	(original description: pacid=37153092 transcript=Phvul.005G001000.1
Phvul.005G02	Chromatin or	component ARP7 of chromatin remodeling complex (original descripti
Phvul.005G07	not assigned.	(original description: pacid=37154333 transcript=Phvul.005G072300.1
Phvul.007G03	Lipid metaboli	base-exchange-type phosphatidylserine synthase (original description:
Phvul.007G03	Lipid metaboli	base-exchange-type phosphatidylserine synthase (original description:
Phvul.007G24	not assigned.	no hits & (original description: pacid=37165375 transcript=Phvul.007
Phvul.007G24	not assigned.	no hits & (original description: pacid=37165375 transcript=Phvul.007
Phvul.007G24	not assigned.	no hits & (original description: pacid=37164381 transcript=Phvul.007
Phvul.008G07	not assigned.	no hits & (original description: pacid=37160757 transcript=Phvul.008
Phvul.008G26	Protein home	chaperone (Hsp110) (original description: pacid=37160259 transcript=
Phvul.008G26	Protein home	chaperone (Hsp110) (original description: pacid=37160259 transcript=
Phvul.008G26	Protein home	chaperone (Hsp110) (original description: pacid=37160259 transcript=
Phvul.008G26	Protein home	chaperone (Hsp110) (original description: pacid=37160259 transcript=
Phvul.009G05	Nutrient upta	NADH-dependent glutamate synthase (original description: pacid=371
Phvul.009G08	not assigned.	(original description: pacid=37152092 transcript=Phvul.009G081900.1
Phvul.009G21	Protein modif	SNF1-related protein kinase (SnRK3) (original description: pacid=3714
Phvul.011G06	Phytohormon	CLE precursor polypeptide (original description: pacid=37155545 trans
Phvul.001G07	not assigned.	no hits & (original description: pacid=37168871 transcript=Phvul.001
Phvul.001G08	not assigned.	(original description: pacid=37168110 transcript=Phvul.001G087700.1
Phvul.001G11	not assigned.	(original description: pacid=37168578 transcript=Phvul.001G117500.1
Phvul.002G00	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37175
Phvul.002G11	Protein modif	receptor-like protein kinase (RLCK-VIIa) (original description: pacid=37
Phvul.002G11	Protein modif	receptor-like protein kinase (RLCK-VIIa) (original description: pacid=37
Phvul.002G16	not assigned.	no hits & (original description: pacid=37178055 transcript=Phvul.002
Phvul.002G16	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37177
Phvul.002G16	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37177
Phvul.002G17	Cell wall orga	AGP hydroxyproline O-galactosyltransferase (original description: paci
Phvul.002G31	not assigned.	no hits & (original description: pacid=37174769 transcript=Phvul.002
Phvul.002G31	not assigned.	no hits & (original description: pacid=37174769 transcript=Phvul.002
Phvul.003G18	not assigned.	(original description: pacid=37144453 transcript=Phvul.003G185300.1
Phvul.003G21	RNA biosynth	transcription factor (DREB) (original description: pacid=37145319 trans
Phvul.004G12	Solute transp	metabolite transporter (DTX) (original description: pacid=37162548 tra
Phvul.006G03	Protein modif	protein kinase (MAPK) (original description: pacid=37172750 transcrip
Phvul.006G03	Protein modif	protein kinase (MAPK) (original description: pacid=37172750 transcrip
Phvul.006G21	not assigned.	no hits & (original description: pacid=37173703 transcript=Phvul.006
Phvul.007G00	RNA processi	scaffold component GANP/SAC3 of TREX-2 mRNP trafficking complex (
Phvul.007G08	RNA biosynth	transcription factor (ERF) (original description: pacid=37165267 transc
Phvul.007G16	not assigned.	(original description: pacid=37166775 transcript=Phvul.007G168600.1
Phvul.008G00	not assigned.	(original description: pacid=37159786 transcript=Phvul.008G002700.1
Phvul.009G06	Cytoskeleton	component GCP5 of gamma-Tubulin ring complex (gamma-TuRC) (orig

Phvul.001G18	DNA damage	bifunctional DNA glycosylase/lyase (ROS1) (original description: pacid=
Phvul.002G02	Multi-process	GTPase effector (BDR) (original description: pacid=37174686 transcript
Phvul.003G20	not assigned.a	(original description: pacid=37147665 transcript=Phvul.003G202300.2
Phvul.003G20	not assigned.a	(original description: pacid=37147665 transcript=Phvul.003G202300.2
Phvul.003G24	not assigned.n	no hits & (original description: pacid=37147737 transcript=Phvul.003G
Phvul.003G24	not assigned.n	no hits & (original description: pacid=37147737 transcript=Phvul.003G
Phvul.003G24	not assigned.n	no hits & (original description: pacid=37147737 transcript=Phvul.003G
Phvul.004G02	not assigned.n	no hits & (original description: pacid=37162719 transcript=Phvul.004G
Phvul.004G07	not assigned.a	(original description: pacid=37163131 transcript=Phvul.004G071800.1
Phvul.004G17	Secondary me	triterpenoid synthase (original description: pacid=37162519 transcript=
Phvul.004G17	Secondary me	triterpenoid synthase (original description: pacid=37162519 transcript=
Phvul.005G17	Solute transpo	subfamily ABCC transporter (original description: pacid=37153148 tran
Phvul.005G17	Solute transpo	subfamily ABCC transporter (original description: pacid=37153148 tran
Phvul.006G05	RNA biosynth	transcription factor (WRKY) (original description: pacid=37171441 tran
Phvul.006G05	RNA biosynth	transcription factor (WRKY) (original description: pacid=37171441 tran
Phvul.006G11	not assigned.n	no hits & (original description: pacid=37173968 transcript=Phvul.006G
Phvul.007G20	Vesicle traffic	component Sec24 of Sec23/24 cargo adaptor subcomplex (original des
Phvul.008G00	not assigned.a	(original description: pacid=37158292 transcript=Phvul.008G006800.1
Phvul.008G03	Enzyme classi	UDP-glycosyltransferase 83A1 OS=Arabidopsis thaliana (sp|q9sga8|u8
Phvul.009G18	not assigned.n	no hits & (original description: pacid=37149447 transcript=Phvul.009G
Phvul.009G18	not assigned.n	no hits & (original description: pacid=37149447 transcript=Phvul.009G

scription: pacid=37161177 transcript=Phvul.008G004800.1 locus=Phvul.008G004800 ID=Phvul.008
locus=Phvul.009G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinosito
locus=Phvul.009G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinosito
315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)
315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)
ranscript=Phvul.004G164800.1 locus=Phvul.004G164800 ID=Phvul.004G164800.1.v2.1 annot-versi
049000.1 locus=Phvul.005G049000 ID=Phvul.005G049000.1.v2.1 annot-version=v2.1)
ription: pacid=37142307 transcript=Phvul.010G108200.1 locus=Phvul.010G108200 ID=Phvul.010G1
143.1 locus=Phvul.L008143 ID=Phvul.L008143.1.v2.1 annot-version=v2.1)
76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 anno
76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 anno
76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 anno
76691 transcript=Phvul.002G189700.4 locus=Phvul.002G189700 ID=Phvul.002G189700.4.v2.1 anno
258800.1 locus=Phvul.002G258800 ID=Phvul.002G258800.1.v2.1 annot-version=v2.1)
script=Phvul.003G202100.1 locus=Phvul.003G202100 ID=Phvul.003G202100.1.v2.1 annot-version=
282800.1 locus=Phvul.003G282800 ID=Phvul.003G282800.1.v2.1 annot-version=v2.1)
161692 transcript=Phvul.004G083900.1 locus=Phvul.004G083900 ID=Phvul.004G083900.1.v2.1 ann
110000.1 locus=Phvul.006G110000 ID=Phvul.006G110000.1.v2.1 annot-version=v2.1)
dopsis thaliana (sp|o23617|tps5_arath : 1388.0) & Enzyme classification.EC_2 transferases.EC_2.4
dopsis thaliana (sp|o23617|tps5_arath : 1388.0) & Enzyme classification.EC_2 transferases.EC_2.4
0 transcript=Phvul.007G094100.1 locus=Phvul.007G094100 ID=Phvul.007G094100.1.v2.1 annot-ver
ginal description: pacid=37159191 transcript=Phvul.008G081700.2 locus=Phvul.008G081700 ID=Ph
201900.1 locus=Phvul.009G201900 ID=Phvul.009G201900.1.v2.1 annot-version=v2.1)
233100.3 locus=Phvul.009G233100 ID=Phvul.009G233100.3.v2.1 annot-version=v2.1)
=Phvul.009G246200.2 locus=Phvul.009G246200 ID=Phvul.009G246200.2.v2.1 annot-version=v2.1)
al description: pacid=37144247 transcript=Phvul.010G125200.1 locus=Phvul.010G125200 ID=Phvul
073400.1 locus=Phvul.011G073400 ID=Phvul.011G073400.1.v2.1 annot-version=v2.1)
tide bond (peptidase)(50.3.4 : 947.8) (original description: pacid=37169558 transcript=Phvul.001G0
pt=Phvul.001G160000.1 locus=Phvul.001G160000 ID=Phvul.001G160000.1.v2.1 annot-version=v2.1
ju9|e1313_arath : 127.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 56.6)
t=Phvul.002G028700.1 locus=Phvul.002G028700 ID=Phvul.002G028700.1.v2.1 annot-version=v2.1)
ript=Phvul.002G185800.1 locus=Phvul.002G185800 ID=Phvul.002G185800.1.v2.1 annot-version=v2
t=Phvul.002G206900.3 locus=Phvul.002G206900 ID=Phvul.002G206900.3.v2.1 annot-version=v2.1)
t=Phvul.002G206900.3 locus=Phvul.002G206900 ID=Phvul.002G206900.3.v2.1 annot-version=v2.1)
078900.1 locus=Phvul.003G078900 ID=Phvul.003G078900.1.v2.1 annot-version=v2.1)
ion: pacid=37144401 transcript=Phvul.003G210500.1 locus=Phvul.003G210500 ID=Phvul.003G210
262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
262300.4 locus=Phvul.003G262300 ID=Phvul.003G262300.4.v2.1 annot-version=v2.1)
162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann
162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann
162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann
162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann
162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann

162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann

162803 transcript=Phvul.004G093900.7 locus=Phvul.004G093900 ID=Phvul.004G093900.7.v2.1 ann

locus=Phvul.004G105600 ID=Phvul.004G105600.1.v2.1 annot-version=v2.1) & Receptor-like prote

nscript=Phvul.004G135400.1 locus=Phvul.004G135400 ID=Phvul.004G135400.1.v2.1 annot-version=

angi : 559.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paire

description: pacid=37161693 transcript=Phvul.004G170000.1 locus=Phvul.004G170000 ID=Phvul.0

locus=Phvul.005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-l

on: pacid=37154025 transcript=Phvul.005G022800.1 locus=Phvul.005G022800 ID=Phvul.005G0228

locus=Phvul.005G072300 ID=Phvul.005G072300.1.v2.1 annot-version=v2.1) & Probable ubiquitin-

: pacid=37167617 transcript=Phvul.007G034000.2 locus=Phvul.007G034000 ID=Phvul.007G034000.

: pacid=37167617 transcript=Phvul.007G034000.2 locus=Phvul.007G034000 ID=Phvul.007G034000.

244033.1 locus=Phvul.007G244033 ID=Phvul.007G244033.1.v2.1 annot-version=v2.1)

244033.1 locus=Phvul.007G244033 ID=Phvul.007G244033.1.v2.1 annot-version=v2.1)

244066.1 locus=Phvul.007G244066 ID=Phvul.007G244066.1.v2.1 annot-version=v2.1)

079000.1 locus=Phvul.008G079000 ID=Phvul.008G079000.1.v2.1 annot-version=v2.1)

Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &

Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &

Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &

Phvul.008G267400.5 locus=Phvul.008G267400 ID=Phvul.008G267400.5.v2.1 annot-version=v2.1) &

50765 transcript=Phvul.009G053900.2 locus=Phvul.009G053900 ID=Phvul.009G053900.2.v2.1 ann

locus=Phvul.009G081900 ID=Phvul.009G081900.1.v2.1 annot-version=v2.1) & F-box/LRR-repeat p

546 transcript=Phvul.009G213000.1 locus=Phvul.009G213000 ID=Phvul.009G213000.1.v2.1 annot-

cript=Phvul.011G065200.2 locus=Phvul.011G065200 ID=Phvul.011G065200.2.v2.1 annot-version=v

079400.1 locus=Phvul.001G079400 ID=Phvul.001G079400.1.v2.1 annot-version=v2.1)

locus=Phvul.001G087700 ID=Phvul.001G087700.1.v2.1 annot-version=v2.1) & Acyltransferase-like

locus=Phvul.001G117500 ID=Phvul.001G117500.1.v2.1 annot-version=v2.1) & 4-alpha-glucanotra

159 transcript=Phvul.002G007100.1 locus=Phvul.002G007100 ID=Phvul.002G007100.1.v2.1 annot-

177142 transcript=Phvul.002G115800.3 locus=Phvul.002G115800 ID=Phvul.002G115800.3.v2.1 an

177142 transcript=Phvul.002G115800.3 locus=Phvul.002G115800 ID=Phvul.002G115800.3.v2.1 an

163600.1 locus=Phvul.002G163600 ID=Phvul.002G163600.1.v2.1 annot-version=v2.1)

986 transcript=Phvul.002G168500.2 locus=Phvul.002G168500 ID=Phvul.002G168500.2.v2.1 annot-

986 transcript=Phvul.002G168500.2 locus=Phvul.002G168500 ID=Phvul.002G168500.2.v2.1 annot-

d=37176445 transcript=Phvul.002G177500.1 locus=Phvul.002G177500 ID=Phvul.002G177500.1.v2.

315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)

315000.2 locus=Phvul.002G315000 ID=Phvul.002G315000.2.v2.1 annot-version=v2.1)

locus=Phvul.003G185300 ID=Phvul.003G185300.1.v2.1 annot-version=v2.1) & PLASMODESMATA

script=Phvul.003G212800.2 locus=Phvul.003G212800 ID=Phvul.003G212800.2.v2.1 annot-version=

nscript=Phvul.004G121900.1 locus=Phvul.004G121900 ID=Phvul.004G121900.1.v2.1 annot-versio

t=Phvul.006G033600.2 locus=Phvul.006G033600 ID=Phvul.006G033600.2.v2.1 annot-version=v2.1)

t=Phvul.006G033600.2 locus=Phvul.006G033600 ID=Phvul.006G033600.2.v2.1 annot-version=v2.1)

219000.1 locus=Phvul.006G219000 ID=Phvul.006G219000.1.v2.1 annot-version=v2.1)

original description: pacid=37164656 transcript=Phvul.007G008100.2 locus=Phvul.007G008100 ID=

ript=Phvul.007G086600.1 locus=Phvul.007G086600 ID=Phvul.007G086600.1.v2.1 annot-version=v2

locus=Phvul.007G168600 ID=Phvul.007G168600.1.v2.1 annot-version=v2.1) & Auxin-binding prote

locus=Phvul.008G002700 ID=Phvul.008G002700.1.v2.1 annot-version=v2.1) & Probable methyltra

inal description: pacid=37149462 transcript=Phvul.009G062500.1 locus=Phvul.009G062500 ID=Phv

=37168174 transcript=Phvul.001G186500.1 locus=Phvul.001G186500 ID=Phvul.001G186500.1.v2.1

t=Phvul.002G028700.1 locus=Phvul.002G028700 ID=Phvul.002G028700.1.v2.1 annot-version=v2.1)

2 locus=Phvul.003G202300 ID=Phvul.003G202300.2.v2.1 annot-version=v2.1) & Protein MODIFIER

2 locus=Phvul.003G202300 ID=Phvul.003G202300.2.v2.1 annot-version=v2.1) & Protein MODIFIER

G248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)

G248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)

G248400.3 locus=Phvul.003G248400 ID=Phvul.003G248400.3.v2.1 annot-version=v2.1)

G024400.1 locus=Phvul.004G024400 ID=Phvul.004G024400.1.v2.1 annot-version=v2.1)

1 locus=Phvul.004G071800 ID=Phvul.004G071800.1.v2.1 annot-version=v2.1) & MLO-like protein 12

=Phvul.004G178500.1 locus=Phvul.004G178500 ID=Phvul.004G178500.1.v2.1 annot-version=v2.1)

=Phvul.004G178500.1 locus=Phvul.004G178500 ID=Phvul.004G178500.1.v2.1 annot-version=v2.1)

nscript=Phvul.005G175600.2 locus=Phvul.005G175600 ID=Phvul.005G175600.2.v2.1 annot-version=

nscript=Phvul.005G175600.2 locus=Phvul.005G175600 ID=Phvul.005G175600.2.v2.1 annot-version=

nscript=Phvul.006G053300.2 locus=Phvul.006G053300 ID=Phvul.006G053300.2.v2.1 annot-version=

nscript=Phvul.006G053300.2 locus=Phvul.006G053300 ID=Phvul.006G053300.2.v2.1 annot-version=

G110000.1 locus=Phvul.006G110000 ID=Phvul.006G110000.1.v2.1 annot-version=v2.1)

scription: pacid=37167521 transcript=Phvul.007G204100.1 locus=Phvul.007G204100 ID=Phvul.007G

1 locus=Phvul.008G006800 ID=Phvul.008G006800.1.v2.1 annot-version=v2.1) & Histone-binding pro

3a1_arath : 307.0) & Enzyme classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 19

G184400.2 locus=Phvul.009G184400 ID=Phvul.009G184400.2.v2.1 annot-version=v2.1)

G184400.2 locus=Phvul.009G184400 ID=Phvul.009G184400.2.v2.1 annot-version=v2.1)

G004800.1.v2.1 annot-version=v2.1) &

ɔl/phosphatidylcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0

ɔl/phosphatidylcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0

ɔn=v2.1) &

108200.1.v2.1 annot-version=v2.1) &

ɔt-version=v2.1) &

ɔt-version=v2.1) &

ɔt-version=v2.1) &

ɔt-version=v2.1) &

v2.1) &

ıot-version=v2.1) &

glycosyltransferase(50.2.4 : 545.4) (original description: pacid=37165866 transcript=Phvul.007G031

glycosyltransferase(50.2.4 : 545.4) (original description: pacid=37165866 transcript=Phvul.007G031

rsion=v2.1) &

vul.008G081700.2.v2.1 annot-version=v2.1) &

&

l.010G125200.1.v2.1 annot-version=v2.1) &

ɔ01700.1 locus=Phvul.001G001700 ID=Phvul.001G001700.1.v2.1 annot-version=v2.1) &

L) &

(original description: pacid=37175571 transcript=Phvul.002G011900.1 locus=Phvul.002G011900 ID

&

2.1) &

&

&

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

ıot-version=v2.1) &

ıot-version=v2.1) &

ıot-version=v2.1) &

ıot-version=v2.1) &

ıot-version=v2.1) &

ıot-version=v2.1) &
ıot-version=v2.1) &
ːin EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 345.0)
=v2.1) &
ːd donor with incorporation or reduction of molecular oxygen(50.1.13 : 407.0) (original description:
04G170000.1.v2.1 annot-version=v2.1) &
like protein G1 OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
00.1.v2.1 annot-version=v2.1) &
conjugating enzyme E2 26 OS=Arabidopsis thaliana (sp|q8gy87|ubc26_arath : 359.0)
.2.v2.1 annot-version=v2.1) &
.2.v2.1 annot-version=v2.1) &

ɔt-version=v2.1) &
ırotein 15 OS=Arabidopsis thaliana (sp|q9smy8|fbl15_arath : 1013.0)
-version=v2.1) &
ı2.1) &

ː protein At3g26840, chloroplastic OS=Arabidopsis thaliana (sp|q9lw26|y3684_arath : 661.0)
nsferase DPE2 OS=Oryza sativa subsp. japonica (sp|q69q02|dpe2_orysj : 394.0)
-version=v2.1) &
ıot-version=v2.1) &
ıot-version=v2.1) &

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

CALLOSE-BINDING PROTEIN 3 OS=Arabidopsis thaliana (sp|q9fz86|pdcb3_arath : 138.0)
v2.1) &
ı=v2.1) &
) &
) &

=Phvul.007G008100.2.v2.1 annot-version=v2.1) &
ː.1) &
ːin T85 OS=Nicotiana tabacum (sp|p33490|abp1_tobac : 271.0)
nsferase PMT19 OS=Arabidopsis thaliana (sp|q9zw75|pmtj_arath : 639.0)
ıul.009G062500.1.v2.1 annot-version=v2.1) &

annot-version=v2.1) &

&

DF SNC1 1 OS=Arabidopsis thaliana (sp|q9sb63|mos1_arath : 429.0)

DF SNC1 1 OS=Arabidopsis thaliana (sp|q9sb63|mos1_arath : 429.0)

2 OS=Arabidopsis thaliana (sp|o80961|mlo12_arath : 669.0)

&

&

=v2.1) &

=v2.1) &

=v2.1) &

=v2.1) &

G204100.1.v2.1 annot-version=v2.1) &

otein MSI1 homolog OS=Oryza sativa subsp. japonica (sp|q10g81|msi1_orysj : 130.0)

95.8) (original description: pacid=37160064 transcript=Phvul.008G034200.2 locus=Phvul.008G0342

)

)

.800.2 locus=Phvul.007G031800 ID=Phvul.007G031800.2.v2.1 annot-version=v2.1) &

.800.2 locus=Phvul.007G031800 ID=Phvul.007G031800.2.v2.1 annot-version=v2.1) &

=Phvul.002G011900.1.v2.1 annot-version=v2.1) &

: pacid=37163295 transcript=Phvul.004G159500.1 locus=Phvul.004G159500 ID=Phvul.004G159500.

00 ID=Phvul.008G034200.2.v2.1 annot-version=v2.1) &

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

miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
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uggaggcagcgg	Phvul.002G112900.2	2.5	-1	1	22
uggaggcagcgg	Phvul.002G112900.1	2.5	-1	1	22
uggaggcagcgg	Phvul.002G112900.2	2.5	-1	1	22
uggaggcagcgg	Phvul.002G112900.1	2.5	-1	1	22
uggaggcagcgg	Phvul.001G016450.1	3	-1	1	22
uggaggcagcgg	Phvul.001G016450.1	3	-1	1	22
uggaggcagcgg	Phvul.002G255100.1	3	-1	1	22
uggaggcagcgg	Phvul.002G255100.1	3	-1	1	22
ucgauaaaccuc	Phvul.002G332500.1	3	-1	1	21
uggaggcagcgg	Phvul.005G022900.2	3	-1	1	22
uggaggcagcgg	Phvul.005G022900.2	3	-1	1	22
uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
uggaggcagcgg	Phvul.005G165300.1	3	-1	1	22
ucgauaaaccuc	Phvul.006G176000.1	3	-1	1	21
ucgauaaaccuc	Phvul.007G172400.1	3	-1	1	21
uggaggcagcgg	Phvul.009G109200.2	3	-1	1	22
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ucgauaaaccuc	Phvul.009G260000.1	3	-1	1	21
uggaggcagcgg	Phvul.003G050000.1	3.5	-1	1	22
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uggaggcagcgg	Phvul.004G050550.1	3.5	-1	1	22
ucgauaaaccuc	Phvul.005G136500.1	3.5	-1	1	21
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uggaggcagcgg	Phvul.006G105000.1	3.5	-1	1	22
uggaggcagcgg	Phvul.007G006700.1	3.5	-1	1	22
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uggaggcagcgg	Phvul.007G216500.4	3.5	-1	1	22
uggaggcagcgg	Phvul.007G216500.3	3.5	-1	1	22
uggaggcagcgg	Phvul.007G216500.1	3.5	-1	1	22
uggaggcagcgg	Phvul.007G216500.4	3.5	-1	1	22
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ucgauaaaccuc	Phvul.008G211500.2	5	-1	1	21
uggaggcagcgg	Phvul.008G250000.1	5	-1	1	22
uggaggcagcgg	Phvul.008G250000.1	5	-1	1	22
uggaggcagcgg	Phvul.009G086300.2	5	-1	1	22
uggaggcagcgg	Phvul.009G086300.1	5	-1	1	22
uggaggcagcgg	Phvul.009G086300.2	5	-1	1	22
uggaggcagcgg	Phvul.009G086300.1	5	-1	1	22
ucgauaaaccuc	Phvul.009G149800.1	5	-1	1	21
uggaggcagcgg	Phvul.009G154300.6	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.5	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.3	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.4	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.1	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.6	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.5	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.3	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.4	5	-1	1	22
uggaggcagcgg	Phvul.009G154300.1	5	-1	1	22
ucgauaaaccuc	Phvul.009G240100.1	5	-1	1	21
uggaggcagcgg	Phvul.011G017800.1	5	-1	1	22

uggaggcagcgg	Phvul.011G017800.1	5	-1	1	22
ucgauaaaccuc	Phvul.011G100200.2	5	-1	1	21
ucgauaaaccuc	Phvul.011G100200.1	5	-1	1	21
ucgauaaaccuc	Phvul.011G108300.1	5	-1	1	21
uggaggcagcgg	Phvul.011G129700.1	5	-1	1	22
uggaggcagcgg	Phvul.011G129700.1	5	-1	1	22
ucgauaaaccuc	Phvul.011G140050.2	5	-1	1	21
ucgauaaaccuc	Phvul.011G140050.1	5	-1	1	21

Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
2888	2907	UCGAUAAAC	::::: ::::::::::.::	GGGGAUG-A	Cleavage	pacid=371763
400	421	UGGAGGCAG	: ::::.:.::.:::.:::.	AACCGAUGG	Cleavage	pacid=371750
400	421	UGGAGGCAG	: ::::.:.::.:::.:::.	AACCGAUGG	Cleavage	pacid=371750
400	421	UGGAGGCAG	: ::::.:.::.:::.:::.	AACCGAUGG	Cleavage	pacid=371750
400	421	UGGAGGCAG	: ::::.:.::.:::.:::.	AACCGAUGG	Cleavage	pacid=371750
187	207	UGGAGGCAG	::: ::::::::::.:.	CCACGA-GAA	Cleavage	pacid=371691
187	207	UGGAGGCAG	::: ::::::::::.:.	CCACGA-GAA	Cleavage	pacid=371691
246	267	UGGAGGCAG	:::::..::.:::.::::	AGCAGAUGA	Cleavage	pacid=371771
246	267	UGGAGGCAG	:::::..::.:::.::::	AGCAGAUGA	Cleavage	pacid=371771
1000	1020	UCGAUAAAC	::.:: :::: :::::::	AAGGGUGGA	Cleavage	pacid=371778
220	241	UGGAGGCAG	: :.::::.:::: ::::::.:	GUUUGAUGG	Cleavage	pacid=371541
220	241	UGGAGGCAG	: :.::::.:::: ::::::.:	GUUUGAUGG	Cleavage	pacid=371541
282	303	UGGAGGCAG	.:: ::::: :::::::::	CUAUGAGGA	Translation	pacid=371526
282	303	UGGAGGCAG	.:: ::::: :::::::::	CUAUGAGGA	Translation	pacid=371526
1116	1136	UCGAUAAAC	::::::::: :::::: ::	GAGGAUGCA	Translation	pacid=371738
473	493	UCGAUAAAC	: ::::: ::::: :::.::	CAGGAUGGA	Cleavage	pacid=371646
315	336	UGGAGGCAG	.:.:: ::::::::.::::	UGUUGACCA	Cleavage	pacid=371495
315	336	UGGAGGCAG	.:.:: ::::::::.::::	UGUUGACCA	Cleavage	pacid=371495
315	336	UGGAGGCAG	.:.:: ::::::::.::::	UGUUGACCA	Cleavage	pacid=371495
315	336	UGGAGGCAG	.:.:: ::::::::.::::	UGUUGACCA	Cleavage	pacid=371495
315	336	UGGAGGCAG	.:.:: ::::::::.::::	UGUUGACCA	Cleavage	pacid=371495
315	336	UGGAGGCAG	.:.:: ::::::::.::::	UGUUGACCA	Cleavage	pacid=371495
3637	3658	UCGAUAA-AC	::::::::::::: ::::::	CUGGAUGCA	Cleavage	pacid=371490
1587	1608	UGGAGGCAG	:.:::::.:::::: ::	AAAAGGUGA	Cleavage	pacid=371459
1587	1608	UGGAGGCAG	:.:::::.:::::: ::	AAAAGGUGA	Cleavage	pacid=371459
3823	3844	UGGAGGCAG	.:. :::.:: ::::::::::	UGUUUAUGG	Translation	pacid=371632
3823	3844	UGGAGGCAG	.:. :::.:: ::::::::::	UGUUUAUGG	Translation	pacid=371632
427	447	UCGAUAAAC	.:: ::::.:::::: .::::	UUGAAUGCG	Cleavage	pacid=371525
2271	2292	UGGAGGCAG	: .:::::.:. :::::::.:	AACUGAUGA	Translation	pacid=371719
2271	2292	UGGAGGCAG	: .:::::.:. :::::::.:	AACUGAUGA	Translation	pacid=371719
694	715	UGGAGGCAG	::::..:.:::::.::..:	UUGGGAUGG	Cleavage	pacid=371667
694	715	UGGAGGCAG	::::..:.:::::.::..:	UUGGGAUGG	Cleavage	pacid=371667
1058	1079	UGGAGGCAG	: :::.::: .::::::::	UGACUAUGG	Translation	pacid=371659
1056	1077	UGGAGGCAG	: :::.::: .::::::::	UGACUAUGG	Translation	pacid=371659
1058	1079	UGGAGGCAG	: :::.::: .::::::::	UGACUAUGG	Translation	pacid=371659
1058	1079	UGGAGGCAG	: :::.::: .::::::::	UGACUAUGG	Translation	pacid=371659
1056	1077	UGGAGGCAG	: :::.::: .::::::::	UGACUAUGG	Translation	pacid=371659
1058	1079	UGGAGGCAG	: :::.::: .::::::::	UGACUAUGG	Translation	pacid=371659
747	767	UCGAUAAAC	:: ::::::::::.:.:.	GAGGCAGCA	Cleavage	pacid=371602
1646	1667	UGGAGGCAG	:: :::::.:..::: .:::::	GACCGAUGG	Cleavage	pacid=371611
1736	1757	UGGAGGCAG	:: :::::.:..::: .:::::	GACCGAUGG	Cleavage	pacid=371611
1646	1667	UGGAGGCAG	:: :::::.:..::: .:::::	GACCGAUGG	Cleavage	pacid=371611
1736	1757	UGGAGGCAG	:: :::::.:..::: .:::::	GACCGAUGG	Cleavage	pacid=371611
2079	2101	UGGAGGCAG	:. ::: :::::::::::::.	GGACGACUG	Cleavage	pacid=371551
2079	2101	UGGAGGCAG	:. ::: :::::::::::::.	GGACGACUG	Cleavage	pacid=371551

427	448	UGGAGGCAG	: : :::: .::.:::::::	UAACAAUGA	Cleavage	pacid=371552
797	818	UGGAGGCAG	: : :::: .::.:::::::	UAACAAUGA	Cleavage	pacid=371552
840	861	UGGAGGCAG	: : :::: .::.:::::::	UAACAAUGA	Cleavage	pacid=371552
427	448	UGGAGGCAG	: : :::: .::.:::::::	UAACAAUGA	Cleavage	pacid=371552
797	818	UGGAGGCAG	: : :::: .::.:::::::	UAACAAUGA	Cleavage	pacid=371552
840	861	UGGAGGCAG	: : :::: .::.:::::::	UAACAAUGA	Cleavage	pacid=371552
543	567	UGGAGGCAG	.::::: :::::::::	CGUCGAUCU	Cleavage	pacid=371679
543	567	UGGAGGCAG	.::::: :::::::::	CGUCGAUCU	Cleavage	pacid=371679
1173	1194	UGGAGGCAG	.:. :::::: :::::::	UGUUAAUGA	Translation	pacid=371679
1173	1194	UGGAGGCAG	.:. :::::: :::::::	UGUUAAUGA	Translation	pacid=371679
336	357	UGGAGGCAG	::::::.::.::: ::::.	ACUCGAUGG	Cleavage	pacid=371687
336	357	UGGAGGCAG	::::::.::.::: ::::.	ACUCGAUGG	Cleavage	pacid=371687
2099	2120	UGGAGGCAG	:. :::::: :::.::.::	UUUUAAUGA	Translation	pacid=371688
2099	2120	UGGAGGCAG	:. :::::: :::.::.::	UUUUAAUGA	Translation	pacid=371688
213	234	UGGAGGCAG	:. :::: ..:::: :.::::	GGCCGAUGC	Cleavage	pacid=371779
213	234	UGGAGGCAG	:. :::: ..:::: :.::::	GGCCGAUGC	Cleavage	pacid=371779
420	441	UGGAGGCAG	::: :: :::::.: :::::	AAUCUAUAA	Cleavage	pacid=371772
420	441	UGGAGGCAG	::: :: :::::.: :::::	AAUCUAUAA	Cleavage	pacid=371772
194	215	UGGAGGCAG	: :: ::.:::::...:.::	UCUAGAAGA	Cleavage	pacid=371769
194	215	UGGAGGCAG	: :: ::.:::::...:.::	UCUAGAAGA	Cleavage	pacid=371769
2119	2140	UGGAGGCAG	: ::.::.::: :: :::::	CACCGGUGG	Translation	pacid=371745
2544	2565	UGGAGGCAG	: ::.::.::: :: :::::	CACCGGUGG	Translation	pacid=371745
2119	2140	UGGAGGCAG	: ::.::.::: :: :::::	CACCGGUGG	Translation	pacid=371745
2544	2565	UGGAGGCAG	: ::.::.::: :: :::::	CACCGGUGG	Translation	pacid=371745
672	693	UGGAGGCAG	:: : :: :::::: :::..:	GAACCAUCAA	Cleavage	pacid=371747
672	693	UGGAGGCAG	:: : :: :::::: :::..:	GAACCAUCAA	Cleavage	pacid=371747
360	380	UCGAUAAAC	: :: .::::::::::.:	GAGAAUUUA	Cleavage	pacid=371457
405	426	UGGAGGCAG	: :::::: .::::::.:.:	CACCGAUGA	Cleavage	pacid=371478
405	426	UGGAGGCAG	: :::::: .::::::.:.:	CACCGAUGA	Cleavage	pacid=371478
286	306	UCGAUAAAC	:::: :::: :::: ::::	CUGGAGGCA	Translation	pacid=371453
350	371	UGGAGGCAG	:.::::: :::: :::: ::::	GGUCGAUAA	Translation	pacid=371453
350	371	UGGAGGCAG	:.::::: :::: :::: ::::	GGUCGAUAA	Translation	pacid=371453
1166	1187	UGGAGGCAG	:. : :.::.:::::::::.	AUUUCAAGG	Cleavage	pacid=371447
1238	1259	UGGAGGCAG	:. : :.::.:::::::::.	AUUUCAAGG	Cleavage	pacid=371447
1166	1187	UGGAGGCAG	:. : :.::.:::::::::.	AUUUCAAGG	Cleavage	pacid=371447
1238	1259	UGGAGGCAG	:. : :.::.:::::::::.	AUUUCAAGG	Cleavage	pacid=371447
344	365	UGGAGGCAG	.:: ::.:: ::::::.::	GUAUGAAGA	Translation	pacid=371461
638	659	UGGAGGCAG	.:: ::.:: ::::::.::	GUAUGAAGA	Translation	pacid=371461
344	365	UGGAGGCAG	.:: ::.:: ::::::.::	GUAUGAAGA	Translation	pacid=371461
638	659	UGGAGGCAG	.:: ::.:: ::::::.::	GUAUGAAGA	Translation	pacid=371461
723	744	UGGAGGCAG	::.:::: ::: ::.::::	UGACGGUGA	Cleavage	pacid=371616
723	744	UGGAGGCAG	::.:::: ::: ::.::::	UGACGGUGA	Cleavage	pacid=371616
589	609	UCGAUAAAC	:::::::.:::: .:::.	CCUGAUGCA	Cleavage	pacid=371545
853	873	UCGAUAAAC	::::::.: :::::::	GCUCAUGCA	Cleavage	pacid=371669
996	1016	UCGAUAAAC	::::::::::: :: ::.:.	AUGGAUGCA	Cleavage	pacid=371667
240	261	UGGAGGCAG	.:.::.::: :::::::	GCGUGGUGG	Translation	pacid=371603

240	261	UGGAGGCAG	.:.::.::: ::::::::	GCGUGGUGG	Translation	pacid=371603
759	779	UCGAUAAAC	:::.:: ::.:::::.:.:	GUGGGUGGA	Cleavage	pacid=371577
1095	1116	UGGAGGCAG	:.::::: :::.::.::.:.	UCUUGAUGA	Cleavage	pacid=371489
1095	1116	UGGAGGCAG	:.::::: :::.::.::.:.	UCUUGAUGA	Cleavage	pacid=371489
1778	1799	UGGAGGCAG	::::::. :::::::::	CGCAAAUGA	Translation	pacid=371487
1778	1799	UGGAGGCAG	::::::. :::::::::	CGCAAAUGA	Translation	pacid=371487
421	441	UCGAUAAAC	:: : ::..:::::::.:::.	CUAGCUGUG	Cleavage	pacid=371439
78	99	UGGAGGCAG	: : ::::: : :::::::::	UAACAAUGA	Translation	pacid=371574
78	99	UGGAGGCAG	: : ::::: : :::::::::	UAACAAUGA	Translation	pacid=371574
719	740	UGGAGGCAG	: :::.: :.:.:::::::.	GCUCGGUCA	Cleavage	pacid=371549
719	740	UGGAGGCAG	: :::.: :.:.:::::::.	GCUCGGUCA	Cleavage	pacid=371549
844	864	UCGAUAAAC	:::::::: :::: ::::	GAAGAUGCA	Translation	pacid=371550
2952	2973	UGGAGGCAG	::::: :.:.:::::::..	AAUCGAGCA	Cleavage	pacid=371569
2952	2973	UGGAGGCAG	::::: :.:.:::::::..	AAUCGAGCA	Cleavage	pacid=371569
2488	2508	UCGAUAAAC	:::::.:::::: : :.:.	UAGGAUGUA	Cleavage	pacid=371678
1245	1266	UGGAGGCAG	::::.::.:::::: ::	AAGGGAUGG	Cleavage	pacid=371677
1269	1290	UGGAGGCAG	::::.::.:::::: ::	AAGGGAUGG	Cleavage	pacid=371677
1245	1266	UGGAGGCAG	::::.::.:::::: ::	AAGGGAUGG	Cleavage	pacid=371677
1269	1290	UGGAGGCAG	::::.::.:::::: ::	AAGGGAUGG	Cleavage	pacid=371677
902	923	UGGAGGCAG	.:::: :.:: ::::::::..	UGAUGAUCA	Translation	pacid=371686
902	923	UGGAGGCAG	.:::: :.:: ::::::::..	UGAUGAUCA	Translation	pacid=371686
252	273	UGGAGGCAG	:: ::::: ...: ::::::::	GAGCGAUGC	Translation	pacid=371759
252	273	UGGAGGCAG	:: ::::: ...: ::::::::	GAGCGAUGC	Translation	pacid=371759
252	273	UGGAGGCAG	:: ::::: ..: ::::::::	GAGCGAUGC	Translation	pacid=371759
252	273	UGGAGGCAG	:: ::::: ..: ::::::::	GAGCGAUGC	Translation	pacid=371759
405	425	UCGAUAAAC	.::::: :::. ::::.:.:.	UUGGAUUCA	Translation	pacid=371779
405	425	UCGAUAAAC	.::::: :::. ::::.:.:.	UUGGAUUCA	Translation	pacid=371779
1306	1326	UCGAUAAAC	::: :::::: :::::.:.	GUGGUGGCA	Cleavage	pacid=371780
819	839	UCGAUAAAC	.:::::::::: ::: .:.:.	UUGGAUGCA	Translation	pacid=371752
521	542	UGGAGGCAG	:::....::::.:::::	GGAACAUGG	Cleavage	pacid=371777
521	542	UGGAGGCAG	:::....::::.:::::	GGAACAUGG	Cleavage	pacid=371777
1039	1060	UGGAGGCAG	:. :::::.::: .::..:::	GGACGAUGG	Translation	pacid=371754
1132	1153	UGGAGGCAG	:. :::::.::: .::..:::	GGACGAUGG	Translation	pacid=371754
1039	1060	UGGAGGCAG	:. :::::.::: .::..:::	GGACGAUGG	Translation	pacid=371754
1132	1153	UGGAGGCAG	:. :::::.::: .::..:::	GGACGAUGG	Translation	pacid=371754
2338	2358	UCGAUAAAC	: :::: :::::: :::::	GUUGAUGAA	Cleavage	pacid=371749
518	539	UGGAGGCAG	.:::::::.:: :: ::.:::.	UGUCGAUGG	Translation	pacid=371782
518	539	UGGAGGCAG	.:::::::.:: :: ::.:::.	UGUCGAUGG	Translation	pacid=371782
1259	1278	UCGAUAAAC	::::::.::::::: :::	GAGGAUGCG	Cleavage	pacid=371466
1050	1069	UCGAUAAAC	.: ::::::::::::: :::.	UUUGAUGCA	Cleavage	pacid=371447
1169	1188	UCGAUAAAC	.: ::::::::::::: :::.	UUUGAUGCA	Cleavage	pacid=371447
1729	1750	UGGAGGCAG	::::::::.::.::...	UUGUUAUGA	Cleavage	pacid=371481
1729	1750	UGGAGGCAG	::::::::.::.::...	UUGUUAUGA	Cleavage	pacid=371481
940	960	UCGAUAAAC	: :::: ::::::::: ::	AUCGAUGAA	Cleavage	pacid=371474
1008	1029	UGGAGGCAG	: ::::.::: ::::::::	AUUAGAUGG	Translation	pacid=371481
1008	1029	UGGAGGCAG	: ::::.::: ::::::::	AUUAGAUGG	Translation	pacid=371481

1713	1733	UCGAUAAAC	:.:::::: ::::::: :	CGUGGUGCA	Translation	pacid=371465
1775	1796	UGGAGGCAG	:::::.:::: .:::::.:...	GAUCGGUGA	Cleavage	pacid=371454
1775	1796	UGGAGGCAG	:::::.:::: .:::::.:...	GAUCGGUGA	Cleavage	pacid=371454
1063	1084	UGGAGGCAG	:. ::::: :::::::::	UCUUAAUGA	Translation	pacid=371483
1063	1084	UGGAGGCAG	:. ::::: :::::::::	UCUUAAUGA	Translation	pacid=371483
330	351	UGGAGGCAG	::::::::::.:.:: :.::	GAUCGAUGA	Cleavage	pacid=371453
330	351	UGGAGGCAG	::::::::::.:.:: :.::	GAUCGAUGA	Cleavage	pacid=371453
1029	1050	UGGAGGCAG	:.:::::::: .: .:::::	AUUUGAUGA	Translation	pacid=371443
1176	1197	UGGAGGCAG	:.:::::::: .: .:::::	AUUUGAUGA	Translation	pacid=371443
1029	1050	UGGAGGCAG	:.:::::::: .: .:::::	AUUUGAUGA	Translation	pacid=371443
1176	1197	UGGAGGCAG	:.:::::::: .: .:::::	AUUUGAUGA	Translation	pacid=371443
2631	2651	UCGAUAAAC	::::::::::::.:.	GACGAUGCA	Cleavage	pacid=371476
2656	2676	UCGAUAAAC	::::::::::::.:.	GACGAUGCA	Cleavage	pacid=371476
354	375	UGGAGGCAG	:. .:.::::::::: :.::.	GGCUGGUGA	Cleavage	pacid=371523
354	375	UGGAGGCAG	:. .:.::::::::: :.::.	GGCUGGUGA	Cleavage	pacid=371523
529	549	UCGAUAAAC	::::.:: ::::: :::: ::	CUGGGUGGA	Cleavage	pacid=371726
607	627	UCGAUAAAC	::::.:: ::::: :::: ::	CUGGGUGGA	Cleavage	pacid=371726
1546	1566	UCGAUAAAC	: ::::: ::::: ::.:.:	CCGGAUGAA	Cleavage	pacid=371664
49	69	UCGAUAAAC	::::.::::: : ::::	UGGGAUGUA	Cleavage	pacid=371660
1650	1671	UGGAGGCAG	.:::::.:::::.:::	GUCUUGUGA	Cleavage	pacid=371649
1650	1671	UGGAGGCAG	.:::::.:::::.:::	GUCUUGUGA	Cleavage	pacid=371649
735	756	UGGAGGCAG	:.:. ::::: ::::::...	ACUUGGGGA	Translation	pacid=371669
735	756	UGGAGGCAG	:.:. ::::: ::::::...	ACUUGGGGA	Translation	pacid=371669
756	777	UGGAGGCAG	::::::.:: ::::::.:	UGUAUAUGA	Cleavage	pacid=371674
756	777	UGGAGGCAG	::::::.:: ::::::.:	UGUAUAUGA	Cleavage	pacid=371674
290	310	UCGAUAAAC	:: :::.:::::.:.::	UCCAAUACA	Cleavage	pacid=371646
1604	1624	UCGAUAAAC	.::::: ::::: :::::. :	UUGGAUUCA	Cleavage	pacid=371645
812	832	UCGAUAAAC	: ::::::.. .:::::: :::	CGGGAUGUG	Cleavage	pacid=371602
293	313	UCGAUAAAC	:::: ::::::: .:.::	AGCGAUGAA	Cleavage	pacid=371609
297	317	UCGAUAAAC	:::: ::::::: .:.::	AGCGAUGAA	Cleavage	pacid=371609
998	1018	UCGAUAAAC	::: :: .:::::: :::.::	CUGAAUUUA	Cleavage	pacid=371607
1005	1025	UCGAUAAAC	::: :: .:::::: :::.::	CUGAAUUUA	Cleavage	pacid=371607
1799	1820	UGGAGGCAG	::: : ::.:.::::::::...	AAUCCAAGA	Cleavage	pacid=371592
1887	1908	UGGAGGCAG	::: : ::.:.::::::::...	AAUCCAAGA	Cleavage	pacid=371592
1799	1820	UGGAGGCAG	::: : ::.:.::::::::...	AAUCCAAGA	Cleavage	pacid=371592
1887	1908	UGGAGGCAG	::: : ::.:.::::::::...	AAUCCAAGA	Cleavage	pacid=371592
280	301	UGGAGGCAG	:.:::: :.:.::.:::. :::	GGUCGAAGG	Cleavage	pacid=371513
352	373	UGGAGGCAG	:.:::: :.:.::.:::. :::	GGUCGAAGG	Cleavage	pacid=371513
280	301	UGGAGGCAG	:.:::: :.:.::.:::. :::	GGUCGAAGG	Cleavage	pacid=371513
352	373	UGGAGGCAG	:.:::: :.:.::.:::. :::	GGUCGAAGG	Cleavage	pacid=371513
678	698	UCGAUAAAC	::::::::: ::::: .:	GGGGAUGCA	Translation	pacid=371503
938	958	UCGAUAAAC	::::::::: ::::: .:	GGGGAUGCA	Translation	pacid=371503
1036	1056	UCGAUAAAC	::::::::: ::::: .:	GGGGAUGCA	Translation	pacid=371503
299	320	UGGAGGCAG	: :::::....:.:::::..	CAACGAUGG	Cleavage	pacid=371518
299	320	UGGAGGCAG	: :::::....:.:::::..	CAACGAUGG	Cleavage	pacid=371518
299	320	UGGAGGCAG	: :::::....:.:::::..	CAACGAUGG	Cleavage	pacid=371518

299	320	UGGAGGCAG	: :::::....:.:::::..	CAACGAUGG	Cleavage	pacid=371518
762	783	UGGAGGCAG	:::: :::: ::::.::: :	UUUCGAAGA	Translation	pacid=371563
762	783	UGGAGGCAG	:::: :::: ::::.::: :	UUUCGAAGA	Translation	pacid=371563
296	317	UGGAGGCAG	::::::::::::::	ACCGUAUGA	Cleavage	pacid=371559
296	317	UGGAGGCAG	::::::::::::::	ACCGUAUGA	Cleavage	pacid=371559
642	661	UCGAUAAAC	:::: ::::::::: :::	GUGGAGGCA	Cleavage	pacid=371710
866	887	UGGAGGCAG	::: ::::::. :.::..:.::	GAUGGAUGA	Translation	pacid=371682
866	887	UGGAGGCAG	::: ::::::. :.::..:.::	GAUGGAUGA	Translation	pacid=371682
647	667	UCGAUAAAC	:: :::: .:::::: ::::	CUUGAUGAG	Cleavage	pacid=371702
1576	1597	UGGAGGCAG	:: :::::.:..: ::..:::	GAGCGAUGG	Cleavage	pacid=371686
1576	1597	UGGAGGCAG	:: :::::.:..: ::..:::	GAGCGAUGG	Cleavage	pacid=371686
1635	1655	UCGAUAAAC	:::::: : :::::::.:.	CUGGAUUCC	Cleavage	pacid=371682
887	908	UGGAGGCAG	:..: :: ::.:.::: :::.::	GGUGGAAGA	Cleavage	pacid=371704
887	908	UGGAGGCAG	:..: :: ::.:.::: :::.::	GGUGGAAGA	Cleavage	pacid=371704
1235	1256	UGGAGGCAG	:: ::.::: .::. ::::::.	GACCGGUGA	Cleavage	pacid=371776
1235	1256	UGGAGGCAG	:: ::.::: .::. ::::::.	GACCGGUGA	Cleavage	pacid=371776
5452	5471	UCGAUAAAC	.:::::: ::::::::::.	UUGGAUG-A	Cleavage	pacid=371766
5464	5483	UCGAUAAAC	.:::::: ::::::::::.	UUGGAUG-A	Cleavage	pacid=371766
384	404	UCGAUAAAC	.::::: :::: :::::::	UUGGAUUCA	Translation	pacid=371776
534	555	UGGAGGCAG	: ::::::.::.:.: .::.:.	GUUUGAUGG	Cleavage	pacid=371781
534	555	UGGAGGCAG	: ::::::.::.:.: .::.:.	GUUUGAUGG	Cleavage	pacid=371781
1036	1056	UCGAUAAAC	::::: :::: ::::::	AAGGAUGAA	Cleavage	pacid=371784
1036	1056	UCGAUAAAC	::::: :::: ::::::	AAGGAUGAA	Cleavage	pacid=371784
653	673	UCGAUAAAC	::::::::::::: :	UGAGAUGCA	Cleavage	pacid=371755
710	731	UGGAGGCAG	:::::::::::::	UUCCCGAAA	Cleavage	pacid=371466
710	731	UGGAGGCAG	:::::::::::::	UUCCCGAAA	Cleavage	pacid=371466
1199	1220	UGGAGGCAG	:::..: :::::::.: .:::::	GAUUGCGGA	Cleavage	pacid=371455
1199	1220	UGGAGGCAG	:::..: :::::::.: .:::::	GAUUGCGGA	Cleavage	pacid=371455
1175	1195	UCGAUAAAC	: :::::.:::: ::. :::	AUAGAUGCG	Cleavage	pacid=371445
1659	1680	UGGAGGCAG	:..:: ::: :..: ::::::::	GGUCUAUGC	Translation	pacid=371461
1953	1974	UGGAGGCAG	:..:: ::: :..: ::::::::	GGUCUAUGC	Translation	pacid=371461
1659	1680	UGGAGGCAG	:..:: ::: :..: ::::::::	GGUCUAUGC	Translation	pacid=371461
1953	1974	UGGAGGCAG	:..:: ::: :..: ::::::::	GGUCUAUGC	Translation	pacid=371461
524	544	UCGAUAAAC	:: :: ::::::::: :: ::	CUUGAGGCA	Cleavage	pacid=371635
503	523	UCGAUAAAC	::.::::::::::: :	CUUUCUGUA	Cleavage	pacid=371540
503	523	UCGAUAAAC	::.::::::::::: :	CUUUCUGUA	Cleavage	pacid=371540
853	875	UGGAGGCAG	: :.::::: ::.::::::.:.:	GCUUGAUGA	Cleavage	pacid=371531
853	875	UGGAGGCAG	: :.::::: ::.::::::.:.:	GCUUGAUGA	Cleavage	pacid=371531
101	121	UCGAUAAAC	::::::::.::. :::::::	CUGGAUGUA	Translation	pacid=371536
713	733	UCGAUAAAC	:::::::::::::: :	UGAGAUGCA	Cleavage	pacid=371532
1276	1296	UCGAUAAAC	:::::::: :: :::.:.:	AUGGAUGCA	Cleavage	pacid=371544
1279	1299	UCGAUAAAC	:::::::: :: :::.:.:	AUGGAUGCA	Cleavage	pacid=371544
1297	1317	UCGAUAAAC	:::::::::::: :: :	ACCUAUGCA	Cleavage	pacid=371714
1228	1249	UGGAGGCAG	::::::: ... .:::::::.:	CAUCGAUGU	Translation	pacid=371721
1228	1249	UGGAGGCAG	::::::: ... .:::::::.:	CAUCGAUGU	Translation	pacid=371721
726	748	UGGAGGCAG	:.:.::: .:.::::::::::	ACUUGGUGA	Cleavage	pacid=371730

726	748	UGGAGGCAG	:.:.::: .:.:::::::::	ACUUGGUGA	Cleavage	pacid=371730
502	523	UGGAGGCAG	::::.::.::::: ::: ::	AAUCGGUGG	Cleavage	pacid=371657
502	523	UGGAGGCAG	::::.::.::::: ::: ::	AAUCGGUGG	Cleavage	pacid=371657
502	523	UGGAGGCAG	::::.::.::::: ::: ::	AAUCGGUGG	Cleavage	pacid=371657
502	523	UGGAGGCAG	::::.::.::::: ::: ::	AAUCGGUGG	Cleavage	pacid=371657
226	246	UCGAUAAAC	.:::::..:::: :::::	UUGGAUGUG	Cleavage	pacid=371662
38	58	UCGAUAAAC	:: :::.::: :::: :.::	AUGAAUGUA	Translation	pacid=371675
37	58	UGGAGGCAG	:.:.:. ::::. .:::::.::	GGUUGGAGA	Translation	pacid=371673
37	58	UGGAGGCAG	:.:.:. ::::. .:::::.::	GGUUGGAGA	Translation	pacid=371673
37	58	UGGAGGCAG	:.:.:. ::::. .:::::.::	GGUUGGAGA	Translation	pacid=371673
37	58	UGGAGGCAG	:.:.:. ::::. .:::::.::	GGUUGGAGA	Translation	pacid=371673
483	505	UGGAGG-CAG	::: ::.::::::: ::::.:	CUUCGUUGG	Cleavage	pacid=371664
483	505	UGGAGG-CAG	::: ::.::::::: ::::.:	CUUCGUUGG	Cleavage	pacid=371664
1346	1366	UCGAUAAAC	:::::.:::: :::::.	GAGGAUGUA	Cleavage	pacid=371674
1498	1518	UCGAUAAAC	:::::::: ::::: ::	UUACAUGCA	Cleavage	pacid=371644
199	220	UGGAGGCAG	:::::. :.. ::.::::::.	GAUCGGAGG	Cleavage	pacid=371654
199	220	UGGAGGCAG	:::::. :.. ::.::::::.	GAUCGGAGG	Cleavage	pacid=371654
2208	2228	UCGAUAAAC	::::: :..::::: .:.:.	CUGGAAGUG	Cleavage	pacid=371593
1369	1390	UGGAGGCAG	::.::: .:..:.::..::.:	CAUUGAUAG	Cleavage	pacid=371605
1369	1390	UGGAGGCAG	::.::: .:..:.::..::.:	CAUUGAUAG	Cleavage	pacid=371605
2716	2736	UCGAUAAAC	:: .::::::.::::	AUUCUUGGG	Cleavage	pacid=371580
309	330	UGGAGGCAG	:..:::: ....:.:::: ::.	GGUCGAUUG	Cleavage	pacid=371606
309	330	UGGAGGCAG	:..:::: ....:.:::: ::.	GGUCGAUUG	Cleavage	pacid=371606
1568	1588	UCGAUAAAC	.:: ::::::::: ::. .::	UUGUAUGCA	Cleavage	pacid=371577
1568	1588	UCGAUAAAC	.:: ::::::::: ::. .::	UUGUAUGCA	Cleavage	pacid=371577
1607	1627	UCGAUAAAC	.:: ::::::::: ::. .::	UUGUAUGCA	Cleavage	pacid=371577
1610	1630	UCGAUAAAC	.:: ::::::::: ::. .::	UUGUAUGCA	Cleavage	pacid=371577
702	724	UGGAGGCAG	:..:.::: :.:..:.:::::.:	GGUUGAUAG	Cleavage	pacid=371599
702	724	UGGAGGCAG	:..:.::: :.:..:.:::::.:	GGUUGAUAG	Cleavage	pacid=371599
1138	1159	UGGAGGCAG	.::::.:::: ::::::	CCCUGAUGG	Cleavage	pacid=371499
1251	1272	UGGAGGCAG	.::::.:::: ::::::	CCCUGAUGG	Cleavage	pacid=371499
1138	1159	UGGAGGCAG	.::::.:::: ::::::	CCCUGAUGG	Cleavage	pacid=371499
1251	1272	UGGAGGCAG	.::::.:::: ::::::	CCCUGAUGG	Cleavage	pacid=371499
363	383	UCGAUAAAC	: :::::: .::::: :::.	AUUGAUGCA	Cleavage	pacid=371495
99	120	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
99	120	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
155	176	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
99	120	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
155	176	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
99	120	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
99	120	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
155	176	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
99	120	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
155	176	UGGAGGCAG	:..:.::::....:.: .:::::	GGUUGAUGG	Cleavage	pacid=371505
199	219	UCGAUAAAC	: :::::::::::::	GGGUAUGCA	Cleavage	pacid=371521
372	393	UGGAGGCAG	:..:. :::::::. ::::::.:	GGUUCUUGA	Cleavage	pacid=371562

372	393	UGGAGGCAG	:.:. :::::::. :::::.:	GGUUCUUGA	Cleavage	pacid=371562
1076	1096	UCGAUAAAC	.: ::: :.:::::::::	UUUGAUCCG	Cleavage	pacid=371558
1076	1096	UCGAUAAAC	.: ::: :.:::::::::	UUUGAUCCG	Cleavage	pacid=371558
110	130	UCGAUAAAC	::::::::::::: :	UGAGAUGCA	Cleavage	pacid=371546
1572	1593	UGGAGGCAG	.:.:.::: :.:.:: ::::	AGUUGGUGA	Cleavage	pacid=371553
1572	1593	UGGAGGCAG	.:.:.::: :.:.:: ::::	AGUUGGUGA	Cleavage	pacid=371553
2490	2510	UCGAUAAAC	::::.:::::::.:.	GACGAUGCG	Cleavage	pacid=371551
2586	2606	UCGAUAAAC	::::.:::::::.:.	GACGAUGCG	Cleavage	pacid=371551

Multiplicity	Target_Acc.	ID	locusName	Pfam	Panther
1	Phvul.002G040800.1	Phvul.002G040800	Phvul.002G04	PF00675,PF05	PTHR11851,P
1	Phvul.002G112900.2	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.002G112900.1	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.002G112900.2	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.002G112900.1	Phvul.002G112900	Phvul.002G11	PF01529	PTHR22883,P
1	Phvul.001G016450.1	Phvul.001G016450	Phvul.001G01	PF13656	PTHR13946,P
1	Phvul.001G016450.1	Phvul.001G016450	Phvul.001G01	PF13656	PTHR13946,P
1	Phvul.002G255100.1	Phvul.002G255100	Phvul.002G25	PF00083	PTHR23505,P
1	Phvul.002G255100.1	Phvul.002G255100	Phvul.002G25	PF00083	PTHR23505,P
1	Phvul.002G332500.1	Phvul.002G332500	Phvul.002G33	0	PTHR10593,P
1	Phvul.005G022900.2	Phvul.005G022900	Phvul.005G02	PF02775,PF13	PTHR18968,P
1	Phvul.005G022900.2	Phvul.005G022900	Phvul.005G02	PF02775,PF13	PTHR18968,P
1	Phvul.005G165300.1	Phvul.005G165300	Phvul.005G16	PF00235	PTHR11604,P
1	Phvul.005G165300.1	Phvul.005G165300	Phvul.005G16	PF00235	PTHR11604,P
1	Phvul.006G176000.1	Phvul.006G176000	Phvul.006G17	PF13837	PTHR31307,P
1	Phvul.007G172400.1	Phvul.007G172400	Phvul.007G17	PF01765	PTHR20982,P
1	Phvul.009G109200.2	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.3	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.1	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.2	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.3	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G109200.1	Phvul.009G109200	Phvul.009G10	PF03055	PTHR10543,P
1	Phvul.009G260000.1	Phvul.009G260000	Phvul.009G26	PF04851,PF14	PTHR14950,P
1	Phvul.003G050000.1	Phvul.003G050000	Phvul.003G05	PF08241	PTHR12176,P
1	Phvul.003G050000.1	Phvul.003G050000	Phvul.003G05	PF08241	PTHR12176,P
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G05	PF13650	PTHR34482,P
1	Phvul.004G050550.1	Phvul.004G050550	Phvul.004G05	PF13650	PTHR34482,P
1	Phvul.005G136500.1	Phvul.005G136500	Phvul.005G13	PF05739	PTHR19957,P
1	Phvul.006G105000.1	Phvul.006G105000	Phvul.006G10	PF13857,PF11	PTHR12447,P
1	Phvul.006G105000.1	Phvul.006G105000	Phvul.006G10	PF13857,PF11	PTHR12447,P
1	Phvul.007G006700.1	Phvul.007G006700	Phvul.007G00	PF01040	PTHR11048,P
1	Phvul.007G006700.1	Phvul.007G006700	Phvul.007G00	PF01040	PTHR11048,P
1	Phvul.007G216500.4	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.3	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.1	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.4	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.3	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.007G216500.1	Phvul.007G216500	Phvul.007G21	PF07786	PTHR31061,P
1	Phvul.008G055300.1	Phvul.008G055300	Phvul.008G05	PF00571	PTHR13780,P
1	Phvul.008G173900.2	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.008G173900.1	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.008G173900.2	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.008G173900.1	Phvul.008G173900	Phvul.008G17	PF13855	PTHR24365,P
1	Phvul.011G132801.1	Phvul.011G132801	Phvul.011G13	0	0
1	Phvul.011G132801.1	Phvul.011G132801	Phvul.011G13	0	0

1	Phvul.011G157600.3	Phvul.011G157600	Phvul.011G15	0	PTHR24067,P
1	Phvul.011G157600.4	Phvul.011G157600	Phvul.011G15	0	PTHR24067,P
1	Phvul.011G157600.2	Phvul.011G157600	Phvul.011G15	0	PTHR24067,P
1	Phvul.011G157600.3	Phvul.011G157600	Phvul.011G15	0	PTHR24067,P
1	Phvul.011G157600.4	Phvul.011G157600	Phvul.011G15	0	PTHR24067,P
1	Phvul.011G157600.2	Phvul.011G157600	Phvul.011G15	0	PTHR24067,P
1	Phvul.001G026200.1	Phvul.001G026200	Phvul.001G02	PF00887	PTHR23310,P
1	Phvul.001G026200.1	Phvul.001G026200	Phvul.001G02	PF00887	PTHR23310,P
1	Phvul.001G141300.1	Phvul.001G141300	Phvul.001G14	PF00076	PTHR24012,P
1	Phvul.001G141300.1	Phvul.001G141300	Phvul.001G14	PF00076	PTHR24012,P
1	Phvul.001G256400.1	Phvul.001G256400	Phvul.001G25	0	PTHR10314,P
1	Phvul.001G256400.1	Phvul.001G256400	Phvul.001G25	0	PTHR10314,P
1	Phvul.001G256600.1	Phvul.001G256600	Phvul.001G25	PF15413,PF01	PTHR10972,P
1	Phvul.001G256600.1	Phvul.001G256600	Phvul.001G25	PF15413,PF01	PTHR10972,P
1	Phvul.002G003600.1	Phvul.002G003600	Phvul.002G00	PF02880,PF00	PTHR22573,P
1	Phvul.002G003600.1	Phvul.002G003600	Phvul.002G00	PF02880,PF00	PTHR22573,P
1	Phvul.002G075900.1	Phvul.002G075900	Phvul.002G07	0	0
1	Phvul.002G075900.1	Phvul.002G075900	Phvul.002G07	0	0
1	Phvul.002G102800.2	Phvul.002G102800	Phvul.002G10	PF00232	PTHR10353,P
1	Phvul.002G102800.2	Phvul.002G102800	Phvul.002G10	PF00232	PTHR10353,P
1	Phvul.002G146600.2	Phvul.002G146600	Phvul.002G14	PF04564	PTHR27003
1	Phvul.002G146600.1	Phvul.002G146600	Phvul.002G14	PF04564	PTHR27003
1	Phvul.002G146600.2	Phvul.002G146600	Phvul.002G14	PF04564	PTHR27003
1	Phvul.002G146600.1	Phvul.002G146600	Phvul.002G14	PF04564	PTHR27003
1	Phvul.002G158200.1	Phvul.002G158200	Phvul.002G15	0	PTHR31798,P
1	Phvul.002G158200.1	Phvul.002G158200	Phvul.002G15	0	PTHR31798,P
1	Phvul.003G013200.2	Phvul.003G013200	Phvul.003G01	PF03171	PTHR10209,P
1	Phvul.003G156333.1	Phvul.003G156333	Phvul.003G15	PF01287	PTHR11673,P
1	Phvul.003G156333.1	Phvul.003G156333	Phvul.003G15	PF01287	PTHR11673,P
1	Phvul.003G179800.1	Phvul.003G179800	Phvul.003G17	0	0
1	Phvul.003G179800.1	Phvul.003G179800	Phvul.003G17	0	0
1	Phvul.003G179800.1	Phvul.003G179800	Phvul.003G17	0	0
1	Phvul.003G261400.2	Phvul.003G261400	Phvul.003G26	PF10018	PTHR13208,P
1	Phvul.003G261400.1	Phvul.003G261400	Phvul.003G26	PF10018	PTHR13208,P
1	Phvul.003G261400.2	Phvul.003G261400	Phvul.003G26	PF10018	PTHR13208,P
1	Phvul.003G261400.1	Phvul.003G261400	Phvul.003G26	PF10018	PTHR13208,P
2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
1	Phvul.004G068900.2	Phvul.004G068900	Phvul.004G06	PF00847	PTHR31677,P
1	Phvul.004G068900.2	Phvul.004G068900	Phvul.004G06	PF00847	PTHR31677,P
1	Phvul.005G069600.1	Phvul.005G069600	Phvul.005G06	PF13771,PF00	PTHR23069,P
1	Phvul.007G157700.1	Phvul.007G157700	Phvul.007G15	PF13041	PTHR24015,P
1	Phvul.007G249600.1	Phvul.007G249600	Phvul.007G24	PF08799,PF00	PTHR19846
1	Phvul.008G111200.1	Phvul.008G111200	Phvul.008G11	PF01612	PTHR13620

1	Phvul.008G111200.1	Phvul.008G111200	Phvul.008G11	PF01612	PTHR13620
1	Phvul.008G230800.1	Phvul.008G230800	Phvul.008G23	PF01535,PF13	PTHR24015
1	Phvul.009G080800.1	Phvul.009G080800	Phvul.009G08	PF02042	PTHR32002
1	Phvul.009G080800.1	Phvul.009G080800	Phvul.009G08	PF02042	PTHR32002
1	Phvul.009G119700.1	Phvul.009G119700	Phvul.009G11	PF00632	PTHR11254,P
1	Phvul.009G119700.1	Phvul.009G119700	Phvul.009G11	PF00632	PTHR11254,P
1	Phvul.010G119500.1	Phvul.010G119500	Phvul.010G11	PF00076	PTHR24012
1	Phvul.011G008600.1	Phvul.011G008600	Phvul.011G00	0	0
1	Phvul.011G008600.1	Phvul.011G008600	Phvul.011G00	0	0
1	Phvul.011G140900.1	Phvul.011G140900	Phvul.011G14	PF12490	PTHR13268,P
1	Phvul.011G140900.1	Phvul.011G140900	Phvul.011G14	PF12490	PTHR13268,P
1	Phvul.011G169222.1	Phvul.011G169222	Phvul.011G16	PF13639	PTHR14155,P
1	Phvul.011G215900.1	Phvul.011G215900	Phvul.011G21	PF01926,PF00	PTHR11566,P
1	Phvul.011G215900.1	Phvul.011G215900	Phvul.011G21	PF01926,PF00	PTHR11566,P
1	Phvul.001G096200.1	Phvul.001G096200	Phvul.001G09	PF12796	PTHR24158,P
1	Phvul.001G104700.2	Phvul.001G104700	Phvul.001G10	PF13906,PF13	PTHR11785,P
1	Phvul.001G104700.1	Phvul.001G104700	Phvul.001G10	PF13906,PF13	PTHR11785,P
1	Phvul.001G104700.2	Phvul.001G104700	Phvul.001G10	PF13906,PF13	PTHR11785,P
1	Phvul.001G104700.1	Phvul.001G104700	Phvul.001G10	PF13906,PF13	PTHR11785,P
1	Phvul.001G211000.1	Phvul.001G211000	Phvul.001G21	PF13632	PTHR13301,P
1	Phvul.001G211000.1	Phvul.001G211000	Phvul.001G21	PF13632	PTHR13301,P
1	Phvul.002G147900.2	Phvul.002G147900	Phvul.002G14	PF01663	PTHR23072,P
1	Phvul.002G147900.1	Phvul.002G147900	Phvul.002G14	PF01663	PTHR23072,P
1	Phvul.002G147900.2	Phvul.002G147900	Phvul.002G14	PF01663	PTHR23072,P
1	Phvul.002G147900.1	Phvul.002G147900	Phvul.002G14	PF01663	PTHR23072,P
1	Phvul.002G182700.2	Phvul.002G182700	Phvul.002G18	PF02746,PF13	PTHR13794,P
1	Phvul.002G182700.1	Phvul.002G182700	Phvul.002G18	PF02746,PF13	PTHR13794,P
1	Phvul.002G202300.1	Phvul.002G202300	Phvul.002G20	PF07800	PTHR31197,P
1	Phvul.002G238000.1	Phvul.002G238000	Phvul.002G23	0	PTHR34669,P
1	Phvul.002G267100.1	Phvul.002G267100	Phvul.002G26	0	PTHR33828,P
1	Phvul.002G267100.1	Phvul.002G267100	Phvul.002G26	0	PTHR33828,P
1	Phvul.002G274400.2	Phvul.002G274400	Phvul.002G27	PF00646	PTHR31370,P
1	Phvul.002G274400.1	Phvul.002G274400	Phvul.002G27	PF00646	PTHR31370,P
1	Phvul.002G274400.2	Phvul.002G274400	Phvul.002G27	PF00646	PTHR31370,P
1	Phvul.002G274400.1	Phvul.002G274400	Phvul.002G27	PF00646	PTHR31370,P
1	Phvul.002G304500.1	Phvul.002G304500	Phvul.002G30	PF07714	PTHR27001,P
1	Phvul.002G327900.1	Phvul.002G327900	Phvul.002G32	PF00462	PTHR10168,P
1	Phvul.002G327900.1	Phvul.002G327900	Phvul.002G32	PF00462	PTHR10168,P
1	Phvul.003G010700.1	Phvul.003G010700	Phvul.003G01	PF00067	PTHR24286,P
1	Phvul.003G023101.2	Phvul.003G023101	Phvul.003G02	PF13906,PF13	PTHR11785,P
1	Phvul.003G023101.1	Phvul.003G023101	Phvul.003G02	PF13906,PF13	PTHR11785,P
1	Phvul.003G044200.1	Phvul.003G044200	Phvul.003G04	PF01536	PTHR11570,P
1	Phvul.003G044200.1	Phvul.003G044200	Phvul.003G04	PF01536	PTHR11570,P
1	Phvul.003G080700.1	Phvul.003G080700	Phvul.003G08	PF03595	PTHR31269,P
1	Phvul.003G090000.2	Phvul.003G090000	Phvul.003G09	PF07714	PTHR27003,P
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1	Phvul.003G113900.1	Phvul.003G113900	Phvul.003G11	0	PTHR36033,P
1	Phvul.003G113900.1	Phvul.003G113900	Phvul.003G11	0	PTHR36033,P
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1	Phvul.003G209900.1	Phvul.003G209900	Phvul.003G20	PF08387	PTHR32212,P
1	Phvul.003G209900.1	Phvul.003G209900	Phvul.003G20	PF08387	PTHR32212,P
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1	Phvul.003G254900.1	Phvul.003G254900	Phvul.003G25	PF00646,PF01	PTHR16517,P
1	Phvul.003G254900.2	Phvul.003G254900	Phvul.003G25	PF00646,PF01	PTHR16517,P
1	Phvul.003G254900.1	Phvul.003G254900	Phvul.003G25	PF00646,PF01	PTHR16517,P
1	Phvul.003G295700.2	Phvul.003G295700	Phvul.003G29	PF01535,PF13	PTHR24015,P
1	Phvul.003G295700.1	Phvul.003G295700	Phvul.003G29	PF01535,PF13	PTHR24015,P
1	Phvul.005G088636.1	Phvul.005G088636	Phvul.005G08	0	0
1	Phvul.005G088636.1	Phvul.005G088636	Phvul.005G08	0	0
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1	Phvul.006G112000.2	Phvul.006G112000	Phvul.006G11	PF01764	PTHR21493,P
1	Phvul.007G015000.1	Phvul.007G015000	Phvul.007G01	PF03634	PTHR31072,P
1	Phvul.007G028800.1	Phvul.007G028800	Phvul.007G02	PF04557,PF03	PTHR11451,P
1	Phvul.007G038000.1	Phvul.007G038000	Phvul.007G03	PF00403	PTHR22814,P
1	Phvul.007G038000.1	Phvul.007G038000	Phvul.007G03	PF00403	PTHR22814,P
1	Phvul.007G062900.1	Phvul.007G062900	Phvul.007G06	PF14306,PF01	PTHR11055,P
1	Phvul.007G062900.1	Phvul.007G062900	Phvul.007G06	PF14306,PF01	PTHR11055,P
1	Phvul.007G100700.1	Phvul.007G100700	Phvul.007G10	PF05512	PTHR33294,P
1	Phvul.007G100700.1	Phvul.007G100700	Phvul.007G10	PF05512	PTHR33294,P
1	Phvul.007G149300.1	Phvul.007G149300	Phvul.007G14	PF10270	PTHR21181
1	Phvul.007G230450.1	Phvul.007G230450	Phvul.007G23	PF07766	PTHR14009,P
1	Phvul.008G046100.1	Phvul.008G046100	Phvul.008G04	PF12854,PF13	PTHR24015,P
1	Phvul.008G177200.1	Phvul.008G177200	Phvul.008G17	0	PTHR35689,P
1	Phvul.008G177200.2	Phvul.008G177200	Phvul.008G17	0	PTHR35689,P
1	Phvul.008G181900.2	Phvul.008G181900	Phvul.008G18	0	PTHR34464
1	Phvul.008G181900.1	Phvul.008G181900	Phvul.008G18	0	PTHR34464
1	Phvul.008G260900.2	Phvul.008G260900	Phvul.008G26	PF00642,PF12	PTHR14493,P
1	Phvul.008G260900.1	Phvul.008G260900	Phvul.008G26	PF00642,PF12	PTHR14493,P
1	Phvul.008G260900.2	Phvul.008G260900	Phvul.008G26	PF00642,PF12	PTHR14493,P
1	Phvul.008G260900.1	Phvul.008G260900	Phvul.008G26	PF00642,PF12	PTHR14493,P
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1	Phvul.009G041100.1	Phvul.009G041100	Phvul.009G04	0	PTHR31789,P
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1	Phvul.009G041100.1	Phvul.009G041100	Phvul.009G04	0	PTHR31789,P
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1	Phvul.009G175100.1	Phvul.009G175100	Phvul.009G17	PF01535,PF13	PTHR24015,P
1	Phvul.009G200500.3	Phvul.009G200500	Phvul.009G20	PF08616	PTHR13677,P
1	Phvul.009G200500.2	Phvul.009G200500	Phvul.009G20	PF08616	PTHR13677,P
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1	Phvul.009G200500.2	Phvul.009G200500	Phvul.009G20	PF08616	PTHR13677,P
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1	Phvul.011G174000.1	Phvul.011G174000	Phvul.011G17	PF13906,PF13	PTHR11785,P
1	Phvul.011G174000.1	Phvul.011G174000	Phvul.011G17	PF13906,PF13	PTHR11785,P
1	Phvul.001G110400.1	Phvul.001G110400	Phvul.001G11	PF04410	PTHR23237
1	Phvul.001G123400.1	Phvul.001G123400	Phvul.001G12	PF05678	PTHR33624,P
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1	Phvul.001G154700.1	Phvul.001G154700	Phvul.001G15	PF00447	PTHR10015,P
1	Phvul.001G179800.1	Phvul.001G179800	Phvul.001G17	PF01535,PF13	PTHR24015,P
1	Phvul.001G179800.1	Phvul.001G179800	Phvul.001G17	PF01535,PF13	PTHR24015,P
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1	Phvul.001G259000.1	Phvul.001G259000	Phvul.001G25	PF00044,PF02	PTHR10836,P
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1	Phvul.002G137100.1	Phvul.002G137100	Phvul.002G13	PF02928,PF02	PTHR10694,P
1	Phvul.002G137200.1	Phvul.002G137200	Phvul.002G13	PF00076	PTHR24012,P
1	Phvul.002G137200.1	Phvul.002G137200	Phvul.002G13	PF00076	PTHR24012,P
1	Phvul.002G139900.2	Phvul.002G139900	Phvul.002G13	PF00076	PTHR24012,P
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1	Phvul.003G252400.1	Phvul.003G252400	Phvul.003G25	PF12171	PTHR10593,P
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1	Phvul.003G265700.1	Phvul.003G265700	Phvul.003G26	0	PTHR34049,P
2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
2	Phvul.003G291600.1	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
2	Phvul.003G291600.2	Phvul.003G291600	Phvul.003G29	PF01039	PTHR22855,P
1	Phvul.004G176100.1	Phvul.004G176100	Phvul.004G17	PF01426,PF00	PTHR10629,P
1	Phvul.005G001500.2	Phvul.005G001500	Phvul.005G00	PF13417	PTHR11260,P
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1	Phvul.005G093400.1	Phvul.005G093400	Phvul.005G09	0	PTHR11017,P
1	Phvul.005G131700.1	Phvul.005G131700	Phvul.005G13	PF00076,PF14	PTHR24012,P
1	Phvul.005G183800.1	Phvul.005G183800	Phvul.005G18	PF01167	PTHR16517,P
1	Phvul.005G183800.2	Phvul.005G183800	Phvul.005G18	PF01167	PTHR16517,P
1	Phvul.006G098700.1	Phvul.006G098700	Phvul.006G09	PF02458	PTHR31642,P
1	Phvul.006G131400.1	Phvul.006G131400	Phvul.006G13	PF11900,PF00	PTHR24413,P
1	Phvul.006G131400.1	Phvul.006G131400	Phvul.006G13	PF11900,PF00	PTHR24413,P
1	Phvul.006G208400.1	Phvul.006G208400	Phvul.006G20	PF00201	PTHR11926,P

1	Phvul.006G208400.1	Phvul.006G208400	Phvul.006G20	PF00201	PTHR11926,P
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1	Phvul.007G043900.2	Phvul.007G043900	Phvul.007G04	PF04484	PTHR31807,P
1	Phvul.007G043900.1	Phvul.007G043900	Phvul.007G04	PF04484	PTHR31807,P
1	Phvul.007G062100.1	Phvul.007G062100	Phvul.007G06	PF00248	PTHR11732,P
1	Phvul.007G067800.1	Phvul.007G067800	Phvul.007G06	PF00447	PTHR10015,P
1	Phvul.007G080900.2	Phvul.007G080900	Phvul.007G08	PF05055	PTHR31113,P
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1	Phvul.007G080900.2	Phvul.007G080900	Phvul.007G08	PF05055	PTHR31113,P
1	Phvul.007G080900.1	Phvul.007G080900	Phvul.007G08	PF05055	PTHR31113,P
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1	Phvul.007G139300.1	Phvul.007G139300	Phvul.007G13	PF00249,PF14	PTHR31499,P
1	Phvul.007G173400.1	Phvul.007G173400	Phvul.007G17	PF04570	PTHR33059,P
1	Phvul.007G246700.1	Phvul.007G246700	Phvul.007G24	PF04043,PF01	PTHR31707,P
1	Phvul.007G274200.1	Phvul.007G274200	Phvul.007G27	PF01248	PTHR23105,P
1	Phvul.007G274200.1	Phvul.007G274200	Phvul.007G27	PF01248	PTHR23105,P
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1	Phvul.008G055500.1	Phvul.008G055500	Phvul.008G05	PF00005	PTHR24220,P
1	Phvul.008G077000.1	Phvul.008G077000	Phvul.008G07	PF03514	PTHR31636,P
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1	Phvul.008G114700.1	Phvul.008G114700	Phvul.008G11	PF03208	PTHR12859
1	Phvul.008G211500.4	Phvul.008G211500	Phvul.008G21	0	PTHR32098,P
1	Phvul.008G211500.3	Phvul.008G211500	Phvul.008G21	0	PTHR32098,P
1	Phvul.008G211500.1	Phvul.008G211500	Phvul.008G21	0	PTHR32098,P
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1	Phvul.008G250000.1	Phvul.008G250000	Phvul.008G25	PF16940	PTHR34935
1	Phvul.008G250000.1	Phvul.008G250000	Phvul.008G25	PF16940	PTHR34935
1	Phvul.009G086300.2	Phvul.009G086300	Phvul.009G08	PF12776	PTHR31704,P
1	Phvul.009G086300.1	Phvul.009G086300	Phvul.009G08	PF12776	PTHR31704,P
1	Phvul.009G086300.2	Phvul.009G086300	Phvul.009G08	PF12776	PTHR31704,P
1	Phvul.009G086300.1	Phvul.009G086300	Phvul.009G08	PF12776	PTHR31704,P
1	Phvul.009G149800.1	Phvul.009G149800	Phvul.009G14	PF00454	PTHR10048,P
1	Phvul.009G154300.6	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G154300.5	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G154300.3	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G154300.4	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G154300.1	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G154300.6	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
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1	Phvul.009G154300.3	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G154300.4	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G154300.1	Phvul.009G154300	Phvul.009G15	PF02146	PTHR11085,P
1	Phvul.009G240100.1	Phvul.009G240100	Phvul.009G24	PF07714	PTHR27001,P
1	Phvul.011G017800.1	Phvul.011G017800	Phvul.011G01	PF12537,PF12	PTHR15948

1	Phvul.011G017800.1	Phvul.011G017800	Phvul.011G01	PF12537,PF12	PTHR15948
1	Phvul.011G100200.2	Phvul.011G100200	Phvul.011G10	0	PTHR34210,P
1	Phvul.011G100200.1	Phvul.011G100200	Phvul.011G10	0	PTHR34210,P
1	Phvul.011G108300.1	Phvul.011G108300	Phvul.011G10	PF14111	0
1	Phvul.011G129700.1	Phvul.011G129700	Phvul.011G12	0	PTHR24006,P
1	Phvul.011G129700.1	Phvul.011G129700	Phvul.011G12	0	PTHR24006,P
1	Phvul.011G140050.2	Phvul.011G140050	Phvul.011G14	PF13041	PTHR24015,P
1	Phvul.011G140050.1	Phvul.011G140050	Phvul.011G14	PF13041	PTHR24015,P

KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
KOG0959	3.4.21.102	0	0	AT5G42390.1	0
0	2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
0	2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
0	2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
0	2.3.1.225	K18932	GO:0008270	AT3G51390.1	0
0	2.7.7.6	0	0	AT2G29540.1	ATRPAC14,AT
0	2.7.7.6	0	0	AT2G29540.1	ATRPAC14,AT
KOG1330	0	0	GO:0055085,	AT5G10190.1	0
KOG1330	0	0	GO:0055085,	AT5G10190.1	0
KOG2462	0	0	0	AT2G01940.1	ATIDD15,SGR
KOG1223	2.2.1.9,4.2.99	K14759	GO:0030976,	AT1G68890.1	0
KOG1223	2.2.1.9,4.2.99	K14759	GO:0030976,	AT1G68890.1	0
KOG1755	0	K05759	0	AT5G56600.1	PFN3,PRF3
KOG1755	0	K05759	0	AT5G56600.1	PFN3,PRF3
KOG4282	0	0	0	AT3G58630.1	0
KOG4759	0	K02838	GO:0006412	AT3G63190.1	AtcpRRF,cpRR
KOG1285	1.13.11.51	0	0	AT3G63520.1	ATCCD1,ATNC
KOG1285	1.13.11.51	0	0	AT3G63520.1	ATCCD1,ATNC
KOG1285	1.13.11.51	0	0	AT3G63520.1	ATCCD1,ATNC
KOG1285	1.13.11.51	0	0	AT3G63520.1	ATCCD1,ATNC
KOG1285	1.13.11.51	0	0	AT3G63520.1	ATCCD1,ATNC
KOG1285	1.13.11.51	0	0	AT3G63520.1	ATCCD1,ATNC
0	3.1.26.3	K11592	GO:0016787,	AT1G01040.1	ASU1,ATDCL1
KOG2352	3.4.24.71	0	GO:0008168,	AT2G31740.1	0
KOG2352	3.4.24.71	0	GO:0008168,	AT2G31740.1	0
0	0	0	0	AT3G29750.1	0
0	0	0	0	AT3G29750.1	0
0	0	K08506	GO:0005515	AT3G09740.1	ATSYP71,SYP7
0	0	0	0	AT3G04470.1	0
0	0	0	0	AT3G04470.1	0
KOG1380	0	K02257	GO:0016021,	AT2G44520.1	COX10
KOG1380	0	K02257	GO:0016021,	AT2G44520.1	COX10
KOG4683	2.3.1.78	K10532	0	AT5G47900.1	0
KOG4683	2.3.1.78	K10532	0	AT5G47900.1	0
KOG4683	2.3.1.78	K10532	0	AT5G47900.1	0
KOG4683	2.3.1.78	K10532	0	AT5G47900.1	0
KOG4683	2.3.1.78	K10532	0	AT5G47900.1	0
KOG4683	2.3.1.78	K10532	0	AT5G47900.1	0
KOG1764	0	0	0	AT1G65320.1	0
0	0	0	GO:0005515	AT1G78230.1	0
0	0	0	GO:0005515	AT1G78230.1	0
0	0	0	GO:0005515	AT1G78230.1	0
0	0	0	GO:0005515	AT1G78230.1	0
0	0	0	0	0	0
0	0	0	0	0	0

0	0	0	0	AT1G53025.1	0
0	0	0	0	AT1G53025.1	0
0	0	0	0	AT1G53025.1	0
0	0	0	0	AT1G53025.1	0
0	0	0	0	AT1G53025.1	0
0	0	0	0	AT1G53025.1	0
KOG0817	0	0	GO:0000062	AT4G24230.6	ACBP3
KOG0817	0	0	GO:0000062	AT4G24230.6	ACBP3
KOG0148,KO	0	K12741	GO:0003676	AT3G15010.2	0
KOG0148,KO	0	K12741	GO:0003676	AT3G15010.2	0
0	4.4.1.15	0	0	AT3G26115.1	0
0	4.4.1.15	0	0	AT3G26115.1	0
0	0	0	0	AT1G13170.1	ORP1D
0	0	0	0	AT1G13170.1	ORP1D
0	5.4.2.3	K01836	GO:0016868,	AT5G18070.1	DRT101
0	5.4.2.3	K01836	GO:0016868,	AT5G18070.1	DRT101
0	0	0	0	AT5G06650.1	GIS2
0	0	0	0	AT5G06650.1	GIS2
0	3.2.1.21	K01188	GO:0005975,	AT1G26560.1	BGLU40
0	3.2.1.21	K01188	GO:0005975,	AT1G26560.1	BGLU40
0	6.3.2.19	0	GO:0016567,	AT5G65500.1	0
0	6.3.2.19	0	GO:0016567,	AT5G65500.1	0
0	6.3.2.19	0	GO:0016567,	AT5G65500.1	0
0	6.3.2.19	0	GO:0016567,	AT5G65500.1	0
0	0	0	0	AT5G52430.1	0
0	0	0	0	AT5G52430.1	0
KOG0143	1.14.11.31	0	GO:0055114,	AT4G25310.1	0
KOG3271	0	K03263	GO:0045905,	AT1G13950.1	ATELF5A-1,EI
KOG3271	0	K03263	GO:0045905,	AT1G13950.1	ATELF5A-1,EI
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	GO:0016592,	AT5G02850.1	0
0	0	0	GO:0016592,	AT5G02850.1	0
0	0	0	GO:0016592,	AT5G02850.1	0
0	0	0	GO:0016592,	AT5G02850.1	0
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	0	K09286	GO:0006355,	AT5G13910.1	LEP
0	0	K09286	GO:0006355,	AT5G13910.1	LEP
0	0	0	GO:0005524	AT3G15120.1	0
0	0	0	0	AT3G53700.1	MEE40
0	0	K12662	GO:0005515	AT2G41500.1	EMB2776,LIS
0	3.6.4.12	0	GO:0008408,	AT4G13870.1	ATWEX,ATWR

0	3.6.4.12	0	GO:0008408,(	AT4G13870.1	ATWEX,ATWR
0	0	0	0	AT2G34400.1	0
0	0	0	0	AT5G16100.1	0
0	0	0	0	AT5G16100.1	0
0	6.3.2.19	K10590	GO:0004842	AT4G38600.1	KAK,UPL3
0	6.3.2.19	K10590	GO:0004842	AT4G38600.1	KAK,UPL3
KOG0131,KOG	0	K13126	GO:0003676	AT1G01080.1	0
0	0	0	0	0	0
0	0	0	0	0	0
KOG2109	0	0	0	AT1G03380.1	ATATG18G,AT
KOG2109	0	0	0	AT1G03380.1	ATATG18G,AT
0	0	0	GO:0008270,(	AT3G05200.1	ATL6
KOG0446	3.6.5.5	K01528	GO:0005525,(	AT1G59610.1	ADL3,CF1,DL3
KOG0446	3.6.5.5	K01528	GO:0005525,(	AT1G59610.1	ADL3,CF1,DL3
KOG0508,KOG	0	0	0	AT5G14230.1	0
KOG1286	0	K13863	GO:0016020,(	AT1G58030.1	CAT2
KOG1286	0	K13863	GO:0016020,(	AT1G58030.1	CAT2
KOG1286	0	K13863	GO:0016020,(	AT1G58030.1	CAT2
KOG1286	0	K13863	GO:0016020,(	AT1G58030.1	CAT2
0	2.4.2.24	K00770	0	AT1G02730.1	ATCSLD5,CSLD
0	2.4.2.24	K00770	0	AT1G02730.1	ATCSLD5,CSLD
KOG2125	0	0	GO:0003824	AT2G22530.1	0
KOG2125	0	0	GO:0003824	AT2G22530.1	0
KOG2125	0	0	GO:0003824	AT2G22530.1	0
KOG2125	0	0	GO:0003824	AT2G22530.1	0
0	0	0	GO:0008152,(	AT3G18270.1	CYP77A5P
0	0	0	GO:0008152,(	AT3G18270.1	CYP77A5P
0	0	0	0	AT1G68140.3	0
0	0	0	0	AT4G28590.1	0
0	0	0	0	AT5G11600.1	0
0	0	0	0	AT5G11600.1	0
0	0	0	GO:0005515	AT5G39450.1	0
0	0	0	GO:0005515	AT5G39450.1	0
0	0	0	GO:0005515	AT5G39450.1	0
0	0	0	GO:0005515	AT5G39450.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G13690.1	0
KOG2824	0	K17479	GO:0045454,(	AT4G10630.1	0
KOG2824	0	K17479	GO:0045454,(	AT4G10630.1	0
0	0	K01723	GO:0055114,(	AT5G42650.1	AOS,CYP74A,D
KOG1286	0	0	GO:0016020,(	AT4G21120.1	AAT1,CAT1
KOG1286	0	0	GO:0016020,(	AT4G21120.1	AAT1,CAT1
KOG0788	4.1.1.50	K01611	GO:0008295,(	AT3G25570.2	0
KOG0788	4.1.1.50	K01611	GO:0008295,(	AT3G25570.2	0
0	0	0	GO:0055085,(	AT1G62280.1	SLAH1
KOG0472	2.7.11.1	0	GO:0006468,(	AT5G49760.1	0
KOG0472	2.7.11.1	0	GO:0006468,(	AT5G49760.1	0

KOG1683	5.1.2.3,1.1.1.3	K10527	GO:0055114,(	AT3G06860.1	ATMFP2,MFP
0	0	0	0	AT3G17030.1	0
0	0	0	0	AT3G17030.1	0
KOG0401	0	K03260	GO:0005515,(	AT5G57870.2	eIFiso4G1
KOG0401	0	K03260	GO:0005515,(	AT5G57870.2	eIFiso4G1
0	0	0	0	AT4G14096.1	0
0	0	0	0	AT4G14096.1	0
KOG2502	0	0	GO:0005515	AT2G18280.2	AtTLP2,TLP2
KOG2502	0	0	GO:0005515	AT2G18280.2	AtTLP2,TLP2
KOG2502	0	0	GO:0005515	AT2G18280.2	AtTLP2,TLP2
KOG2502	0	0	GO:0005515	AT2G18280.2	AtTLP2,TLP2
0	0	0	0	AT4G04790.1	0
0	0	0	0	AT4G04790.1	0
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	GO:0006629	AT1G02660.1	0
0	0	0	GO:0006629	AT1G02660.1	0
0	0	0	0	AT5G23280.1	0
0	6.1.1.18	K01886	GO:0006425,(	AT1G25350.1	OVA9
KOG1603	0	0	GO:0046872,(	AT1G23000.1	0
KOG1603	0	0	GO:0046872,(	AT1G23000.1	0
0	2.7.7.4	K13811	GO:0004781	AT3G22890.1	APS1
0	2.7.7.4	K13811	GO:0004781	AT3G22890.1	APS1
0	0	0	0	AT1G04560.1	0
0	0	0	0	AT1G04560.1	0
0	0	0	0	AT5G03345.1	0
KOG1043	0	0	0	AT3G11560.4	0
0	0	0	0	AT2G44880.1	0
0	0	0	0	AT4G09060.1	0
0	0	0	0	AT4G09060.1	0
0	0	0	0	AT4G38060.2	0
0	0	0	0	AT4G38060.2	0
KOG1595	0	0	GO:0046872	AT5G58620.1	0
KOG1595	0	0	GO:0046872	AT5G58620.1	0
KOG1595	0	0	GO:0046872	AT5G58620.1	0
KOG1595	0	0	GO:0046872	AT5G58620.1	0
0	0	0	0	AT3G54190.1	0
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0	0	0	0	AT3G54190.1	0
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0	0	0	0	AT1G64310.1	0
0	0	0	0	AT1G64310.1	0
0	0	0	0	AT1G64310.1	0
0	0	0	0	AT1G73930.2	0
0	0	0	0	AT1G73930.2	0
0	0	0	0	AT1G73930.2	0

0	0	0	0	AT1G73930.2	0
0	0	0	GO:0043565,(	AT1G08000.2	GATA10
0	0	0	GO:0043565,(	AT1G08000.2	GATA10
KOG1286	0	K03294	GO:0016020,(	AT1G17120.1	CAT8
KOG1286	0	K03294	GO:0016020,(	AT1G17120.1	CAT8
0	0	K11128	GO:0042254,(	AT3G03920.1	0
0	0	0	0	AT2G41180.1	0
0	0	0	0	AT2G41180.1	0
KOG0627	0	K09419	GO:0043565,(	AT3G22830.1	AT-HSFA6B,HS
0	0	0	0	AT5G37570.1	0
0	0	0	0	AT5G37570.1	0
0	0	0	GO:0005515	AT1G03910.1	0
KOG0657	1.2.1.12	K00134	GO:0055114,(	AT3G04120.1	GAPC,GAPC-1
KOG0657	1.2.1.12	K00134	GO:0055114,(	AT3G04120.1	GAPC,GAPC-1
0	0	0	0	AT5G66730.1	0
0	0	0	0	AT5G66730.1	0
0	2.7.1.150	K00921	GO:0005524,(	AT1G71010.1	FAB1C
0	2.7.1.150	K00921	GO:0005524,(	AT1G71010.1	FAB1C
0	1.14.11.27	0	0	AT5G46910.1	0
0	0	0	GO:0003676	0	0
0	0	0	GO:0003676	0	0
0	0	0	GO:0003676	AT5G46840.1	0
0	0	0	GO:0003676	AT5G46840.1	0
0	0	0	0	0	0
0	0	K13947	GO:0055085,(	AT1G70940.1	ATPIN3,PIN3
0	0	K13947	GO:0055085,(	AT1G70940.1	ATPIN3,PIN3
0	0	0	0	AT5G66730.1	0
0	0	0	0	AT5G66730.1	0
0	0	0	0	AT4G35930.1	0
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	6.4.1.4	K01969	0	AT4G34030.1	MCCB
0	2.1.1.37	K00558	GO:0003682	AT1G69770.1	CMT3
0	0	0	GO:0005515	AT4G10000.1	0
0	0	0	GO:0005515	AT4G10000.1	0
KOG1254	2.3.3.8	K01648	0	AT1G60810.1	ACLA-2
KOG1254	2.3.3.8	K01648	0	AT1G60810.1	ACLA-2
KOG4579	0	0	0	AT1G69550.1	0
0	0	0	GO:0003676	0	0
KOG2502	0	0	0	AT1G16070.1	AtTLP8,TLP8
KOG2502	0	0	0	AT1G16070.1	AtTLP8,TLP8
0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
0	0	K14508	GO:0005515	AT5G45110.1	ATNPR3,NPR3
0	0	K14508	GO:0005515	AT5G45110.1	ATNPR3,NPR3
0	2.4.1.273	0	GO:0016758,(	AT2G22590.1	0

0	2.4.1.273	0	GO:0016758,(	AT2G22590.1	0
0	0	0	0	AT1G49890.1	0
0	0	0	0	AT1G49890.1	0
0	0	0	0	AT1G49890.1	0
0	0	0	0	AT1G49890.1	0
KOG1575	1.1.1.317	0	0	AT1G60710.1	ATB2
0	0	K09419	GO:0043565,(	AT5G62020.1	AT-HSFB2A,H
0	0	0	0	AT1G20180.1	0
0	0	0	0	AT1G20180.1	0
0	0	0	0	AT1G20180.1	0
0	0	0	0	AT1G20180.1	0
0	0	0	0	AT3G24120.1	0
0	0	0	0	AT3G24120.1	0
0	0	0	0	AT3G22550.1	0
0	3.1.1.11	K01051	GO:0004857,(	AT4G02330.1	ATPMEPCRB
KOG3166	0	K02936	0	AT3G62870.1	0
KOG3166	0	K02936	0	AT3G62870.1	0
0	3.1.3.16	K18999	0	AT2G33540.1	ATCPL3,CPL3
0	3.6.3.25	0	GO:0016887,(	AT1G65410.1	ATNAP11,NA
0	3.6.3.25	0	GO:0016887,(	AT1G65410.1	ATNAP11,NA
0	0	0	0	AT3G54220.1	SCR,SGR1
KOG4050	0	0	0	AT5G02040.2	PRA1.A1
KOG4050	0	0	0	AT5G02040.2	PRA1.A1
0	5.5.1.19	0	0	AT2G32640.1	0
0	5.5.1.19	0	0	AT2G32640.1	0
0	5.5.1.19	0	0	AT2G32640.1	0
0	5.5.1.19	0	0	AT2G32640.1	0
0	0	0	0	AT1G06950.1	ATTIC110,TIC
0	0	0	0	AT1G06950.1	ATTIC110,TIC
0	0	0	0	AT2G24960.2	0
0	0	0	0	AT2G24960.2	0
0	0	0	0	AT2G24960.2	0
0	0	0	0	AT2G24960.2	0
0	2.7.1.67	K00888	GO:0016773,(	AT5G64070.1	PI-4KBETA1,P
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG2683	3.5.1.98	K11414	GO:0070403	AT5G09230.7	AtSRT2,SRT2
KOG1187	2.7.11.1	0	GO:0006468,(	AT2G18890.1	0
0	0	0	GO:0016020	AT4G27630.2	GTG2

	0	0	0	GO:0016020	AT4G27630.2	GTG2
	0	0	0	0	AT5G22040.2	0
	0	0	0	0	AT5G22040.2	0
	0	0	0	0	0	0
KOG1947		0	0	0	AT2G42620.1	MAX2,ORE9,P
KOG1947		0	0	0	AT2G42620.1	MAX2,ORE9,P
	0	0	0	0	AT4G04790.1	0
	0	0	0	0	AT4G04790.1	0

arabi-defline	ID	Annot_defline	IDENTIFIER	NAME
Insulinase (Peptidase family M16) family	Phvul.002G04	PTHR11851:S	Phvul.002G04	Protein modif
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:S	Phvul.002G11	not assigned.
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:S	Phvul.002G11	not assigned.
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:S	Phvul.002G11	not assigned.
DHHC-type zinc finger family protein	Phvul.002G11	PTHR22883:S	Phvul.002G11	not assigned.
RNApolymerase 14 kDa subunit	Phvul.001G01	PTHR13946:S	Phvul.001G01	RNA biosynth
RNApolymerase 14 kDa subunit	Phvul.001G01	PTHR13946:S	Phvul.001G01	RNA biosynth
Major facilitator superfamily protein	Phvul.002G25	KOG1330 - Su	Phvul.002G25	Solute transp
Major facilitator superfamily protein	Phvul.002G25	KOG1330 - Su	Phvul.002G25	Solute transp
C2H2-like zinc finger protein	Phvul.002G33	PTHR10593:S	Phvul.002G33	RNA biosynth
magnesium ion binding;thiamin pyroph	Phvul.005G02	K14759 - isoc	Phvul.005G02	Coenzyme me
magnesium ion binding;thiamin pyroph	Phvul.005G02	K14759 - isoc	Phvul.005G02	Coenzyme me
profilin 3	Phvul.005G16	K05759 - profi	Phvul.005G16	Cytoskeleton
profilin 3	Phvul.005G16	K05759 - profi	Phvul.005G16	Cytoskeleton
sequence-specific DNA binding transcrip	Phvul.006G17	KOG4282 - Tr	Phvul.006G17	RNA biosynth
ribosome recycling factor, chloroplast p	Phvul.007G17	PTHR20982:S	Phvul.007G17	Protein biosyn
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//	Phvul.009G10	Enzyme classi
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//	Phvul.009G10	Enzyme classi
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//	Phvul.009G10	Enzyme classi
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//	Phvul.009G10	Enzyme classi
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//	Phvul.009G10	Enzyme classi
carotenoid cleavage dioxygenase 1	Phvul.009G10	PTHR10543//	Phvul.009G10	Enzyme classi
dicer-like 1	Phvul.009G26	PTHR14950:S	Phvul.009G26	RNA processi
S-adenosyl-L-methionine-dependent me	Phvul.003G05	PTHR12176:S	Phvul.003G05	not assigned.
S-adenosyl-L-methionine-dependent me	Phvul.003G05	PTHR12176:S	Phvul.003G05	not assigned.
Eukaryotic aspartyl protease family prot	Phvul.004G05	PF13650 - Asp	Phvul.004G05	not assigned.
Eukaryotic aspartyl protease family prot	Phvul.004G05	PF13650 - Asp	Phvul.004G05	not assigned.
syntaxin of plants 71	Phvul.005G13	K08506 - synt	Phvul.005G13	Vesicle traffic
Ankyrin repeat family protein	Phvul.006G10	PTHR12447:S	Phvul.006G10	not assigned.
Ankyrin repeat family protein	Phvul.006G10	PTHR12447:S	Phvul.006G10	not assigned.
cytochrome c oxidase 10	Phvul.007G00	K02257 - prot	Phvul.007G00	not assigned.
cytochrome c oxidase 10	Phvul.007G00	K02257 - prot	Phvul.007G00	not assigned.
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.
Protein of unknown function (DUF1624)	Phvul.007G21	K10532 - hep	Phvul.007G21	not assigned.
Cystathionine beta-synthase (CBS) famil	Phvul.008G05	PTHR13780:S	Phvul.008G05	not assigned.
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:S	Phvul.008G17	not assigned.
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:S	Phvul.008G17	not assigned.
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:S	Phvul.008G17	not assigned.
Outer arm dynein light chain 1 protein	Phvul.008G17	PTHR24365:S	Phvul.008G17	not assigned.
0	0	0	Phvul.011G13	not assigned.
0	0	0	Phvul.011G13	not assigned.

Ubiquitin-conjugating enzyme family pr	Phvul.011G15	PTHR24067:S	Phvul.011G15	not assigned.
Ubiquitin-conjugating enzyme family pr	Phvul.011G15	PTHR24067:S	Phvul.011G15	not assigned.
Ubiquitin-conjugating enzyme family pr	Phvul.011G15	PTHR24067:S	Phvul.011G15	not assigned.
Ubiquitin-conjugating enzyme family pr	Phvul.011G15	PTHR24067:S	Phvul.011G15	not assigned.
Ubiquitin-conjugating enzyme family pr	Phvul.011G15	PTHR24067:S	Phvul.011G15	not assigned.
Ubiquitin-conjugating enzyme family pr	Phvul.011G15	PTHR24067:S	Phvul.011G15	not assigned.
acyl-CoA-binding domain 3	Phvul.001G02	PTHR23310:S	Phvul.001G02	not assigned.
acyl-CoA-binding domain 3	Phvul.001G02	PTHR23310:S	Phvul.001G02	not assigned.
RNA-binding (RRM/RBD/RNP motifs) fa	Phvul.001G14	KOG0148//K	Phvul.001G14	not assigned.
RNA-binding (RRM/RBD/RNP motifs) fa	Phvul.001G14	KOG0148//K	Phvul.001G14	not assigned.
Pyridoxal-5\'-phosphate-dependent enz	Phvul.001G25	PTHR10314//	Phvul.001G25	not assigned.
Pyridoxal-5\'-phosphate-dependent enz	Phvul.001G25	PTHR10314//	Phvul.001G25	not assigned.
OSBP(oxysterol binding protein)-related	Phvul.001G25	PTHR10972:S	Phvul.001G25	not assigned.
OSBP(oxysterol binding protein)-related	Phvul.001G25	PTHR10972:S	Phvul.001G25	not assigned.
phosphoglucosamine mutase-related	Phvul.002G00	5.4.2.3 - Phos	Phvul.002G00	Carbohydrate
phosphoglucosamine mutase-related	Phvul.002G00	5.4.2.3 - Phos	Phvul.002G00	Carbohydrate
C2H2 and C2HC zinc fingers superfamily	0	0	Phvul.002G07	RNA biosynth
C2H2 and C2HC zinc fingers superfamily	0	0	Phvul.002G07	RNA biosynth
beta glucosidase 40	Phvul.002G10	PTHR10353:S	Phvul.002G10	Enzyme classi
beta glucosidase 40	Phvul.002G10	PTHR10353:S	Phvul.002G10	Enzyme classi
U-box domain-containing protein kinase	Phvul.002G14	PTHR27003:S	Phvul.002G14	not assigned.
U-box domain-containing protein kinase	Phvul.002G14	PTHR27003:S	Phvul.002G14	not assigned.
U-box domain-containing protein kinase	Phvul.002G14	PTHR27003:S	Phvul.002G14	not assigned.
U-box domain-containing protein kinase	Phvul.002G14	PTHR27003:S	Phvul.002G14	not assigned.
hydroxyproline-rich glycoprotein family	0	0	Phvul.002G15	not assigned.
hydroxyproline-rich glycoprotein family	0	0	Phvul.002G15	not assigned.
2-oxoglutarate (2OG) and Fe(II)-depend	Phvul.003G01	PTHR10209:S	Phvul.003G01	Enzyme classi
eukaryotic elongation factor 5A-1	Phvul.003G15	K03263 - tran	Phvul.003G15	Protein biosy
eukaryotic elongation factor 5A-1	Phvul.003G15	K03263 - tran	Phvul.003G15	Protein biosy
0	0	0	Phvul.003G17	not assigned.
0	0	0	Phvul.003G17	not assigned.
0	0	0	Phvul.003G17	not assigned.
hydroxyproline-rich glycoprotein family	Phvul.003G26	PTHR13208 -	Phvul.003G26	RNA biosynth
hydroxyproline-rich glycoprotein family	Phvul.003G26	PTHR13208 -	Phvul.003G26	RNA biosynth
hydroxyproline-rich glycoprotein family	Phvul.003G26	PTHR13208 -	Phvul.003G26	RNA biosynth
hydroxyproline-rich glycoprotein family	Phvul.003G26	PTHR13208 -	Phvul.003G26	RNA biosynth
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-m	Phvul.003G29	Amino acid m
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-m	Phvul.003G29	Amino acid m
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-m	Phvul.003G29	Amino acid m
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-m	Phvul.003G29	Amino acid m
Integrase-type DNA-binding superfamily	Phvul.004G06	PTHR31677:S	Phvul.004G06	RNA biosynth
Integrase-type DNA-binding superfamily	Phvul.004G06	PTHR31677:S	Phvul.004G06	RNA biosynth
P-loop containing nucleoside triphospha	Phvul.005G06	PTHR23069//	Phvul.005G06	DNA damage
Pentatricopeptide repeat (PPR) superfa	Phvul.007G15	PF13041 - PP	Phvul.007G15	not assigned.
WD-40 repeat family protein / small nuc	Phvul.007G24	K12662 - U4/	Phvul.007G24	RNA processi
Werner syndrome-like exonuclease	Phvul.008G11	PTHR13620 -	Phvul.008G11	not assigned.

Werner syndrome-like exonuclease	Phvul.008G11	PTHR13620 -	Phvul.008G11	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G23	PF01535//PF1	Phvul.008G23	not assigned.a
0	Phvul.009G08	PF02042 - RW	Phvul.009G08	not assigned.r
0	Phvul.009G08	PF02042 - RW	Phvul.009G08	not assigned.r
HEAT repeat ;HECT-domain (ubiquitin-tr	Phvul.009G11	PTHR11254:S	Phvul.009G11	Protein home
HEAT repeat ;HECT-domain (ubiquitin-tr	Phvul.009G11	PTHR11254:S	Phvul.009G11	Protein home
RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.010G11	KOG0131//KC	Phvul.010G11	not assigned.a
0	0	0	Phvul.011G00	not assigned.r
0	0	0	Phvul.011G00	not assigned.r
homolog of yeast autophagy 18 (ATG18)	Phvul.011G14	PTHR13268:S	Phvul.011G14	Protein home
homolog of yeast autophagy 18 (ATG18)	Phvul.011G14	PTHR13268:S	Phvul.011G14	Protein home
RING/U-box superfamily protein	Phvul.011G16	PTHR14155:S	Phvul.011G16	not assigned.r
dynamin-like 3	Phvul.011G21	PTHR11566//	Phvul.011G21	Vesicle traffic
dynamin-like 3	Phvul.011G21	PTHR11566//	Phvul.011G21	Vesicle traffic
0	Phvul.001G09	KOG0508//KC	Phvul.001G09	not assigned.r
cationic amino acid transporter 2	Phvul.001G10	K13863 - solu	Phvul.001G10	Solute transp
cationic amino acid transporter 2	Phvul.001G10	K13863 - solu	Phvul.001G10	Solute transp
cationic amino acid transporter 2	Phvul.001G10	K13863 - solu	Phvul.001G10	Solute transp
cationic amino acid transporter 2	Phvul.001G10	K13863 - solu	Phvul.001G10	Solute transp
cellulose synthase-like D5	Phvul.001G21	K00770 - 1,4-	Phvul.001G21	Cell wall orga
cellulose synthase-like D5	Phvul.001G21	K00770 - 1,4-	Phvul.001G21	Cell wall orga
Alkaline-phosphatase-like family protein	Phvul.002G14	K05310 - etha	Phvul.002G14	not assigned.r
Alkaline-phosphatase-like family protein	Phvul.002G14	K05310 - etha	Phvul.002G14	not assigned.r
Alkaline-phosphatase-like family protein	Phvul.002G14	K05310 - etha	Phvul.002G14	not assigned.r
Alkaline-phosphatase-like family protein	Phvul.002G14	K05310 - etha	Phvul.002G14	not assigned.r
cytochrome P450, family 77, subfamily	Phvul.002G18	PTHR13794 -	Phvul.002G18	not assigned.a
cytochrome P450, family 77, subfamily	Phvul.002G18	PTHR13794 -	Phvul.002G18	not assigned.a
Protein of unknown function (DUF1644)	Phvul.002G20	PF07800 - Pro	Phvul.002G20	not assigned.r
0	0	0	Phvul.002G23	not assigned.a
0	0	0	Phvul.002G26	not assigned.r
0	0	0	Phvul.002G26	not assigned.r
F-box family protein	Phvul.002G27	PF00646 - F-b	Phvul.002G27	not assigned.a
F-box family protein	Phvul.002G27	PF00646 - F-b	Phvul.002G27	not assigned.a
F-box family protein	Phvul.002G27	PF00646 - F-b	Phvul.002G27	not assigned.a
F-box family protein	Phvul.002G27	PF00646 - F-b	Phvul.002G27	not assigned.a
Protein kinase protein with adenine nuc	Phvul.002G30	2.7.11.1 - Non	Phvul.002G30	Protein modif
Glutaredoxin family protein	Phvul.002G32	PTHR10168:S	Phvul.002G32	not assigned.a
Glutaredoxin family protein	Phvul.002G32	PTHR10168:S	Phvul.002G32	not assigned.a
allene oxide synthase	Phvul.003G01	K01723 - hydr	Phvul.003G01	Phytohormon
amino acid transporter 1	Phvul.003G02	PTHR11785:S	Phvul.003G02	Solute transp
amino acid transporter 1	Phvul.003G02	PTHR11785:S	Phvul.003G02	Solute transp
Adenosylmethionine decarboxylase fam	Phvul.003G04	4.1.1.50 - Ade	Phvul.003G04	Polyamine me
Adenosylmethionine decarboxylase fam	Phvul.003G04	4.1.1.50 - Ade	Phvul.003G04	Polyamine me
SLAC1 homologue 1	Phvul.003G08	PF03595 - Vol	Phvul.003G08	Solute transp
Leucine-rich repeat protein kinase famil	Phvul.003G09	PTHR27003:S	Phvul.003G09	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.003G09	PTHR27003:S	Phvul.003G09	Protein modif

multifunctional protein 2	Phvul.003G09	1.1.1.35//4.2.	Phvul.003G09	Lipid metaboli
Nucleic acid-binding proteins superfamil	Phvul.003G11	PTHR36033:S	Phvul.003G11	not assigned.n
Nucleic acid-binding proteins superfamil	Phvul.003G11	PTHR36033:S	Phvul.003G11	not assigned.n
MIF4G domain-containing protein / MA	Phvul.003G15	PTHR23253//	Phvul.003G15	Protein biosyn
MIF4G domain-containing protein / MA	Phvul.003G15	PTHR23253//	Phvul.003G15	Protein biosyn
F-box/RNI-like superfamily protein	Phvul.003G20	PF08387 - FB	Phvul.003G20	not assigned.n
F-box/RNI-like superfamily protein	Phvul.003G20	PF08387 - FB	Phvul.003G20	not assigned.n
tubby like protein 2	Phvul.003G25	PTHR16517:S	Phvul.003G25	RNA biosynth
tubby like protein 2	Phvul.003G25	PTHR16517:S	Phvul.003G25	RNA biosynth
tubby like protein 2	Phvul.003G25	PTHR16517:S	Phvul.003G25	RNA biosynth
tubby like protein 2	Phvul.003G25	PTHR16517:S	Phvul.003G25	RNA biosynth
Tetratricopeptide repeat (TPR)-like supe	Phvul.003G29	PF01535//PF1	Phvul.003G29	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.003G29	PF01535//PF1	Phvul.003G29	not assigned.a
0	0	0	Phvul.005G08	not assigned.a
0	0	0	Phvul.005G08	not assigned.a
alpha/beta-Hydrolases superfamily prot	Phvul.006G11	PTHR21493//	Phvul.006G11	Lipid metaboli
alpha/beta-Hydrolases superfamily prot	Phvul.006G11	PTHR21493//	Phvul.006G11	Lipid metaboli
TCP family transcription factor	Phvul.007G01	PTHR31072:S	Phvul.007G01	Multi-process
glutamine-tRNA ligase, putative / glutam	Phvul.007G02	6.1.1.18 - Glut	Phvul.007G02	Protein biosyn
Heavy metal transport/detoxification su	Phvul.007G03	PTHR22814//	Phvul.007G03	not assigned.a
Heavy metal transport/detoxification su	Phvul.007G03	PTHR22814//	Phvul.007G03	not assigned.a
ATP sulfurylase 1	Phvul.007G06	2.7.7.4 - Sulfa	Phvul.007G06	Nutrient uptak
ATP sulfurylase 1	Phvul.007G06	2.7.7.4 - Sulfa	Phvul.007G06	Nutrient uptak
AWPM-19-like family protein	Phvul.007G10	PTHR33294:S	Phvul.007G10	not assigned.a
AWPM-19-like family protein	Phvul.007G10	PTHR33294:S	Phvul.007G10	not assigned.a
0	Phvul.007G14	PF10270 - Me	Phvul.007G14	Solute transpo
LETM1-like protein	Phvul.007G23	PTHR14009:S	Phvul.007G23	not assigned.n
Pentatricopeptide repeat (PPR-like) supe	Phvul.008G04	PF01535//PF1	Phvul.008G04	RNA processin
0	Phvul.008G17	PTHR35689:S	Phvul.008G17	not assigned.n
0	Phvul.008G17	PTHR35689:S	Phvul.008G17	not assigned.n
0	0	0	Phvul.008G18	not assigned.n
0	0	0	Phvul.008G18	not assigned.n
zinc finger (CCCH-type) family protein	Phvul.008G26	PTHR14493:S	Phvul.008G26	RNA processin
zinc finger (CCCH-type) family protein	Phvul.008G26	PTHR14493:S	Phvul.008G26	RNA processin
zinc finger (CCCH-type) family protein	Phvul.008G26	PTHR14493:S	Phvul.008G26	RNA processin
zinc finger (CCCH-type) family protein	Phvul.008G26	PTHR14493:S	Phvul.008G26	RNA processin
Transducin/WD40 repeat-like superfami	0	0	Phvul.009G04	not assigned.n
Transducin/WD40 repeat-like superfami	0	0	Phvul.009G04	not assigned.n
Transducin/WD40 repeat-like superfami	0	0	Phvul.009G04	not assigned.n
Transducin/WD40 repeat-like superfami	0	0	Phvul.009G04	not assigned.n
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G17	PF01535//PF1	Phvul.009G17	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G17	PF01535//PF1	Phvul.009G17	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G17	PF01535//PF1	Phvul.009G17	not assigned.a
0	Phvul.009G20	PTHR13677:S	Phvul.009G20	not assigned.n
0	Phvul.009G20	PTHR13677:S	Phvul.009G20	not assigned.n
0	Phvul.009G20	PTHR13677:S	Phvul.009G20	not assigned.n

0	Phvul.009G20	PTHR13677:SI	Phvul.009G20	not assigned.r
GATA transcription factor 10	Phvul.011G08	PTHR10071:SI	Phvul.011G08	RNA biosynthe
GATA transcription factor 10	Phvul.011G08	PTHR10071:SI	Phvul.011G08	RNA biosynthe
cationic amino acid transporter 8	Phvul.011G17	PTHR11785:SI	Phvul.011G17	Solute transpo
cationic amino acid transporter 8	Phvul.011G17	PTHR11785:SI	Phvul.011G17	Solute transpo
H/ACA ribonucleoprotein complex, subu	Phvul.001G11	K11128 - H/A(	Phvul.001G11	Protein biosyr
VQ motif-containing protein	Phvul.001G12	PTHR33624:SI	Phvul.001G12	External stimu
VQ motif-containing protein	Phvul.001G12	PTHR33624:SI	Phvul.001G12	External stimu
heat shock transcription factor A6B	Phvul.001G15	PTHR10015//I	Phvul.001G15	RNA biosynthe
Pentatricopeptide repeat (PPR-like) supe	Phvul.001G17	PF01535//PF1	Phvul.001G17	not assigned.a
Pentatricopeptide repeat (PPR-like) supe	Phvul.001G17	PF01535//PF1	Phvul.001G17	not assigned.a
0	Phvul.001G18	PTHR21737:SI	Phvul.001G18	not assigned.a
glyceraldehyde-3-phosphate dehydroge	Phvul.001G25	PTHR10836:SI	Phvul.001G25	Cellular respir
glyceraldehyde-3-phosphate dehydroge	Phvul.001G25	PTHR10836:SI	Phvul.001G25	Cellular respir
C2H2-like zinc finger protein	Phvul.002G02	PTHR10593:SI	Phvul.002G02	RNA biosynthe
C2H2-like zinc finger protein	Phvul.002G02	PTHR10593:SI	Phvul.002G02	RNA biosynthe
FORMS APLOID AND BINUCLEATE CELLS	Phvul.002G09	PTHR11353:SI	Phvul.002G09	Multi-process
FORMS APLOID AND BINUCLEATE CELLS	Phvul.002G09	PTHR11353:SI	Phvul.002G09	Multi-process
Transcription factor jumonji (jmj) family	Phvul.002G13	PTHR10694:SI	Phvul.002G13	RNA biosynthe
0	Phvul.002G13	PF00076 - RN/	Phvul.002G13	not assigned.r
0	Phvul.002G13	PF00076 - RN/	Phvul.002G13	not assigned.r
RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.002G13	K14837 - nucl	Phvul.002G13	not assigned.r
RNA-binding (RRM/RBD/RNP motifs) fan	Phvul.002G13	K14837 - nucl	Phvul.002G13	not assigned.r
0	Phvul.002G15	PF14111 - Dor	Phvul.002G15	not assigned.r
Auxin efflux carrier family protein	Phvul.003G03	K13947 - auxi	Phvul.003G03	Solute transpo
Auxin efflux carrier family protein	Phvul.003G03	K13947 - auxi	Phvul.003G03	Solute transpo
C2H2-like zinc finger protein	Phvul.003G25	PTHR10593:SI	Phvul.003G25	RNA biosynthe
C2H2-like zinc finger protein	Phvul.003G25	PTHR10593:SI	Phvul.003G25	RNA biosynthe
F-box family protein	0	0	Phvul.003G26	not assigned.a
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-me	Phvul.003G29	Amino acid me
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-me	Phvul.003G29	Amino acid me
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-me	Phvul.003G29	Amino acid me
3-methylcrotonyl-CoA carboxylase	Phvul.003G29	K01969 - 3-me	Phvul.003G29	Amino acid me
chromomethylase 3	Phvul.004G17	PTHR10629:SI	Phvul.004G17	Chromatin org
Thioredoxin family protein	Phvul.005G00	PTHR11260:SI	Phvul.005G00	not assigned.r
Thioredoxin family protein	Phvul.005G00	PTHR11260:SI	Phvul.005G00	not assigned.r
ATP-citrate lyase A-2	Phvul.005G04	KOG1254 - AT	Phvul.005G04	Lipid metaboli
ATP-citrate lyase A-2	Phvul.005G04	KOG1254 - AT	Phvul.005G04	Lipid metaboli
disease resistance protein (TIR-NBS-LRR	Phvul.005G09	PTHR11017//I	Phvul.005G09	not assigned.a
0	Phvul.005G13	PF00076//PF1	Phvul.005G13	not assigned.r
tubby like protein 8	Phvul.005G18	PTHR16517:SI	Phvul.005G18	RNA biosynthe
tubby like protein 8	Phvul.005G18	PTHR16517:SI	Phvul.005G18	RNA biosynthe
HXXXD-type acyl-transferase family prot	Phvul.006G09	PTHR31642:SI	Phvul.006G09	Enzyme classif
NPR1-like protein 3	Phvul.006G13	PTHR24413:SI	Phvul.006G13	Phytohormon
NPR1-like protein 3	Phvul.006G13	PTHR24413:SI	Phvul.006G13	Phytohormon
UDP-Glycosyltransferase superfamily pr	Phvul.006G20	PTHR11926//I	Phvul.006G20	Enzyme classif

UDP-Glycosyltransferase superfamily pr	Phvul.006G20	PTHR11926//	Phvul.006G20	Enzyme classi
Family of unknown function (DUF566)	Phvul.007G04	PTHR31807:S	Phvul.007G04	not assigned.
Family of unknown function (DUF566)	Phvul.007G04	PTHR31807:S	Phvul.007G04	not assigned.
Family of unknown function (DUF566)	Phvul.007G04	PTHR31807:S	Phvul.007G04	not assigned.
Family of unknown function (DUF566)	Phvul.007G04	PTHR31807:S	Phvul.007G04	not assigned.
NAD(P)-linked oxidoreductase superfam	Phvul.007G06	PTHR11732//	Phvul.007G06	Enzyme classi
heat shock transcription factor B2A	Phvul.007G06	PTHR10015:S	Phvul.007G06	RNA biosynth
Protein of unknown function (DUF677)	Phvul.007G08	PF05055 - Pro	Phvul.007G08	not assigned.
Protein of unknown function (DUF677)	Phvul.007G08	PF05055 - Pro	Phvul.007G08	not assigned.
Protein of unknown function (DUF677)	Phvul.007G08	PF05055 - Pro	Phvul.007G08	not assigned.
Protein of unknown function (DUF677)	Phvul.007G08	PF05055 - Pro	Phvul.007G08	not assigned.
Homeodomain-like superfamily protein	Phvul.007G13	PTHR31499:S	Phvul.007G13	RNA biosynth
Homeodomain-like superfamily protein	Phvul.007G13	PTHR31499:S	Phvul.007G13	RNA biosynth
Protein of unknown function (DUF581)	Phvul.007G17	PF04570 - zin	Phvul.007G17	Multi-process
Plant invertase/pectin methylesterase i	Phvul.007G24	PTHR31707:S	Phvul.007G24	Cell wall orga
Ribosomal protein L7Ae/L30e/S12e/Gad	Phvul.007G27	K02936 - larg	Phvul.007G27	Protein biosy
Ribosomal protein L7Ae/L30e/S12e/Gad	Phvul.007G27	K02936 - larg	Phvul.007G27	Protein biosy
C-terminal domain phosphatase-like 3	Phvul.008G01	PTHR23081:S	Phvul.008G01	Protein modif
non-intrinsic ABC protein 11	Phvul.008G05	PTHR24220:S	Phvul.008G05	Lipid metabol
non-intrinsic ABC protein 11	Phvul.008G05	PTHR24220:S	Phvul.008G05	Lipid metabol
GRAS family transcription factor	Phvul.008G07	PTHR31636:S	Phvul.008G07	External stimu
prenylated RAB acceptor 1.A1	Phvul.008G11	PTHR12859 -	Phvul.008G11	Vesicle traffic
prenylated RAB acceptor 1.A1	Phvul.008G11	PTHR12859 -	Phvul.008G11	Vesicle traffic
Lycopene beta/epsilon cyclase protein	Phvul.008G21	PTHR32098:S	Phvul.008G21	not assigned.
Lycopene beta/epsilon cyclase protein	Phvul.008G21	PTHR32098:S	Phvul.008G21	not assigned.
Lycopene beta/epsilon cyclase protein	Phvul.008G21	PTHR32098:S	Phvul.008G21	not assigned.
Lycopene beta/epsilon cyclase protein	Phvul.008G21	PTHR32098:S	Phvul.008G21	not assigned.
translocon at the inner envelope memb	Phvul.008G25	PF16940 - Chl	Phvul.008G25	Protein transl
translocon at the inner envelope memb	Phvul.008G25	PF16940 - Chl	Phvul.008G25	Protein transl
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.
phosphatidylinositol 4-OH kinase beta1	Phvul.009G14	K00888 - phos	Phvul.009G14	Multi-process
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
sirtuin 2	Phvul.009G15	PTHR11085:S	Phvul.009G15	Protein modif
Protein kinase superfamily protein	Phvul.009G24	2.7.11.1 - Non	Phvul.009G24	Multi-process
GPCR-type G protein 2	Phvul.011G01	PTHR15948 -	Phvul.011G01	External stimu

GPCR-type G protein 2	Phvul.011G01	PTHR15948 -	Phvul.011G01	External stim
0	0	0	Phvul.011G10	not assigned.
0	0	0	Phvul.011G10	not assigned.
0	Phvul.011G10	PF14111 - Do	Phvul.011G10	not assigned.
RNI-like superfamily protein	Phvul.011G12	PTHR24006:S	Phvul.011G12	Phytohormon
RNI-like superfamily protein	Phvul.011G12	PTHR24006:S	Phvul.011G12	Phytohormon
Tetratricopeptide repeat (TPR)-like supe	Phvul.011G14	PF13041 - PP	Phvul.011G14	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.011G14	PF13041 - PP	Phvul.011G14	not assigned.

DESCRIPTION
stromal processing peptidase (SPP) (original description: pacid=37176362 transcript=Phvul.002G04
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subunit 11 of RNA polymerase (original description: pacid=37169148 transcript=Phvul.001G01645
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C2H2 zinc finger transcription factor (original description: pacid=37177813 transcript=Phvul.002G3
multifunctional phylloquinone biosynthesis protein (PHYLLO) (original description: pacid=3715411
multifunctional phylloquinone biosynthesis protein (PHYLLO) (original description: pacid=3715411
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transcription factor (Trihelix) (original description: pacid=37173860 transcript=Phvul.006G176000.
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Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) &
Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) &
Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) &
Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) &
Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) &
Carotenoid 9,10(9,10)-cleavage dioxygenase 1 OS=Pisum sativum (sp|q8lp17|ccd1_pea : 232.0) &
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N-acetylglucosamine-phosphate mutase (original description: pacid=37177997 transcript=Phvul.00
N-acetylglucosamine-phosphate mutase (original description: pacid=37177997 transcript=Phvul.00
C2H2 zinc finger transcription factor (original description: pacid=37177254 transcript=Phvul.002G0
C2H2 zinc finger transcription factor (original description: pacid=37177254 transcript=Phvul.002G0
Beta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0|bgl40_arath : 833.0) & Enzyme classificati
Beta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0|bgl40_arath : 833.0) & Enzyme classificati
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Probable 2-oxoglutarate/Fe(II)-dependent dioxygenase OS=Papaver somniferum (sp|d4n501|diox
poly-P/G elongation factor (eEF5/eIF5A) (original description: pacid=37147810 transcript=Phvul.00
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component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
component MED4 of middle module of MEDIATOR transcription co-activator complex (original des
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
transcription factor (ERF) (original description: pacid=37161639 transcript=Phvul.004G068900.2 lo
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component BRCA1|BARD1 of BRCA1,ÄìBARD1 DNA-damage response heterodimer (original descri
(original description: pacid=37166946 transcript=Phvul.007G157700.1 locus=Phvul.007G157700 ID
protein factor PRPF4 of U4/U6 small nuclear ribonucleoprotein particle (snRNP) (original descriptio
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monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37148701 transcript=Phvul.009G

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component ATG18 of autophagosome ATG9-2-18 membrane shuttling complex (original descriptio

component ATG18 of autophagosome ATG9-2-18 membrane shuttling complex (original descriptio

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DRP2-type clathrin coated vesicle dynamin (original description: pacid=37156922 transcript=Phvul.

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cationic amino acid transporter (CAT) (original description: pacid=37167733 transcript=Phvul.001G

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mannan synthase (CSLD) (original description: pacid=37168697 transcript=Phvul.001G211000.1 loc

mannan synthase (CSLD) (original description: pacid=37168697 transcript=Phvul.001G211000.1 loc

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allene oxidase synthase (AOS) (original description: pacid=37146668 transcript=Phvul.003G010700

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S-adenosyl methionine decarboxylase (original description: pacid=37148102 transcript=Phvul.003G

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protein kinase (LRR-VIII-1) (original description: pacid=37148128 transcript=Phvul.003G090000.2 lo

protein kinase (LRR-VIII-1) (original description: pacid=37148128 transcript=Phvul.003G090000.2 lo

multifunctional enzyme (MFP) (original description: pacid=37146564 transcript=Phvul.003G09650
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magnesium cation transporter (MMgT) (original description: pacid=37164628 transcript=Phvul.007
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NAD-dependent glyceraldehyde 3-phosphate dehydrogenase (original description: pacid=3717044
NAD-dependent glyceraldehyde 3-phosphate dehydrogenase (original description: pacid=3717044
C2H2 zinc finger transcription factor (original description: pacid=37177695 transcript=Phvul.002G0
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phosphatidylinositol 3-phosphate 5-kinase (FAB1) (original description: pacid=37176675 transcript
phosphatidylinositol 3-phosphate 5-kinase (FAB1) (original description: pacid=37176675 transcript
transcription factor (JUMONJI) (original description: pacid=37177660 transcript=Phvul.002G1371
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auxin efflux transporter (PIN) (original description: pacid=37146616 transcript=Phvul.003G032500.
auxin efflux transporter (PIN) (original description: pacid=37146616 transcript=Phvul.003G032500.
C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript=Phvul.003G2
C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript=Phvul.003G2
(original description: pacid=37144586 transcript=Phvul.003G265700.1 locus=Phvul.003G265700 ID
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
subunit beta of methylcrotonoyl-CoA carboxylase complex (original description: pacid=37146169 t
DNA chromomethylase (CMT) (original description: pacid=37163557 transcript=Phvul.004G176100
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alpha chain of ATP-dependent citrate lyase complex (original description: pacid=37153149 transcri
alpha chain of ATP-dependent citrate lyase complex (original description: pacid=37153149 transcri
(original description: pacid=37153683 transcript=Phvul.005G093400.1 locus=Phvul.005G093400 ID
no hits & (original description: pacid=37153235 transcript=Phvul.005G131700.1 locus=Phvul.005G
transcription factor (TUB) (original description: pacid=37154406 transcript=Phvul.005G183800.2 lo
transcription factor (TUB) (original description: pacid=37154406 transcript=Phvul.005G183800.2 lo
Benzyl alcohol O-benzoyltransferase OS=Nicotiana tabacum (sp|q8gt20|bebt_tobac : 533.0) & Enz
receptor protein (NPR3|4) (original description: pacid=37172197 transcript=Phvul.006G131400.1 l
receptor protein (NPR3|4) (original description: pacid=37172197 transcript=Phvul.006G131400.1 l
Soyasaponin III rhamnosyltransferase OS=Glycine max (sp|d4q9z5|sgt3_soybn : 536.0) & Enzyme c

Soyasaponin III rhamnosyltransferase OS=Glycine max (sp|d4q9z5|sgt3_soybn : 536.0) & Enzyme c

(original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 I

(original description: pacid=37165774 transcript=Phvul.007G043900.2 locus=Phvul.007G043900 I

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Perakine reductase OS=Rauvolfia serpentina (sp|q3l181|perr_rause : 490.0) & Enzyme classificatio

transcription factor (HSF) (original description: pacid=37167531 transcript=Phvul.007G067800.1 lo

(original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 I

(original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 I

(original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 I

(original description: pacid=37167319 transcript=Phvul.007G080900.2 locus=Phvul.007G080900 I

G2-like GARP transcription factor (original description: pacid=37166422 transcript=Phvul.007G139

G2-like GARP transcription factor (original description: pacid=37166422 transcript=Phvul.007G139

SnRK1-interacting factor (FLZ) (original description: pacid=37167409 transcript=Phvul.007G173400

pectin methylesterase (original description: pacid=37164403 transcript=Phvul.007G246700.1 locus

component RPL7a of LSU proteome component (original description: pacid=37165435 transcript=P

component RPL7a of LSU proteome component (original description: pacid=37165435 transcript=P

subcluster H/CPL3-4 phosphatase (original description: pacid=37159302 transcript=Phvul.008G019

ATPase component TGD3 of TGD lipid importer complex (original description: pacid=37160544 tra

ATPase component TGD3 of TGD lipid importer complex (original description: pacid=37160544 tra

SCR gravity signalling transcription factor (original description: pacid=37158083 transcript=Phvul.0

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A-class Rab-GDF protein (original description: pacid=37160643 transcript=Phvul.008G114700.1 loc

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component Tic110 of inner envelope TIC translocation system (original description: pacid=371599

component Tic110 of inner envelope TIC translocation system (original description: pacid=371599

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(original description: pacid=37149910 transcript=Phvul.009G086300.2 locus=Phvul.009G086300 I

phosphatidylinositol 4-kinase (PI4K-beta) (original description: pacid=37149528 transcript=Phvul.0

sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G15430

sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G15430

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sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G15430

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sirtuin-type lysine deacetylase (original description: pacid=37150532 transcript=Phvul.009G15430

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GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37152122 transcript=Phvu

cold sensor (COLD1) (original description: pacid=37156295 transcript=Phvul.011G017800.1 locus=P cold sensor (COLD1) (original description: pacid=37156295 transcript=Phvul.011G017800.1 locus=

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MAX2 strigolactone signal transducer (original description: pacid=37155383 transcript=Phvul.011G

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1 locus=Phvul.006G176000 ID=Phvul.006G176000.1.v2.1 annot-version=v2.1) &

07G172400.1 locus=Phvul.007G172400 ID=Phvul.007G172400.1.v2.1 annot-version=v2.1) &

Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxidoreductase acting on single donor with in

Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxidoreductase acting on single donor with in

Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxidoreductase acting on single donor with in

Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxidoreductase acting on single donor with in

Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxidoreductase acting on single donor with in

Enzyme classification.EC_1 oxidoreductases.EC_1.13 oxidoreductase acting on single donor with in

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173900 ID=Phvul.008G173900.2.v2.1 annot-version=v2.1)

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D=Phvul.001G256400.1.v2.1 annot-version=v2.1) & D-cysteine desulfhydrase 2, mitochondrial OS=A

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2G003600.1 locus=Phvul.002G003600 ID=Phvul.002G003600.1.v2.1 annot-version=v2.1) &

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ion.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 434.9) (original description: pacid=37176972 transc

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D=Phvul.002G158200.1.v2.1 annot-version=v2.1) & Uncharacterized protein At1g76660 OS=Arabid

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2_papso : 230.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on p

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cription: pacid=37144783 transcript=Phvul.003G261400.2 locus=Phvul.003G261400 ID=Phvul.003G

cription: pacid=37144783 transcript=Phvul.003G261400.2 locus=Phvul.003G261400 ID=Phvul.003G

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ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versi

ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versi

ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versi

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cus=Phvul.004G068900 ID=Phvul.004G068900.2.v2.1 annot-version=v2.1) &

cus=Phvul.004G068900 ID=Phvul.004G068900.2.v2.1 annot-version=v2.1) &

ption: pacid=37154570 transcript=Phvul.005G069600.1 locus=Phvul.005G069600 ID=Phvul.005G06

D=Phvul.007G157700.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At

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=Phvul.008G111200.1.v2.1 annot-version=v2.1) & Werner Syndrome-like exonuclease OS=Arabido
=Phvul.008G230800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At
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=Phvul.002G182700.2.v2.1 annot-version=v2.1) & L-Ala-D/L-amino acid epimerase OS=Populus tri
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202300 ID=Phvul.002G202300.1.v2.1 annot-version=v2.1)
=Phvul.002G238000.1.v2.1 annot-version=v2.1) & Thioredoxin-like fold domain-containing protein
267100 ID=Phvul.002G267100.1.v2.1 annot-version=v2.1)
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113900 ID=Phvul.003G113900.1.v2.1 annot-version=v2.1)

cript=Phvul.003G154900.1 locus=Phvul.003G154900 ID=Phvul.003G154900.1.v2.1 annot-version=v

cript=Phvul.003G154900.1 locus=Phvul.003G154900 ID=Phvul.003G154900.1.v2.1 annot-version=v

209900 ID=Phvul.003G209900.1.v2.1 annot-version=v2.1)

209900 ID=Phvul.003G209900.1.v2.1 annot-version=v2.1)

cus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &

cus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &

cus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &

cus=Phvul.003G254900 ID=Phvul.003G254900.2.v2.1 annot-version=v2.1) &

=Phvul.003G295700.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At

=Phvul.003G295700.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At

=Phvul.005G088636.1.v2.1 annot-version=v2.1) & Ribosomal protein S1, mitochondrial OS=March

=Phvul.005G088636.1.v2.1 annot-version=v2.1) & Ribosomal protein S1, mitochondrial OS=March

2000.2 locus=Phvul.006G112000 ID=Phvul.006G112000.2.v2.1 annot-version=v2.1) &

2000.2 locus=Phvul.006G112000 ID=Phvul.006G112000.2.v2.1 annot-version=v2.1) &

015000.1 locus=Phvul.007G015000 ID=Phvul.007G015000.1.v2.1 annot-version=v2.1) &

=Phvul.007G028800 ID=Phvul.007G028800.1.v2.1 annot-version=v2.1) &

=Phvul.007G038000.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant pro

=Phvul.007G038000.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenylated plant pro

.007G062900 ID=Phvul.007G062900.1.v2.1 annot-version=v2.1) &

.007G062900 ID=Phvul.007G062900.1.v2.1 annot-version=v2.1) &

=Phvul.007G100700.1.v2.1 annot-version=v2.1) & Membrane protein PM19L OS=Oryza sativa sub

=Phvul.007G100700.1.v2.1 annot-version=v2.1) & Membrane protein PM19L OS=Oryza sativa sub

G149300.1 locus=Phvul.007G149300 ID=Phvul.007G149300.1.v2.1 annot-version=v2.1) &

230450 ID=Phvul.007G230450.1.v2.1 annot-version=v2.1)

locus=Phvul.008G046100 ID=Phvul.008G046100.1.v2.1 annot-version=v2.1) &

177200 ID=Phvul.008G177200.2.v2.1 annot-version=v2.1)

177200 ID=Phvul.008G177200.2.v2.1 annot-version=v2.1)

181900 ID=Phvul.008G181900.2.v2.1 annot-version=v2.1)

181900 ID=Phvul.008G181900.2.v2.1 annot-version=v2.1)

260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &

260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &

260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &

260900.2 locus=Phvul.008G260900 ID=Phvul.008G260900.2.v2.1 annot-version=v2.1) &

041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)

041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)

041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)

041100 ID=Phvul.009G041100.2.v2.1 annot-version=v2.1)

=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing p

=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing p

=Phvul.009G175100.3.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing p

200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)

200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)

200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)

200500 ID=Phvul.009G200500.3.v2.1 annot-version=v2.1)
locus=Phvul.011G080200 ID=Phvul.011G080200.1.v2.1 annot-version=v2.1) &
locus=Phvul.011G080200 ID=Phvul.011G080200.1.v2.1 annot-version=v2.1) &
174000.1 locus=Phvul.011G174000 ID=Phvul.011G174000.1.v2.1 annot-version=v2.1) &
174000.1 locus=Phvul.011G174000 ID=Phvul.011G174000.1.v2.1 annot-version=v2.1) &
n complex (original description: pacid=37171084 transcript=Phvul.001G110400.1 locus=Phvul.001G
00.1 locus=Phvul.001G123400 ID=Phvul.001G123400.1.v2.1 annot-version=v2.1) &
00.1 locus=Phvul.001G123400 ID=Phvul.001G123400.1.v2.1 annot-version=v2.1) &
cus=Phvul.001G154700 ID=Phvul.001G154700.1.v2.1 annot-version=v2.1) &
=Phvul.001G179800.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing p
=Phvul.001G179800.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat-containing p
=Phvul.001G184000.1.v2.1 annot-version=v2.1) & Cactin OS=Arabidopsis thaliana (sp|f4i2j8|catin_
2 transcript=Phvul.001G259000.1 locus=Phvul.001G259000 ID=Phvul.001G259000.1.v2.1 annot-ver
2 transcript=Phvul.001G259000.1 locus=Phvul.001G259000 ID=Phvul.001G259000.1.v2.1 annot-ver
28100.1 locus=Phvul.002G028100 ID=Phvul.002G028100.1.v2.1 annot-version=v2.1) &
28100.1 locus=Phvul.002G028100 ID=Phvul.002G028100.1.v2.1 annot-version=v2.1) &
=Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvul.002G092900.2.v2.1 annot-version=v2.1)
=Phvul.002G092900.2 locus=Phvul.002G092900 ID=Phvul.002G092900.2.v2.1 annot-version=v2.1)
0.1 locus=Phvul.002G137100 ID=Phvul.002G137100.1.v2.1 annot-version=v2.1) &
137200 ID=Phvul.002G137200.1.v2.1 annot-version=v2.1)
137200 ID=Phvul.002G137200.1.v2.1 annot-version=v2.1)
139900 ID=Phvul.002G139900.2.v2.1 annot-version=v2.1)
139900 ID=Phvul.002G139900.2.v2.1 annot-version=v2.1)
156300 ID=Phvul.002G156300.1.v2.1 annot-version=v2.1)
.1 locus=Phvul.003G032500 ID=Phvul.003G032500.1.v2.1 annot-version=v2.1) &
.1 locus=Phvul.003G032500 ID=Phvul.003G032500.1.v2.1 annot-version=v2.1) &
52400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1) &
52400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1) &
=Phvul.003G265700.1.v2.1 annot-version=v2.1) & F-box protein At4g35930 OS=Arabidopsis thalia
ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versi
ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versi
ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versi
ranscript=Phvul.003G291600.2 locus=Phvul.003G291600 ID=Phvul.003G291600.2.v2.1 annot-versi
.1 locus=Phvul.004G176100 ID=Phvul.004G176100.1.v2.1 annot-version=v2.1) &
001500 ID=Phvul.005G001500.2.v2.1 annot-version=v2.1)
001500 ID=Phvul.005G001500.2.v2.1 annot-version=v2.1)
pt=Phvul.005G043500.1 locus=Phvul.005G043500 ID=Phvul.005G043500.1.v2.1 annot-version=v2.1
pt=Phvul.005G043500.1 locus=Phvul.005G043500 ID=Phvul.005G043500.1.v2.1 annot-version=v2.1
=Phvul.005G093400.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP5 OS=Arabidopsi
131700 ID=Phvul.005G131700.1.v2.1 annot-version=v2.1)
cus=Phvul.005G183800 ID=Phvul.005G183800.2.v2.1 annot-version=v2.1) &
cus=Phvul.005G183800 ID=Phvul.005G183800.2.v2.1 annot-version=v2.1) &
yme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 37.5) (original description: paci
ocus=Phvul.006G131400 ID=Phvul.006G131400.1.v2.1 annot-version=v2.1) &
ocus=Phvul.006G131400 ID=Phvul.006G131400.1.v2.1 annot-version=v2.1) &
classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 134.3) (original description: paci

classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 134.3) (original description: paci

D=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t

D=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t

D=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t

D=Phvul.007G043900.2.v2.1 annot-version=v2.1) & Protein SNOWY COTYLEDON 3 OS=Arabidopsis t

on.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting on CH-OH group of donor(50.1.1 : 438.7) (or

cus=Phvul.007G067800 ID=Phvul.007G067800.1.v2.1 annot-version=v2.1) &

D=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis tha

D=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis tha

D=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis tha

D=Phvul.007G080900.2.v2.1 annot-version=v2.1) & UPF0496 protein At1g20180 OS=Arabidopsis tha

300.1 locus=Phvul.007G139300 ID=Phvul.007G139300.1.v2.1 annot-version=v2.1) &

300.1 locus=Phvul.007G139300 ID=Phvul.007G139300.1.v2.1 annot-version=v2.1) &

0.1 locus=Phvul.007G173400 ID=Phvul.007G173400.1.v2.1 annot-version=v2.1) &

s=Phvul.007G246700 ID=Phvul.007G246700.1.v2.1 annot-version=v2.1) &

Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &

Phvul.007G274200.1 locus=Phvul.007G274200 ID=Phvul.007G274200.1.v2.1 annot-version=v2.1) &

9000.1 locus=Phvul.008G019000 ID=Phvul.008G019000.1.v2.1 annot-version=v2.1) &

nscript=Phvul.008G055500.1 locus=Phvul.008G055500 ID=Phvul.008G055500.1.v2.1 annot-version=

nscript=Phvul.008G055500.1 locus=Phvul.008G055500 ID=Phvul.008G055500.1.v2.1 annot-version=

08G077000.1 locus=Phvul.008G077000 ID=Phvul.008G077000.1.v2.1 annot-version=v2.1) &

us=Phvul.008G114700 ID=Phvul.008G114700.1.v2.1 annot-version=v2.1) &

us=Phvul.008G114700 ID=Phvul.008G114700.1.v2.1 annot-version=v2.1) &

G211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)

G211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)

G211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)

G211500 ID=Phvul.008G211500.4.v2.1 annot-version=v2.1)

29 transcript=Phvul.008G250000.1 locus=Phvul.008G250000 ID=Phvul.008G250000.1.v2.1 annot-ve

29 transcript=Phvul.008G250000.1 locus=Phvul.008G250000 ID=Phvul.008G250000.1.v2.1 annot-ve

D=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein

D=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein

D=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein

D=Phvul.009G086300.2.v2.1 annot-version=v2.1) & L10-interacting MYB domain-containing protein

09G149800.1 locus=Phvul.009G149800 ID=Phvul.009G149800.1.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

0.6 locus=Phvul.009G154300 ID=Phvul.009G154300.6.v2.1 annot-version=v2.1) &

ul.009G240100.1 locus=Phvul.009G240100 ID=Phvul.009G240100.1.v2.1 annot-version=v2.1) &

Phvul.011G017800 ID=Phvul.011G017800.1.v2.1 annot-version=v2.1) &

Phvul.011G017800 ID=Phvul.011G017800.1.v2.1 annot-version=v2.1) &
100200 ID=Phvul.011G100200.2.v2.1 annot-version=v2.1)
100200 ID=Phvul.011G100200.2.v2.1 annot-version=v2.1)
108300 ID=Phvul.011G108300.1.v2.1 annot-version=v2.1)
129700.1 locus=Phvul.011G129700 ID=Phvul.011G129700.1.v2.1 annot-version=v2.1) &
129700.1 locus=Phvul.011G129700 ID=Phvul.011G129700.1.v2.1 annot-version=v2.1) &
D=Phvul.011G140050.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At
D=Phvul.011G140050.2.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-containing protein At

aliana (sp|q7xa86|zdh11_arath : 318.0)
aliana (sp|q7xa86|zdh11_arath : 318.0)
aliana (sp|q7xa86|zdh11_arath : 318.0)
aliana (sp|q7xa86|zdh11_arath : 318.0)

sion=v2.1) &
sion=v2.1) &

corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=3714957
corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=3714957
corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=3714957
corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=3714957
corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=3714957
corporation of molecular oxygen (oxygenase)(50.1.12 : 199.5) (original description: pacid=3714957
1.v2.1 annot-version=v2.1) &

al OS=Arabidopsis thaliana (sp|o64886|cox10_arath : 442.0)
al OS=Arabidopsis thaliana (sp|o64886|cox10_arath : 442.0)

idopsis thaliana (sp|q8gza4|cbsx6_arath : 500.0)

DS=Arabidopsis thaliana (sp|q9stx1|acbp3_arath : 116.0)
DS=Arabidopsis thaliana (sp|q9stx1|acbp3_arath : 116.0)
liana (sp|q9lka4|uba2c_arath : 175.0)
liana (sp|q9lka4|uba2c_arath : 175.0)
Arabidopsis thaliana (sp|a1l4v7|dcyd2_arath : 443.0)
Arabidopsis thaliana (sp|a1l4v7|dcyd2_arath : 443.0)
S=Arabidopsis thaliana (sp|q9saf0|orp1d_arath : 1151.0)
S=Arabidopsis thaliana (sp|q9saf0|orp1d_arath : 1151.0)

cript=Phvul.002G102800.2 locus=Phvul.002G102800 ID=Phvul.002G102800.2.v2.1 annot-version=v
cript=Phvul.002G102800.2 locus=Phvul.002G102800 ID=Phvul.002G102800.2.v2.1 annot-version=v
S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)
S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)
S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)
S=Arabidopsis thaliana (sp|q9fgd7|pub50_arath : 342.0)
opsis thaliana (sp|q9sre5|y1666_arath : 119.0)
opsis thaliana (sp|q9sre5|y1666_arath : 119.0)
paired donor with incorporation or reduction of molecular oxygen(50.1.13 : 122.3) (original descript

i261400.2.v2.1 annot-version=v2.1) &
i261400.2.v2.1 annot-version=v2.1) &
i261400.2.v2.1 annot-version=v2.1) &
i261400.2.v2.1 annot-version=v2.1) &
on=v2.1) &
on=v2.1) &
on=v2.1) &
on=v2.1) &

9600.1.v2.1 annot-version=v2.1) &
3g53700, chloroplastic OS=Arabidopsis thaliana (sp|q9lff1|pp281_arath : 948.0)
)0.1.v2.1 annot-version=v2.1) &
opsis thaliana (sp|q84lh3|wex_arath : 98.6)

psis thaliana (sp|q84lh3|wex_arath : 98.6)
2g34400 OS=Arabidopsis thaliana (sp|o64705|pp184_arath : 608.0)

bidopsis thaliana (sp|q39061|cp33_arath : 102.0)

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

chocarpa (sp|b9i2j6|axep_poptr : 565.0)
chocarpa (sp|b9i2j6|axep_poptr : 565.0)

MRL7, chloroplastic OS=Arabidopsis thaliana (sp|f4jlc1|mrl7_arath : 334.0)

na (sp|q8rwd6|fb271_arath : 511.0)
na (sp|q8rwd6|fb271_arath : 511.0)
na (sp|q8rwd6|fb271_arath : 511.0)
na (sp|q8rwd6|fb271_arath : 511.0)

psis thaliana (sp|q9fle8|y5986_arath : 127.0)
psis thaliana (sp|q9fle8|y5986_arath : 127.0)

2.1) &

2.1) &

4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304_arath : 449.0)

4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304_arath : 449.0)

antia polymorpha (sp|p26863|rt01_marpo : 94.7)

antia polymorpha (sp|p26863|rt01_marpo : 94.7)

tein 37 OS=Arabidopsis thaliana (sp|a2rvm8|hip37_arath : 113.0)

tein 37 OS=Arabidopsis thaliana (sp|a2rvm8|hip37_arath : 113.0)

sp. japonica (sp|q6l4d2|pm19l_orysj : 166.0)

sp. japonica (sp|q6l4d2|pm19l_orysj : 166.0)

rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104_arath : 473.0)

rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104_arath : 473.0)

rotein At1g64310 OS=Arabidopsis thaliana (sp|q9c7v5|pp104_arath : 473.0)

110400 ID=Phvul.001G110400.1.v2.1 annot-version=v2.1) &

rotein At5g37570 OS=Arabidopsis thaliana (sp|q9fhr3|pp403_arath : 574.0)
rotein At5g37570 OS=Arabidopsis thaliana (sp|q9fhr3|pp403_arath : 574.0)
_arath : 759.0)
rsion=v2.1) &
rsion=v2.1) &

&
&

na (sp|q5xf11|fb248_arath : 202.0)
n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &

1) &
1) &
thaliana (sp|f4jnb7|rpp5_arath : 109.0)

id=37171403 transcript=Phvul.006G098700.1 locus=Phvul.006G098700 ID=Phvul.006G098700.1.v2

id=37173062 transcript=Phvul.006G208400.1 locus=Phvul.006G208400 ID=Phvul.006G208400.1.v2.

id=37173062 transcript=Phvul.006G208400.1 locus=Phvul.006G208400 ID=Phvul.006G208400.1.v2.
thaliana (sp|q8gxd9|sco3_arath : 320.0)
thaliana (sp|q8gxd9|sco3_arath : 320.0)
thaliana (sp|q8gxd9|sco3_arath : 320.0)
thaliana (sp|q8gxd9|sco3_arath : 320.0)
riginal description: pacid=37166204 transcript=Phvul.007G062100.1 locus=Phvul.007G062100 ID=Pl

aliana (sp|q6dye5|u496k_arath : 151.0)
aliana (sp|q6dye5|u496k_arath : 151.0)
aliana (sp|q6dye5|u496k_arath : 151.0)
aliana (sp|q6dye5|u496k_arath : 151.0)

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=v2.1) &

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4g04790, mitochondrial OS=Arabidopsis thaliana (sp|q6nq81|pp304_arath : 558.0)

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2.1) &

2.1) &

ion: pacid=37145792 transcript=Phvul.003G013200.2 locus=Phvul.003G013200 ID=Phvul.003G0132

.1 annot-version=v2.1) &

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.1 annot-version=v2.1) &

hvul.007G062100.1.v2.1 annot-version=v2.1) &

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

miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
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ggaaucuugaug	Phvul.001G174400.1	0.5	-1	1	21
ggaaucuugaug	Phvul.001G174400.1	0.5	-1	1	21
ggaaucuugaug	Phvul.001G174400.1	0.5	-1	1	21
ggaaucuugaug	Phvul.001G174400.1	0.5	-1	1	21
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ggaaucuugaug	Phvul.001G174400.1	0.5	-1	1	21
ggaaucuugaug	Phvul.001G174400.1	0.5	-1	1	24
ggaaucuugaug	Phvul.002G016900.1	0.5	-1	1	21
ggaaucuugaug	Phvul.002G016900.1	0.5	-1	1	21
ggaaucuugaug	Phvul.002G016900.1	0.5	-1	1	21
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uggaaucuugau	Phvul.007G252700.1	5	-1	1	22
ggaaucuugaug	Phvul.008G003900.1	5	-1	1	24
uggaaucuugau	Phvul.008G003900.1	5	-1	1	22
ggaaucuugaug	Phvul.008G041600.1	5	-1	1	21
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uggaaucuugau	Phvul.008G081500.1	5	-1	1	22
uggaaucuugau	Phvul.008G093200.1	5	-1	1	22
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ggaaucuugaug	Phvul.010G053600.1	5	-1	1	24
ggaaucuugaug	Phvul.011G035700.2	5	-1	1	21
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uggaaucuugau	Phvul.011G082801.1	5	-1	1	22
uggaaucuugau	Phvul.011G147000.1	5	-1	1	22
ggaaucuugaug	Phvul.011G152100.3	5	-1	1	21
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ggaaucuugaug	Phvul.011G152100.1	5	-1	1	24

Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1508	1528	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371695
1505	1528	GGAAUCUUG	:: ::::::::::::::.:::	CUACUGCAG	Cleavage	pacid=371695
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1869	1889	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371755
1866	1889	GGAAUCUUG	:::::::::::::::::.:::	CUGCUGCAG	Cleavage	pacid=371755
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1939	1959	GGAAUCUUG	::::::::::::::.::::::	CUGCAGCAU	Cleavage	pacid=371483
1936	1959	GGAAUCUUG	:::::::::::::::::.:::	CUGCUGCAG	Cleavage	pacid=371483
1752	1772	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1797	1817	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1752	1772	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1797	1817	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1752	1772	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1797	1817	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1752	1772	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1797	1817	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1752	1772	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1797	1817	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1752	1772	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1797	1817	GGAAUCUUG	::::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574

1752	1772	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1797	1817	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1752	1772	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1797	1817	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1752	1772	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1797	1817	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1752	1772	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1797	1817	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371574
1749	1772	GGAAUCUUG/	:::::::::::::::::.:::	CUGCUGCAG(	Cleavage	pacid=371574
1794	1817	GGAAUCUUG/	:::::::::::::::::.:::	CUGCUGCAG(	Cleavage	pacid=371574
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1428	1448	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1473	1493	GGAAUCUUG/	::::::::::::::.:::::.	CUGCAGCAU(	Cleavage	pacid=371484
1425	1448	GGAAUCUUG/	:: ::::::::::::::.:::	CUACUGCAG(	Cleavage	pacid=371484
1470	1493	GGAAUCUUG/	:: ::::::::::::::.:::	CUACUGCAG(	Cleavage	pacid=371484
1508	1529	UGGAAUCUU(	::::::::::::::.::::::	CUGCAGCAU(	Cleavage	pacid=371695
1869	1890	UGGAAUCUU(	::::::::::::::.::::::	CUGCAGCAU(	Cleavage	pacid=371755
1939	1960	UGGAAUCUU(	::::::::::::::.::::::	CUGCAGCAU(	Cleavage	pacid=371483
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539
764	784	GGAAUCUUG/	::.::::::::::::::::	AUGUAGCAU(	Cleavage	pacid=371539

764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	784	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
761	784	GGAAUCUUG	: : ::.::::::::::::::	CGGAUGUAG	Cleavage	pacid=371539
761	784	GGAAUCUUG	: : ::.::::::::::::::	CGGAUGUAG	Cleavage	pacid=371539
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1503	1523	GGAAUCUUG	: ::::::::::::.::::	CAGCAGCAU	Cleavage	pacid=371641
1500	1523	GGAAUCUUG	::: ::::::::::::.::::	AUGCAGCAG	Cleavage	pacid=371641
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
873	893	GGAAUCUUG	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
870	893	GGAAUCUUG	: : ::.::::::::::::::	CGGAUGUAG	Cleavage	pacid=371559
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703

445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
445	465	GGAAUCUUG	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703
442	465	GGAAUCUUG	: : :: ::::::::::::::	CCGGUGGAG	Cleavage	pacid=371703
442	465	GGAAUCUUG	: : :: ::::::::::::::	CCGGUGGAG	Cleavage	pacid=371703
1752	1773	UGGAAUCUU	:::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1797	1818	UGGAAUCUU	:::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371574
1428	1449	UGGAAUCUU	:::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371484
1473	1494	UGGAAUCUU	:::::::::::::.:::::.	CUGCAGCAU	Cleavage	pacid=371484
261	282	UGGAAUCUU	:::: :::::::::::.:	CAAAAGCAG	Cleavage	pacid=371448
1430	1451	UGGAAUCUU	:: ::::::::::: :::	UCUCACCAU	Cleavage	pacid=371544
1399	1420	UGGAAUCUU	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1497	UGGAAUCUU	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1690	1711	UGGAAUCUU	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
147	167	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
403	423	GGAAUCUUG	:: :::::::::.:::.:::	GUGGAGCAU	Cleavage	pacid=371678
144	167	GGAAUCUUG	:: :::::::::.:::.::	AUUGUGGAG	Cleavage	pacid=371678
400	423	GGAAUCUUG	:: :::::::::.:::.::	AUUGUGGAG	Cleavage	pacid=371678
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693

13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
13	33	GGAAUCUUG	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
10	33	GGAAUCUUG	:::::::: :::::::	UUUCCUCAG	Translation	pacid=371693
13	34	UGGAAUCUU	:::::::: ::::::::.	CCUCAGCAUC	Translation	pacid=371693
657	678	UGGAAUCUU	:::: .::::.:::::..	AGUCAGCAG	Cleavage	pacid=371678
725	746	UGGAAUCUU	:::: .::::.:::::..	AGUCAGCAG	Cleavage	pacid=371678
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
460	480	GGAAUCUUG	:: :::: :::::::::.	GCGCUGCAU	Cleavage	pacid=371786
637	658	UGGAAUCUU	::::::: ::: ::::::	GAUCAGCAU	Translation	pacid=371757
251	272	UGGAAUCUU	.: :.::.::: :.::::::::	UUUCGGCGU	Translation	pacid=371760
446	467	UGGAAUCUU	.: :::: :::: :::::::.:	UUCCAGCUU	Translation	pacid=371756
672	693	UGGAAUCUU	.: :::: :::: :::::::.:	UUCCAGCUU	Translation	pacid=371756
186	207	UGGAAUCUU	::::.::::...:.::.:.	CACCAGCGUC	Cleavage	pacid=371456
165	186	UGGAAUCUU	::::.::::...:.::.:.	CACCAGCGUC	Cleavage	pacid=371462
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1854	1874	GGAAUCUUG	::.: : ::::::::::::.	AUGUAUCUU	Cleavage	pacid=371541
1851	1874	GGAAUCUUG	:: ::.: : :::::::::::	CUUAUGUAU	Cleavage	pacid=371541
1854	1875	UGGAAUCUU	::.: : ::::::::::::.:	AUGUAUCUU	Cleavage	pacid=371541
1903	1924	UGGAAUCUU	.: .: : ::::::::::::.:	UUUUAUCUU	Cleavage	pacid=371531
2017	2038	UGGAAUCUU	.: .: : ::::::::::::.:	UUUUAUCUU	Cleavage	pacid=371531
2016	2037	UGGAAUCUU	.: .: : ::::::::::::.:	UUUUAUCUU	Cleavage	pacid=371531
1836	1857	UGGAAUCUU	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523

18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
18	38	GGAAUCUUG	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
15	38	GGAAUCUUG	:: :: ::::.:::::.::	UGGCAUCAU	Cleavage	pacid=371523
18	39	UGGAAUCUU	:: ::::.:::::.::::	CAUCAUCAU	Cleavage	pacid=371523
764	785	UGGAAUCUU	::.:::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
764	785	UGGAAUCUU	::.:::::::::::::::	AUGUAGCAU	Cleavage	pacid=371539
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
604	623	GGAAUCUUG	:::::. ::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
601	623	GGAAUCUUG	: :::::. ::::::::::	AAGGUGCAG	Cleavage	pacid=371730
1503	1524	UGGAAUCUU	: ::::::::::::.:::::	CAGCAGCAUC	Cleavage	pacid=371641
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.:::::	CUCCGCCAUC	Cleavage	pacid=371597

339	359	GGAAUCUUG	:: :. ::::::::.::::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.::::::	CUCCGCCAUC	Cleavage	pacid=371597
342	362	GGAAUCUUG	:: :. ::::::::.::::::	CUCCGCCAUC	Cleavage	pacid=371597
339	359	GGAAUCUUG	:: :. ::::::::.::::::	CUCCGCCAUC	Cleavage	pacid=371597
339	362	GGAAUCUUG	: :: :. ::::::::.::::	AUCCUCCGCC	Cleavage	pacid=371597
339	362	GGAAUCUUG	: :: :. ::::::::.::::	AUCCUCCGCC	Cleavage	pacid=371597
336	359	GGAAUCUUG	: :: :. ::::::::.::::	AUCCUCCGCC	Cleavage	pacid=371597
342	363	UGGAAUCUU	:: :. ::::::::.::::::	CUCCGCCAUC	Cleavage	pacid=371597
342	363	UGGAAUCUU	:: :. ::::::::.::::::	CUCCGCCAUC	Cleavage	pacid=371597
339	360	UGGAAUCUU	:: :. ::::::::.::::::	CUCCGCCAUC	Cleavage	pacid=371597
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
467	487	GGAAUCUUG	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
464	487	GGAAUCUUG	:..:::: ::::::::::	GCGGAGUGG	Cleavage	pacid=371506
151	172	UGGAAUCUU	:: :::::::: :::..::	CAUCAUCAU	Cleavage	pacid=371511
873	894	UGGAAUCUU	::.::::::::::::::::	AUGUAGCAU	Cleavage	pacid=371559
1868	1889	UGGAAUCUU	:: .: : ::::::::::::.:	CUUUAUCUU	Cleavage	pacid=371556
1850	1871	UGGAAUCUU	:: .: : ::::::::::::.:	CUUUAUCUU	Cleavage	pacid=371565
1850	1871	UGGAAUCUU	:: .: : ::::::::::::.:	CUUUAUCUU	Cleavage	pacid=371565
1832	1853	UGGAAUCUU	:: .: : ::::::::::::.:	CUAUAUCUU	Cleavage	pacid=371556
1914	1935	UGGAAUCUU	:: .: : ::::::::::::.:	CUAUAUCUU	Cleavage	pacid=371556
1917	1938	UGGAAUCUU	:: .: : ::::::::::::.:	CUAUAUCUU	Cleavage	pacid=371556
1935	1956	UGGAAUCUU	:: .: : ::::::::::::.:	CUUUAUCUU	Cleavage	pacid=371563
1839	1860	UGGAAUCUU	:: .: : ::::::::::::.:	CUUUAUCUU	Cleavage	pacid=371559
147	168	UGGAAUCUU	:: ::::::::.:::.::: :	GUGGAGCAU	Cleavage	pacid=371678
403	424	UGGAAUCUU	:: ::::::::.:::.::: :	GUGGAGCAU	Cleavage	pacid=371678
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
132	152	GGAAUCUUG	::: ::::: :::.:.::::	GUGCUGCAU	Translation	pacid=371702
129	152	GGAAUCUUG	::: ::::: :::.:.::	AUCGUGCUG	Translation	pacid=371702
132	153	UGGAAUCUU	::: ::::: :::.:.:::::	GUGCUGCAU	Cleavage	pacid=371702
445	466	UGGAAUCUU	:: :::::::::::::::	GUGGAGCAU	Cleavage	pacid=371703

445	466	UGGAAUCUU(	:: :::::::::::::::::	GUGGAGCAU(	Cleavage	pacid=371703
460	481	UGGAAUCUU(	:: :::: ::::::::::..	GCGCUGCAU/	Cleavage	pacid=371786
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
1391	1411	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCUGCAAC	Cleavage	pacid=371748
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2480	2500	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2557	2577	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2662	2682	GGAAUCUUG/	: ::.:::::::. ::.::.:	CGGCGGCAU(	Cleavage	pacid=371765
2477	2500	GGAAUCUUG/	::: ::.:::::::. ::.::	GUGCGGCGG(	Cleavage	pacid=371765
2554	2577	GGAAUCUUG/	::: ::.:::::::. ::.::	GUGCGGCGG(	Cleavage	pacid=371765
2659	2682	GGAAUCUUG/	::: ::.:::::::. ::.::	GUGCGGCGG(	Cleavage	pacid=371765
17	37	GGAAUCUUG/	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783

17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
17	37	GGAAUCUUG	: :: ::: ::::::::::..	CAGCCGCAAC	Cleavage	pacid=371783
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2361	2381	GGAAUCUUG	::..::::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2358	2381	GGAAUCUUG	.:: ::..:::::::::::::	UUGGUGUGG	Cleavage	pacid=371461
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12225	12245	GGAAUCUUG	: ::.:: ::. :::::::::	CAGCGGCUU	Translation	pacid=371454
12222	12245	GGAAUCUUG	.::: ::.:: ::. :::::::	UUGCAGCGG	Translation	pacid=371454
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
539	559	GGAAUCUUG	: :: :.:: ::::::::::.	CCGCUGUAU	Cleavage	pacid=371473
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456

186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
186	206	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371456
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
165	185	GGAAUCUUG	::::.:::::..:.::.:	CACCAGCGUC	Cleavage	pacid=371462
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1430	1450	GGAAUCUUG	:: ::::::::::: ::	UCUCACCAUC	Cleavage	pacid=371544
1096	1117	UGGAAUCUU	:: :: .: ::::.::::::.	CUUCACUACC	Cleavage	pacid=371722
1247	1268	UGGAAUCUU	:: :: .: ::::.::::::.	CUUCACUACC	Cleavage	pacid=371722
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
1203	1223	GGAAUCUUG	:..:: :.:::::::::..	GGGUGGCCU	Cleavage	pacid=371734
195	216	UGGAAUCUU	::::::::::::::.:	UCAAGACAUC	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729

1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
1892	1912	GGAAUCUUG	.:: .: ::::.:::.::::	UUGGGGAAU	Cleavage	pacid=371729
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
564	584	GGAAUCUUG	: ::::: ::::.:::: :.	CCGCAGCUU	Cleavage	pacid=371649
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1704	1724	GGAAUCUUG	:::: ::::::: :.::.:	CUGCAUCAU	Cleavage	pacid=371666
1701	1724	GGAAUCUUG	:::: ::::::: :.::	CCUCUGCAU	Cleavage	pacid=371666
1704	1725	UGGAAUCUU	:::: ::::::: :.::.::	CUGCAUCAU	Cleavage	pacid=371666
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1399	1419	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1476	1496	GGAAUCUUG	:: .: : ::::::::::::	CUUUAUCUU	Cleavage	pacid=371593
1396	1419	GGAAUCUUG	:: :: .: : ::::::::::	CUUCUUUAU	Cleavage	pacid=371593
1473	1496	GGAAUCUUG	:: :: .: : ::::::::::	CUUCUUUAU	Cleavage	pacid=371593

1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1174	GGAAUCUUG	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1044	1064	GGAAUCUUG	:::: .::..::::::::..	CUGCAAUAU	Cleavage	pacid=371487
1041	1064	GGAAUCUUG	:::: .::..::::::::	UGCCUGCAA	Cleavage	pacid=371487
467	488	UGGAAUCUU	:..::: ::::::::::.:	GAGUGGCAC	Cleavage	pacid=371506
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
286	306	GGAAUCUUG	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
283	306	GGAAUCUUG	:::::::: ::::.::	AGCAUGCAG	Translation	pacid=371433
286	307	UGGAAUCUU	:::::::: ::::.::::	AUGCAGCAU	Translation	pacid=371433
1306	1327	UGGAAUCUU	:::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
2984	3004	GGAAUCUUG	:::..::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569

2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2984	3004	GGAAUCUUG	:::..::::::::::.::: :.	CUGUGGCAU	Cleavage	pacid=371569
2981	3004	GGAAUCUUG	:::..::::::::::.:::	CAUCUGUGG	Cleavage	pacid=371569
2984	3005	UGGAAUCUU	:::..::::::::::.::: :.:	CUGUGGCAU	Cleavage	pacid=371569
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	453	GGAAUCUUG	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
433	454	UGGAAUCUU	:::.:::: .::::::::	UGACAGUAU	Translation	pacid=371555
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1941	1961	GGAAUCUUG	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1690	1710	GGAAUCUUG	:: .: : :::::::::::::	CUUUAUCUU	Cleavage	pacid=371564
1687	1710	GGAAUCUUG	:: :: .: : :::::::::::	CUUCUUUAU	Cleavage	pacid=371564
1876	1897	UGGAAUCUU	:: .: : ::::::.::::::.:	CUUUAUCUU	Cleavage	pacid=371558
1876	1897	UGGAAUCUU	:: .: : ::::::.::::::.:	CUUUAUCUU	Cleavage	pacid=371558
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485

1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1397	1417	GGAAUCUUG	.:::: :.:..:::::::..	UUGCACCGU	Cleavage	pacid=371485
1394	1417	GGAAUCUUG	.: .:::: :.:..:::::::	UUAUUGCAC	Cleavage	pacid=371485
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
249	271	GGAAUCUUG	:::::::::: ::::::::	AAGCAGCAU	Cleavage	pacid=371446
246	271	GGAAUCUUG	:::::::::: :::::	AGAAAGCAG	Cleavage	pacid=371446
249	272	UGGAAUCUU	:::::::::: ::::::::	AAGCAGCAU	Translation	pacid=371446
1104	1125	UGGAAUCUU	:.:::::.:::::.::	AUUUUGUAU	Cleavage	pacid=371685
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
311	331	GGAAUCUUG	::.:..:: :::::::..	UCGCGGUGU	Translation	pacid=371712
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
154	174	GGAAUCUUG	::::::::::.: .::.:	CCUCAGCAUC	Cleavage	pacid=371703
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678

725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
657	677	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
725	745	GGAAUCUUG	::::: .::::.:::::.	AGUCAGCAG	Cleavage	pacid=371678
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1546	1566	GGAAUCUUG	::: :::::: :::::: ::	CUGAAGCAU	Translation	pacid=371686
1543	1566	GGAAUCUUG	: ::: :::::: :::::::	GUUCUGAAG	Translation	pacid=371686
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689

1163	1183	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1521	1541	GGAAUCUUG	.:: : :::: :::.::::::	UUGGAACAU	Translation	pacid=371689
1163	1184	UGGAAUCUU	.:: : :::: :::.:::::::	UUGGAACAU	Cleavage	pacid=371689
1521	1542	UGGAAUCUU	.:: : :::: :::.:::::::	UUGGAACAU	Cleavage	pacid=371689
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371707
1599	1622	GGAAUCUUG	.:::.:::::.:::::. :	UCUUUGCGG	Cleavage	pacid=371707
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1602	1622	GGAAUCUUG	.:::.:::::.:::::. :..	UUGCGGCAU	Cleavage	pacid=371685
1599	1622	GGAAUCUUG	.:::.:::::.:::::. :	UCUUUGCGG	Cleavage	pacid=371685
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
637	657	GGAAUCUUG	::::::: ::: ::::	GAUCAGCAU	Translation	pacid=371757
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760
251	271	GGAAUCUUG	.: :.::.::: :.::::::	UUUCGGCGU	Translation	pacid=371760

248	271	GGAAUCUUG	:.: :.::.::: :.::::::	UCGUUUCGG	Translation	pacid=371760
1999	2020	UGGAAUCUU	:: .:: .:..:.:::::::.	CUCUAGAGU	Cleavage	pacid=371787
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
446	466	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
672	692	GGAAUCUUG	.: :::: :::: :::::::.	UUCCAGCUU	Cleavage	pacid=371756
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
261	281	GGAAUCUUG	:::: :::::::::::.	CAAAAGCAGC	Cleavage	pacid=371448
12225	12246	UGGAAUCUU	: ::.:: ::. :::::::::.	CAGCGGCUU	Translation	pacid=371454
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2133	2153	GGAAUCUUG	: ::::::.. ::: :::::	CGGCAGCAU	Translation	pacid=371445
2130	2153	GGAAUCUUG	: ::::::.. ::: :::	CCCCGGCAGC	Translation	pacid=371445
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476

1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1083	1103	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1216	1236	GGAAUCUUG	::..::::.:: :.:::::.	GUGUGGCAU	Cleavage	pacid=371476
1080	1103	GGAAUCUUG	.:: ::..::::.:: :.::::	UUGGUGUGG	Cleavage	pacid=371476
1213	1236	GGAAUCUUG	.:: ::..::::.:: :.::::	UUGGUGUGG	Cleavage	pacid=371476
485	506	UGGAAUCUU	.:::::.:::::::..	GAAAUGUAU	Cleavage	pacid=371481
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
532	552	GGAAUCUUG	:::.::.::::.:: :::	CGCCAGUAU	Cleavage	pacid=371476
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445

401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
401	421	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
512	532	GGAAUCUUG	:::.::.::::. :::::	CGUCAGUAU	Cleavage	pacid=371445
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: :::::::::::. ::.:	CAGCAGCAU	Cleavage	pacid=371444
276	296	GGAAUCUUG	: ::::::::::: ::.:	CAGCAGCAU	Cleavage	pacid=371444
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
3082	3102	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
4114	4134	GGAAUCUUG	..:.::::.:::.::.:	AGAUGGUAU	Cleavage	pacid=371450
381	401	GGAAUCUUG	.::: :::: ::.:::::	UUGCUUCAU	Translation	pacid=371633

381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
381	401	GGAAUCUUG	.::: :::: ::.::::::	UUGCUUCAU	Translation	pacid=371633
378	401	GGAAUCUUG	:: .::: :::: ::.::::	CUUUUGCUU	Translation	pacid=371633
1146	1167	UGGAAUCUU	.: :::.: : :.:::::::.:	UUCCAGUAC	Cleavage	pacid=371632
1151	1172	UGGAAUCUU	.: :::.: : :.:::::::.:	UUCCAGUAC	Cleavage	pacid=371631
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1181	1201	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1262	1282	GGAAUCUUG	::::::::::. ::: :.:	GUGCAGCAU	Cleavage	pacid=371529
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1836	1856	GGAAUCUUG	:: .: : ::::::.::::::	CUCUACCUU	Cleavage	pacid=371538
1833	1856	GGAAUCUUG	:: :: .: : ::::::.::::	CUUCUCUAC	Cleavage	pacid=371538
888	908	GGAAUCUUG	:: :. :::..:::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..:::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..:::::::.:	CUUCGUCAU	Cleavage	pacid=371540

899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
888	908	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	919	GGAAUCUUG	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
885	908	GGAAUCUUG	::: :. :::..::::::::	AGGCUUCGU	Cleavage	pacid=371540
896	919	GGAAUCUUG	::: :. :::..::::::::	AGGCUUCGU	Cleavage	pacid=371540
888	909	UGGAAUCUU	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
899	920	UGGAAUCUU	:: :. :::..::::::::.:	CUUCGUCAU	Cleavage	pacid=371540
2636	2659	GGAAUCUUG	::: :::::::::: :::	AUGCGGCAG	Cleavage	pacid=371722
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2152	GGAAUCUUG	:::::.:::: ::::.:: :	AUGCAGUAU	Translation	pacid=371732
2132	2153	UGGAAUCUU	:::::.:::: ::::.:: ::	AUGCAGUAU	Translation	pacid=371732
604	624	UGGAAUCUU	:::::. :::::::::::.:	GUGCAGU-UC	Cleavage	pacid=371730
1892	1913	UGGAAUCUU	.:: .: ::::.:::.::::.	UUGGGGAAU	Cleavage	pacid=371729
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
803	823	GGAAUCUUG	:::::.::::: ::::	CCAAAGCAU	Cleavage	pacid=371668
910	931	UGGAAUCUU	::::::::.::::.::	CCCUCUCAUC	Cleavage	pacid=371652

249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
249	270 GGAAU-CUUG	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
246	270 GGAAU-CUUG	.:::::: :::::::::: ::	UUGCUGCUG	Cleavage	pacid=371645
249	271 UGGAAU-CU	:::: :::::::::: ::::	CUGCUGCAU	Cleavage	pacid=371645
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
143	163 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
204	224 GGAAUCUUG	::.::. :.:::::::::.	AUGUAGUUU	Cleavage	pacid=371666
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
230	250 GGAAUCUUG	:::::: ::: :::::::::	CUGCAGAAU	Translation	pacid=371577
227	250 GGAAUCUUG	: ::::::: ::: :::::::	CAGCUGCAG	Translation	pacid=371577
741	761 GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761 GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761 GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604

741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
741	761	GGAAUCUUG	.:: :::.:.::::.::::.	UUGGAGCGU	Cleavage	pacid=371604
738	761	GGAAUCUUG	.:: :::.:.::::.::::	UCUUUGGAG	Cleavage	pacid=371604
738	761	GGAAUCUUG	.:: :::.:.::::.::::	UCUUUGGAG	Cleavage	pacid=371604
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2506	GGAAUCUUG	:: :::::: :: :::::	AUGGAGCAU	Translation	pacid=371593
2486	2507	UGGAAUCUU	:: :::::: :: ::::::	AUGGAGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
556	576	GGAAUCUUG	: ::.::::.: ::.:.:::.	CGGCGGCAU	Translation	pacid=371593
553	576	GGAAUCUUG	: :: ::.::::.: ::.:.::	CGGCGGCGG	Translation	pacid=371593
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614

1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1448	1469	GGAAUCUUG	.::.: :.::.:::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1445	1469	GGAAUCUUG	.::.: :.::.::::::::	UACUUGUAU	Cleavage	pacid=371614
1044	1065	UGGAAUCUU	::::: .::..::::::::...	CUGCAAUAU	Cleavage	pacid=371487
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
65	85	GGAAUCUUG	.::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423
329	350	UGGAAUCUU	.::::::: :: :::::::::	UUGCAGCAG	Translation	pacid=371436
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	122	GGAAUCUUG	: :::::: ::::::::: :	CAGCAGCAG	Cleavage	pacid=371568
102	123	UGGAAUCUU	: :::::: ::::::::: : :	CAGCAGCAG	Cleavage	pacid=371568
695	716	UGGAAUCUU	::::::::::.::.::	ACUCCCCAUC	Cleavage	pacid=371547
695	716	UGGAAUCUU	::::::::::.::.::	ACUCCCCAUC	Cleavage	pacid=371547
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
1306	1326	GGAAUCUUG	::::: : :: :::::::::	AUGCAGGAC	Translation	pacid=371570
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553

426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
426	446	GGAAUCUUG	:::..::: .::::::::	UGACAGUGU	Translation	pacid=371553
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1868	1888	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371556
1865	1888	GGAAUCUUG	:: :: .: : :::::::::::	CUUCUUUAU	Cleavage	pacid=371556
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1850	1870	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371565
1847	1870	GGAAUCUUG	:: :: .: : :::::::::::	CUUCUUUAU	Cleavage	pacid=371565
1847	1870	GGAAUCUUG	:: :: .: : :::::::::::	CUUCUUUAU	Cleavage	pacid=371565
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556

1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1832	1852	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1914	1934	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1917	1937	GGAAUCUUG	:: .: : ::::::::::::.	CUAUAUCUU	Cleavage	pacid=371556
1829	1852	GGAAUCUUG	:: :: .: : :::::::::::	CUACUAUAU	Cleavage	pacid=371556
1911	1934	GGAAUCUUG	:: :: .: : :::::::::::	CUACUAUAU	Cleavage	pacid=371556
1914	1937	GGAAUCUUG	:: :: .: : :::::::::::	CUACUAUAU	Cleavage	pacid=371556
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1935	1955	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371563
1932	1955	GGAAUCUUG	:: :: .: : :::::::::::	CUUCUUUAU	Cleavage	pacid=371563
1756	1777	UGGAAUCUU	.::.: : :::::::::::.:	UUGUAUCUC	Cleavage	pacid=371555
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559

1839	1859	GGAAUCUUG	:: .: : ::::::::::::.	CUUUAUCUU	Cleavage	pacid=371559
1836	1859	GGAAUCUUG	:: :: .: : ::::::::::	CUUCUUUAU	Cleavage	pacid=371559
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1756	1776	GGAAUCUUG	.::.: : :::::::::::	UUGUAUCUA	Cleavage	pacid=371549
1753	1776	GGAAUCUUG	:: .::.: : ::::::::::	CUUUUGUAU	Cleavage	pacid=371549
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
839	859	GGAAUCUUG	::::::::..:::. :: ::	GUGCAGCAU	Cleavage	pacid=371676
836	859	GGAAUCUUG	.:: ::::::::..:::. ::	UUGGUGCAG	Cleavage	pacid=371676
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1024	1043	GGAAUCUUG	::..:::::::::: :::.	AUGUGGCAU	Cleavage	pacid=371687
1021	1043	GGAAUCUUG	.:: ::..:::::::::: ::	UUGAUGUGG	Cleavage	pacid=371687
1602	1623	UGGAAUCUU	.:::.:::::.:::::. :...	UUGCGGCAU	Cleavage	pacid=371707
1602	1623	UGGAAUCUU	.:::.:::::.:::::. :...	UUGCGGCAU	Cleavage	pacid=371685
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743
2180	2200	GGAAUCUUG	.::: ::::..:::. :::.:	UUGCUGCAU	Cleavage	pacid=371743

2180	2200	GGAAUCUUG	.::: ::::..:::. ::::.:	UUGCUGCAU	Cleavage	pacid=371743
2177	2200	GGAAUCUUG	: :.::: ::::..:::. :::	CCGUUGCUG	Cleavage	pacid=371743
2180	2201	UGGAAUCUU	.::: ::::..:::. :::.::	UUGCUGCAU	Cleavage	pacid=371743
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1718	1739	GGAAUCUUG	:::::::: :::::: ::::	AUGCAGCAU	Cleavage	pacid=371750
1715	1739	GGAAUCUUG	:::::::: :::::: ::	AAAAUGCAG	Cleavage	pacid=371750
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
134	154	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371766
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
113	133	GGAAUCUUG	:::::: ::::.:. ::::	AUGCAGCUU	Cleavage	pacid=371768
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1999	2019	GGAAUCUUG	:: .:: .:..:.:::::::	CUCUAGAGU	Cleavage	pacid=371787
1996	2019	GGAAUCUUG	:::: .:: .:..:.::::::	AUGCUCUAG	Cleavage	pacid=371787
2480	2501	UGGAAUCUU	: ::.:::::::. ::.::.:	CGGCGGCAU	Cleavage	pacid=371765

2557	2578	UGGAAUCUU	: ::.:::::::. ::.::.:	CGGCGGCAU	Cleavage	pacid=371765
2662	2683	UGGAAUCUU	: ::.:::::::. ::.::.:	CGGCGGCAU	Cleavage	pacid=371765
965	986	UGGAAUCUU	::::: . .::::.::::::	CUGCAUAGC	Cleavage	pacid=371781
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	359	GGAAUCUUG	.:::. :::: :: :::::::	UUGCGCCAU	Translation	pacid=371780
339	360	UGGAAUCUU	.:::. :::: :: ::::::::	UUGCGCCAU	Cleavage	pacid=371780
339	360	UGGAAUCUU	.:::. :::: :: ::::::::	UUGCGCCAU	Cleavage	pacid=371780
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1433	1453	GGAAUCUUG	:::::::.:: .::::.:	AUGCAGCAU	Cleavage	pacid=371454
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468

1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1542	1562	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
1731	1751	GGAAUCUUG	::::::: :.::: :::: ::	CUGCAGCUU	Cleavage	pacid=371468
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
2495	2515	GGAAUCUUG	:: :: :::. :::.::::::	CUCCAACAUU	Translation	pacid=371476
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
128	148	GGAAUCUUG	.::::::::.. ::::::.:	UUGCAGCAU	Translation	pacid=371454
125	148	GGAAUCUUG	::.:::::::::.. ::::::	GUGUUGCAG	Translation	pacid=371454
1083	1104	UGGAAUCUU	::..::::.:: :.:::::..	GUGUGGCAU	Translation	pacid=371476
1216	1237	UGGAAUCUU	::..::::.:: :.:::::..	GUGUGGCAU	Translation	pacid=371476
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
485	505	GGAAUCUUG	:.:::::.:::::::.	GAAAUGUAU	Cleavage	pacid=371481
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621

718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
718	738	GGAAUCUUG	.: ..::::. :::::.::::	UUUUGGCAU	Translation	pacid=371621
715	738	GGAAUCUUG	:: .: ..::::. :::::.::	CUUUUUUGG	Translation	pacid=371621
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
1703	1723	GGAAUCUUG	::: .:. :.:::::::::..	CUGAGGUUU	Cleavage	pacid=371526
338	359	UGGAAUCUU	:::::: :::::::: .::	GUGCAGCCU	Cleavage	pacid=371531
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2329	2349	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371736
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716

2135	2155	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
2296	2316	GGAAUCUUG	:::: :. ::::::.::::.	CUGCUGUUU	Cleavage	pacid=371716
177	198	UGGAAUCUU	.:::::.. .:::::: ::.:	UUGCAGUGG	Cleavage	pacid=371720
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1372	1392	GGAAUCUUG	:::.: . :::::::::: ::	CUGUAAUCU	Cleavage	pacid=371717
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1096	1116	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
1247	1267	GGAAUCUUG	:: :: .: :::::.::::::	CUUCACUACC	Cleavage	pacid=371722
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
308	328	GGAAUCUUG	::::: : ::::::::. ::.	CUGCACCCUC	Cleavage	pacid=371717
305	328	GGAAUCUUG	:::::: : ::::::::. :	AUGCUGCACC	Cleavage	pacid=371717
2106	2126	GGAAUCUUG	:: ::::::::: :::..	AAUCAACAUC	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: ::::::::: :::..	AAUCAACAUC	Cleavage	pacid=371734

2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
2106	2126	GGAAUCUUG	:: :::::::: :::..	AAUCAACAU	Cleavage	pacid=371734
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
195	215	GGAAUCUUG	:::::::::::::.	UCAAGACAU	Cleavage	pacid=371729
494	515	UGGAAUCUU	: : :::::..::::: ::	GGACCGGAU	Cleavage	pacid=371666
555	576	UGGAAUCUU	: : :::::..::::: ::	GGACCGGAU	Cleavage	pacid=371666
188	209	UGGAAUCUU	:: :::::.:::::: : .::	CUCCAGCGU	Cleavage	pacid=371655
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610

836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
833	853	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
836	856	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
938	958	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371610
941	961	GGAAUCUUG	.::: ::: :::::.::::.	UUGCUGCAG	Cleavage	pacid=371609
830	853	GGAAUCUUG	:.::: ::: :::::.::::	UGGUUGCUG	Cleavage	pacid=371610
833	856	GGAAUCUUG	:.::: ::: :::::.::::	UGGUUGCUG	Cleavage	pacid=371610
935	958	GGAAUCUUG	:.::: ::: :::::.::::	UGGUUGCUG	Cleavage	pacid=371610
938	961	GGAAUCUUG	:.::: ::: :::::.::::	UGGUUGCUG	Cleavage	pacid=371609
833	854	UGGAAUCUU	.::: ::: :::::.::::. :	UUGCUGCAG	Cleavage	pacid=371610
836	857	UGGAAUCUU	.::: ::: :::::.::::. :	UUGCUGCAG	Cleavage	pacid=371610
938	959	UGGAAUCUU	.::: ::: :::::.::::. :	UUGCUGCAG	Cleavage	pacid=371610
941	962	UGGAAUCUU	.::: ::: :::::.::::. :	UUGCUGCAG	Cleavage	pacid=371609
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
504	525	GGAAUCUUG	.::::: .:::::. ::::::	UUGCAGAUA	Cleavage	pacid=371614
501	525	GGAAUCUUG	:.::::: .:::::. ::::	GAGUUGCAG	Cleavage	pacid=371614
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
746	766	GGAAUCUUG	.::..::::. ::::: ::::	UUGUGGCAU	Translation	pacid=371578
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAAC	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAAC	Translation	pacid=371576

20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
20	40	GGAAUCUUG	:::::::: : :::::.::..	CUGCAGCAA	Translation	pacid=371576
17	40	GGAAUCUUG	.: :::::::: : :::::.::	UUUCUGCAG	Translation	pacid=371576
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
567	587	GGAAUCUUG	::: :::::..:.:: ::::.	CUGGAGCAU	Cleavage	pacid=371598
564	587	GGAAUCUUG	:::: :::::..:.:: :::	AGGCUGGAG	Cleavage	pacid=371598
567	588	UGGAAUCUU	::: :::::..:.:: ::::.:	CUGGAGCAU	Cleavage	pacid=371598
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
627	646	GGAAUCUUG	.:: :::::::::::: :::.	UUGAAGCAU	Cleavage	pacid=371604
1448	1470	UGGAAUCUU	.:::.: :.::.::::::::::.	UUGUAUGUA	Cleavage	pacid=371614
1154	1175	UGGAAUCUU	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
1154	1175	UGGAAUCUU	:::. :::::::.:.::::	AUGCGAAAU	Cleavage	pacid=371505
94	114	UGGAAUCUU	: ::::::::: ::: ::::::	CAGCAGCAU	Translation	pacid=371511
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
1001	1021	GGAAUCUUG	.: ::::::.::. .::::.:	UUACAGCAU	Cleavage	pacid=371502
65	86	UGGAAUCUU	.:::::::::::::: :	UGAUAGCAU	Cleavage	pacid=371423

441	462	UGGAAUCUU	:::: :::..:::: .:::.:	GUGCAACAU	Cleavage	pacid=371565
1075	1096	UGGAAUCUU	.::.: ::: :::::::	GGUUAGUAA	Translation	pacid=371565
1075	1096	UGGAAUCUU	.::.: ::: :::::::	GGUUAGUAA	Translation	pacid=371565
1397	1418	UGGAAUCUU	.:::: :.:..::::::::..	UUGCACCGU	Cleavage	pacid=371485
119	141	UGGAAUCUU	:::::: :. :..::::::	GUGCAGCAG	Cleavage	pacid=371694
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1408	1428	GGAAUCUUG	.:::: :::.::..:::::	UUGCACCAU	Cleavage	pacid=371688
1981	2001	UGGAAUCUU	.:::::::::.:..: ::::.:	UUGCAGCAU	Cleavage	pacid=371683
1989	2009	UGGAAUCUU	.:::::::::.:..: ::::.:	UUGCAGCAU	Cleavage	pacid=371683
1996	2016	UGGAAUCUU	.:::::::::.:..: ::::.:	UUGCAGCAU	Cleavage	pacid=371683
1546	1567	UGGAAUCUU	::: :::::: :::::: ::	CUGAAGCAU	Cleavage	pacid=371686
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1080	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371777
1061	1081	UGGAAUCUU	::::.::::..::::: ::::	CUGCGGCAU	Cleavage	pacid=371777
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1249	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371779
1230	1250	UGGAAUCUU	::::.::::..::::: ::::	CUGCGGCAU	Cleavage	pacid=371779
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765

1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1216	1235	GGAAUCUUG	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1213	1235	GGAAUCUUG	::::::.::::..::::: ::	AUGCUGCGG	Cleavage	pacid=371765
1216	1236	UGGAAUCUU	::::.::::..::::: :::.	CUGCGGCAU	Cleavage	pacid=371765
1402	1425	GGAAUCUUG	: :: :::::: :::::.:.::	CAGCAGCAG	Cleavage	pacid=371771
1490	1513	GGAAUCUUG	: :: :::::: :::::.:.::	CAGCAGCAG	Cleavage	pacid=371771
1603	1626	GGAAUCUUG	: :: :::::: :::::.:.::	CAGCAGCAG	Cleavage	pacid=371771
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
976	996	GGAAUCUUG	::: ::::::: :::::::	CUGAAGCAU	Translation	pacid=371783
973	996	GGAAUCUUG	::: ::::::: :::::::	UAACUGAAG	Translation	pacid=371783
2361	2382	UGGAAUCUU	::...:::::::::::: :	GUGUGGCAU	Cleavage	pacid=371461
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2388	2408	GGAAUCUUG	:::: :.:::. ::::.:::	CUGCCGUAU	Translation	pacid=371483
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2271	2291	GGAAUCUUG	::::::: :: .::::::.:	CUGCAGCUU	Translation	pacid=371450
2268	2291	GGAAUCUUG	.::::::::: :: .::::::	UUGCUGCAG	Translation	pacid=371450
2271	2292	UGGAAUCUU	::::::: :: .::::::.::	CUGCAGCUU	Translation	pacid=371450
188	209	GGAAUCUUG	::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG	::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460

188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
188	209	GGAAUCUUG-	:::::::. :::: ::::::::.	CUGCAGUCU	Cleavage	pacid=371460
185	209	GGAAUCUUG-	:: ::::::. :::: ::::::	CUCCUGCAG	Cleavage	pacid=371460
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1479	1499	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371632
1484	1504	GGAAUCUUG	::::: :::..::::: ::.	CUGCAUCAU	Cleavage	pacid=371631
1476	1499	GGAAUCUUG	:::::: :::..::::: ::	AGGCUGCAU	Cleavage	pacid=371632
1481	1504	GGAAUCUUG	:::::: :::..::::: ::	AGGCUGCAU	Cleavage	pacid=371631
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1200	1220	GGAAUCUUG	.::::::: :: .::::::.	UUGCAGCAG	Translation	pacid=371615
1197	1220	GGAAUCUUG	::.::::::: :: .:::::::	AUGUUGCAG	Translation	pacid=371615
1200	1221	UGGAAUCUU	.::::::: :: .::::::. :	UUGCAGCAG	Translation	pacid=371615
1703	1724	UGGAAUCUU	::: .:. :.:::::::::...	CUGAGGUUU	Cleavage	pacid=371526
1181	1203	UGGAA-UCU	:::::::::::. ::: ::::	GUGCAGCAU	Cleavage	pacid=371529
1262	1284	UGGAA-UCU	:::::::::::. ::: ::::	GUGCAGCAU	Cleavage	pacid=371529

239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
239	259	GGAAUCUUG	::: .::::. ::::::::.	CUGAGGCAU	Translation	pacid=371721
2329	2350	UGGAAUCUU	:::: :. ::::::.::::. :	CUGCUGUUU	Cleavage	pacid=371736
2296	2317	UGGAAUCUU	:::: :. ::::::.::::. :	CUGCUGUUU	Cleavage	pacid=371716
2135	2156	UGGAAUCUU	:::: :. ::::::.::::. :	CUGCUGUUU	Cleavage	pacid=371716
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
177	197	GGAAUCUUG	.:::::.. .:::::: ::.	UUGCAGUGG	Cleavage	pacid=371720
174	197	GGAAUCUUG	::.:::::.. .:::::: :	GUGUUGCAG	Cleavage	pacid=371720
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
101	121	GGAAUCUUG	:: .::::: ::: ::::.	CUCUAGCAU	Translation	pacid=371731
308	329	UGGAAUCUU	::::: : ::::::::. ::..	CUGCACCCUC	Cleavage	pacid=371717
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
41	61	GGAAUCUUG	:: ..::::.:::.::: ::.	CUCUGGCAU	Cleavage	pacid=371664
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673

764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
764	784	GGAAUCUUG	.::::::::.::. : .::.:	UUGCAGCAU	Cleavage	pacid=371673
1518	1539	UGGAAUCUU	.:::::.: :::... .:::::	UUGCAGUAC	Cleavage	pacid=371650
2961	2984	GGAAUCUUG	::::::::.::..: :	UUUAUGCAG	Cleavage	pacid=371581
2964	2985	UGGAAUCUU	::::::::.::..: : :.:	AUGCAGCAU	Cleavage	pacid=371581
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1707	GGAAUCUUG	:::..: : :::::::::.	CUGUGGGAA	Cleavage	pacid=371596
1687	1708	UGGAAUCUU	:::..: : :::::::::. :	CUGUGGGAA	Cleavage	pacid=371596
230	251	UGGAAUCUU	::::: ::: ::::::::	CUGCAGAAU	Translation	pacid=371577
20	41	UGGAAUCUU	::::::: : :::::.::.	CUGCAGCAA	Cleavage	pacid=371576
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
203	223	GGAAUCUUG	:::: ::::::.: ::::.	CUGCAACAU	Cleavage	pacid=371610
471	493	GGAAUCUUG	.:::::::: ::.::. ::::	UUGCUGCAG-	Cleavage	pacid=371584
474	494	UGGAAUCUU	::::: ::.::. ::::::.:	CUGCAG-AUU	Cleavage	pacid=371584
163	186	GGAAUCUUG	:::: ::: .::::::: ::	CUGCAGCAA	Cleavage	pacid=371613
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: ::::	UUGCUGCAU	Cleavage	pacid=371498

1986	2007	GGAAU-CUUG	.::: :::::::..:: :::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2007	GGAAU-CUUG	.::: :::::::..:: :::::	UUGCUGCAU	Cleavage	pacid=371498
1986	2008	UGGAAU-CU	.::: :::::::..:: :::::	UUGCUGCAU	Cleavage	pacid=371498
3055	3078	GGAAUCUUG	.:: :::: ::.::::::::::	UUGAUGCAA	Cleavage	pacid=371424
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
1147	1167	GGAAUCUUG	:::: ::::.:::. :.:::	CUGCUGCAU	Cleavage	pacid=371560
2140	2162	UGGAAUCUU	:: .::: :::::::::. :.:	CUAUAGCUA	Cleavage	pacid=371559
1941	1962	UGGAAUCUU	::.: : :::::::::::	AUGUACCUU	Cleavage	pacid=371568
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1075	1095	GGAAUCUUG	.::.: ::: :::::::	GGUUAGUAA	Cleavage	pacid=371565
1072	1095	GGAAUCUUG	.::.: ::: ::::::	UAAGGUUAG	Cleavage	pacid=371565
1072	1095	GGAAUCUUG	.::.: ::: ::::::	UAAGGUUAG	Cleavage	pacid=371565

Multiplicity	Target_Acc.	ID	locusName	Pfam	Panther
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.003G241900.1	Phvul.003G241900	Phvul.003G24	PF00847	PTHR32467,P
1	Phvul.003G241900.1	Phvul.003G241900	Phvul.003G24	PF00847	PTHR32467,P
1	Phvul.003G241900.1	Phvul.003G241900	Phvul.003G24	PF00847	PTHR32467,P
1	Phvul.003G241900.1	Phvul.003G241900	Phvul.003G24	PF00847	PTHR32467,P
1	Phvul.003G241900.1	Phvul.003G241900	Phvul.003G24	PF00847	PTHR32467,P
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1	Phvul.003G241900.1	Phvul.003G241900	Phvul.003G24	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P

1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
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1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.2	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.011G071100.1	Phvul.011G071100	Phvul.011G07	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
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1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
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1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.2	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.L000308.1	Phvul.L000308	Phvul.L00030	PF00847	PTHR32467,P
1	Phvul.001G174400.1	Phvul.001G174400	Phvul.001G17	PF00847	PTHR32467,P
1	Phvul.002G016900.1	Phvul.002G016900	Phvul.002G01	PF00847	PTHR32467,P
1	Phvul.003G241900.1	Phvul.003G241900	Phvul.003G24	PF00847	PTHR32467,P
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1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0	0
1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
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1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0	0
1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0	0
1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
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1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
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1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
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1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
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1	Phvul.005G132300.2	Phvul.005G132300	Phvul.005G13	0	0
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1	Phvul.005G132300.1	Phvul.005G132300	Phvul.005G13	0	0
1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24	PF00847	PTHR32467,P
1	Phvul.007G240200.1	Phvul.007G240200	Phvul.007G24	PF00847	PTHR32467,P
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1	Phvul.001G233200.2	Phvul.001G233200	Phvul.001G23	0	0
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1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03	PF10258	PTHR13135
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1	Phvul.002G330500.1	Phvul.002G330500	Phvul.002G33	0	PTHR14513
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1	Phvul.008G033900.3	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
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1	Phvul.008G033900.2	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
1	Phvul.008G033900.3	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
1	Phvul.008G033900.1	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
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1	Phvul.008G033900.3	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P

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1	Phvul.008G033900.3	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
1	Phvul.008G033900.1	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
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1	Phvul.008G033900.3	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
1	Phvul.008G033900.1	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
1	Phvul.008G033900.2	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
1	Phvul.008G033900.3	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
1	Phvul.008G033900.1	Phvul.008G033900	Phvul.008G03	0	PTHR13890,P
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1	Phvul.009G130700.1	Phvul.009G130700	Phvul.009G13	PF00651	PTHR24413,P
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1	Phvul.009G130700.1	Phvul.009G130700	Phvul.009G13	PF00651	PTHR24413,P
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2	Phvul.011G082801.1	Phvul.011G082801	Phvul.011G08	0	0
1	Phvul.011G150950.1	Phvul.011G150950	Phvul.011G15	PF11883,PF0	PTHR27002,P
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2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15	PF08276,PF0	PTHR27002,P
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1	Phvul.011G152400.1	Phvul.011G152400	Phvul.011G15	PF11883,PF08	PTHR27002,P
1	Phvul.011G168400.2	Phvul.011G168400	Phvul.011G16	PF08276,PF0	PTHR27002,P
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1	Phvul.001G033700.2	Phvul.001G033700	Phvul.001G03	PF10258	PTHR13135
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1	Phvul.002G276700.2	Phvul.002G276700	Phvul.002G27	PF00130,PF0	PTHR11255,P
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1	Phvul.002G276700.3	Phvul.002G276700	Phvul.002G27	PF00130,PF0	PTHR11255,P
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1	Phvul.006G181200.1	Phvul.006G181200	Phvul.006G18	PF02362,PF06	PTHR31384,P
1	Phvul.006G181200.1	Phvul.006G181200	Phvul.006G18	PF02362,PF06	PTHR31384,P
1	Phvul.006G181200.1	Phvul.006G181200	Phvul.006G18	PF02362,PF06	PTHR31384,P

1	Phvul.006G181200.1	Phvul.006G181200	Phvul.006G18	PF02362,PF06	PTHR31384,P
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1	Phvul.007G234200.1	Phvul.007G234200	Phvul.007G23	PF02485	PTHR31042,P
1	Phvul.007G236400.1	Phvul.007G236400	Phvul.007G23	PF13857,PF11	PTHR12447
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1	Phvul.008G058700.2	Phvul.008G058700	Phvul.008G05	PF01657,PF07	PTHR27002,P
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1	Phvul.008G058700.2	Phvul.008G058700	Phvul.008G05	PF01657,PF07	PTHR27002,P
1	Phvul.008G058700.1	Phvul.008G058700	Phvul.008G05	PF01657,PF07	PTHR27002,P
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1	Phvul.008G058700.2	Phvul.008G058700	Phvul.008G05	PF01657,PF07	PTHR27002,P
1	Phvul.008G058700.1	Phvul.008G058700	Phvul.008G05	PF01657,PF07	PTHR27002,P
1	Phvul.008G058700.2	Phvul.008G058700	Phvul.008G05	PF01657,PF07	PTHR27002,P
1	Phvul.008G058700.1	Phvul.008G058700	Phvul.008G05	PF01657,PF07	PTHR27002,P

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1	Phvul.009G014600.2	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.1	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.2	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.1	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
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1	Phvul.009G014600.1	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.2	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
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1	Phvul.009G014600.2	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.1	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.2	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
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1	Phvul.009G014600.2	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.1	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
1	Phvul.009G014600.2	Phvul.009G014600	Phvul.009G01	PF00561	PTHR10992,P
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1	Phvul.001G169200.1	Phvul.001G169200	Phvul.001G16	PF15511	PTHR10484
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1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428	PTHR23012,P
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1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.1	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.1	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.1	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.1	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
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1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
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1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
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1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
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1	Phvul.001G212400.2	Phvul.001G212400	Phvul.001G21	PF12428		PTHR23012,P
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1	Phvul.001G232300.2	Phvul.001G232300	Phvul.001G23	PF07714		PTHR27001,P
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1	Phvul.001G232300.2	Phvul.001G232300	Phvul.001G23	PF07714		PTHR27001,P
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1	Phvul.003G260000.1	Phvul.003G260000	Phvul.003G26	PF05577	PTHR11010,P
1	Phvul.003G260000.3	Phvul.003G260000	Phvul.003G26	PF05577	PTHR11010,P
1	Phvul.003G260000.2	Phvul.003G260000	Phvul.003G26	PF05577	PTHR11010,P
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1	Phvul.008G089600.3	Phvul.008G089600	Phvul.008G08	PF14938	PTHR13768,P
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1	Phvul.008G089600.3	Phvul.008G089600	Phvul.008G08	PF14938	PTHR13768,P
1	Phvul.008G089600.4	Phvul.008G089600	Phvul.008G08	PF14938	PTHR13768,P
1	Phvul.008G089600.3	Phvul.008G089600	Phvul.008G08	PF14938	PTHR13768,P
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1	Phvul.011G152400.1	Phvul.011G152400	Phvul.011G15	PF11883,PF08	PTHR27002,P
1	Phvul.011G152400.1	Phvul.011G152400	Phvul.011G15	PF11883,PF08	PTHR27002,P
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1	Phvul.011G168400.2	Phvul.011G168400	Phvul.011G16	PF08276,PF00	PTHR27002,P
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1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
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1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
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1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G32	PF14226,PF03	PTHR10209,P
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1	Phvul.003G189300.1	Phvul.003G189300	Phvul.003G18	PF02701	PTHR31089,P
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1	Phvul.003G189300.1	Phvul.003G189300	Phvul.003G18	PF02701	PTHR31089,P
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1	Phvul.003G189300.1	Phvul.003G189300	Phvul.003G18	PF02701	PTHR31089,P
1	Phvul.003G189300.2	Phvul.003G189300	Phvul.003G18	PF02701	PTHR31089,P
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1	Phvul.006G106400.1	Phvul.006G106400	Phvul.006G10	PF00512,PF01	PTHR24423,P
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1	Phvul.006G106400.1	Phvul.006G106400	Phvul.006G10	PF00512,PF01	PTHR24423,P

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1	Phvul.006G136700.3	Phvul.006G136700	Phvul.006G13	PF03765,PF0	PTHR23324,P
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1	Phvul.006G136700.3	Phvul.006G136700	Phvul.006G13	PF03765,PF0	PTHR23324,P
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1	Phvul.006G136700.3	Phvul.006G136700	Phvul.006G13	PF03765,PF0	PTHR23324,P
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1	Phvul.006G136700.3	Phvul.006G136700	Phvul.006G13	PF03765,PF0	PTHR23324,P
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1	Phvul.006G136700.3	Phvul.006G136700	Phvul.006G13	PF03765,PF0	PTHR23324,P
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1	Phvul.006G136700.3	Phvul.006G136700	Phvul.006G13	PF03765,PF0	PTHR23324,P
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1	Phvul.008G048600.2	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.3	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.2	Phvul.008G048600	Phvul.008G04	0	0
1	Phvul.008G048600.1	Phvul.008G048600	Phvul.008G04	0	0
1	Phvul.008G048600.3	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.3	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.1	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.4	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.3	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.2	Phvul.008G048600	Phvul.008G04	0	0
1	Phvul.008G048600.1	Phvul.008G048600	Phvul.008G04	0	0
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1	Phvul.008G048600.4	Phvul.008G048600	Phvul.008G04	0	0
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2	Phvul.011G152100.3	Phvul.011G152100	Phvul.011G15	PF08276,PF0	PTHR27002,P
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2	Phvul.011G152100.1	Phvul.011G152100	Phvul.011G15	PF08276,PF0	PTHR27002,P
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KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
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0	0	K09284	GO:0006355,(	AT4G36920.2	AP2,FL1,FLO2
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0	0	K09284	GO:0006355,(	AT2G28550.2	RAP2.7,TOE1
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0	5.3.99.6	K10525	GO:0016853,(	AT3G25780.1	AOC3
KOG0374	3.1.3.16	0	GO:0005515,(	AT2G27210.1	BSL3
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
0	0	K14291	0	AT3G20430.1	0
0	0	K14291	0	AT3G20430.1	0
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0	0	0	0	AT1G06590.1	0
0	0	0	0	AT1G02610.1	0
0	0	0	0	AT1G02610.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT5G67380.1	ATCKA1,CKA1
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0	2.7.11.1	K03097	GO:0006468,(	AT5G67380.1	ATCKA1,CKA1
0	2.7.11.1	K03097	GO:0006468,(	AT5G67380.1	ATCKA1,CKA1
0	2.3.1.45	0	0	AT2G34410.2	0
0	4.4.1.19	0	GO:0019295	AT4G21320.1	HSA32
0	0	0	GO:0043047,(	AT5G06310.1	AtPOT1b
0	0	0	GO:0043047,(	AT5G06310.1	AtPOT1b
KOG1558	0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558	0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
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0	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48

KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
KOG1282	3.4.16.5	K16298	GO:0006508,(	AT3G45010.1	scpl48
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KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
KOG1441	0	0	GO:0055085	AT3G11320.1	0
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KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1	0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
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KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
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0	0	K15032	GO:0006355,(	AT2G03050.1	EMB93,SOLDAT1(
0	0	K15032	GO:0006355,(	AT2G03050.1	EMB93,SOLDAT1(
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0	0	K15032	GO:0006355,(	AT2G03050.1	EMB93,SOLDAT1(
0	0	K15032	GO:0006355,(	AT2G03050.1	EMB93,SOLDAT1(
0	0	K15032	GO:0006355,(	AT2G03050.1	EMB93,SOLDAT1(
0	0	K15032	GO:0006355,(	AT2G03050.1	EMB93,SOLDAT1(
0	0	K15032	GO:0006355,(	AT2G03050.1	EMB93,SOLDAT1(
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2

KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
KOG1399	1.14.13.168	K11816	0	AT4G13260.1	YUC2
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
KOG1809	0	0	0	AT1G48090.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
0	2.7.11.1	K03097	GO:0006468,(	AT3G50000.1	ATCKA2,CKA2
KOG1558	0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558	0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558	0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558	0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558	0	K14709	GO:0055085,(	AT1G31260.1	ZIP10

KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG1558		0	K14709	GO:0055085,(	AT1G31260.1	ZIP10
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG0374	3.1.3.16		0	GO:0005515,(	AT2G27210.1	BSL3
KOG1471		0	0	0	AT5G47730.1	0
KOG1471		0	0	0	AT5G47730.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
	0	0	0	0	AT5G03170.1	ATFLA11,FLA11
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
	0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT

0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
0	0	K14486	GO:0003677,(	AT2G33860.1	ARF3,ETT
0	0	0	GO:0016020,(	AT3G52060.2	0
0	0	0	GO:0016020,(	AT3G52060.2	0
0	0	0	GO:0016020,(	AT3G52060.2	0
0	0	0	GO:0016020,(	AT3G52060.2	0
0	0	0	GO:0016020,(	AT3G52060.2	0
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0	0	0	GO:0016020,(	AT3G52060.2	0
0	0	0	GO:0016020,(	AT3G52060.2	0
0	0	0	GO:0016020,(	AT3G52060.2	0
KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
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KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
KOG0522	0	0	0	AT1G04780.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29
KOG1187	2.7.11.1	0	GO:0006468,(	AT4G21410.1	CRK29

KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	0	0	AT5G17690.1	LHP1,TFL2
0	0	K10523	GO:0005515	AT4G08455.1	0
0	0	0	0	AT3G50140.1	0
0	0	0	0	AT3G50140.1	0
0	0	0	0	AT3G50140.1	0
0	0	0	0	AT3G50140.1	0
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0	0	0	0	AT3G50140.1	0
0	0	0	0	AT3G50140.1	0
0	0	0	0	AT3G50140.1	0
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0	0	0	0	AT3G50140.1	0
0	0	0	0	AT3G50140.1	0
0	0	0	0	AT3G50140.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2	0
0	0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV

	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
	0		0	K09338		GO:0003677,(	AT5G60690.1	IFL,IFL1,REV	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543		3.4.22.33			0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0048544,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0004674,(	AT4G27290.1		0
KOG1187		2.7.11.1			0	GO:0004674,(	AT4G27290.1		0
	0	3.1.1.3			0	GO:0016788	AT5G33370.1		0

	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
	0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
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KOG2275	3.5.1.14	K14677	GO:0016787,(	AT4G38220.1	0
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KOG3467	0	K11254	0	AT2G28740.1	HIS4
KOG3467	0	K11254	0	AT2G28740.1	HIS4
KOG3467	0	K11254	0	AT2G28740.1	HIS4
KOG3467	0	K11254	0	AT2G28740.1	HIS4
KOG3467	0	K11254	0	AT2G28740.1	HIS4
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KOG3467	0	K11254	0	AT2G28740.1	HIS4
KOG3467	0	K11254	0	AT2G28740.1	HIS4
KOG3467	0	K11254	0	AT2G28740.1	HIS4
0	0	0	0	AT3G53320.1	0
0	0	0	0	AT3G53320.1	0
0	0	0	0	AT3G53320.1	0
0	0	0	0	AT3G53320.1	0
0	0	0	0	AT3G53320.1	0
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0	0	0	0	AT1G02610.1	0
0	0	0	0	AT1G02610.1	0
0	0	0	0	AT1G02610.1	0

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	0	0	0	0	AT1G02610.1	0
	0	0	0	0	AT1G02610.1	0
KOG2231		0	0	0	AT3G62240.1	0
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KOG2231		0	0	0	AT3G62240.1	0
KOG2231		0	0	0	AT3G62240.1	0
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KOG2231		0	0	0	AT3G62240.1	0
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KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
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KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
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KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B
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KOG1187	2.7.11.1,2.7.1		0	GO:0006468,	AT2G28930.1	APK1B,PK1B

KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT2G28930.1	APK1B,PK1B
KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT2G28930.1	APK1B,PK1B
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0	2.3.1.45	0	0	AT2G34410.2	0
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0	2.3.1.45	0	0	AT2G34410.2	0
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0	4.4.1.19	0	GO:0019295	AT4G21320.1	HSA32
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	0		0		0	GO:0006355,(		AT5G46590.1	anac096,NAC096	
	0		0		0	GO:0006355,(		AT5G46590.1	anac096,NAC096	

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KOG2182	3.4.21.26		0	GO:0008236,(	AT4G36195.1		0
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KOG2182	3.4.21.26		0	GO:0008236,(	AT4G36195.1		0
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KOG2182	3.4.21.26		0	GO:0008236,(	AT4G36195.1		0
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
KOG4742	3.2.1.14	K01183		GO:0008061,(	AT3G12500.1	ATHCHIB,B-CHI,C	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	0	AT4G13750.1	NOV	
	0	0	0	GO:0016020	AT3G01100.1	ATHYP1,HYP1	

	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0016020	AT3G01100.1	ATHYP1,HYP1
	0	0		0	GO:0005515	AT5G22720.1	0
	0	0		0	GO:0005515	AT5G22720.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
	0	0	K19041		GO:0008270,(	AT1G53190.1	0
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG1187	2.7.11.1			0	GO:0004674,(	AT4G21380.1	ARK3,RK3
KOG0645		0		0	GO:0005515	AT1G52360.1	0
KOG0645		0		0	GO:0005515	AT1G52360.1	0
KOG0645		0		0	GO:0005515	AT1G52360.1	0

KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
KOG0645			0		0	GO:0005515	AT1G52360.1	0
	0		0		0	GO:0006886,(	AT2G38020.1	EMB258,MAN,VC
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1902			0	K14404		0	AT1G30460.1	ATCPSF30,CPSF3(
KOG1441			0		0	GO:0055085	AT3G11320.1	0
	0		0	K14486		GO:0003677,(	AT2G33860.1	ARF3,ETT
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
KOG1187		2.7.11.1			0	GO:0005515,(	AT1G68400.1	0
	0	2.1.1.193			0	GO:0008168,(	AT1G50000.1	0

0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
0	0	0	GO:0006355,(	AT4G09620.1	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
0	0	0	0	AT2G38570.1	0
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS

KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG1586	0	0	GO:0006886	AT3G56190.1	ALPHA-SNAP2,AS
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
KOG0192	2.7.11.1	0	GO:0005515,(	AT3G24715.1	0
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	1.3.3.3	K00228	GO:0055114,(	AT1G03475.1	ATCPO-I,HEMF1,L
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1

0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1	
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1	
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1	
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1	
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1	
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1	
0	0	0	0	AT5G17690.1	LHP1,TFL2	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	GO:0016788	AT1G53920.1	GLIP5	
0	0	0	0	AT3G02645.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G51990.1		0
0	0	K07399	0	AT1G49380.1		0
0	0	K07399	0	AT1G49380.1		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1187	2.7.11.1	0	GO:0006468,(	AT3G14840.2		0
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	

KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12	
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
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0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
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0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
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0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
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0	2.7.11.1	0	GO:0048544,(	AT4G27290.1		0
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KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
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KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
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KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27290.1	0
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KOG1187	2.7.11.1	0	GO:0004674,(	AT4G27300.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
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KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0

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KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
KOG1187	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	K10268	GO:0005515	AT4G02760.2	0
0	0	0	0	AT5G03150.1	JKD
0	0	0	0	AT5G03150.1	JKD
0	0	0	0	AT5G03150.1	JKD
0	0	0	0	AT5G03150.1	JKD
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0	0	0	0	AT5G03150.1	JKD
0	0	0	0	AT5G03150.1	JKD
0	1.10.3.3	0	GO:0055114,(	AT1G55570.1	sks12
0	1.10.3.3	0	GO:0055114,(	AT1G55570.1	sks12
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
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0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49

0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	5.2.1.8	K10598	GO:0006457,(	AT5G67530.1	ATPUB49,PUB49
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
0	1.3.3.8	0	GO:0055114,(	AT2G34790.1	EDA28,MEE23
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10530.1	0
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1235	3.6.3.46	0	0	AT5G64940.1	ATATH13,ATH13,
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2

KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
KOG1169	2.7.1.107	0	GO:0035556,(	AT5G63770.2	ATDGK2,DGK2
0	0	0	GO:0004519	AT2G15820.1	OTP51
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
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KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
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KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EFE
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
KOG0748	0	K07297	GO:0016021	AT5G20270.1	HHP1
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0	0	0	GO:0006355,(	AT3G47500.1	CDF3
0	0	0	GO:0006355,(	AT3G47500.1	CDF3
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0	0	0	GO:0006355,(	AT3G47500.1	CDF3
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0	0	0	GO:0006355,(	AT3G47500.1	CDF3
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0	0	0	GO:0006355,(	AT3G47500.1	CDF3

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0	0	0	GO:0006355,(	AT3G47500.1	CDF3
0	0	0	GO:0006355,(	AT3G47500.1	CDF3
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
KOG0472	2.7.11.1	0	GO:0005515	AT4G20140.1	GSO1
0	0	0	0	AT5G14410.1	0
0	0	0	0	AT5G14410.1	0
0	0	0	0	AT5G14410.1	0
0	0	0	0	AT5G14410.1	0
0	0	0	0	AT5G14410.1	0
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0	0	0	0	AT5G14410.1	0
0	0	0	0	AT5G14410.1	0
0	0	0	0	AT5G14410.1	0
0	0	0	GO:0006355,(	AT5G46590.1	anac096,NAC096
0	0	0	GO:0006355,(	AT5G46590.1	anac096,NAC096
0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
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0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
0	2.7.11.1	K03097	GO:0006468,(	AT2G23070.1	0
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0	0	0	GO:0007165,(	AT5G17680.1	0
0	0	0	GO:0007165,(	AT5G17680.1	0

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0	2.4.1.142	K03842	GO:0016757	AT1G16570.1		0
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0	2.4.1.142	K03842	GO:0016757	AT1G16570.1		0
0	2.4.1.142	K03842	GO:0016757	AT1G16570.1		0
0	0	0	GO:0005089	AT1G79860.1	ATROPGEF12,ME	
KOG0519	2.7.11.1	K14509	GO:0005515,(	AT3G04580.2	EIN4	
KOG0519	2.7.11.1	K14509	GO:0005515,(	AT3G04580.2	EIN4	
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KOG0519	2.7.11.1	K14509	GO:0005515,(	AT3G04580.2	EIN4	
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KOG0519	2.7.11.1	K14509	GO:0005515,(	AT3G04580.2	EIN4	
KOG0519	2.7.11.1	K14509	GO:0005515,(	AT3G04580.2	EIN4	
KOG0519	2.7.11.1	K14509	GO:0005515,(	AT3G04580.2	EIN4	
KOG0519	2.7.11.1	K14509	GO:0005515,(	AT3G04580.2	EIN4	
KOG0519	2.7.11.1	0	GO:0007165,(	AT3G04580.1	EIN4	
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KOG0519	2.7.11.1	0	GO:0007165,(	AT3G04580.1	EIN4	
KOG0519	2.7.11.1	0	GO:0007165,(	AT3G04580.1	EIN4	
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KOG0519	2.7.11.1	0	GO:0007165,(	AT3G04580.1	EIN4	
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KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG0039	1.16.1.7		0	GO:0055114,(	AT5G49740.1	ATFRO7,FRO7
KOG1471		0	0	0	AT5G47730.1	0
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KOG1471		0	0	0	AT5G47730.1	0
KOG1471		0	0	0	AT5G47730.1	0
	0	0	0	0	AT2G45180.1	0
	0	0	0	0	AT2G45180.1	0
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KOG1919	5.4.99.24		0	GO:0009982,(	AT4G21770.1	0
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KOG1919	5.4.99.24	0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24	0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24	0	GO:0009982,(	AT4G21770.1	0
KOG1919	5.4.99.24	0	GO:0009982,(	AT4G21770.1	0
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0	0	0	0	AT5G03170.1	ATFLA11,FLA11
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0	0	0	0	AT5G03170.1	ATFLA11,FLA11
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
KOG4793	2.7.7.7	0	0	AT5G26940.3	0
0	0	0	0	AT3G01680.1	0
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0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
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0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
0	2.5.1.55	K01627	GO:0009058,(	AT1G79500.4	AtkdsA1
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KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0

KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG1187	2.7.11.1	0	GO:0005515,(	AT3G47570.1	0
KOG2913	0	K12386	0	AT5G40670.1	0
KOG2913	0	K12386	0	AT5G40670.1	0
KOG2913	0	K12386	0	AT5G40670.1	0
KOG2913	0	K12386	0	AT5G40670.1	0
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KOG2913	0	K12386	0	AT5G40670.1	0
KOG2913	0	K12386	0	AT5G40670.1	0
KOG0143	1.14.11.32	0	GO:0055114,(	AT5G58660.1	0
KOG0143	1.14.11.32	0	GO:0055114,(	AT5G58660.1	0
KOG0143	1.14.11.32	0	GO:0055114,(	AT5G58660.1	0
KOG0143	1.14.11.32	0	GO:0055114,(	AT5G58660.1	0
KOG0143	1.14.11.32	0	GO:0055114,(	AT5G58660.1	0
KOG0143	1.14.11.32	0	GO:0055114,(	AT5G58660.1	0
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KOG0143	1.14.11.32	0	GO:0055114,(	AT5G58660.1	0
0	2.7.7.15	0	GO:0009058,(	AT2G32260.1	ATCCT1,CCT1
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
KOG4409	2.3.1.51	0	0	AT4G24160.1	0
0	0	0	GO:0046983	AT4G00120.1	EDA33,GT140,IN
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
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KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
KOG1305	0	K14207	GO:0003333	AT3G30390.2	0
0	0	0	GO:0016788	AT1G53920.1	GLIP5

KOG1430	1.1.1.170	K07748	GO:0050662,(	AT2G43420.1	0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
0	2.7.11.1	0	GO:0048544,(	AT4G27290.1	0
0	3.1.1.3	0	GO:0016788	AT5G33370.1	0
0	0	0	0	AT4G36550.1	0
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
0	3.1.1.3	K14674	GO:0006629,(	AT5G04040.1	SDP1
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0	0	0	GO:0007010,(	AT2G41740.1	ATVLN2,VLN2
0	0	0	GO:0007010,(	AT2G41740.1	ATVLN2,VLN2
KOG2231	0	0	0	AT3G62240.1	0
0	0	0	GO:0006629	AT4G16070.1	0
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KOG1471	0	0	0	AT4G36490.1	ATSFH12,SFH12
KOG1471	0	0	0	AT4G36490.1	ATSFH12,SFH12
KOG1471	0	0	0	AT4G36490.1	ATSFH12,SFH12
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
KOG1138	0	K13146	GO:0032039,(	AT3G07530.1	0
0	2.4.1.15,3.1.3	K16055	GO:0005992,(	AT1G60140.1	ATTPS10,TPS10
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1028	0	0	GO:0005515	AT1G74720.1	QKY
KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
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KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
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KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
KOG1973	2.3.1.48	0	GO:0005515	AT4G14920.1	0
KOG2826	0	K05758	GO:0034314,(	AT1G30825.1	ARPC2A,DIS2
KOG2826	0	K05758	GO:0034314,(	AT1G30825.1	ARPC2A,DIS2

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	0	0	K19041	GO:0008270,(	AT1G53190.1	0
	0	0	K19041	GO:0008270,(	AT1G53190.1	0

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KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
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KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
KOG0809	0	0	GO:0005515	AT3G05710.2	ATSYP43,SYP43
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0	2.5.1.36	K09833	GO:0016021,	AT2G18950.1	ATHPT,HPT1,TPT
0	2.5.1.36	K09833	GO:0016021,	AT2G18950.1	ATHPT,HPT1,TPT
0	6.6.1.1	K03403	GO:0016851,	AT5G13630.1	ABAR,CCH,CCH1,
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0	0	0	0	AT5G13390.1	NEF1
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KOG1187	2.7.11.1	0	GO:0005515,	AT3G47570.1	0
0	2.5.1.54	K01626	GO:0009073,	AT1G22410.1	0
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arabi-defline	ID	Annot_defline
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related to AP2.7	Phvul.001G17	K09284 - AP2-
related to AP2.7	Phvul.001G17	K09284 - AP2-
Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
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Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.002G01	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.003G24	PTHR32467:S
Integrase-type DNA-binding superfamily protein	Phvul.003G24	PTHR32467:S
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Integrase-type DNA-binding superfamily protein	Phvul.003G24	PTHR32467:S
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Integrase-type DNA-binding superfamily protein	Phvul.003G24	PTHR32467:S
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related to AP2.7		Phvul.011G07	PTHR32467:S
related to AP2.7		Phvul.011G07	PTHR32467:S
related to AP2.7		Phvul.L00030	PTHR32467:S
related to AP2.7		Phvul.L00030	PTHR32467:S
allene oxide cyclase 3		Phvul.003G11	K10525 - allen
BRI1 suppressor 1 (BSU1)-like 3		Phvul.005G11	PTHR11668//
cysteine-rich RLK (RECEPTOR-like protein kinase) 29		Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29		Phvul.008G05	PTHR27002:S
S-locus lectin protein kinase family protein		Phvul.011G15	PTHR27002:S
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
	0	0	0
	0	0	0
	0	0	0
	0	0	0
	0	0	0
	0	0	0

	0	0	0
	0	0	0
	0	0	0
	0	0	0
	0	0	0
	0	0	0
RING/FYVE/PHD zinc finger superfamily protein		Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein		Phvul.001G21	PTHR23012:S
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
casein kinase alpha 1		Phvul.002G01	K03097 - case
O-acetyltransferase family protein		Phvul.002G19	PTHR13533:S
Aldolase-type TIM barrel family protein		Phvul.002G21	4.4.1.19 - Pho
Nucleic acid-binding, OB-fold-like protein		Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein		Phvul.002G33	PTHR14513 -
zinc transporter 10 precursor		Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor		Phvul.003G26	PTHR11040:S
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G03	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G08	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G08	PF00954//PF
S-locus lectin protein kinase family protein		Phvul.005G08	PF00954//PF
receptor kinase 3		Phvul.005G08	PF00954//PF
serine carboxypeptidase-like 48		Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48		Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48		Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48		Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48		Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48		Phvul.005G13	K16298 - seri

serine carboxypeptidase-like 48	Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48	Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48	Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48	Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48	Phvul.005G13	K16298 - seri
serine carboxypeptidase-like 48	Phvul.005G13	K16298 - seri
0	0	0
0	0	0
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//
related to AP2.7	Phvul.007G24	PTHR32467:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S
magnesium transporter 4	Phvul.008G03	PTHR13890:S

magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
magnesium transporter 4		Phvul.008G03	PTHR13890:S
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
BTB/POZ domain-containing protein		Phvul.009G13	K10523 - spec
Tetratricopeptide repeat (TPR)-like superfamily protein		Phvul.009G24	PF01535//PF1
	0	0	0
S-locus lectin protein kinase family protein		Phvul.011G15	PF00954//PF0
S-locus lectin protein kinase family protein		Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein		Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein		Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein		Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein		Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein		Phvul.011G15	PF00954//PF0
S-locus lectin protein kinase family protein		Phvul.011G16	PTHR27002:S
	0	Phvul.001G03	PTHR13135 -
	0	Phvul.001G03	PTHR13135 -
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
Plant protein of unknown function (DUF247)		Phvul.001G18	PF03140 - Pla
	0	0	0

0	0	0
casein kinase alpha 1	Phvul.002G01	K03097 - case
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
Mitochondrial transcription termination factor family protein	Phvul.002G08	PTHR13068//
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:SF
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//

Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
Flavin-binding monooxygenase family protein	Phvul.002G31	PTHR23023//
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
trehalose phosphate synthase	Phvul.003G05	2.4.1.15//3.1.
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
casein kinase II, alpha chain 2	Phvul.003G23	K03097 - case
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S

zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
zinc transporter 10 precursor	Phvul.003G26	PTHR11040:S
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
BRI1 suppressor 1 (BSU1)-like 3	Phvul.005G11	PTHR11668//
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S
FASCICLIN-like arabinogalactan-protein 11	Phvul.006G17	PTHR32077:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S

Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.007G23	PTHR31042:S
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
Ankyrin repeat family protein	Phvul.007G23	PF11904//PF1
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S
cysteine-rich RLK (RECEPTOR-like protein kinase) 29	Phvul.008G05	PTHR27002:S

alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 - (
BTB/POZ domain-containing protein	Phvul.009G13	K10523 - spec
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Plant protein of unknown function (DUF247)	Phvul.010G00	PF03140 - Plai
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME

Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
Homeobox-leucine zipper family protein / lipid-binding STAR	Phvul.011G07	PF08670 - ME
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
senescence-associated gene 12	Phvul.011G12	PTHR12411//I
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PFC
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:SI
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//I

GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
Peptidase M20/M25/M40 family protein	Phvul.003G00	3.5.1.14 - N-a
resistance to phytophthora 1	Phvul.001G14	PTHR36359:S
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
histone H4	Phvul.001G16	K11254 - hist
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S

RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/FYVE/PHD zinc finger superfamily protein	Phvul.001G21	PTHR23012:S
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.

protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
protein kinase 1B	Phvul.001G23	2.7.10.2//2.7.
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
O-acetyltransferase family protein	Phvul.002G19	PTHR13533:S
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho
Aldolase-type TIM barrel family protein	Phvul.002G21	4.1.1.19 - Pho

Aldolase-type TIM barrel family protein	Phvul.002G21	4.4.1.19 - Pho
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
Nucleic acid-binding, OB-fold-like protein	Phvul.002G33	PTHR14513 -
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
allene oxide cyclase 3	Phvul.003G11	K10525 - allen
calcium-dependent lipid-binding family protein	Phvul.003G11	PTHR16166:S
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
Leucine-rich receptor-like protein kinase family protein	Phvul.003G20	PF00069//PF
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S

NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G25	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe
Serine carboxypeptidase S28 family protein	Phvul.003G26	3.4.14.2 - Dipe

Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
Serine carboxypeptidase S28 family protein	Phvul.003G263.4.14.2 - Dip	
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
basic chitinase	Phvul.003G26	PTHR22595:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase fam	Phvul.003G29	PTHR32387:S
hypothetical protein 1	Phvul.004G03	PTHR13018//

hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
hypothetical protein 1	Phvul.004G03	PTHR13018//I
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 u
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
receptor kinase 3	Phvul.005G08	PF00954//PF0
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KO
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KO
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KO

Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
Coatomer, beta\' subunit	Phvul.005G17	KOG0265//KC
vacuoleless1 (VCL1)	Phvul.006G02	PTHR12811 - \
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
cleavage and polyadenylation specificity factor 30	Phvul.006G13	PTHR12357:SI
Nucleotide-sugar transporter family protein	Phvul.006G13	PTHR11132//I
Transcriptional factor B3 family protein / auxin-responsive fa	Phvul.006G18	PTHR31384:SI
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
leucine-rich repeat transmembrane protein kinase family prc	Phvul.007G02	PF00560//PFC
methyltransferases	Phvul.007G04	2.1.1.193 - 16

Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Mitochondrial transcription termination factor family protei	Phvul.007G08	PTHR13068:S
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily	Phvul.007G19	KOG4793 - Th
0	0	0
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0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
0	0	0
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph

alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
alpha-soluble NSF attachment protein 2	Phvul.008G08	K15296 - alph
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Protein kinase superfamily protein with octicosapeptide/Phc	Phvul.008G12	PTHR23257//I
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
Coproporphyrinogen III oxidase	Phvul.008G28	1.3.3.3 - Copr
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho

phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
like heterochromatin protein (LHP1)	Phvul.009G11	PTHR22812 -
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:S
Plant protein of unknown function (DUF247)	Phvul.010G15	PF03140 - Pla
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
Protein kinase superfamily protein	Phvul.011G01	2.7.11.1 - Non
cytochrome c biogenesis protein family	Phvul.011G04	K07399 - cyto
cytochrome c biogenesis protein family	Phvul.011G04	K07399 - cyto
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
Leucine-rich repeat transmembrane protein kinase	Phvul.011G06	PF00069//PF1
senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//

senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//
senescence-associated gene 12	Phvul.011G12	PTHR12411//
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S

S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S

S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G16	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G20	PF00954//PF
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
RNI-like superfamily protein	Phvul.001G15	K10268 - F-bo
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
C2H2-like zinc finger protein	Phvul.001G17	PTHR10593:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
SKU5 similar 12	Phvul.001G26	PTHR11709:S
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept

plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
plant U-box 49	Phvul.002G01	K10598 - pept
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
FAD-binding Berberine family protein	Phvul.002G19	1.3.3.8 - Tetra
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PTHR27007:S
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
Concanavalin A-like lectin protein kinase family protein	Phvul.002G21	PF00139//PF
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
ABC2 homolog 13	Phvul.002G26	PTHR10566:S
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:S

diacylglycerol kinase 2	Phvul.002G27	PTHR11255:S
diacylglycerol kinase 2	Phvul.002G27	PTHR11255:S
endonucleases	Phvul.002G30	PF03161 - LA
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
ethylene-forming enzyme	Phvul.002G32	K05933 - ami
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
heptahelical transmembrane protein1	Phvul.003G17	PTHR20855//
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S
cycling DOF factor 3	Phvul.003G18	PTHR31089:S

cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
cycling DOF factor 3	Phvul.003G18	PTHR31089:S	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
Leucine-rich repeat transmembrane protein kinase	Phvul.003G20	PF00560//PF	
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NAC domain containing protein 96	Phvul.003G22	PTHR31989:S	
NAC domain containing protein 96	Phvul.003G22	PTHR31989:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
Protein kinase superfamily protein	Phvul.003G23	PTHR24054:S	
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//	
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//	
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//	
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//	

disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//
disease resistance protein (TIR-NBS-LRR class), putative	Phvul.004G04	PTHR11017//
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
RHO guanyl-nucleotide exchange factor 12	Phvul.005G16	PF03759 - PR
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy

Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
ferric reduction oxidase 7	Phvul.006G13	1.16.1.7 - Ferr
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Sec14p-like phosphatidylinositol transfer family protein	Phvul.006G13	PTHR23324//I
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:SI

Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
Pseudouridine synthase family protein		Phvul.006G15	PTHR11079:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
FASCICLIN-like arabinogalactan-protein 11		Phvul.006G17	PTHR32077:SI
Polynucleotidyl transferase, ribonuclease H-like superfamily		Phvul.007G19	KOG4793 - Th
Polynucleotidyl transferase, ribonuclease H-like superfamily		Phvul.007G19	KOG4793 - Th
	0	Phvul.007G28	PF14577 - Sie
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Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de
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Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PF0
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PF0

Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PFC
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
PQ-loop repeat family protein / transmembrane family prote	Phvul.008G14	K12386 - cysti
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.008G26	PTHR10209:SI
phosphorylcholine cytidylyltransferase	Phvul.008G29	2.7.7.15 - Cho
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
alpha/beta-Hydrolases superfamily protein	Phvul.009G01	PTHR10992//I
basic helix-loop-helix (bHLH) DNA-binding superfamily protei	Phvul.009G14	PTHR12565:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
Transmembrane amino acid transporter family protein	Phvul.009G19	PTHR22950:SI
GDSL-motif lipase 5	Phvul.010G12	PTHR22835:SI

3-beta hydroxysteroid dehydrogenase/isomerase family prot	Phvul.011G05	PTHR10366:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.L00233	PTHR22835//
ARM repeat superfamily protein	Phvul.001G01	PTHR22849:S
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
Patatin-like phospholipase family protein	Phvul.001G12	K14674 - TAG
villin 2	Phvul.001G13	PTHR11977:S
villin 2	Phvul.001G13	PTHR11977:S
villin 2	Phvul.001G13	PTHR11977:S
RING/U-box superfamily protein	Phvul.001G21	PTHR22938 -
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.002G13	PTHR21493//

Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3		Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3		Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3		Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3		Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3		Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3		Phvul.002G13	PTHR21493//
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3		Phvul.002G13	PTHR21493//
SEC14-like 12		Phvul.002G16	PTHR23324:S
SEC14-like 12		Phvul.002G16	PTHR23324:S
SEC14-like 12		Phvul.002G16	PTHR23324:S
	0	Phvul.002G28	K13146 - inte
	0	Phvul.002G28	K13146 - inte
	0	Phvul.002G28	K13146 - inte
	0	Phvul.002G28	K13146 - inte
	0	Phvul.002G28	K13146 - inte
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	0	Phvul.002G28	K13146 - inte
	0	Phvul.002G28	K13146 - inte
	0	Phvul.002G28	K13146 - inte
trehalose phosphate synthase		Phvul.003G05	2.4.1.15//3.1.
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
C2 calcium/lipid-binding plant phosphoribosyltransferase far		Phvul.003G19	PTHR10024:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc fi		Phvul.003G22	PTHR24098:S
Arp2/3 complex, 34 kD subunit p34-Arc		Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc		Phvul.003G27	K05758 - acti

Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
Arp2/3 complex, 34 kD subunit p34-Arc	Phvul.003G27	K05758 - acti
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
F-box/RNI-like superfamily protein	Phvul.004G11	PF00646 - F-b
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
Nucleotide-diphospho-sugar transferases superfamily protei	Phvul.004G17	PTHR12726 -
UDP-Glycosyltransferase superfamily protein	Phvul.005G05	2.4.1.142 - Ch
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 ul
RING/U-box superfamily protein	Phvul.005G06	K19041 - E3 ul

Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Ribosomal protein L19 family protein	Phvul.006G05	PTHR15680:SI
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
Signal transduction histidine kinase, hybrid-type, ethylene se	Phvul.006G10	K14509 - ethy
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
lipid transfer protein 3	Phvul.006G11	PF00234 - Pro
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Bifunctional inhibitor/lipid-transfer protein/seed storage 2S	Phvul.006G13	PTHR31731:SI
syntaxin of plants 43	Phvul.007G19	K08489 - synt
syntaxin of plants 43	Phvul.007G19	K08489 - synt
syntaxin of plants 43	Phvul.007G19	K08489 - synt
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syntaxin of plants 43	Phvul.007G19	K08489 - synt
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih

homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
homogentisate phytyltransferase 1	Phvul.007G22	2.5.1.36 - Trih
magnesium-chelatase subunit chlH, chloroplast, putative /	Phvul.007G25	K03403 - mag
no exine formation 1	Phvul.008G00	PTHR35313:S
no exine formation 1	Phvul.008G00	PTHR35313:S
Protein of unknown function (DUF1666)	Phvul.008G04	PTHR10759//
Protein of unknown function (DUF1666)	Phvul.008G04	PTHR10759//
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Protein of unknown function (DUF1666)	Phvul.008G04	PTHR10759//
Protein of unknown function (DUF1666)	Phvul.008G04	PTHR10759//
Protein of unknown function (DUF1666)	Phvul.008G04	PTHR10759//
Protein of unknown function (DUF1666)	Phvul.008G04	PTHR10759//
Protein of unknown function (DUF1666)	Phvul.008G04	PTHR10759//
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Leucine-rich repeat protein kinase family protein	Phvul.008G09	PF00069//PF
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Class-II DAHP synthetase family protein	Phvul.008G17	2.5.1.54 - 3-d
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.008G19	PTHR13343:S
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.008G19	PTHR13343:S
Lateral organ boundaries (LOB) domain family protein	Phvul.008G25	PTHR31301:S
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
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epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//

epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
epsin N-terminal homology (ENTH) domain-containing prote	Phvul.009G09	PTHR22951//
Vacuolar sorting protein 39	Phvul.010G05	PTHR12894:S
Basic-leucine zipper (bZIP) transcription factor family protein	Phvul.011G03	PTHR23334 -
Basic-leucine zipper (bZIP) transcription factor family protein	Phvul.011G03	PTHR23334 -
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Basic-leucine zipper (bZIP) transcription factor family protein	Phvul.011G03	PTHR23334 -
Basic-leucine zipper (bZIP) transcription factor family protein	Phvul.011G03	PTHR23334 -
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Basic-leucine zipper (bZIP) transcription factor family protein	Phvul.011G03	PTHR23334 -
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S-locus lectin protein kinase family protein	Phvul.011G14	PF00954//PF
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
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S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
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S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S
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S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S

IDENTIFIER	NAME	DESCRIPTION
Phvul.001G17	RNA biosynth	transcription factor (AP2) (original description: pacid=37169523 transc
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Phvul.007G24	RNA biosynth	transcription factor (AP2) (original description: pacid=37164176 transc
Phvul.007G24	RNA biosynth	transcription factor (AP2) (original description: pacid=37164176 transc
Phvul.007G24	RNA biosynth	transcription factor (AP2) (original description: pacid=37164176 transc
Phvul.007G24	RNA biosynth	transcription factor (AP2) (original description: pacid=37164176 transc
Phvul.007G24	RNA biosynth	transcription factor (AP2) (original description: pacid=37164176 transc
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Phvul.L00030	RNA biosynth	transcription factor (AP2) (original description: pacid=37148483 transc
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tra
Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=
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Phvul.001G17	not assigned.a	(original description: pacid=37169336 transcript=Phvul.001G172501.1
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Phvul.001G17	not assigned.a	(original description: pacid=37169336 transcript=Phvul.001G172501.1
Phvul.001G17	not assigned.a	(original description: pacid=37169336 transcript=Phvul.001G172501.1
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Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G01	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.002G19	Cell wall orgar	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G21	not assigned.a	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
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Phvul.007G24	RNA biosynth	transcription factor (AP2) (original description: pacid=37164176 transc
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Phvul.009G24	not assigned.a	(original description: pacid=37151143 transcript=Phvul.009G249300.1
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37155680 transcript=
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Phvul.001G23	not assigned.n	no hits & (original description: pacid=37170395 transcript=Phvul.001G

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Phvul.002G08	RNA biosynth	transcription factor (mTERF) (original description: pacid=37174803 tra
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Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367

Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.002G31	Phytohormon	flavin monooxygenase (YUCCA) (original description: pacid=37178367
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
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Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
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Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G26	Solute transp	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transp	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transp	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transp	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transp	metal cation transporter (ZIP) (original description: pacid=37145610 tr

Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37145610 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37145610 tr
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Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
Phvul.003G26	Solute transpo	metal cation transporter (ZIP) (original description: pacid=37146252 tr
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Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=P
Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=P
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Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=P
Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=P
Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=P
Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=P
Phvul.005G11	Protein modif	phosphatase (PPKL) (original description: pacid=37154472 transcript=P
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Phvul.006G13	not assigned.a	(original description: pacid=37172219 transcript=Phvul.006G136700.3
Phvul.006G13	not assigned.a	(original description: pacid=37172219 transcript=Phvul.006G136700.3
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
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Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
Phvul.006G17	Cell wall orga	fasciclin-type arabinogalactan protein (original description: pacid=3717
Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
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Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc

Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.006G18	RNA biosynth	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37164938 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37164938 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37164938 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37164938 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37164938 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37164938 transcript=Phvul.007
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Phvul.007G23	not assigned.r	no hits & (original description: pacid=37164938 transcript=Phvul.007
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Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
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Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.007G23	not assigned.r	no hits & (original description: pacid=37166658 transcript=Phvul.007
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
Phvul.008G05	Protein modif	protein kinase (SD-1) (original description: pacid=37159381 transcript=
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Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
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Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.009G13	not assigned.	(original description: pacid=37150692 transcript=Phvul.009G130700.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
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Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.010G00	not assigned.	(original description: pacid=37143326 transcript=Phvul.010G002600.1
Phvul.011G06	Protein modif	protein kinase (LRR-VIII-2) (original description: pacid=37157071 trans
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t

Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
Phvul.011G07	RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 t
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Phvul.011G12	Protein home	protease (Papain) (original description: pacid=37155572 transcript=Ph
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Phvul.011G12	Protein home	protease (Papain) (original description: pacid=37155572 transcript=Ph
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G14	Protein modif	protein kinase (SD-1) (original description: pacid=37156823 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156493 transcript=
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Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P

Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
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Phvul.L00233	Cell wall orga	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.003G00	Enzyme classi	Enzyme classification.EC_3 hydrolases.EC_3.5 hydrolase acting on carb
Phvul.001G14	not assigned.	(original description: pacid=37168555 transcript=Phvul.001G147500.1
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G16	Chromatin or	histone (H4) (original description: pacid=37171228 transcript=Phvul.0
Phvul.001G17	Cytoskeleton	MT plus-end-tracking protein (GPT) (original description: pacid=37170
Phvul.001G17	Cytoskeleton	MT plus-end-tracking protein (GPT) (original description: pacid=37170
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Phvul.001G17	Cytoskeleton	MT plus-end-tracking protein (GPT) (original description: pacid=37170
Phvul.001G17	Cytoskeleton	MT plus-end-tracking protein (GPT) (original description: pacid=37170
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Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript

Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	Protein home	RING-v-class E3 ligase (original description: pacid=37167834 transcript
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G21	RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37168
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
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Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
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Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stimu	protein kinase (BIK1) (original description: pacid=37168984 transcript=

Phvul.001G23	External stim	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stim	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stim	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G23	External stim	protein kinase (BIK1) (original description: pacid=37168984 transcript=
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G19	Cell wall orga	O-acetyltransferase (RWA) (original description: pacid=37175788 trans
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G21	not assigned.	(original description: pacid=37176061 transcript=Phvul.002G218300.1

Phvul.002G21	not assigned.a	(original description: pacid=37176061 transcript=Phvul.002G218300.1
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
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Phvul.002G33	Cell cycle orga	associated component POT of telomerase ribonucleoprotein complex (
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	Phytohormon	allene oxidase cyclase (AOC) (original description: pacid=37144852 tran
Phvul.003G11	not assigned.r	no hits & (original description: pacid=37145453 transcript=Phvul.003G
Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
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Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
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Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
Phvul.003G20	Protein modif	protein kinase (LRR-XI) (original description: pacid=37144508 transcrip
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc

Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
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Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
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Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G25	Protein home	S28-class serine carboxypeptidase (original description: pacid=371476
Phvul.003G25	Protein home	S28-class serine carboxypeptidase (original description: pacid=371476
Phvul.003G25	Protein home	S28-class serine carboxypeptidase (original description: pacid=371476
Phvul.003G25	Protein home	S28-class serine carboxypeptidase (original description: pacid=371476
Phvul.003G25	Protein home	S28-class serine carboxypeptidase (original description: pacid=371476
Phvul.003G25	Protein home	S28-class serine carboxypeptidase (original description: pacid=371476
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Phvul.003G26	Protein home	S28-class serine carboxypeptidase (original description: pacid=371445
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Phvul.005G08	Protein modif	protein kinase (SD-1) (original description: pacid=37153816 transcript=
Phvul.005G08	Protein modif	protein kinase (SD-1) (original description: pacid=37153816 transcript=
Phvul.005G08	Protein modif	protein kinase (SD-1) (original description: pacid=37153816 transcript=
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Phvul.006G02	Vesicle traffick	component VPS16/VCL1 of HOPS/CORVET membrane tethering comple
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	RNA processir	component CPSF30/Yth1 of Cleavage and Polyadenylation Specificity F
Phvul.006G13	not assigned.a	(original description: pacid=37173088 transcript=Phvul.006G137900.1
Phvul.006G18	RNA biosynthe	transcription factor (ARF) (original description: pacid=37172907 transc
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
Phvul.007G02	Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcrip
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Phvul.008G12	Protein modif	protein kinase (MAP3K-RAF) (original description: pacid=37159336 tra
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Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
Phvul.008G28	Coenzyme me	oxygen-dependent coproporphyrinogen III oxidase (HemF) (original de
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Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid

Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.009G11	Chromatin or	modification reader component Pc of PRC1 histone mono-ubiquitinati
Phvul.010G12	not assigned.	(original description: pacid=37142336 transcript=Phvul.010G124800.1
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Phvul.010G12	not assigned.	(original description: pacid=37142336 transcript=Phvul.010G124800.1
Phvul.010G12	not assigned.	(original description: pacid=37142336 transcript=Phvul.010G124800.1
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Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G01	Enzyme classi	Serine/threonine-protein kinase-like protein At3g51990 OS=Arabidops
Phvul.011G04	Photosynthesi	assembly factor CcsB of CCS cytochrome f/c6 maturation system (syste
Phvul.011G04	Photosynthesi	assembly factor CcsB of CCS cytochrome f/c6 maturation system (syste
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Phvul.011G12	Protein home	protease (Papain) (original description: pacid=37155382 transcript=Ph
Phvul.011G12	Protein home	protease (Papain) (original description: pacid=37155382 transcript=Ph
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Phvul.001G26	Enzyme classi	L-ascorbate oxidase homolog OS=Brassica napus (sp|q00624|asol_bra
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Phvul.002G19	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase act
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Phvul.002G19	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase act
Phvul.002G19	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase act
Phvul.002G19	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase act
Phvul.002G19	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase act
Phvul.002G19	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase act
Phvul.002G19	Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase act
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Phvul.002G21	Protein modif	protein kinase (L-lectin) (original description: pacid=37176614 transcri
Phvul.002G21	Protein modif	protein kinase (L-lectin) (original description: pacid=37176614 transcri
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Phvul.002G21	Protein modif	protein kinase (L-lectin) (original description: pacid=37176821 transcri
Phvul.002G21	Protein modif	protein kinase (L-lectin) (original description: pacid=37176821 transcri
Phvul.002G21	Protein modif	protein kinase (L-lectin) (original description: pacid=37176821 transcri
Phvul.002G21	Protein modif	protein kinase (L-lectin) (original description: pacid=37176821 transcri
Phvul.002G21	Protein modif	protein kinase (L-lectin) (original description: pacid=37176821 transcri
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G26	Protein modif	protein kinase (ABC1) (original description: pacid=37178758 transcript
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=

Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G27	Lipid metaboli	diacylglycerol kinase (original description: pacid=37176586 transcript=
Phvul.002G30	RNA processi	OTP51 plastidial RNA splicing factor (original description: pacid=37178
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.002G32	Phytohormon	1-aminocyclopropane-1-carboxylate (ACC) oxidase (original descriptio
Phvul.003G17	not assigned.	(original description: pacid=37145410 transcript=Phvul.003G170000.1
Phvul.003G17	not assigned.	(original description: pacid=37145410 transcript=Phvul.003G170000.1
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Phvul.003G17	not assigned.	(original description: pacid=37145410 transcript=Phvul.003G170000.1
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc

Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G18	RNA biosynth	transcription factor (DOF) (original description: pacid=37146863 transc
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	Phytohormon	CIF-peptide receptor (GSO) (original description: pacid=37147649 tran
Phvul.003G20	not assigned.	no hits & (original description: pacid=37145436 transcript=Phvul.003G
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Phvul.003G20	not assigned.	no hits & (original description: pacid=37145436 transcript=Phvul.003G
Phvul.003G20	not assigned.	no hits & (original description: pacid=37145436 transcript=Phvul.003G
Phvul.003G20	not assigned.	no hits & (original description: pacid=37145436 transcript=Phvul.003G
Phvul.003G20	not assigned.	no hits & (original description: pacid=37145436 transcript=Phvul.003G
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G22	RNA biosynth	transcription factor (NAC) (original description: pacid=37147699 transc
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.003G23	Protein modif	catalytic subunit alpha of CK-II protein kinase (original description: pac
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip

Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.004G04	External stimu	effector receptor (NLR) (original description: pacid=37162120 transcrip
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G05	Protein modif	beta-1,4-mannosyl-transferase (ALG1) (original description: pacid=371
Phvul.005G16	Multi-process	PRONE-type RopGEF guanine nucleotide exchange factor (original desc
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37

Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
Phvul.006G11	not assigned.	no hits & (original description: pacid=37172023 transcript=Phvul.006
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
Phvul.006G13	Nutrient upta	metal ion-chelate reductase (FRO) (original description: pacid=371717
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Phvul.006G13	not assigned.	(original description: pacid=37172219 transcript=Phvul.006G136700.3
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Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
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Phvul.006G15	not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1
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Phvul.006G17	Cell wall orgar	fasciclin-type arabinogalactan protein (original description: pacid=3717
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Phvul.006G17	Cell wall orgar	fasciclin-type arabinogalactan protein (original description: pacid=3717
Phvul.006G17	Cell wall orgar	fasciclin-type arabinogalactan protein (original description: pacid=3717
Phvul.007G19	not assigned.a	(original description: pacid=37166614 transcript=Phvul.007G199800.2
Phvul.007G19	not assigned.a	(original description: pacid=37166614 transcript=Phvul.007G199800.2
Phvul.007G28	not assigned.a	(original description: pacid=37165505 transcript=Phvul.007G280600.1
Phvul.008G04	not assigned.r	no hits & (original description: pacid=37161002 transcript=Phvul.008G
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Phvul.008G04	not assigned.r	no hits & (original description: pacid=37161002 transcript=Phvul.008G
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Phvul.008G04	not assigned.r	no hits & (original description: pacid=37161002 transcript=Phvul.008G
Phvul.008G04	not assigned.r	no hits & (original description: pacid=37161002 transcript=Phvul.008G
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Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
Phvul.008G04	Cell wall orga	KDO-8-phosphate synthase (original description: pacid=37161420 tran
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Phvul.008G04	not assigned.	no hits & (original description: pacid=37157873 transcript=Phvul.008
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Phvul.008G04	not assigned.	no hits & (original description: pacid=37157873 transcript=Phvul.008
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Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcri

Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
Phvul.008G09	Protein modif	protein kinase (LRR-XII) (original description: pacid=37157650 transcrip
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Phvul.008G14	not assigned.a	(original description: pacid=37159888 transcript=Phvul.008G145800.1
Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
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Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
Phvul.008G26	Enzyme classi	no description available(sp|q7xp65|g2ox6_orysj : 123.0) & Enzyme cla
Phvul.008G29	Lipid metaboli	CTP:phosphorylcholine cytidylyltransferase (original description: pacid
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G01	Lipid metaboli	cardiolipin deacylase (original description: pacid=37150511 transcript=
Phvul.009G14	RNA biosynth	transcription factor (bHLH) (original description: pacid=37151166 trans
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
Phvul.009G19	Solute transpo	solute transporter (AAAP) (original description: pacid=37150292 transc
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
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Phvul.L00233	Cell wall orgar	cutin synthase (CD) (original description: pacid=37148519 transcript=P
Phvul.001G01	not assigned.a	(original description: pacid=37169408 transcript=Phvul.001G013800.1
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Phvul.001G12	Lipid metaboli	Patatin-type lipase (original description: pacid=37168813 transcript=P
Phvul.001G12	Lipid metaboli	Patatin-type lipase (original description: pacid=37168813 transcript=P
Phvul.001G12	Lipid metaboli	Patatin-type lipase (original description: pacid=37168813 transcript=P
Phvul.001G12	Lipid metaboli	Patatin-type lipase (original description: pacid=37168813 transcript=P
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Phvul.001G12	Lipid metaboli	Patatin-type lipase (original description: pacid=37168813 transcript=P
Phvul.001G12	Lipid metaboli	Patatin-type lipase (original description: pacid=37168813 transcript=P
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Phvul.002G13	not assigned.r	no hits & (original description: pacid=37177944 transcript=Phvul.002
Phvul.002G13	not assigned.r	no hits & (original description: pacid=37177944 transcript=Phvul.002
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Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.002G28	RNA processir	component DSP4 of DSP snRNA processing complex (original descriptio
Phvul.003G05	Enzyme classi	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10
Phvul.003G19	not assigned.a	(original description: pacid=37148323 transcript=Phvul.003G192500.1
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Phvul.003G19	not assigned.a	(original description: pacid=37148323 transcript=Phvul.003G192500.1
Phvul.003G19	not assigned.a	(original description: pacid=37148323 transcript=Phvul.003G192500.1
Phvul.003G19	not assigned.a	(original description: pacid=37148323 transcript=Phvul.003G192500.1
Phvul.003G19	not assigned.a	(original description: pacid=37148323 transcript=Phvul.003G192500.1
Phvul.003G19	not assigned.a	(original description: pacid=37148323 transcript=Phvul.003G192500.1
Phvul.003G19	not assigned.a	(original description: pacid=37148323 transcript=Phvul.003G192500.1
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Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
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Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
Phvul.003G22	RNA biosynth	PHD finger transcription factor (original description: pacid=37145047 t
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Phvul.003G27	Cytoskeleton (	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton (	component ArpC2 of Arp2/3 actin polymerization initiation complex (o

Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
Phvul.003G27	Cytoskeleton	component ArpC2 of Arp2/3 actin polymerization initiation complex (o
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Phvul.004G11	not assigned.	(original description: pacid=37163202 transcript=Phvul.004G118500.5
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Phvul.004G11	not assigned.	(original description: pacid=37163202 transcript=Phvul.004G118500.5
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Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
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Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
Phvul.004G17	Lipid metaboli	ceramide glucosyltransferase (original description: pacid=37161552 tra
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Phvul.005G06	not assigned.	(original description: pacid=37152944 transcript=Phvul.005G068800.2

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Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
Phvul.006G05	Protein biosyr	component mtRPL19 of large ribosomal subunit proteome (original de
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Phvul.006G10	Phytohormon	ETR/ERS-type ethylene receptor protein (original description: pacid=37
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Phvul.006G11	not assigned.r	no hits & (original description: pacid=37172023 transcript=Phvul.006
Phvul.006G11	not assigned.r	no hits & (original description: pacid=37172023 transcript=Phvul.006
Phvul.006G11	not assigned.r	no hits & (original description: pacid=37172023 transcript=Phvul.006
Phvul.006G11	not assigned.r	no hits & (original description: pacid=37172023 transcript=Phvul.006
Phvul.006G11	not assigned.r	no hits & (original description: pacid=37172023 transcript=Phvul.006
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Phvul.007G19	Vesicle traffic	SYP4-group Qa-type SNARE component (original description: pacid=37
Phvul.007G19	Vesicle traffic	SYP4-group Qa-type SNARE component (original description: pacid=37
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Phvul.007G22	Redox homeo	homogentisate phytyltransferase (VTE2/HPT) (original description: pac
Phvul.007G22	Redox homeo	homogentisate phytyltransferase (VTE2/HPT) (original description: pac
Phvul.007G22	Redox homeo	homogentisate phytyltransferase (VTE2/HPT) (original description: pac
Phvul.007G22	Redox homeo	homogentisate phytyltransferase (VTE2/HPT) (original description: pac
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Phvul.007G22	Redox homeo	homogentisate phytyltransferase (VTE2/HPT) (original description: pac
Phvul.007G22	Redox homeo	homogentisate phytyltransferase (VTE2/HPT) (original description: pac
Phvul.007G22	Redox homeo	homogentisate phytyltransferase (VTE2/HPT) (original description: pac
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Phvul.007G25	Phytohormon	ABAR chloroplast envelope-localized abscisic acid receptor (original de
Phvul.008G00	Cell wall orga	exine patterning factor (NEF1) (original description: pacid=37158156 t
Phvul.008G00	Cell wall orga	exine patterning factor (NEF1) (original description: pacid=37158156 t
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Phvul.008G04	not assigned.	no hits & (original description: pacid=37159608 transcript=Phvul.008G
Phvul.008G04	not assigned.	no hits & (original description: pacid=37159608 transcript=Phvul.008G
Phvul.008G04	not assigned.	no hits & (original description: pacid=37159608 transcript=Phvul.008G
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Phvul.008G08	not assigned.	no hits & (original description: pacid=37157729 transcript=Phvul.008G
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Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G17	Amino acid m	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase (origi
Phvul.008G19	not assigned.	(original description: pacid=37158415 transcript=Phvul.008G199500.1
Phvul.008G19	not assigned.	(original description: pacid=37158415 transcript=Phvul.008G199500.1
Phvul.008G25	RNA biosynth	transcription factor (AS2/LOB) (original description: pacid=37161314 t
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffic	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d

Phvul.009G09	Vesicle traffick	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffick	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.009G09	Vesicle traffick	component CAP1/ECA4 of TPLATE AP-2 co-adaptor complex (original d
Phvul.010G05	Vesicle traffick	CORVET-specific component VPS3 of HOPS/CORVET membrane tetheri
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
Phvul.011G03	RNA biosynth	transcription factor (bZIP19/23/24) (original description: pacid=37156
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
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Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=
Phvul.011G15	Protein modif	protein kinase (SD-1) (original description: pacid=37156554 transcript=

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epeat-containing protein At5g50990 OS=Arabidopsis thaliana (sp|q9fi49|pp428_arath : 614.0)

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attachment protein OS=Vitis vinifera (sp|p93798|snaa_vitvi : 260.0)
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G117500 ID=Phvul.009G117500.1.v2.1 annot-version=v2.1) &
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nol or related substance as donor(50.1.10 : 138.7) (original description: pacid=37170741 transcript=
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l/phosphatidylcholine transfer protein SFH2 OS=Arabidopsis thaliana (sp|f4jva9|sfh2_arath : 95.1)
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protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
protein DC2.15 OS=Daucus carota (sp|p14009|14kd_dauca : 82.8)
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synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
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synthase 6, chloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)
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chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
chloroplastic/mitochondrial OS=Arabidopsis thaliana (sp|q682u6|dpd1_arath : 218.0)
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l/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana (sp|q9si13|sfh10_arath : 53
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l/phosphatidylcholine transfer protein SFH10 OS=Arabidopsis thaliana (sp|q9si13|sfh10_arath : 53
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miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
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Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
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419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
306	326	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
419	439	UUCCACAGCU	:: :::::::::::::::..:	AAGCUCAAGA	Cleavage	pacid=371471
305	326	UUCCACAGCU	:: :::::::::::::::..:	GAAGCUCAAG	Cleavage	pacid=371471
418	439	UUCCACAGCU	:: :::::::::::::::..:	GAAGCUCAAG	Cleavage	pacid=371471
1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
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1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
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1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
1050	1070	UUCCACAGCU	..:::::::::::::: ::::	UGGUUCAAGA	Cleavage	pacid=371599
1049	1070	UUCCACAGCU	:..:::::::::::::: :::	AUGGUUCAAG	Cleavage	pacid=371599
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455

36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
36	56	UUCCACAGCU	:.:::::: ::::::::::.:	CGGUUCAAUA	Cleavage	pacid=371455
35	56	UUCCACAGCU	.:.:::::: ::::::::::.	GCGGUUCAAU	Cleavage	pacid=371455
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
140	160	UUCCACAGCU	::: .:::::::.::::::	AAGUGUAAGA	Cleavage	pacid=371666
139	160	UUCCACAGCU	::: .:::::::.:::::::	GAAGUGUAA	Cleavage	pacid=371666
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
712	732	UUCCACAGCU	:::::::.:::::::::	GACGUCAAGA	Cleavage	pacid=371702
711	732	UUCCACAGCU	:::::::.:::::::::	CGACGUCAA	Cleavage	pacid=371702
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1552	1572	UUCCACAGCU	: ::..::::.:::::::::	AAAUUUGAGA	Cleavage	pacid=371752
1551	1572	UUCCACAGCU	: ::..::::.:::::::::	GAAAUUUGA	Cleavage	pacid=371752
2054	2074	UUCCACAGCU	.: : :::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGCU	.: : :::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGCU	.: : :::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGCU	.: : :::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGCU	.: : :::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGCU	.: : :::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGCU	.: : :::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633

2054	2074	UUCCACAGC	.: : ::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGC	.: : ::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGC	.: : ::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2054	2074	UUCCACAGC	.: : ::::.:::::::::	GGGGUGAAG	Cleavage	pacid=371633
2053	2074	UUCCACAGC	: .: : ::::.::::::::::	AGGGGUGAA	Cleavage	pacid=371633
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2613	2633	UUCCACAGC	:::: :::::::.:::::	CAGUUAAAG	Cleavage	pacid=371610
2612	2633	UUCCACAGC	:::: :::::::.::::::	UCAGUUAAA	Cleavage	pacid=371610
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
212	232	UUCCACAGC	::::::::.:: :::::.	AUGUUCAAG	Cleavage	pacid=371562
211	232	UUCCACAGC	::::::::.:: :::::.	AAUGUUCAA	Cleavage	pacid=371562
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1046	1067	UUCCACA-GC	:::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371692
1045	1067	UUCCACA-GC	:. :::::::::: :::::	AUCGUUCAA	Cleavage	pacid=371692
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706

814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
814	834	UUCCACAGC	.:::.:::::::::: :::	AGGUUUAAG	Cleavage	pacid=371706
813	834	UUCCACAGC	.:::.:::::::::: :::	UAGGUUUAA	Cleavage	pacid=371706
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
361	381	UUCCACAGC	:: ::::::::. ::::::	GCGUGCAAG	Cleavage	pacid=371679
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
722	743	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371693
721	743	UUCCACA-GC	:: :::::::::::: :::::	ACCGUUCAA	Cleavage	pacid=371693
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782

235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
235	256	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
670	691	UUCCACA-GC	:::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371782
234	256	UUCCACA-GC	:. :::::::::::: :::::	AUCGUUCAA	Cleavage	pacid=371782
669	691	UUCCACA-GC	:. :::::::::::: :::::	AUCGUUCAA	Cleavage	pacid=371782
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
794	814	UUCCACAGC	:.::::::::: .:::::..	CGGUUCAAG	Cleavage	pacid=371752
793	814	UUCCACAGC	:.::::::::: .::::::..	CCGGUUCAA	Cleavage	pacid=371752
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
496	517	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371780
495	517	UUCCACA-GC	:: :::::::::::: :::::	ACCGUUCAA	Cleavage	pacid=371780
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
483	503	UUCCACAGC	::::::::::::: :::.	CUCUUCAAG	Cleavage	pacid=371758
482	503	UUCCACAGC	::::::::::::: ::::.	GCUCUUCAA	Cleavage	pacid=371758
906	926	UUCCACAGC	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGC	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778

906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
906	926	UUCCACAGCU	:: :.:::.:::::::::	GUGUACGAG	Cleavage	pacid=371778
905	926	UUCCACAGCU	:: :.:::.:::::::::	CGUGUACGA	Cleavage	pacid=371778
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
973	993	UUCCACAGCU	: :::. :::.:::::::::	GAAUUCGUG	Cleavage	pacid=371746
972	993	UUCCACAGCU	: :::. :::.:::::::::	GGAAUUCGU	Cleavage	pacid=371746
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
734	754	UUCCACAGCU	.:::: ::.:.:::::::	AGGUUCCAG	Cleavage	pacid=371476
733	754	UUCCACAGCU	.:::: ::.:.:::::::	GAGGUUCCA	Cleavage	pacid=371476
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
798	819	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371464
797	819	UUCCACA-GC	:: ::::::::::: :::::	ACCGUUCAA	Cleavage	pacid=371464

1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1720	1740	UUCCACAGC	:: :..::::.::::::::.	AAGAUUGAG	Cleavage	pacid=371469
1719	1740	UUCCACAGC	:: :..::::.::::::::.	GAAGAUUGA	Cleavage	pacid=371469
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1421	1441	UUCCACAGC	:::::.:.:::::: ::.	GCGUUCAGG	Cleavage	pacid=371722
1420	1441	UUCCACAGC	:::::.:.:::::: ::.	UGCGUUCAG	Cleavage	pacid=371722
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
701	721	UUCCACAGC	::: ::::.:: ::::::::	GAGUACAAG	Cleavage	pacid=371724
700	721	UUCCACAGC	::: ::::.:: ::::::::	UGAGUACAA	Cleavage	pacid=371724
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661

640	661	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371661
639	661	UUCCACA-GC	:: ::::::::::: :::::	ACCGUUCAA	Cleavage	pacid=371661
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1081	1101	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371593
1080	1101	UUCCACAGC	:..::::::::::::: :::	AUGGUUCAA	Cleavage	pacid=371593
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1213	1233	UUCCACAGC	..::::::::::::: ::::	UGGUUCAAG	Cleavage	pacid=371578
1212	1233	UUCCACAGC	..::::::::::::: ::::	CUGGUUCAA	Cleavage	pacid=371578
394	415	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: ::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509

394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509

860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
349	370	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
394	415	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
860	881	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
862	883	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1029	1050	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1032	1053	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1028	1049	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
1031	1052	UUCCACA-GC	: :::::::::::: ::::::	CCGUUCAAG	Cleavage	pacid=371509
393	415	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
348	370	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
393	415	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
859	881	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
861	883	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
1028	1050	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
1031	1053	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
1027	1049	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
1030	1052	UUCCACA-GC	: :::::::::::: ::::::	CCCGUUCAA	Cleavage	pacid=371509
1177	1197	UUCCACAGC	:: ::::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: ::::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: ::::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: ::::::::::::::	CCCUUAAAG	Cleavage	pacid=371498

1177	1197	UUCCACAGC	:: :::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: :::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: :::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: :::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: :::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: :::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1177	1197	UUCCACAGC	:: :::::::::::::	CCCUUAAAG	Cleavage	pacid=371498
1176	1197	UUCCACAGC	:: :: :::::::::::::	ACCCUUAAA	Cleavage	pacid=371498
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
504	525	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
558	579	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371490
503	525	UUCCACA-GC	:. ::::::::::: ::::::	AUCGUUCAA	Cleavage	pacid=371490
557	579	UUCCACA-GC	:. ::::::::::: ::::::	AUCGUUCAA	Cleavage	pacid=371490
760	781	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	::::::::::: :::::::	UCGUUCAAG	Cleavage	pacid=371425

760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371426
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
760	781	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
766	787	UUCCACA-GC	:::::::::::: ::::::	UCGUUCAAG	Cleavage	pacid=371425
759	781	UUCCACA-GC	:. :::::::::::: :::::	AUCGUUCAA	Cleavage	pacid=371426
765	787	UUCCACA-GC	:. :::::::::::: :::::	AUCGUUCAA	Cleavage	pacid=371425
759	781	UUCCACA-GC	:. :::::::::::: :::::	AUCGUUCAA	Cleavage	pacid=371425
765	787	UUCCACA-GC	:. :::::::::::: :::::	AUCGUUCAA	Cleavage	pacid=371425
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1938	1959	UUCCACA-GC	: :::::::::::: :::::	CCGUUCAAG	Cleavage	pacid=371432
1937	1959	UUCCACA-GC	:: :::::::::::: :::::	ACCGUUCAA	Cleavage	pacid=371432

928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
928	948	UUCCACAGCU	..:: :::.:::.::::::	UGGUGGAAG	Cleavage	pacid=371442
927	948	UUCCACAGCU	..:: :::.:::.::::::	UUGGUGGAA	Cleavage	pacid=371442
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
625	646	UUCCACA-GCU	: :::::::::: :::::	CCGUUCAAGA	Cleavage	pacid=371562
624	646	UUCCACA-GCU	:: :::::::::: ::::	ACCGUUCAAG	Cleavage	pacid=371562
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
959	979	UUCCACAGCU	.:::..::.:.: ::::::	GGGUUUGAG	Cleavage	pacid=371678
958	979	UUCCACAGCU	.:::..::.:.: ::::::	UGGGUUUGA	Cleavage	pacid=371678
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704
378	398	UUCCACAGCU	.: ::: .::::::::::	UAUUUCCGGA	Cleavage	pacid=371704

378	398	UUCCACAGCL	.: ::: .::::::::::::	UAUUUCCGG/	Cleavage	pacid=371704
377	398	UUCCACAGCL	..: ::: .::::::::::::	GUAUUUCCG(	Cleavage	pacid=371704
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
235	255	UUCCACAGCL	.: ::..:::::::::::::.	UAUUUUGAG	Cleavage	pacid=371773
234	255	UUCCACAGCL	.: ::..:::::::::::::.	UUAUUUUGA	Cleavage	pacid=371773
234	255	UUCCACAGCL	.: ::..:::::::::::::.	UUAUUUUGA	Cleavage	pacid=371773
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1487	1507	UUCCACAGCL	:::.:::::::::: : :	GUGUUUAAG	Cleavage	pacid=371747
1486	1507	UUCCACAGCL	:::.:::::::::: : :	GGUGUUUAA	Cleavage	pacid=371747
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777
579	599	UUCCACAGCL	::: :::.::::::::::	GUCCUCAUG/	Cleavage	pacid=371777

579	599	UUCCACAGC	::: :::.::::::::	GUCCUCAUG	Cleavage	pacid=371777
579	599	UUCCACAGC	::: :::.::::::::	GUCCUCAUG	Cleavage	pacid=371777
579	599	UUCCACAGC	::: :::.::::::::	GUCCUCAUG	Cleavage	pacid=371777
930	951	UUCCACAGC	:...:::. :::.::::::::.	AUGGUUUUC	Cleavage	pacid=371771
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
591	611	UUCCACAGC	::::::::::.::: ::.	GUAUUCAAG	Cleavage	pacid=371446
590	611	UUCCACAGC	::::::::::.::: ::.	AGUAUUCAA	Cleavage	pacid=371446
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
2330	2350	UUCCACAGC	::::::::: :::: :::.	AUGUUCAAG	Translation	pacid=371449
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452

942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
540	560	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
942	962	UUCCACAGC	:.:::::::.:::::: : ::	CGGUUCAAG	Cleavage	pacid=371452
539	560	UUCCACAGC	:.:::::::.:::::: : ::	UCGGUUCAA	Cleavage	pacid=371452
941	962	UUCCACAGC	:.:::::::.:::::: : ::	UCGGUUCAA	Cleavage	pacid=371452
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
984	1004	UUCCACAGC	:: ::: :.::::::::::	GAGCUCAUG	Cleavage	pacid=371455
983	1004	UUCCACAGC	:: ::: :.::::::::::	CGAGCUCAU	Cleavage	pacid=371455
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1055	1075	UUCCACAGC	::::.:::::::::::	AUGGCCAAG	Cleavage	pacid=371618
1054	1075	UUCCACAGC	::::.:::::::::::	AAUGGCCAA	Cleavage	pacid=371618
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
149	169	UUCCACAGC	::::::::.::: ::::: :	AAGUUCAAG	Cleavage	pacid=371545
148	169	UUCCACAGC	::::::::.::: ::::: :	UAAGUUCAA	Cleavage	pacid=371545
574	594	UUCCACAGC	::: :..::::::::: ::::	CAGAUUGAG	Cleavage	pacid=371713
574	594	UUCCACAGC	::: :..::::::::: ::::	CAGAUUGAG	Cleavage	pacid=371713
574	594	UUCCACAGC	::: :..::::::::: ::::	CAGAUUGAG	Cleavage	pacid=371713
574	594	UUCCACAGC	::: :..::::::::: ::::	CAGAUUGAG	Cleavage	pacid=371713
574	594	UUCCACAGC	::: :..::::::::: ::::	CAGAUUGAG	Cleavage	pacid=371713

574	594	UUCCACAGCU	::: :..::::::::: ::::	CAGAUUGAG/	Cleavage	pacid=371713
574	594	UUCCACAGCU	::: :..::::::::: ::::	CAGAUUGAG/	Cleavage	pacid=371713
574	594	UUCCACAGCU	::: :..::::::::: ::::	CAGAUUGAG/	Cleavage	pacid=371713
574	594	UUCCACAGCU	::: :..::::::::: ::::	CAGAUUGAG/	Cleavage	pacid=371713
574	594	UUCCACAGCU	::: :..::::::::: ::::	CAGAUUGAG/	Cleavage	pacid=371713
574	594	UUCCACAGCU	::: :..::::::::: ::::	CAGAUUGAG/	Cleavage	pacid=371713
573	594	UUCCACAGCU	::: :..::::::::: ::::	UCAGAUUGA(	Cleavage	pacid=371713
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
1411	1431	UUCCACAGCU	.::: .::.:.::::::::	AGGUUGGAG	Cleavage	pacid=371667
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
394	414	UUCCACAGCU	.::: .::.:.::::::::	GGGUUGGAG	Cleavage	pacid=371647
393	414	UUCCACAGCU	.::: .::.:.::::::::	UGGGUUGGA	Cleavage	pacid=371647
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
985	1005	UUCCACAGCU	:::::::::: ::::::	GGUAUCAAG/	Cleavage	pacid=371660
984	1005	UUCCACAGCU	:::::::::: ::::::	AGGUAUCAA(	Cleavage	pacid=371660
704	724	UUCCACAGCU	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCU	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCU	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCU	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671

704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
704	724	UUCCACAGCL	.:::::::::::::::	GCUGCUAAG/	Cleavage	pacid=371671
703	724	UUCCACAGCL	.:::::::::::::::	AGCUGCUAA(	Cleavage	pacid=371671
703	724	UUCCACAGCL	.:::::::::::::::	AGCUGCUAA(	Cleavage	pacid=371671
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
616	636	UUCCACAGCL	::::::: :::.:: ::::.:	CAGUUCAUG/	Cleavage	pacid=371646
615	636	UUCCACAGCL	::::::: :::.:: ::::.:	CCAGUUCAU(	Cleavage	pacid=371646
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
84	104	UUCCACAGCL	.: ::.::::.:::: ::::	GGGCUCGAG/	Cleavage	pacid=371584
537	557	UUCCACAGCL	.: :::: .:.:::::::::	AGGCUCAAA(	Cleavage	pacid=371587
537	557	UUCCACAGCL	.: :::: .:.:::::::::	AGGCUCAAA(	Cleavage	pacid=371587
537	557	UUCCACAGCL	.: :::: .:.:::::::::	AGGCUCAAA(	Cleavage	pacid=371587

537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
537	557	UUCCACAGC	.: :::: .:.::::::::::	AGGCUCAAA	Cleavage	pacid=371587
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGC	::: :: :::.:.:::::::.	AAGUGCAUG	Cleavage	pacid=371582

621	641	UUCCACAGCU	::: :: :::.:.:::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGCU	::: :: :::.:.:::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGCU	::: :: :::.:.:::::.	AAGUGCAUG	Cleavage	pacid=371582
621	641	UUCCACAGCU	::: :: :::.:.:::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGCU	::: :: :::.:.:::::.	AAGUGCAUG	Cleavage	pacid=371582
620	640	UUCCACAGCU	::: :: :::.:.:::::.	AAGUGCAUG	Cleavage	pacid=371582
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
703	723	UUCCACAGCU	:: :::::::.::::::	UCAUUGAAG	Cleavage	pacid=371578
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
286	306	UUCCACAGCU	:.::: .::.:.::::::::	CGGUUGGAG	Cleavage	pacid=371520
285	306	UUCCACAGCU	.:.::: .::.:.::::::::	GCGGUUGGA	Cleavage	pacid=371520
285	306	UUCCACAGCU	.:.::: .::.:.::::::::	GCGGUUGGA	Cleavage	pacid=371520
275	295	UUCCACAGCU	::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492

275	295	UUCCACAGCU	:::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	:::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	:::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	:::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	:::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
275	295	UUCCACAGCU	:::::::::::::: ::.	UUGUUCAAG	Cleavage	pacid=371492
274	295	UUCCACAGCU	:::::::::::::: ::.	GUUGUUCAA	Cleavage	pacid=371492
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
1786	1806	UUCCACAGCU	:::::::.:::: :::::	UUGUUCAAG	Cleavage	pacid=371519
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
104	124	UUCCACAGCU	..: ::::::.:: :::::.:	UGGCUCAAG	Cleavage	pacid=371486
103	124	UUCCACAGCU	..: ::::::.:: :::::.:	UUGGCUCAA	Cleavage	pacid=371486
103	124	UUCCACAGCU	..: ::::::.:: :::::.:	UUGGCUCAA	Cleavage	pacid=371486
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG	Cleavage	pacid=371499

1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1035	1055	UUCCACAGCU	: ::.::::.:::: ::::	AAUUUUAAG/	Cleavage	pacid=371499
1034	1055	UUCCACAGCU	: ::.::::.:::: ::::	UAAUUUUAA(	Cleavage	pacid=371499
1034	1055	UUCCACAGCU	: ::.::::.:::: ::::	UAAUUUUAA(	Cleavage	pacid=371499
2163	2184	UUCCACAGCU	:...:: :::.:::.::::::.	AUGGUGGAA(	Cleavage	pacid=371432
2114	2135	UUCCACAGCU	:...:: ::::::.::::::.	AUGGUGGAA(	Cleavage	pacid=371441
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
1212	1232	UUCCACAGCU	:::::: :..:.:::::.:	GCGUUCAAA/	Cleavage	pacid=371573
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
67	87	UUCCACAGCU	::::::::.:::::::	UCCACCAAGA	Cleavage	pacid=371562
66	87	UUCCACAGCU	::::::::.::::::::	AUCCACCAAG	Cleavage	pacid=371562
646	666	UUCCACAGCU	::::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703

651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
646	666	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
651	671	UUCCACAGCL	:::::::.:::: ::::	ACCCUCAAGA	Cleavage	pacid=371703
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
778	798	UUCCACAGCL	..:::::::.:: ::::: .:	UGGUUCAAG(	Cleavage	pacid=371708
777	798	UUCCACAGCL	..:::::::.:: ::::: .:	UUGGUUCAA(	Cleavage	pacid=371708
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
702	722	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371694
603	623	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	:::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687

603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
603	623	UUCCACAGCL	::::.:::::::: ::	AUUGUCAAG(	Cleavage	pacid=371687
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1212	1232	UUCCACAGCL	::::.::::.: ::::::	GAGUUCGAG/	Cleavage	pacid=371707
1211	1232	UUCCACAGCL	::::.::::.: ::::::	CGAGUUCGA(	Cleavage	pacid=371707
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698

796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
796	816	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
894	914	UUCCACAGCL	: ::::. .:::.::::::	AAAUUCAGU(	Cleavage	pacid=371698
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
903	923	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1168	1188	UUCCACAGCL	::::::.:::::: :::	GUUUUCAAG(	Cleavage	pacid=371770
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
1138	1158	UUCCACAGCL	::: ::::::.: ::::::	AAGUACAAG/	Cleavage	pacid=371774
255	275	UUCCACAGCL	.:::::::.:.:: :::: :	AGGUUCAAG(	Cleavage	pacid=371780
255	275	UUCCACAGCL	.:::::::.:.:: :::: :	AGGUUCAAG(	Cleavage	pacid=371780
255	275	UUCCACAGCL	.:::::::.:.:: :::: :	AGGUUCAAG(	Cleavage	pacid=371780
255	275	UUCCACAGCL	.:::::::.:.:: :::: :	AGGUUCAAG(	Cleavage	pacid=371780
255	275	UUCCACAGCL	.:::::::.:.:: :::: :	AGGUUCAAG(	Cleavage	pacid=371780

255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
255	275	UUCCACAGC	.:::::::.:.:: :::: :	AGGUUCAAG	Cleavage	pacid=371780
254	275	UUCCACAGC	: .:::::::.:.:: :::: :	AAGGUUCAA	Cleavage	pacid=371780
254	275	UUCCACAGC	: .:::::::.:.:: :::: :	AAGGUUCAA	Cleavage	pacid=371780
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
574	594	UUCCACAGC	:::: .:::::::::::	ACCAUCAAAG	Cleavage	pacid=371463
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1181	1201	UUCCACAGC	::: :::::::: ::::::	AAGUACAAG	Cleavage	pacid=371451
1180	1201	UUCCACAGC	::: :::::::: ::::::	CAAGUACAA	Cleavage	pacid=371451
489	509	UUCCACAGC	::: :: ::.::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.::::: ::::	CAGCUCCAG	Cleavage	pacid=371447

489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
489	509	UUCCACAGC	::: :: ::.:::::: ::::	CAGCUCCAG	Cleavage	pacid=371447
488	509	UUCCACAGC	::: :: ::.:::::: ::::	UCAGCUCCA	Cleavage	pacid=371447
488	509	UUCCACAGC	::: :: ::.:::::: ::::	UCAGCUCCA	Cleavage	pacid=371447
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
702	722	UUCCACAGC	: :::::::::: :::: :	GAAUUCAAG	Cleavage	pacid=371470
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463

491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
491	511	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
750	770	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
790	810	UUCCACAGC	:.::::::::: . ::::.:	CGGUUCAAG	Cleavage	pacid=371463
490	511	UUCCACAGC	:.::::::::: . ::::.:	UCGGUUCAA	Cleavage	pacid=371463
749	770	UUCCACAGC	:.::::::::: . ::::.:	UCGGUUCAA	Cleavage	pacid=371463
789	810	UUCCACAGC	:.::::::::: . ::::.:	UCGGUUCAA	Cleavage	pacid=371463
2392	2413	UUCCACAGC	:.::: .: ::::::::::::	AUAGUGAGA	Cleavage	pacid=371483
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
556	576	UUCCACAGC	:: :::.:.:: .::::::	AAGAUCAGG	Cleavage	pacid=371476
555	576	UUCCACAGC	: :: :::.:.:: .::::::	AAAGAUCAG	Cleavage	pacid=371476
3519	3540	UUCCACAGC	:: :::::::::.::: :: .:	ACUGUUCAA	Cleavage	pacid=371474
3671	3692	UUCCACAGC	:: :::::::::.::: :: .:	ACUGUUCAA	Cleavage	pacid=371451
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
812	832	UUCCACAGC	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455

812	832	UUCCACAGCU	:::::.::::.::: :: ::	GAGUUCGAG	Cleavage	pacid=371455
811	832	UUCCACAGCU	: :::::.::::.::: :: ::	AGAGUUCGA	Cleavage	pacid=371455
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1754	1774	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1794	1814	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
2002	2022	UUCCACAGCU	:: :::: .::::::::::	CAUUUCAUU	Cleavage	pacid=371530
1753	1774	UUCCACAGCU	::: :::: .:::::::::::	ACAUUUCAU	Cleavage	pacid=371530
1793	1814	UUCCACAGCU	::: :::: .:::::::::::	ACAUUUCAU	Cleavage	pacid=371530
2001	2022	UUCCACAGCU	::: :::: .:::::::::::	ACAUUUCAU	Cleavage	pacid=371530
1951	1972	UUCCACAGCU	:...: ::.::::.::::: .:	AUGGCUCGA	Cleavage	pacid=371719
1639	1659	UUCCACAGCU	:::: .:::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .:::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .:::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .:::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .:::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .:::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .:::::: :::::	GAGUUAGAG	Cleavage	pacid=371737

1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1639	1659	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1783	1803	UUCCACAGCU	:::: .::::::: :::::	GAGUUAGAG	Cleavage	pacid=371737
1638	1659	UUCCACAGCU	: :::: .::::::: :::::	AGAGUUAGA	Cleavage	pacid=371737
1782	1803	UUCCACAGCU	: :::: .::::::: :::::	AGAGUUAGA	Cleavage	pacid=371737
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
4015	4036	UUCCACAGCU	:::: .:::.:::.::::::.	GAGUUGUAA	Cleavage	pacid=371668
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
59	81	UUCCACAGCU	..:::: :: ::::::::::	UGGUUCGAA	Cleavage	pacid=371647
730	750	UUCCACAGCU	::::. .::.:: :::::::	GAGUUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCU	::::. .::.:: :::::::	GAGUUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCU	::::. .::.:: :::::::	GAGUUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCU	::::. .::.:: :::::::	GAGUUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCU	::::. .::.:: :::::::	GAGUUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCU	::::. .::.:: :::::::	GAGUUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCU	::::. .::.:: :::::::	GAGUUUUGG	Cleavage	pacid=371642

730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
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730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
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730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
730	750	UUCCACAGCL	::::. .::.:: :::::::	GAGUUUGG	Cleavage	pacid=371642
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644

963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
945	965	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
963	983	UUCCACAGCL	..:::.:. .:::.:::::.:	UGGUUUAGU	Cleavage	pacid=371644
944	965	UUCCACAGCL	..:::.:. .:::.:::::.:	CUGGUUUAG	Cleavage	pacid=371644
962	983	UUCCACAGCL	..:::.:. .:::.:::::.:	CUGGUUUAG	Cleavage	pacid=371644
944	965	UUCCACAGCL	..:::.:. .:::.:::::.:	CUGGUUUAG	Cleavage	pacid=371644
962	983	UUCCACAGCL	..:::.:. .:::.:::::.:	CUGGUUUAG	Cleavage	pacid=371644
908	928	UUCCACAGCL	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGCL	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGCL	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGCL	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGCL	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGCL	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGCL	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658

908	928	UUCCACAGC	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGC	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGC	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
908	928	UUCCACAGC	.:::..::.:.: ::::::.	GGGUUUGAG	Cleavage	pacid=371658
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
486	506	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
482	502	UUCCACAGC	:.:::::: :.:::::: :.:	CGGUUCAAA	Cleavage	pacid=371606
485	506	UUCCACAGC	.:.:::::: :.:::::: :.:	GCGGUUCAA	Cleavage	pacid=371606
481	502	UUCCACAGC	.:.:::::: :.:::::: :.:	GCGGUUCAA	Cleavage	pacid=371606
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
327	347	UUCCACAGC	:: :..::::: :::::::.	AAGCUUGAG	Cleavage	pacid=371579
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592

1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1064	1085	UUCCACAGC	::::: :::::.::: :::::	GAGUUCCAA	Cleavage	pacid=371592
1063	1085	UUCCACAGC	: ::::: :::::.::: ::::	AGAGUUCCA	Cleavage	pacid=371592
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1314	1334	UUCCACAGC	:...:::::::::::.	GAAAUUGGG	Cleavage	pacid=371578
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1184	1204	UUCCACAGC	:::::.:::::: :::::.	GAGUUCGAG	Cleavage	pacid=371607
1183	1204	UUCCACAGC	:::::.:::::: :::::	GGAGUUCGA	Cleavage	pacid=371607
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
136	156	UUCCACAGC	::::::::.:::::.:	AUUGACAAG	Cleavage	pacid=371489
135	156	UUCCACAGC	::::::::.:::::.:	AAUUGACAA	Cleavage	pacid=371489
917	937	UUCCACAGC	::: :::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGC	::: :::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGC	::: :::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGC	::: :::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGC	::: :::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGC	::: :::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497

917	937	UUCCACAGCU	::: ::::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGCU	::: ::::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGCU	::: ::::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGCU	::: ::::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
917	937	UUCCACAGCU	::: ::::::: :::: :::	GAGUACAAG	Cleavage	pacid=371497
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
844	864	UUCCACAGCU	::::::: ::.:: :::::.	GAGUUCAAA	Cleavage	pacid=371504
843	864	UUCCACAGCU	::::::: ::.:: :::::.	UGAGUUCAA	Cleavage	pacid=371504
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
581	601	UUCCACAGCU	:.::: .:::: :.:::::.:	CGGUUGGAG	Translation	pacid=371515
580	601	UUCCACAGCU	.:.::: .:::: :.:::::.:	GCGGUUGGA	Translation	pacid=371515
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
618	638	UUCCACAGCU	::: ::::.:.:::::: :.	AAGUCCAAG	Cleavage	pacid=371510
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG	Cleavage	pacid=371504

160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
160	180	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
152	172	UUCCACAGCU	.:::::.:::::: : :::.	AGGUUCAGG/	Cleavage	pacid=371504
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
375	395	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371432
374	395	UUCCACAGCU	:: ::::: :.::::::::	UGAGAUCAA(	Cleavage	pacid=371432
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
394	414	UUCCACAGCU	:: ::::: :.::::::::	GAGAUCAAG(	Cleavage	pacid=371434
393	414	UUCCACAGCU	:: ::::: :.::::::::	UGAGAUCAA(	Cleavage	pacid=371434
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423

892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
892	912	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
994	1014	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
1474	1494	UUCCACAGCU	::.::::.:.::::::.	AUUAUCGAG/	Cleavage	pacid=371423
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
430	450	UUCCACAGCU	:::: :::::::::::.	ACCAUCAACA	Cleavage	pacid=371556
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564
291	311	UUCCACAGCU	:..::.::::::::::.	CCUAUUGAG(	Cleavage	pacid=371564

291	311	UUCCACAGC	:..::.::::::::::.	CCUAUUGAG	Cleavage	pacid=371564
291	311	UUCCACAGC	:..::.::::::::::.	CCUAUUGAG	Cleavage	pacid=371564
291	311	UUCCACAGC	:..::.::::::::::.	CCUAUUGAG	Cleavage	pacid=371564
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
292	312	UUCCACAGC	::: : .:::::: :::::::	CAGCUGGAG	Cleavage	pacid=371562
291	312	UUCCACAGC	.::: : .:::::: :::::::	GCAGCUGGA	Cleavage	pacid=371562
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1161	1180	UUCCACAGC	::: :::.:::: :::::::	CAGAUCAGG	Cleavage	pacid=371690
1160	1180	UUCCACAGC	.::: :::.:::: :::::::	GCAGAUCAG	Cleavage	pacid=371690
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.:::: :: ::	AAGUUUGAG	Cleavage	pacid=371710

977	997	UUCCACAGC	::::..::.::::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.::::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
977	997	UUCCACAGC	::::..::.::::: :: ::	AAGUUUGAG	Cleavage	pacid=371710
976	997	UUCCACAGC	: ::::..::.::::: :: ::	AAAGUUUGA	Cleavage	pacid=371710
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
881	901	UUCCACAGC	::::::::::.: .::: ::.	CAGUUCAAG	Cleavage	pacid=371698
880	901	UUCCACAGC	.::::::::::.: .::: ::.	GCAGUUCAA	Cleavage	pacid=371698
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1843	1863	UUCCACAGC	:::: ..::::.::: ::::.	CAGUAUGAG	Cleavage	pacid=371746
1842	1863	UUCCACAGC	.:::: ..::::.::: ::::.	GCAGUAUGA	Cleavage	pacid=371746
907	929	UUCCACAGC	::.:::. .::.::::::::	ACGGUUUUU	Cleavage	pacid=371787
843	865	UUCCACAGC	::.:::. .::.::::::::	ACGGUUUUU	Cleavage	pacid=371787
706	727	UUCCACAGC	.:.:::.. ::..:.:::::..	GCGGUUUGU	Cleavage	pacid=371782
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1805	1825	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1805	1825	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1805	1825	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1805	1825	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1805	1825	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1805	1825	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1805	1825	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449
1806	1826	UUCCACAGC	::::::.:::.:::: : :.	AAGUUCAGG	Cleavage	pacid=371449

1805	1825	UUCCACAGCU	::::::.:::.:::: : :.	AAGUUCAGG/	Cleavage	pacid=371449
1806	1826	UUCCACAGCU	::::::.:::.:::: : :.	AAGUUCAGG/	Cleavage	pacid=371449
1805	1825	UUCCACAGCU	::::::.:::.:::: : :.	AAGUUCAGG/	Cleavage	pacid=371449
1806	1826	UUCCACAGCU	::::::.:::.:::: : :.	AAGUUCAGG/	Cleavage	pacid=371449
1805	1825	UUCCACAGCU	::::::.:::.:::: : :.	AAGUUCAGG/	Cleavage	pacid=371449
1806	1826	UUCCACAGCU	::::::.:::.:::: : :.	AAGUUCAGG/	Cleavage	pacid=371449
1805	1825	UUCCACAGCU	::::::.:::.:::: : :.	AAGUUCAGG/	Cleavage	pacid=371449
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1736	1756	UUCCACAGCU	::::: .::::::: :::::	CAGUUAGAG/	Cleavage	pacid=371484
1735	1756	UUCCACAGCU	:::::: .:::::::: :::::	ACAGUUAGA(	Cleavage	pacid=371484
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1891	1911	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1928	1948	UUCCACAGCU	:..: :::::::::::::	AACCUUGAU/	Cleavage	pacid=371447
1890	1911	UUCCACAGCU	:..: :::::::::::::	UAACCUUGAU	Cleavage	pacid=371447
1927	1948	UUCCACAGCU	:..: :::::::::::::	UAACCUUGAU	Cleavage	pacid=371447
1105	1126	UUCCACAGCU	::::: :: ::..:::::: :	ACAGUGCAU(	Cleavage	pacid=371479
1131	1152	UUCCACAGCU	:.: ::::.::::: :::.	AUAUCUCAA(	Cleavage	pacid=371448
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAG/	Cleavage	pacid=371624

715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
627	647	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
715	735	UUCCACAGCU	::: ::::::::: : ::.:	CAGAUCAAGA	Cleavage	pacid=371624
626	647	UUCCACAGCU	.::: ::::::::: : ::.:	GCAGAUCAAG	Cleavage	pacid=371624
714	735	UUCCACAGCU	.::: ::::::::: : ::.:	GCAGAUCAAG	Cleavage	pacid=371624
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
352	372	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
413	433	UUCCACAGCU	.::::::.:::. .: :::::	UAGUUCAGGA	Cleavage	pacid=371540
351	372	UUCCACAGCU	:.::::::.:::. .: :::::	AUAGUUCAGG	Cleavage	pacid=371540

412	433	UUCCACAGC	:.:::::::.:::. .: :::::	AUAGUUCAG	Cleavage	pacid=371540
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1224	1244	UUCCACAGC	::: :.:.::.:::: :::.	CAGCUUAGG	Cleavage	pacid=371714
1223	1244	UUCCACAGC	::: :.:.::.:::: :::.	UCAGCUUAG	Cleavage	pacid=371714
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
283	303	UUCCACAGC	.::::..:.:::.:::::	AGGUUCGGG	Cleavage	pacid=371729
282	303	UUCCACAGC	.::::..:.:::.:::::	CAGGUUCGG	Cleavage	pacid=371729
1264	1285	UUCCACAGC	:..: ::::::::.::::: ::	AUAUUUCAA	Cleavage	pacid=371673
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611

280	300	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
451	471	UUCCACAGC	:::::::.:.:: .:::: ::	CAGUUCAGG	Cleavage	pacid=371611
279	300	UUCCACAGC	:::::::.:.:: .:::: ::	UCAGUUCAG	Cleavage	pacid=371611
450	471	UUCCACAGC	:::::::.:.:: .:::: ::	UCAGUUCAG	Cleavage	pacid=371611
160	181	UUCCACAGC	:..:::::. .:::. :::::	AUGGUUCAG	Cleavage	pacid=371588
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1072	1092	UUCCACAGC	::::: .:::::::: ::: :	CAGUUGGAG	Cleavage	pacid=371593
1071	1092	UUCCACAGC	.::::: .:::::::: ::: :	GCAGUUGGA	Cleavage	pacid=371593
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
545	566	UUCCACAGC	:::::.: :::::.::: :::	CAGUUUAGA	Cleavage	pacid=371604
544	566	UUCCACAGC	:::::.: :::::.::: ::	UCAGUUUAG	Cleavage	pacid=371604
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
359	378	UUCCACAGC	:.:::::::.: ::::::::	CGGUUCAAG	Translation	pacid=371579
358	378	UUCCACAGC	::.:::::::.: ::::::::	ACGGUUCAA	Translation	pacid=371579
1689	1709	UUCCACAGC	:::::.:. ::::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. ::::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. ::::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. ::::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. ::::: :::::.	CAGUUUAGA	Cleavage	pacid=371615

1689	1709	UUCCACAGC	:::::.:. :::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. :::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. :::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. :::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. :::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1689	1709	UUCCACAGC	:::::.:. :::: :::::.	CAGUUUAGA	Cleavage	pacid=371615
1688	1709	UUCCACAGC	::::::.:. :::: :::::.	ACAGUUUAG	Cleavage	pacid=371615
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
804	823	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
917	936	UUCCACAGC	:.::::::::: :::: :::	CGGUUCAAG	Cleavage	pacid=371499
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1777	1797	UUCCACAGC	.: ::::::::.:. ::::	UACUUCAAG	Cleavage	pacid=371502
1776	1797	UUCCACAGC	..: ::::::::.:. ::::	GUACUUCAA	Cleavage	pacid=371502
690	711	UUCCACAGC	:.: ::::::::.::: ::::	AUAUUUCAA	Cleavage	pacid=371425
1065	1086	UUCCAC-AGC	::::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	::::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	::::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	::::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431

1065	1086	UUCCAC-AGC	:::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	:::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	:::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	:::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	:::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	:::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1065	1086	UUCCAC-AGC	:::::: ::.:::: :::::	CAGUUCAUG	Cleavage	pacid=371431
1064	1086	UUCCAC-AGC	::::::: ::.:::: ::::	ACAGUUCAU	Cleavage	pacid=371431
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
2014	2034	UUCCACAGC	::::.:: .: ::::::::.	AAGUUUAAU	Translation	pacid=371548
841	863	UUCCACAGC	:..:: :...:.:::.:::::	AUGGUGUUG	Cleavage	pacid=371566
841	863	UUCCACAGC	:..:: :...:.:::.:::::	AUGGUGUUG	Cleavage	pacid=371566
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
1959	1979	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
2129	2149	UUCCACAGC	:::::..:::: ::: :::.	AAGUUCGGG	Cleavage	pacid=371561
3332	3353	UUCCACAGC	:::::: :::.:: . ::::::	ACAGUUAAA	Cleavage	pacid=371475
3430	3451	UUCCACAGC	:::::: :::.:: . ::::::	ACAGUUAAA	Cleavage	pacid=371475
1254	1275	UUCCACAGC	.::::: .::.:.:.:::: :.	GCAGUUGGA	Cleavage	pacid=371454

132	153	UUCCACAGCL	.:::::: .::: :. ::::::	GCAGUUCUG(	Translation	pacid=371477
132	153	UUCCACAGCL	.:::::: .::: :. ::::::	GCAGUUCUG(	Translation	pacid=371477
696	717	UUCCACAGCL	:..:::..::.:::.:: ::.	AUGGUUGA	Cleavage	pacid=371632
696	717	UUCCACAGCL	:..:::..::.:::.:: ::.	AUGGUUGA	Cleavage	pacid=371632
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
448	468	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371523
447	468	UUCCACAGCL	:::::.:::.::::::::	CCAGUUUAA(	Cleavage	pacid=371523
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
422	442	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
525	545	UUCCACAGCL	:::::.:::.::::::::	CAGUUUAAG(	Cleavage	pacid=371533
421	442	UUCCACAGCL	:::::.:::.::::::::	CCAGUUUAA(	Cleavage	pacid=371533
524	545	UUCCACAGCL	:::::.:::.::::::::	CCAGUUUAA(	Cleavage	pacid=371533
631	651	UUCCACAGCL	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCL	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCL	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCL	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCL	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCL	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526

631	651	UUCCACAGCU	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCU	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCU	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCU	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
631	651	UUCCACAGCU	:: :::::::::.:::::	CAUCUCAAGA	Cleavage	pacid=371526
630	651	UUCCACAGCU	:: :::::::::.:::::	UCAUCUCAAG	Cleavage	pacid=371526
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1758	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	CAGUUCGAG	Cleavage	pacid=371726
1757	1778	UUCCACAGCU	::::::.::.:.:.:: : ::	UCAGUUCGA	Cleavage	pacid=371726
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
863	884	UUCCACAGCU	:: ::::: :.:::::::::.:	CAUUUCAAU	Cleavage	pacid=371722
862	884	UUCCACAGCU	::: ::::: :.:::::::::.	ACAUUUCAAU	Cleavage	pacid=371722
939	960	UUCCACAGCU	.:::::: .::..:. :::::.	GCAGUUCCG	Cleavage	pacid=371713
603	623	UUCCACAGCU	:.::::.::::::: :::: :	AUAGUUUAA	Cleavage	pacid=371643
644	664	UUCCACAGCU	:.::::.::::::: :::: :	AUAGUUUAA	Cleavage	pacid=371643
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
4525	4545	UUCCACAGCU	:.: :::::::::.::: :..	CGGAACAAGA	Cleavage	pacid=371668
1780	1801	UUCCACAGCU	::::: :::::::::.: :: .:	ACAGUACAAG	Cleavage	pacid=371656
1898	1919	UUCCACAGCU	::::: :::::::::.: :: .:	ACAGUACAAG	Cleavage	pacid=371656

2394	2415	UUCCACAGC	::::: ::::::::.: :: .:	ACAGUACAA	Cleavage	pacid=371656
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
836	856	UUCCACAGC	.::::::::.:.::::	AGGUUCAAG	Cleavage	pacid=371658
835	856	UUCCACAGC	: .::::::::.:.::::	AAGGUUCAA	Cleavage	pacid=371658
417	438	UUCCACAGC	.:::::. : ::::: ::::.	GCAGUUCGU	Cleavage	pacid=371599
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1414	1434	UUCCACAGC	::::::::..:. ::: :.	CAGUUCAAG	Cleavage	pacid=371425
1413	1434	UUCCACAGC	:::::::::..:. ::: :.	ACAGUUCAA	Cleavage	pacid=371425
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
596	616	UUCCACAGC	:::::.:.:::::. ::::.	CAGUUUAGG	Cleavage	pacid=371443
595	616	UUCCACAGC	::::::.:.:::::. ::::.	ACAGUUUAG	Cleavage	pacid=371443
1484	1505	UUCCACAGC	:::::: :::.::::: ::	ACAGUUCCU	Cleavage	pacid=371428
685	703	UUCCACAGC	::::: :::.::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.::::::::.:	CAGUU--AGA	Cleavage	pacid=371569

685	703	UUCCACAGC	::::: :::.:::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.:::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.:::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
685	703	UUCCACAGC	::::: :::.:::::::::.:	CAGUU--AGA	Cleavage	pacid=371569
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1397	1417	UUCCACAGC	:.::::..::::::::::	CGGUUCGGG	Cleavage	pacid=371790
1396	1417	UUCCACAGC	:.::::..::::::::::	UCGGUUCGG	Cleavage	pacid=371790

Multiplicity	Target_Acc.	ID	locusName	Pfam
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1	Phvul.003G168301.1	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.2	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.1	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.2	Phvul.003G168301	Phvul.003G168301	0
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1	Phvul.003G168301.2	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.1	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.2	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.1	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.2	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.003G168301.1	Phvul.003G168301	Phvul.003G168301	0
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1	Phvul.003G168301.1	Phvul.003G168301	Phvul.003G168301	0
1	Phvul.008G204300.1	Phvul.008G204300	Phvul.008G204300	PF13962
1	Phvul.008G204300.1	Phvul.008G204300	Phvul.008G204300	PF13962
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1	Phvul.007G253900.1	Phvul.007G253900	Phvul.007G253900	0
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1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879

1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.2	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G041800.1	Phvul.002G041800	Phvul.002G041800	PF08879
1	Phvul.002G061900.1	Phvul.002G061900	Phvul.002G061900	PF00854
1	Phvul.002G061900.1	Phvul.002G061900	Phvul.002G061900	PF00854
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1	Phvul.002G061900.1	Phvul.002G061900	Phvul.002G061900	PF00854
1	Phvul.002G061900.1	Phvul.002G061900	Phvul.002G061900	PF00854
1	Phvul.002G131700.1	Phvul.002G131700	Phvul.002G131700	PF08880,PF08
1	Phvul.002G131700.1	Phvul.002G131700	Phvul.002G131700	PF08880,PF08
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1	Phvul.002G147600.1	Phvul.002G147600	Phvul.002G147600	PF01486,PF00
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1	Phvul.002G162900.1	Phvul.002G162900	Phvul.002G162900	PF13181,PF02
1	Phvul.002G162900.1	Phvul.002G162900	Phvul.002G162900	PF13181,PF02

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1	Phvul.002G162900.1	Phvul.002G162900	Phvul.002G162900	PF13181,PF02
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1	Phvul.003G014900.1	Phvul.003G014900	Phvul.003G014900	PF13041,PF01
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1	Phvul.006G102400.1	Phvul.006G102400	Phvul.006G102400	PF00515,PF13
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1	Phvul.006G191600.1	Phvul.006G191600	Phvul.006G191600	PF05739,PF0
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1	Phvul.009G047000.4	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.009G047000.5	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.009G047000.9	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.8	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.009G047000.4	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.009G047000.6	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.5	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.2	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.3	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.9	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.8	Phvul.009G047000	Phvul.009G047000	PF08880,PF08

1	Phvul.009G047000.7	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.009G047000.5	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.2	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.3	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.9	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.8	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.7	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.4	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.1	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.6	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.5	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.2	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.009G047000.9	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.8	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.7	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
1	Phvul.009G047000.4	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.009G047000.4	Phvul.009G047000	Phvul.009G047000	PF08880,PF08
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1	Phvul.007G225200.1	Phvul.007G225200	Phvul.007G225200	PF02987
1	Phvul.007G225200.2	Phvul.007G225200	Phvul.007G225200	PF02987
1	Phvul.007G225200.1	Phvul.007G225200	Phvul.007G225200	PF02987
1	Phvul.007G280800.1	Phvul.007G280800	Phvul.007G280800	PF02458
1	Phvul.007G280800.1	Phvul.007G280800	Phvul.007G280800	PF02458
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1	Phvul.008G020700.1	Phvul.008G020700	Phvul.008G020700	PF13855,PF00
1	Phvul.008G020700.1	Phvul.008G020700	Phvul.008G020700	PF13855,PF00
1	Phvul.008G020700.1	Phvul.008G020700	Phvul.008G020700	PF13855,PF00
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1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041
1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041

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1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041	
1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041	
1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041	
1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041	
1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041	
1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041	
1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041	
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1	Phvul.008G046300.1	Phvul.008G046300	Phvul.008G046300	PF13041	
1	Phvul.008G046300.2	Phvul.008G046300	Phvul.008G046300	PF13041	
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1	Phvul.008G118100.3	Phvul.008G118100	Phvul.008G118100		0
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1	Phvul.008G118100.2	Phvul.008G118100	Phvul.008G118100		0
1	Phvul.008G118100.3	Phvul.008G118100	Phvul.008G118100		0
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1	Phvul.008G118100.2	Phvul.008G118100	Phvul.008G118100		0
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1	Phvul.008G118100.1	Phvul.008G118100	Phvul.008G118100		0
1	Phvul.008G118100.2	Phvul.008G118100	Phvul.008G118100		0
1	Phvul.008G118100.3	Phvul.008G118100	Phvul.008G118100		0
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1	Phvul.008G118100.2	Phvul.008G118100	Phvul.008G118100		0
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1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
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1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
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1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
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1	Phvul.009G019500.2	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
1	Phvul.009G019500.1	Phvul.009G019500	Phvul.009G019500	PF01479,PF00	
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1	Phvul.011G087500.1	Phvul.011G087500	Phvul.011G087500	PF00125
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501

1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
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1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
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1	Phvul.001G021800.1	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G021800.2	Phvul.001G021800	Phvul.001G021800	PF01501
1	Phvul.001G055000.1	Phvul.001G055000	Phvul.001G055000	PF14226,PF03
1	Phvul.001G055000.1	Phvul.001G055000	Phvul.001G055000	PF14226,PF03
1	Phvul.001G055000.1	Phvul.001G055000	Phvul.001G055000	PF14226,PF03
1	Phvul.001G055000.1	Phvul.001G055000	Phvul.001G055000	PF14226,PF03
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1	Phvul.001G103833.1	Phvul.001G103833	Phvul.001G103833	PF08502
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1	Phvul.001G109780.2	Phvul.001G109780	Phvul.001G109780	PF08502

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1	Phvul.001G261800.2	Phvul.001G261800	Phvul.001G261800	PF05755
1	Phvul.001G261800.1	Phvul.001G261800	Phvul.001G261800	PF05755
1	Phvul.001G261800.2	Phvul.001G261800	Phvul.001G261800	PF05755

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1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
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1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03

1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
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1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
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1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
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1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.1	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
1	Phvul.002G326600.2	Phvul.002G326600	Phvul.002G326600	PF14226,PF03
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2	Phvul.003G195900.2	Phvul.003G195900	Phvul.003G195900	0
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2	Phvul.003G195900.2	Phvul.003G195900	Phvul.003G195900		0
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2	Phvul.003G195900.1	Phvul.003G195900	Phvul.003G195900		0
2	Phvul.003G195900.2	Phvul.003G195900	Phvul.003G195900		0
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1	Phvul.003G218500.3	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.3	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.3	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.3	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854	
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1	Phvul.003G218500.3	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854	
1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854	

1	Phvul.003G218500.3	Phvul.003G218500	Phvul.003G218500	PF00854
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1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854
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1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854
1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854
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1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854
1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854
1	Phvul.003G218500.3	Phvul.003G218500	Phvul.003G218500	PF00854
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1	Phvul.003G218500.2	Phvul.003G218500	Phvul.003G218500	PF00854
1	Phvul.003G218500.1	Phvul.003G218500	Phvul.003G218500	PF00854
1	Phvul.003G225400.1	Phvul.003G225400	Phvul.003G225400	PF00588
1	Phvul.003G240800.1	Phvul.003G240800	Phvul.003G240800	PF08246,PF00
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1	Phvul.003G248700.1	Phvul.003G248700	Phvul.003G248700	0
1	Phvul.003G249000.1	Phvul.003G249000	Phvul.003G249000	0
1	Phvul.003G273400.1	Phvul.003G273400	Phvul.003G273400	PF03765,PF00
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1	Phvul.003G273400.1	Phvul.003G273400	Phvul.003G273400	PF03765,PF00
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1	Phvul.003G273400.1	Phvul.003G273400	Phvul.003G273400	PF03765,PF00

1	Phvul.003G273400.1	Phvul.003G273400	Phvul.003G273400	PF03765,PF00
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1	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.1	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.3	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
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1	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.1	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.3	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.1	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
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1	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
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1	Phvul.005G101400.3	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.1	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.3	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
1	Phvul.005G101400.2	Phvul.005G101400	Phvul.005G101400	PF00122,PF12
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1	Phvul.006G060500.3	Phvul.006G060500	Phvul.006G060500	PF16529
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
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1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00

1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
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1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
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1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.2	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
1	Phvul.006G174400.1	Phvul.006G174400	Phvul.006G174400	PF08263,PF00
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1	Phvul.007G161800.2	Phvul.007G161800	Phvul.007G161800	PF03741
1	Phvul.007G161800.2	Phvul.007G161800	Phvul.007G161800	PF03741
1	Phvul.007G161800.2	Phvul.007G161800	Phvul.007G161800	PF03741
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1	Phvul.007G166500.5	Phvul.007G166500	Phvul.007G166500	PF13365
1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
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1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
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1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
1	Phvul.007G166500.6	Phvul.007G166500	Phvul.007G166500	PF13365
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1	Phvul.007G166500.4	Phvul.007G166500	Phvul.007G166500	PF13365
1	Phvul.007G166500.3	Phvul.007G166500	Phvul.007G166500	PF13365
1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.3	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400

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1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.3	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.3	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.3	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.5	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G184400.6	Phvul.007G184400	Phvul.007G184400	PF00400
1	Phvul.007G184400.2	Phvul.007G184400	Phvul.007G184400	PF00400
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1	Phvul.007G207200.1	Phvul.007G207200	Phvul.007G207200	PF00098,PF08
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1	Phvul.008G012100.2	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
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1	Phvul.008G012100.1	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
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1	Phvul.008G012100.2	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
1	Phvul.008G012100.1	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
1	Phvul.008G012100.2	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
1	Phvul.008G012100.1	Phvul.008G012100	Phvul.008G012100	PF02969,PF07
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1	Phvul.010G066900.1	Phvul.010G066900	Phvul.010G066900	PF00141
1	Phvul.010G066900.1	Phvul.010G066900	Phvul.010G066900	PF00141
1	Phvul.010G066900.1	Phvul.010G066900	Phvul.010G066900	PF00141
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01

1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.2	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.1	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
1	Phvul.010G073200.3	Phvul.010G073200	Phvul.010G073200	PF16278,PF01
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1	Phvul.011G077500.1	Phvul.011G077500	Phvul.011G077500	PF00808
1	Phvul.011G077500.1	Phvul.011G077500	Phvul.011G077500	PF00808
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1	Phvul.001G024500.1	Phvul.001G024500	Phvul.001G024500	PF00396,PF08
1	Phvul.001G024500.1	Phvul.001G024500	Phvul.001G024500	PF00396,PF08
1	Phvul.001G024500.1	Phvul.001G024500	Phvul.001G024500	PF00396,PF08
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13

1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.2	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G095200.3	Phvul.001G095200	Phvul.001G095200	PF12854,PF13
1	Phvul.001G198800.1	Phvul.001G198800	Phvul.001G198800	PF04576
1	Phvul.001G198800.1	Phvul.001G198800	Phvul.001G198800	PF04576
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1	Phvul.002G119401.1	Phvul.002G119401	Phvul.002G119401	PF04434,PF10
1	Phvul.002G119401.1	Phvul.002G119401	Phvul.002G119401	PF04434,PF10
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1	Phvul.002G119401.1	Phvul.002G119401	Phvul.002G119401	PF04434,PF10
1	Phvul.002G123300.1	Phvul.002G123300	Phvul.002G123300	PF03759
1	Phvul.002G123300.2	Phvul.002G123300	Phvul.002G123300	PF03759
1	Phvul.002G327900.1	Phvul.002G327900	Phvul.002G327900	PF00462
1	Phvul.003G136300.2	Phvul.003G136300	Phvul.003G136300	PF01985
1	Phvul.003G136300.1	Phvul.003G136300	Phvul.003G136300	PF01985
1	Phvul.003G136300.2	Phvul.003G136300	Phvul.003G136300	PF01985
1	Phvul.003G136300.1	Phvul.003G136300	Phvul.003G136300	PF01985
1	Phvul.003G136300.2	Phvul.003G136300	Phvul.003G136300	PF01985
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1	Phvul.003G136300.2	Phvul.003G136300	Phvul.003G136300	PF01985
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1	Phvul.003G136300.2	Phvul.003G136300	Phvul.003G136300	PF01985

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1	Phvul.003G136300.2	Phvul.003G136300	Phvul.003G136300	PF01985
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2	Phvul.003G195900.2	Phvul.003G195900	Phvul.003G195900	0
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2	Phvul.003G195900.1	Phvul.003G195900	Phvul.003G195900	0
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1	Phvul.003G292800.1	Phvul.003G292800	Phvul.003G292800	PF13812,PF01
1	Phvul.004G026100.2	Phvul.004G026100	Phvul.004G026100	PF01145

1	Phvul.004G026100.1	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.2	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.1	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.2	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.1	Phvul.004G026100	Phvul.004G026100	PF01145
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1	Phvul.004G026100.2	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.1	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.2	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.1	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.2	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.1	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.2	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.004G026100.1	Phvul.004G026100	Phvul.004G026100	PF01145
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.005G172300.2	Phvul.005G172300	Phvul.005G172300	PF00534,PF16

1	Phvul.005G172300.1	Phvul.005G172300	Phvul.005G172300	PF00534,PF16
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
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1	Phvul.006G052200.1	Phvul.006G052200	Phvul.006G052200	PF00664,PF00
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1	Phvul.006G056000.2	Phvul.006G056000	Phvul.006G056000	0
1	Phvul.006G056000.2	Phvul.006G056000	Phvul.006G056000	0
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1	Phvul.006G056000.2	Phvul.006G056000	Phvul.006G056000	0
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1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923

1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.2	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G003600.1	Phvul.008G003600	Phvul.008G003600	PF00923
1	Phvul.008G055200.1	Phvul.008G055200	Phvul.008G055200	PF03547
1	Phvul.008G162900.1	Phvul.008G162900	Phvul.008G162900	PF13245,PF13
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1	Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
1	Phvul.008G283700.1	Phvul.008G283700	Phvul.008G283700	PF17048,PF04
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1	Phvul.009G140900.1	Phvul.009G140900	Phvul.009G140900	PF00860
1	Phvul.010G131100.2	Phvul.010G131100	Phvul.010G131100	PF00067
1	Phvul.010G140600.2	Phvul.010G140600	Phvul.010G140600	PF00664,PF0
1	Phvul.010G140600.2	Phvul.010G140600	Phvul.010G140600	PF00664,PF0
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1	Phvul.011G031600.2	Phvul.011G031600	Phvul.011G031600	PF00168
1	Phvul.011G031600.1	Phvul.011G031600	Phvul.011G031600	PF00168
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1	Phvul.011G092600.1	Phvul.011G092600	Phvul.011G092600	PF02225,PF00
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1	Phvul.011G092600.1	Phvul.011G092600	Phvul.011G092600	PF02225,PF00
1	Phvul.011G092600.2	Phvul.011G092600	Phvul.011G092600	PF02225,PF00
1	Phvul.011G092600.1	Phvul.011G092600	Phvul.011G092600	PF02225,PF00
1	Phvul.011G092600.2	Phvul.011G092600	Phvul.011G092600	PF02225,PF00
1	Phvul.011G092600.1	Phvul.011G092600	Phvul.011G092600	PF02225,PF00
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Panther	KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
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PTHR22904,P	KOG0548,KO	0	K09527	0	AT5G65160.1	0
PTHR22904,P	KOG0548,KO	0	K09527	0	AT5G65160.1	0
PTHR22904,P	KOG0548,KO	0	K09527	0	AT5G65160.1	0
PTHR22904,P	KOG0548,KO	0	K09527	0	AT5G65160.1	0
PTHR24093,P	0	3.6.3.8	K01537	GO:0046872,	AT3G22910.1	0
PTHR24093,P	0	3.6.3.8	K01537	GO:0046872,	AT3G22910.1	0
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PTHR24093,P	0	3.6.3.8	K01537	GO:0046872,	AT3G22910.1	0
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PTHR24093,P	0	3.6.3.8	K01537	GO:0046872,	AT3G22910.1	0
PTHR24093,P	0	3.6.3.8	K01537	GO:0046872,	AT3G22910.1	0

PTHR24093,P	0	3.6.3.8	K01537	GO:0046872,(	AT3G22910.1	0
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PTHR24093,P	0	3.6.3.8	K01537	GO:0046872,(	AT3G22910.1	0
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PTHR11361,P	0	0	0	GO:0030983,(	AT5G54090.1	0
PTHR11361,P	0	0	0	GO:0030983,(	AT5G54090.1	0
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PTHR11361,P	0	0	0	GO:0030983,(	AT5G54090.1	0
PTHR11361,P	0	0	0	GO:0030983,(	AT5G54090.1	0
PTHR12217,P	0	0	K15027	GO:0006413,(	AT1G71350.1	0
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PTHR12217,P	0	0	K15027	GO:0006413,(	AT1G71350.1	0
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PTHR12217,P	0	0	K15027	GO:0006413,(	AT1G71350.1	0
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PTHR31602,P	0	0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1
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PTHR16019,P	0	0	0	0	AT1G03350.1	0
PTHR16019,P	0	0	0	0	AT1G03350.1	0
PTHR16019,P	0	0	0	0	AT1G03350.1	0

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PTHR16019,P	0	0	0	0	AT1G03350.1	0
PTHR16019,P	0	0	0	0	AT1G03350.1	0
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PTHR16019,P	0	0	0	0	AT1G03350.1	0
PTHR12640,P	KOG2447	2.4.99.18	K12667	GO:0016021,	AT4G21150.3	HAP6
PTHR12640,P	KOG2447	2.4.99.18	K12667	GO:0016021,	AT4G21150.3	HAP6
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PTHR31602,P	0	0	0	GO:0006355,	AT3G52910.1	AtGRF4,GRF4
PTHR31602,P	0	0	0	GO:0006355,	AT3G52910.1	AtGRF4,GRF4
PTHR31602,P	0	0	0	GO:0006355,	AT3G52910.1	AtGRF4,GRF4
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2

PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,(	AT4G37740.1	AtGRF2,GRF2
PTHR11654,P	0	3.6.3.26	K14638	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	0	3.6.3.26	K14638	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
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PTHR11654,P	0	3.6.3.26	K14638	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	0	3.6.3.26	K14638	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	0	3.6.3.26	K14638	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	0	3.6.3.26	K14638	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
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PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
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PTHR11246,P	0	0	K12869	GO:0005515,(	AT5G41770.1	0
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PTHR23086,P	0	2.7.1.68	K00889	GO:0046488,(	AT1G10900.1	0
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PTHR24015,P	0	0	0	0	AT1G31430.1	0
PTHR24015,P	0	0	0	0	AT1G31430.1	0
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PTHR31602,P	0	0	0	GO:0006355,(	AT3G13960.1	AtGRF5,GRF5
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PTHR31602,P	0	0	0	GO:0006355,(	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,(	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,(	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,(	AT3G13960.1	AtGRF5,GRF5
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PTHR31602,P	0	0	0	GO:0006355,(	AT3G13960.1	AtGRF5,GRF5

PTHR19375,P	0	0	K03283		0	AT1G16030.1	Hsp70b	
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PTHR19375,P	0	0	K03283		0	AT1G16030.1	Hsp70b	
PTHR19375,P	0	0	K03283		0	AT1G16030.1	Hsp70b	
PTHR19375,P	0	0	K03283		0	AT1G16030.1	Hsp70b	
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PTHR22904,P	KOG4412	0		0	GO:0005515	AT3G04710.3		0
PTHR22904,P	KOG4412	0		0	GO:0005515	AT3G04710.3		0
PTHR22904,P	KOG4412	0		0	GO:0005515	AT3G04710.3		0
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PTHR22904,P	KOG4412	0		0	GO:0005515	AT3G04710.3		0
PTHR22904,P	KOG4412	0		0	GO:0005515	AT3G04710.3		0
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
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PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
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PTHR19957,P	KOG0810	0	K08486		GO:0005515,(	AT1G61290.1	ATSYP124,SYP	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	
PTHR31602,P	0	0		0	GO:0006355,(	AT2G36400.1	AtGRF3,GRF3	

PTHR31602,P	0	0	0	GO:0006355,	AT2G36400.1	AtGRF3,GRF3
PTHR31602,P	0	0	0	GO:0006355,	AT2G36400.1	AtGRF3,GRF3
PTHR24177	KOG4214	0	0	GO:0008270	AT3G54070.1	0
PTHR24177	KOG4214	0	0	GO:0008270	AT3G54070.1	0
PTHR24177	KOG4214	0	0	GO:0008270	AT3G54070.1	0
PTHR24177	KOG4214	0	0	GO:0008270	AT3G54070.1	0
PTHR24177	KOG4214	0	0	GO:0008270	AT3G54070.1	0
PTHR24177	KOG4214	0	0	GO:0008270	AT3G54070.1	0
PTHR24177	KOG4214	0	0	GO:0008270	AT3G54070.1	0
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PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR24177	0	0	0	0	AT3G54070.1	0
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2

PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT4G37740.1	AtGRF2,GRF2

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PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,(	AT4G37740.1	AtGRF2,GRF2
PTHR12948,P	KOG2561	0	0	0	AT2G12550.1	0
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PTHR12948,P	KOG2561		0	0	0	AT2G12550.1	0
PTHR31602,P		0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P		0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
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PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
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PTHR31602,P		0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2

PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0032502,	AT4G37740.1	AtGRF2,GRF2
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5

PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	0	GO:0055114,	AT1G55020.1	ATLOX1,LOX1
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR31602,P	0	0	0	GO:0006355,	AT3G13960.1	AtGRF5,GRF5
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	0	GO:0016787,	AT5G26742.2	emb1138
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3

PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR32409,P	0	0	0	GO:0045040,	AT3G27080.1	TOM20-3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR10589	KOG1415	3.4.19.12	0	GO:0006511,	AT4G17510.1	UCH3
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR11727,P	KOG0820	2.1.1.183	K14191	0	AT5G66360.2	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0

PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR14003	0	0	0	0	AT4G06634.1	0
PTHR11102,P	KOG1550	0	K14026	0	AT1G18260.1	0
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR11946,P	0	6.1.1.5	K01870	GO:0006418,(	AT5G49030.3	OVA2
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24115,P	KOG0242	3.6.4.4	K11498	GO:0008017,(	AT3G43210.1	ATNACK2,NAC
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,(	AT5G57110.2	ACA8,AT-ACA

PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,	AT5G57110.2	ACA8,AT-ACA
PTHR24093,P	0	3.6.3.8	K01537	GO:0005516,	AT5G57110.2	ACA8,AT-ACA
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR23115,P	0	3.6.5.3	K02358	GO:0005525	AT4G20360.1	ATRAB8D,ATR
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR24092,P	0	3.6.3.1	K01530	GO:0046872,	AT3G27870.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
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PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR33178,P	0	0	0	0	AT5G22580.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0

PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR18359	0	0	K14553	GO:0005515	AT5G14050.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
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PTHR24015,P	0	0	0	0	AT3G11460.1	0
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PTHR24015,P	0	0	0	0	AT3G11460.1	0
PTHR24015,P	0	0	0	0	AT3G11460.1	0
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PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR24096,P	0	6.2.1.3	K01897	GO:0008152,(	AT2G47240.1	CER8,LACS1
PTHR23241,P	KOG4744	0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744	0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744	0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744	0	0	0	AT3G53040.1	0

PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
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PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR23241,P	KOG4744		0	0	0	AT3G53040.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
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PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR31642,P		0	2.3.1.196	0	GO:0016747	AT5G17540.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,(	AT4G10780.1	0
PTHR24015,P		0	0	0	0	AT4G19890.1	0
PTHR24015,P		0	0	0	0	AT4G19890.1	0
PTHR24015,P		0	0	0	0	AT4G19890.1	0

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PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
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PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
PTHR24015,P	0	0	0	0	AT4G19890.1		0
0	0	0	0	0	AT5G02130.1	NDP1	
0	0	0	0	0	AT5G02130.1	NDP1	
0	0	0	0	0	AT5G02130.1	NDP1	
0	0	0	0	0	AT5G02130.1	NDP1	
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0	0	0	0	0	AT5G02130.1	NDP1
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0	0	0	0	0	AT5G02130.1	NDP1
PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
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PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
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PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
PTHR13522	KOG3102	0	0	GO:0034477,	AT5G51170.1	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11079,P	KOG1919	5.4.99.23	0	GO:0003723,	AT1G76050.2	0
PTHR11945,P	KOG0014	0	0	GO:0006355,	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,	AT2G22540.1	AGL22,SVP
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PTHR11945,P	KOG0014	0	0	GO:0006355,	AT2G22540.1	AGL22,SVP

PTHR11945,P	KOG0014	0	0	GO:0006355,(	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,(	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,(	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,(	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,(	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,(	AT2G22540.1	AGL22,SVP
PTHR11945,P	KOG0014	0	0	GO:0006355,(	AT2G22540.1	AGL22,SVP
PTHR24015,P	0	0	0	0	AT2G04860.1	0
PTHR24015,P	0	0	0	0	AT2G04860.1	0
PTHR24015,P	0	0	0	0	AT2G04860.1	0
PTHR24015,P	0	0	0	0	AT2G04860.1	0
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PTHR24015,P	0	0	0	0	AT2G04860.1	0
PTHR24015,P	0	0	0	0	AT2G04860.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
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PTHR31115,P	0	0	0	0	AT4G29790.1	0
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PTHR31115,P	0	0	0	0	AT4G29790.1	0
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PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
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PTHR31115,P	0	0	0	0	AT4G29790.1	0
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PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR31115,P	0	0	0	0	AT4G29790.1	0
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4

PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR13780,P	0	0	0	0	AT1G09020.1	ATSNF4,SNF4
PTHR11771,P	0	1.13.11.58	K15718	GO:0005515,	AT1G55020.1	ATLOX1,LOX1
PTHR11771,P	0	1.13.11.58	K15718	GO:0005515,	AT1G55020.1	ATLOX1,LOX1
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR13878,P	0	1.5.99.12	K00279	GO:0055114,	AT3G63440.1	ATCKX6,ATCK
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR23428	KOG1744	0	K11252	GO:0003677,	AT1G08170.1	0
PTHR11183,P	KOG1950	2.4.1.17	0	GO:0016757,	AT4G33330.2	GUX2,PGSIP3

PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
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PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR11183,P	KOG1950	2.4.1.17			0	GO:0016757,(	AT4G33330.2	GUX2,PGSIP3
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10209,P	KOG0143		0	K04124		GO:0055114,(	AT1G15550.1	ATGA3OX1,G
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.13			0	GO:0009098,(	AT1G18500.1	IPMS1,MAML
PTHR10277,P	0	2.3.3.14			0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,M
PTHR10277,P	0	2.3.3.14			0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,M

PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR10277,P	0	2.3.3.14	0	GO:0009098,(	AT1G74040.1	IMS1,IPMS2,N
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
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PTHR33732,P	0	0	0	0	AT1G67360.2	0
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PTHR33732,P	0	0	0	0	AT1G67360.2	0
PTHR33732,P	0	0	0	0	AT1G67360.2	0
PTHR33732,P	0	0	0	0	AT1G67360.2	0
PTHR33732,P	0	0	0	0	AT1G67360.2	0
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PTHR33732,P	0	0	0	0	AT1G67360.2	0
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PTHR33732,P	0	0	0	0	AT1G67360.2	0

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PTHR33732,P	0	0	0	0	AT1G67360.2	0
PTHR31113,P	0	0	0	0	AT2G18630.1	0
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PTHR31113,P	0	0	0	0	AT2G18630.1	0
PTHR31113,P	0	0	0	0	AT2G18630.1	0
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PTHR11679,P	0	0	0	GO:0016192,(	AT2G17980.1	ATSLY1
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF

PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
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PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR10209,P	KOG0143	1.14.17.4	K05933	GO:0055114,(	AT1G05010.1	ACO4,EAT1,EF
PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
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PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
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PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
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PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
PTHR31235,P	0	1.11.1.7	K00430	GO:0055114,(	AT4G21960.1	PRXR1
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34949,P	0	0	0	GO:0048193,(	AT4G30240.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0

PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR12626,P	0	0	0	0	AT5G63190.1	0
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26	0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C

PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR11654,P	KOG1237	3.6.3.26		0	GO:0016020,(	AT1G12110.1	ATNRT1,B-1,C
PTHR12029,P	0	2.1.1.34		0	GO:0008173,(	AT4G17610.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
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PTHR12411,P	KOG1543	3.4.22.14		0	GO:0008234,(	AT3G19390.1	0
PTHR14237,P	0	2.8.1.9		0	0	AT2G23520.1	0
PTHR14237,P	0	2.8.1.9		0	0	AT2G23520.1	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0
PTHR23324,P	KOG1471		0	0	0	AT1G55690.3	0

PTHR23324,P	KOG1471			0		0		0	AT1G55690.3		0
PTHR23324,P	KOG1471			0		0		0	AT1G55690.3		0
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
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PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
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PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
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PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
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PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
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PTHR24092,P		0	3.6.3.1		K01530		GO:0046872,(		AT5G44240.2	ALA2	
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PTHR15598,P		0		0	K12616			0	AT3G13300.1	VCS	
PTHR27001,P	KOG1187		2.7.11.1			0	GO:0006468,(		AT5G45780.1		0
PTHR27001,P	KOG1187		2.7.11.1			0	GO:0006468,(		AT5G45780.1		0
PTHR27001,P	KOG1187		2.7.11.1			0	GO:0006468,(		AT5G45780.1		0
PTHR27001,P	KOG1187		2.7.11.1			0	GO:0006468,(		AT5G45780.1		0
PTHR27001,P	KOG1187		2.7.11.1			0	GO:0006468,(		AT5G45780.1		0
PTHR27001,P	KOG1187		2.7.11.1			0	GO:0006468,(		AT5G45780.1		0
PTHR27001,P	KOG1187		2.7.11.1			0	GO:0006468,(		AT5G45780.1		0

PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
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PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G45780.1	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
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PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR30238,P	0	0	0	GO:0016021	AT5G12130.1	ATTERC,PDE1
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2

PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR22939,P	KOG1320	3.4.21.107	0	0	AT2G47940.1	DEGP2
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1

PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR19862,P	KOG0279	0	0	GO:0005515	AT3G05090.1	LRS1
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138

PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR24031,P	KOG0331	3.6.4.13	K16911	GO:0008270,(	AT5G26742.2	emb1138
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR10221,P	KOG2549	0	K03131	GO:0006352,(	AT1G04950.1	ATTAF6,TAF6,
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR36795,P	0	0	0	0	AT5G14410.1	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0

PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24012,P	KOG0131	0	K12741	GO:0003676	AT2G41060.2	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR24015,P	0	0	0	0	AT3G02650.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
PTHR13683,P	KOG1339	3.4.23.12	0	GO:0006508,(	AT1G66180.1	0
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0	0	0	0	0	0	0
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0	0	0	0	0	0	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0

PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR10445,P	KOG2905	3.6.4.12	K03139	GO:0006367,(	AT1G75510.1	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR24015,P	0	0	0	0	AT1G05670.2	0
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR10410,P	0	3.4.25.1	K09613	GO:0005515	AT1G71230.1	AJH2,CSN5,CS
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR26312,P	0	0	0	0	AT4G39470.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0

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PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR24015,P	0	0	0	0	AT1G79540.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR31388,P	0	1.11.1.7	K00430	GO:0055114,(	AT5G05340.1	0
PTHR12486,P	KOG0562	0	0	GO:0033699,(	AT5G01310.1	APTX
PTHR12486,P	KOG0562	0	0	GO:0033699,(	AT5G01310.1	APTX
PTHR12486,P	KOG0562	0	0	GO:0033699,(	AT5G01310.1	APTX
PTHR12486,P	KOG0562	0	0	GO:0033699,(	AT5G01310.1	APTX
PTHR12486,P	KOG0562	0	0	GO:0033699,(	AT5G01310.1	APTX
PTHR12486,P	KOG0562	0	0	GO:0033699,(	AT5G01310.1	APTX

PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
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PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR12486,P	KOG0562			0		0	GO:0033699,(		AT5G01310.1	APTX
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR10252,P		0	2.7.7.7			0		0	AT1G07980.1	NF-YC10
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1
PTHR31633		0		0	K14763		GO:0042254,(		AT1G03530.1	ATNAF1,NAF1

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PTHR31633	0	0	K14763	GO:0042254,(	AT1G03530.1	ATNAF1,NAF1
PTHR31633	0	0	K14763	GO:0042254,(	AT1G03530.1	ATNAF1,NAF1
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR24326,P	0	0	0	GO:0003677	AT5G53980.1	ATHB52,HB52
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR12411,P	KOG1543	3.4.22.14	0	GO:0008234,(	AT1G47128.1	RD21,RD21A
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0

PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR24015,P	0	0	0	0	AT3G04130.2	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31422,P	0	0	0	0	AT5G06560.1	0
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR31669,P	0	0	0	GO:0008270,(	AT4G38180.1	FRS5
PTHR33101,P	0	0	0	GO:0005089	AT1G31650.1	ATROPGEF14,
PTHR33101,P	0	0	0	GO:0005089	AT1G31650.1	ATROPGEF14,
PTHR10168,P	KOG2824	0	K17479	GO:0045454,(	AT4G10630.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
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PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
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PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0

PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
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PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR31846,P	KOG1990	0	0	GO:0003723	AT4G29750.1	0
PTHR24015,P	0	0	0	0	AT4G30700.1	0
PTHR24015,P	0	0	0	0	AT4G30700.1	0
PTHR24015,P	0	0	0	0	AT4G30700.1	0
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PTHR24015,P	0	0	0	0	AT4G30700.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
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PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
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PTHR34778,P	0	0	0	0	AT1G19010.1	0
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PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR34778,P	0	0	0	0	AT1G19010.1	0
PTHR31009,P	0	2.1.1.274	K08241	GO:0008168	AT5G04380.1	0
PTHR24015,P	0	0	0	0	AT2G15690.1	0
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1

PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR10264,P	KOG2620	0	0	GO:0016020	AT5G62740.1	ATHIR1,HIR1
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
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PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0

PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G13080.1	ATMRP3,MRP
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
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0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
0	0	0	0	0	0	0
PTHR11817,P	0	2.7.1.40	K00873	GO:0030955,(	AT3G52990.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0

PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR10683,P	KOG2772	2.2.1.2	0	GO:0005975	AT5G13420.1	0
PTHR31752,P	0	0	K13947	GO:0055085,	AT5G16530.1	PIN5
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
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PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR10887,P	KOG1801	0	K10706	0	AT4G15570.1	MAA3
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RS
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR31321,P	0	3.1.1.11	K01051	GO:0042545,	AT5G55590.1	QRT1
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0

PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR12670,P	0	3.5.1.23	K12349	0	AT1G07380.1	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR31704,P	0	0	0	0	AT2G24960.2	0
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR11119,P	0	0	K06901	GO:0055085,(	AT3G10960.1	ATAZG1,AZG1
PTHR24286,P	0	0	0	GO:0055114,(	AT1G05160.1	ATKAO1,CYP8
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44	0	GO:0055085,(	AT3G60160.1	ATMRP9,MRP

PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR24223,P	0	3.6.3.44		0	GO:0055085,	AT3G60160.1	ATMRP9,MRP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR22953,P	KOG1378	3.1.4.1		0	GO:0016787	AT4G24890.1	ATPAP24,PAP
PTHR10774,P	0		0	0	GO:0005515	AT3G19830.1	NTMC2T5.2,N
PTHR10774,P	0		0	0	GO:0005515	AT3G19830.1	NTMC2T5.2,N
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR10795,P	0	3.4.14.10		0	GO:0006508,	AT2G04160.1	AIR3
PTHR22870,P	KOG1427		0	0	GO:0046872	AT1G69710.1	0
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PTHR23070,P	0		0	K08900	GO:0005524,	AT5G57480.1	0

PTHR11746,P	KOG1509			0	0	GO:0005737	AT5G66550.1	0
PTHR11746,P	KOG1509			0	0	GO:0005737	AT5G66550.1	0
PTHR27000,P	KOG1187		2.7.11.1		0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2
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PTHR21330,P		0	3.4.22.16		0	GO:0030915,(	AT3G15150.1	ATMMS21,HP
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PTHR21330,P		0	3.4.22.16		0	GO:0030915,(	AT3G15150.1	ATMMS21,HP
PTHR21330,P		0	3.4.22.16		0	GO:0030915,(	AT3G15150.1	ATMMS21,HP
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PTHR31852,P		0		0	0	0	AT2G35460.1	0
PTHR31852,P		0		0	0	0	AT2G35460.1	0

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PTHR24006,P	KOG1947	0	K10268	GO:0005515	AT4G15475.1	0
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PTHR31422,P	0	0	0	0	AT1G18265.1	0
PTHR11532,P	KOG2649	3.4.17.22	0	0	AT1G71696.1	SOL1
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PTHR22849,P	KOG0279	2.7.11.7	0	GO:0005515,(	AT3G06880.2	0
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PTHR31549,P	0	0	0	0	AT4G31980.1	0
PTHR24031,P	0	3.6.4.13	K17679	GO:0016787,(	AT5G08610.1	0
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PTHR11851,P	0	1.10.2.2,3.4.2	K01412	0	AT1G51980.1	0
PTHR23029,P	KOG0235	3.1.3.63	K15634	0	AT5G22620.1	0
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arabi-defline	ID	Annot_defline	IDENTIFIER	NAME
0	0	0	Phvul.003G16	not assigned.r
0	0	0	Phvul.003G16	not assigned.r
0	0	0	Phvul.003G16	not assigned.r
0	0	0	Phvul.003G16	not assigned.r
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0	0	0	Phvul.003G16	not assigned.r
0	0	0	Phvul.003G16	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
Ankyrin-repeat containing protein	Phvul.008G20	PF13962 - Dor	Phvul.008G20	not assigned.r
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0	0	0	Phvul.007G25	Cell cycle orga
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0	0	0	Phvul.007G25	Cell cycle orga
0	0	0	Phvul.007G25	Cell cycle orga
0	0	0	Phvul.007G25	Cell cycle orga
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.001G15	PF00689//PFC	Phvul.001G15	Solute transpo
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
tetratricopeptide repeat (TPR)-containir	Phvul.002G25	KOG0548//KC	Phvul.002G25	not assigned.a
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PFC	Phvul.004G04	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PFC	Phvul.004G04	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PFC	Phvul.004G04	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PFC	Phvul.004G04	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PFC	Phvul.004G04	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PFC	Phvul.004G04	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PFC	Phvul.004G04	Solute transpo

ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PF	Phvul.004G04	Solute transp
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PF	Phvul.004G04	Solute transp
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PF	Phvul.004G04	Solute transp
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PF	Phvul.004G04	Solute transp
ATPase E1-E2 type family protein / halo	Phvul.004G04	PF00122//PF	Phvul.004G04	Solute transp
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
DNA mismatch repair protein MutS, typ	Phvul.008G18	PTHR11361:S	Phvul.008G18	not assigned.a
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
eukaryotic translation initiation factor S	Phvul.011G21	K15027 - tran	Phvul.011G21	not assigned.
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth

BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
BSD domain-containing protein	Phvul.001G14	PTHR16019 -	Phvul.001G14	RNA biosynth
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
ribophorin II (RPN2) family protein	Phvul.001G16	K12667 - olig	Phvul.001G16	Protein modif
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 4	Phvul.001G18	PTHR31602:S	Phvul.001G18	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth
growth-regulating factor 2	Phvul.002G04	PF08879//PF	Phvul.002G04	RNA biosynth

growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
growth-regulating factor 2	Phvul.002G04	PF08879//PF0	Phvul.002G04	RNA biosynthe
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
nitrate transporter 1.1	Phvul.002G06	PTHR11654:SF	Phvul.002G06	Solute transpo
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
growth-regulating factor 2	Phvul.002G13	PF08879//PF0	Phvul.002G13	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
K-box region and MADS-box transcriptio	Phvul.002G14	PTHR11945:SF	Phvul.002G14	RNA biosynthe
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processin
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processin

crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
crooked neck protein, putative / cell cyc	Phvul.002G16	K12869 - croo	Phvul.002G16	RNA processi
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Phosphatidylinositol-4-phosphate 5-kin	Phvul.002G25	PTHR23086:S	Phvul.002G25	Multi-process
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.003G01	PF01535//PF1	Phvul.003G01	not assigned.
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth
growth-regulating factor 5	Phvul.003G13	PF08879//PF	Phvul.003G13	RNA biosynth

heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
heat shock protein 70B	Phvul.003G15	PTHR19375:S	Phvul.003G15	Protein home
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
ankyrin repeat family protein	Phvul.006G10	PTHR22904//	Phvul.006G10	not assigned.
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
syntaxin of plants 124	Phvul.006G19	PTHR19957//	Phvul.006G19	Vesicle traffic
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth

growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
growth-regulating factor 3	Phvul.007G22	PTHR31602:S	Phvul.007G22	RNA biosynth
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF01529//PF1	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
Ankyrin repeat family protein	Phvul.008G20	PF13962 - Do	Phvul.008G20	not assigned.
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth

growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth

growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
growth-regulating factor 2	Phvul.009G04	PF08879//PF	Phvul.009G04	RNA biosynth
ubiquitin-associated (UBA)/TS-N domai	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.
ubiquitin-associated (UBA)/TS-N domai	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.
ubiquitin-associated (UBA)/TS-N domai	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.
ubiquitin-associated (UBA)/TS-N domai	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.

ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
ubiquitin-associated (UBA)/TS-N domair	Phvul.009G21	PTHR12948 - I	Phvul.009G21	not assigned.r
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 5	Phvul.009G22	PF08879//PF0	Phvul.009G22	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe
growth-regulating factor 2	Phvul.010G04	PTHR31602:SI	Phvul.010G04	RNA biosynthe

growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 2	Phvul.010G04	PTHR31602:S	Phvul.010G04	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth
growth-regulating factor 5	Phvul.010G13	PTHR31602:S	Phvul.010G13	RNA biosynth

lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	1.13.11.58 - Li	Phvul.010G13	Enzyme classi
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
growth-regulating factor 5	Phvul.011G01	PF08879//PF	Phvul.011G01	RNA biosynth
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
DEAD box RNA helicase (RH3)	Phvul.001G22	PTHR24031:S	Phvul.001G22	RNA processi
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl

translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
translocase of outer membrane 20 kDa	Phvul.001G26	PTHR32409:S	Phvul.001G26	Protein transl
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
ubiquitin C-terminal hydrolase 3	Phvul.002G00	K05609 - ubiq	Phvul.002G00	Protein home
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
Ribosomal RNA adenine dimethylase fa	Phvul.002G16	PTHR11727:S	Phvul.002G16	Protein biosy
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth

zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
zinc finger (C2H2 type) family protein	Phvul.002G24	PTHR14003 -	Phvul.002G24	RNA biosynth
HCP-like superfamily protein	Phvul.002G33	K14026 - SEL1	Phvul.002G33	Protein home
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
tRNA synthetase class I (I, L, M and V) fa	Phvul.003G10	6.1.1.5 - Isole	Phvul.003G10	Protein biosy
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
ATP binding microtubule motor family p	Phvul.003G12	PTHR24115:S	Phvul.003G12	Cytoskeleton
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF	Phvul.003G14	Solute transp

autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF0	Phvul.003G14	Solute transpo
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF0	Phvul.003G14	Solute transpo
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF0	Phvul.003G14	Solute transpo
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF0	Phvul.003G14	Solute transpo
autoinhibited Ca2+ -ATPase, isoform 8	Phvul.003G14	PF00122//PF0	Phvul.003G14	Solute transpo
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
RAB GTPase homolog E1B	Phvul.003G20	PTHR23115//I	Phvul.003G20	Protein biosyn
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
ATPase E1-E2 type family protein / halo	Phvul.004G01	PTHR24092:S	Phvul.004G01	Solute transpo
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Stress responsive A/B Barrel Domain	Phvul.005G12	PF07876 - Str	Phvul.005G12	not assigned.
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyn
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyn
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyn
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyn
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyn

Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyr
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyr
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyr
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyr
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyr
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyr
Transducin/WD40 repeat-like superfami	Phvul.006G20	K14553 - U3 s	Phvul.006G20	Protein biosyr
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	RNA processir
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.007G18	PF01535//PF1	Phvul.007G18	not assigned.a
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
AMP-dependent synthetase and ligase f	Phvul.007G21	PTHR24096:SI	Phvul.007G21	Enzyme classi
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:SI	Phvul.007G22	not assigned.r
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:SI	Phvul.007G22	not assigned.r
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:SI	Phvul.007G22	not assigned.r
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:SI	Phvul.007G22	not assigned.r

late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
late embryogenesis abundant protein, p	Phvul.007G22	PTHR23241:S	Phvul.007G22	not assigned.
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
HXXXD-type acyl-transferase family prot	Phvul.007G28	PTHR31642:S	Phvul.007G28	Enzyme classi
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
LRR and NB-ARC domains-containing dis	Phvul.008G02	PTHR23155//	Phvul.008G02	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.

Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.008G04	PF13041 - PP	Phvul.008G04	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r

Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
Tetratricopeptide repeat (TPR)-like supe	0	0	Phvul.008G11	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
0	Phvul.008G14	KOG3102 - Un	Phvul.008G14	not assigned.r
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
Pseudouridine synthase family protein	Phvul.009G01	PTHR11079:SI	Phvul.009G01	RNA processir
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:SI	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:SI	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:SI	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:SI	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:SI	Phvul.009G03	RNA biosynth

K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:S	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:S	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:S	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:S	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:S	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:S	Phvul.009G03	RNA biosynth
K-box region and MADS-box transcriptic	Phvul.009G03	PTHR11945:S	Phvul.009G03	RNA biosynth
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G06	PF01535//PF1	Phvul.009G06	not assigned.
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
0	Phvul.009G23	PTHR31115:S	Phvul.009G23	RNA biosynth
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//	Phvul.009G24	not assigned.
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//	Phvul.009G24	not assigned.
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//	Phvul.009G24	not assigned.
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//	Phvul.009G24	not assigned.

homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
homolog of yeast sucrose nonfermentin	Phvul.009G24	PTHR13780//I	Phvul.009G24	not assigned.a
lipoxygenase 1	Phvul.010G13	K15718 - linol	Phvul.010G13	Enzyme classi
lipoxygenase 1	Phvul.010G13	K15718 - linol	Phvul.010G13	Enzyme classi
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
cytokinin oxidase/dehydrogenase 6	Phvul.011G01	PTHR13878:SI	Phvul.011G01	Phytohormon
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
Histone superfamily protein	Phvul.011G08	K11252 - histc	Phvul.011G08	Chromatin org
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:SI	Phvul.001G02	Cell wall orgar

plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
plant glycogenin-like starch initiation pr	Phvul.001G02	PTHR11183:S	Phvul.001G02	Cell wall orga
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
gibberellin 3-oxidase 1	Phvul.001G05	K04124 - gibb	Phvul.001G05	Phytohormon
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
methylthioalkylmalate synthase-like 4	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.

2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
2-isopropylmalate synthase 1	Phvul.001G10	2.3.3.13 - 2-is	Phvul.001G10	not assigned.a
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Eukaryotic aspartyl protease family prot	Phvul.001G22	PTHR13683:S	Phvul.001G22	Protein home
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Ru	Phvul.001G26	Lipid metaboli

Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Rubber elongation factor protein (REF)	Phvul.001G26	PF05755 - Rub	Phvul.001G26	Lipid metaboli
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Protein of unknown function (DUF677)	Phvul.002G02	PF05055 - Pro	Phvul.002G02	Cytoskeleton
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
Sec1/munc18-like (SM) proteins superfa	Phvul.002G20	PTHR11679:S	Phvul.002G20	not assigned.
ethylene-forming enzyme	Phvul.002G32	K05933 - ami	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - ami	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - ami	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - ami	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - ami	Phvul.002G32	Phytohormon

ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
ethylene-forming enzyme	Phvul.002G32	K05933 - amir	Phvul.002G32	Phytohormon
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Peroxidase superfamily protein	Phvul.003G07	PTHR31235:SI	Phvul.003G07	not assigned.a
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
Syntaxin/t-SNARE family protein	Phvul.003G14	PF09177 - Syn	Phvul.003G14	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r

	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
	0	0	0	Phvul.003G19	not assigned.r
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
MA3 domain-containing protein		Phvul.003G20	PTHR12626:SI	Phvul.003G20	Multi-process
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo
nitrate transporter 1.1		Phvul.003G21	PTHR11654:SI	Phvul.003G21	Solute transpo

nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
nitrate transporter 1.1	Phvul.003G21	PTHR11654:S	Phvul.003G21	Solute transpo
tRNA/rRNA methyltransferase (SpoU) fa	Phvul.003G22	PTHR12029//	Phvul.003G22	RNA processin
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.003G24	PTHR12411//	Phvul.003G24	Enzyme classi
Pyridoxal phosphate (PLP)-dependent tr	Phvul.003G24	PTHR14237:S	Phvul.003G24	not assigned.a
Pyridoxal phosphate (PLP)-dependent tr	Phvul.003G24	PTHR14237:S	Phvul.003G24	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:S	Phvul.003G27	not assigned.a

Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:SI	Phvul.003G27	not assigned.a
Sec14p-like phosphatidylinositol transfe	Phvul.003G27	PTHR23324:SI	Phvul.003G27	not assigned.a
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
aminophospholipid ATPase 2	Phvul.005G10	K01530 - phos	Phvul.005G10	Solute transpo
Transducin/WD40 repeat-like superfami	Phvul.006G06	K12616 - enha	Phvul.006G06	RNA processir
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PFC	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PFC	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PFC	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PFC	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PFC	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PFC	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PFC	Phvul.006G17	Protein modif

Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Leucine-rich repeat protein kinase famil	Phvul.006G17	PF00069//PF	Phvul.006G17	Protein modif
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
integral membrane TerC family protein	Phvul.007G16	PTHR30238 -	Phvul.007G16	Photosynthesi
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home

DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
DEGP protease 2	Phvul.007G16	PTHR22939:S	Phvul.007G16	Protein home
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r

Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
Transducin/WD40 repeat-like superfami	Phvul.007G18	K15361 - WD	Phvul.007G18	not assigned.r
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir

DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
DEAD box RNA helicase (RH3)	Phvul.007G20	K16911 - ATP-	Phvul.007G20	RNA processir
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
TATA BOX ASSOCIATED FACTOR II 59	Phvul.008G01	K03131 - trans	Phvul.008G01	RNA biosynth
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
0	0	0	Phvul.008G15	not assigned.r
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:SI	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:SI	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:SI	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:SI	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:SI	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:SI	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:SI	Phvul.008G20	not assigned.a

RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:S	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:S	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:S	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:S	Phvul.008G20	not assigned.a
RNA-binding (RRM/RBD/RNP motifs) far	Phvul.008G20	PTHR24012:S	Phvul.008G20	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.008G21	PF01535//PF1	Phvul.008G21	not assigned.a
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
Eukaryotic aspartyl protease family prot	Phvul.008G23	PTHR13683:S	Phvul.008G23	Protein home
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
0	0	0	Phvul.009G01	not assigned.r
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth

Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Transcription initiation factor IIF, beta s	Phvul.009G01	K03139 - tran	Phvul.009G01	RNA biosynth
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
Pentatricopeptide repeat (PPR-like) sup	Phvul.009G08	PTHR24015:S	Phvul.009G08	not assigned.a
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
COP9-signalosome 5B	Phvul.009G10	K09613 - COP	Phvul.009G10	Protein home
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.009G13	PF13371//PF1	Phvul.009G13	not assigned.a
Pentatricopeptide repeat (PPR) superfa	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfa	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfa	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfa	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfa	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfa	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a

Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.009G14	PF01535//PF1	Phvul.009G14	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
Peroxidase superfamily protein	Phvul.010G06	1.11.1.7 - Per	Phvul.010G06	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a

APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
APRATAXIN-like	Phvul.010G07	K10863 - apra	Phvul.010G07	not assigned.a
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear factor Y, subunit C10	Phvul.011G07	PTHR10252:S	Phvul.011G07	RNA biosynth
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy

nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
nuclear assembly factor 1	Phvul.011G11	K14763 - H/A	Phvul.011G11	Protein biosy
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
homeobox protein 52	Phvul.011G15	PTHR24326:S	Phvul.011G15	RNA biosynth
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Granulin repeat cysteine protease famil	Phvul.001G02	PTHR12411//	Phvul.001G02	Enzyme classi
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.

Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.a
Tetratricopeptide repeat (TPR)-like supe	Phvul.001G09	PF12854//PF1	Phvul.001G09	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
Protein of unknown function, DUF593	Phvul.001G19	PTHR31422:S	Phvul.001G19	not assigned.a
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
FAR1-related sequence 5	Phvul.002G11	PTHR31669:S	Phvul.002G11	RNA biosynth
RHO guanyl-nucleotide exchange factor	Phvul.002G12	PTHR33101:S	Phvul.002G12	Multi-process
RHO guanyl-nucleotide exchange factor	Phvul.002G12	PTHR33101:S	Phvul.002G12	Multi-process
Glutaredoxin family protein	Phvul.002G32	PTHR10168:S	Phvul.002G32	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:S	Phvul.003G13	not assigned.a

CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:SI	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:SI	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:SI	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:SI	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:SI	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:SI	Phvul.003G13	not assigned.a
CRS1 / YhbY (CRM) domain-containing p	Phvul.003G13	PTHR31846:SI	Phvul.003G13	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
Pentatricopeptide repeat (PPR) superfar	Phvul.003G15	PF01535//PF1	Phvul.003G15	not assigned.a
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
0	0	0	Phvul.003G19	not assigned.r
S-adenosyl-L-methionine-dependent me	Phvul.003G25	2.1.1.274 - Sal	Phvul.003G25	Enzyme classi
Tetratricopeptide repeat (TPR)-like supe	Phvul.003G29	PF01535//PF1	Phvul.003G29	RNA processir
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a

SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
SPFH/Band 7/PHB domain-containing m	Phvul.004G02	PTHR10264//I	Phvul.004G02	not assigned.a
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r

UDP-Glycosyltransferase superfamily pr	Phvul.005G17	PTHR12526//I	Phvul.005G17	not assigned.r
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
multidrug resistance-associated protein	Phvul.006G05	PTHR24223:SI	Phvul.006G05	Solute transpo
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
0	0	0	Phvul.006G05	not assigned.r
Pyruvate kinase family protein	Phvul.007G24	PTHR11817//I	Phvul.007G24	Enzyme classi
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate

Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Aldolase-type TIM barrel family protein	Phvul.008G00	K00616 - tran	Phvul.008G00	Carbohydrate
Auxin efflux carrier family protein	Phvul.008G05	PTHR31752:S	Phvul.008G05	Solute transp
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
P-loop containing nucleoside triphospha	Phvul.008G16	PTHR10887:S	Phvul.008G16	not assigned.a
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
RAD-like 6	Phvul.008G19	PTHR24078:S	Phvul.008G19	RNA biosynth
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Pectin lyase-like superfamily protein	Phvul.008G27	PTHR31321:S	Phvul.008G27	Cell wall orga
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli

Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
Neutral/alkaline non-lysosomal ceramid	Phvul.008G28	K12349 - neut	Phvul.008G28	Lipid metaboli
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
0	Phvul.009G08	PF12776 - My	Phvul.009G08	not assigned.a
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
AZA-guanine resistant1	Phvul.009G14	K06901 - puta	Phvul.009G14	Solute transpo
cytochrome P450, family 88, subfamily	Phvul.010G13	PTHR24286:S	Phvul.010G13	Enzyme classi
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo

multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
multidrug resistance-associated protein	Phvul.010G14	PTHR24223:S	Phvul.010G14	Solute transpo
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
purple acid phosphatase 24	Phvul.011G01	PTHR22953:S	Phvul.011G01	not assigned.a
Calcium-dependent lipid-binding (CaLB	Phvul.011G03	PTHR10774//	Phvul.011G03	not assigned.r
Calcium-dependent lipid-binding (CaLB	Phvul.011G03	PTHR10774//	Phvul.011G03	not assigned.r
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Subtilisin-like serine endopeptidase fam	Phvul.011G09	PTHR10795//	Phvul.011G09	not assigned.a
Regulator of chromosome condensation	Phvul.003G06	PTHR22870:S	Phvul.003G06	not assigned.a
Regulator of chromosome condensation	Phvul.003G06	PTHR22870:S	Phvul.003G06	not assigned.a
P-loop containing nucleoside triphospha	Phvul.003G14	PTHR23070:S	Phvul.003G14	not assigned.a

Maf-like protein	Phvul.003G25	K06287 - sept	Phvul.003G25	not assigned.
Maf-like protein	Phvul.003G25	K06287 - sept	Phvul.003G25	not assigned.
receptor-like protein kinase 2	Phvul.004G03	PTHR27000:S	Phvul.004G03	Protein modif
receptor-like protein kinase 2	Phvul.004G03	PTHR27000:S	Phvul.004G03	Protein modif
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G02	PTHR21330:S	Phvul.005G02	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
RING/U-box superfamily protein	Phvul.005G07	3.4.22.16 - Ca	Phvul.005G07	Protein home
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.

Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
Late embryogenesis abundant (LEA) hyd	Phvul.005G10	PF03168 - Lat	Phvul.005G10	not assigned.
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
inositol transporter 4	Phvul.006G14	K08150 - MFS	Phvul.006G14	Solute transp
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
F-box/RNI-like superfamily protein	Phvul.006G15	PTHR24006:S	Phvul.006G15	not assigned.
Protein of unknown function, DUF593	Phvul.006G20	PTHR31422:S	Phvul.006G20	not assigned.
carboxypeptidase D, putative	Phvul.007G08	3.4.17.22 - M	Phvul.007G08	Protein home
carboxypeptidase D, putative	Phvul.007G08	3.4.17.22 - M	Phvul.007G08	Protein home
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Transducin/WD40 repeat-like superfami	Phvul.007G13	PTHR22849//	Phvul.007G13	External stim
Beige/BEACH domain ;WD domain, G-b	Phvul.007G17	PTHR13743:S	Phvul.007G17	not assigned.
Beige/BEACH domain ;WD domain, G-b	Phvul.007G17	PTHR13743:S	Phvul.007G17	not assigned.

Beige/BEACH domain ;WD domain, G-be	Phvul.007G17	PTHR13743:S	Phvul.007G17	not assigned.a
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
WRKY DNA-binding protein 21	Phvul.007G17	PTHR31282:S	Phvul.007G17	RNA biosynth
0	Phvul.008G10	PF03140 - Pla	Phvul.008G10	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
P-loop containing nucleoside triphospha	Phvul.010G11	PTHR24031:S	Phvul.010G11	not assigned.a
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
ARID/BRIGHT DNA-binding domain-cont	Phvul.010G12	PF01388 - ARI	Phvul.010G12	RNA biosynth
Insulinase (Peptidase family M16) prote	Phvul.010G14	3.4.24.64 - Mi	Phvul.010G14	Protein modif
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthesi
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthesi
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthesi
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthesi
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthesi
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthesi
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthesi

phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthes
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthes
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthes
phosphoglycerate/bisphosphoglycerate	Phvul.011G09	PTHR23029:S	Phvul.011G09	Photosynthes
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home
RING/U-box superfamily protein with A	Phvul.L00161	PTHR23315:S	Phvul.L00161	Protein home

DESCRIPTION
no hits & (original description: pacid=37147189 transcript=Phvul.003G168301.2 locus=Phvul.003G
no hits & (original description: pacid=37147189 transcript=Phvul.003G168301.2 locus=Phvul.003G
no hits & (original description: pacid=37147189 transcript=Phvul.003G168301.2 locus=Phvul.003G
no hits & (original description: pacid=37147189 transcript=Phvul.003G168301.2 locus=Phvul.003G
no hits & (original description: pacid=37147189 transcript=Phvul.003G168301.2 locus=Phvul.003G
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Pyruvate kinase 1, cytosolic OS=Oryza sativa subsp. japonica (sp|q2rak2|kpyc1_orysj : 915.0) & En

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corporation of molecular oxygen (oxygenase)(50.1.12 : 1091.2) & Seed linoleate 9S-lipoxygenase OS
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lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

lassification.EC_3 hydrolases.EC_3.4 hydrolase acting on peptide bond (peptidase)(50.3.4 : 359.5) (c

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ıe max (sp|q39891|leu1_soybn : 313.0)
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=v2.1) &
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original description: pacid=37147951 transcript=Phvul.003G255900.1 locus=Phvul.003G255900 ID=

Arabidopsis thaliana (sp|q9car7|hir2_arath : 450.0)

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(50.2.7 : 376.0) (original description: pacid=37167361 transcript=Phvul.007G244900.1 locus=Phvul.

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hzb2|bcha1_arath : 4995.0)

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ucuucccuacaccucccauacc	Phvul.008G061300.2	2	-1	1
ucuucccuacaccucccauacc	Phvul.008G061300.1	2	-1	1
ucuucccaauuccgcccauucc	Phvul.002G079200.1	2.5	-1	1
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ucuucccuacaccucccauacc	Phvul.001G133100.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.001G133100.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.001G133101.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.001G133101.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.001G185400.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.001G185400.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.001G217800.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.002G063500.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.002G063500.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.002G104200.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.002G104200.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.002G279500.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G050200.2	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G050200.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G076900.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G076900.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G104900.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G104900.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G157600.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G158700.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G158700.1	4.5	-1	1

ucuucccaauuccgcccauucc	Phvul.003G162300.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G209600.2	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G209600.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G288300.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.003G288300.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.004G011400.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.004G064300.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.004G064300.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.004G131300.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.004G131300.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.005G031200.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.005G071300.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.005G071300.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.006G057000.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.006G057100.5	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.006G057100.4	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.006G057700.2	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.006G066800.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.006G066800.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.007G086300.2	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.007G086300.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.008G014700.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.008G014700.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.008G072032.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.008G072032.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.008G168300.2	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.008G168300.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.009G039200.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.009G079700.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.009G079700.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.009G180800.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.009G180800.2	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.009G180800.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.009G180800.2	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.009G249500.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G025000.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G025700.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G063700.2	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G101700.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G141400.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.010G149500.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.010G149500.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G015000.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G181500.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G181500.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G198000.1	4.5	-1	1

ucuucccuacaccucccauacc	Phvul.011G198000.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G200880.2	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G200880.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G201000.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G201000.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G201101.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G201101.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G202366.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.011G202366.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.L004500.1	4.5	-1	1
ucuucccuacaccucccauacc	Phvul.L004500.1	4.5	-1	1
ucuucccaauuccgcccauucc	Phvul.001G183400.2	5	-1	1
ucuucccaauuccgcccauucc	Phvul.001G183400.3	5	-1	1
ucuucccaauuccgcccauucc	Phvul.001G183400.4	5	-1	1
ucuucccaauuccgcccauucc	Phvul.001G183400.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G089800.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G089800.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.002G171400.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G244900.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G244900.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.5	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.4	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.3	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.2	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.5	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.4	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.3	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.002G245000.2	5	-1	1
ucuucccuacaccucccauacc	Phvul.003G002200.5	5	-1	1
ucuucccuacaccucccauacc	Phvul.003G002200.4	5	-1	1
ucuucccuacaccucccauacc	Phvul.003G002200.3	5	-1	1
ucuucccuacaccucccauacc	Phvul.003G002200.5	5	-1	1
ucuucccuacaccucccauacc	Phvul.003G002200.4	5	-1	1
ucuucccuacaccucccauacc	Phvul.003G002200.3	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G050200.2	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G050200.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G244225.3	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G244225.2	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G244225.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G282200.3	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G282200.2	5	-1	1
ucuucccaauuccgcccauucc	Phvul.003G282250.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.004G011100.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.004G086300.2	5	-1	1

ucuucccaauuccgcccauucc	Phvul.004G086300.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.005G041300.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.005G041300.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.005G069700.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.005G069700.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.005G072000.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.006G027500.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.006G027500.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.006G100600.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.006G126400.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.006G126400.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.006G170700.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.008G107400.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.008G107400.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.008G206300.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.009G103100.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G008500.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G013500.1	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.3	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
ucuucccuacaccucccauacc	Phvul.010G044000.2	5	-1	1
ucuucccaauuccgcccauucc	Phvul.010G145600.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G181700.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G200820.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G202100.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G202300.1	5	-1	1
ucuucccaauuccgcccauucc	Phvul.011G203100.1	5	-1	1

miRNA_end	Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition
22	667	688	UCUUCCCAAL	::::::::::::.::::::::	GGAAUGGGC	Cleavage
22	1158	1179	UCUUCCCUAC	:::: .::::.::::::	UAUAUGGCG	Cleavage
22	993	1014	UCUUCCCUAC	:::: .::::.::::::	UAUAUGGCG	Cleavage
22	1158	1179	UCUUCCCUAC	:::: .::::.::::::	UAUAUGGCG	Cleavage
22	993	1014	UCUUCCCUAC	:::: .::::.::::::	UAUAUGGCG	Cleavage
22	1110	1131	UCUUCCCUAC	:::: .::::.::::::	UAUAUGGCG	Cleavage
22	1110	1131	UCUUCCCUAC	:::: .::::.::::::	UAUAUGGCG	Cleavage
22	1023	1044	UCUUCCCUAC	::::::::.:::::::: :::	GGUAUGGGG	Cleavage
22	1520	1541	UCUUCCCUAC	::::::::.:::::::: :::	GGUAUGGGG	Cleavage
22	1023	1044	UCUUCCCUAC	::::::::.:::::::: :::	GGUAUGGGG	Cleavage
22	1520	1541	UCUUCCCUAC	::::::::.:::::::: :::	GGUAUGGGG	Cleavage
22	863	884	UCUUCCCAAL	::::::::.:::.:::: :::	GGAAUGGGU	Cleavage
22	104	125	UCUUCCCAAL	: .::: .:::.:::::::.::	UGUGUGGUU	Cleavage
22	2120	2141	UCUUCCCUAC	:.::::::::::. :::.::	AUUGUGGGA	Cleavage
22	2120	2141	UCUUCCCUAC	:.::::::::::. :::.::	AUUGUGGGA	Cleavage
22	782	803	UCUUCCCAAL	::.:::::.::..:::: :::	GGGAUGGGU	Cleavage
22	2213	2234	UCUUCCCAAL	.::::: : .::::::::::	CAGAUGGGG	Cleavage
22	2213	2234	UCUUCCCAAL	.::::: : .::::::::::	CAGAUGGGG	Cleavage
22	2209	2230	UCUUCCCAAL	.::::: : .::::::::::	CAGAUGGGG	Cleavage
22	763	784	UCUUCCCAAL	::::: ::.::::: ::::::	GGAAUAGGU	Cleavage
22	986	1007	UCUUCCCAAL	: ..::::.:::: :::::.::	GAGGUGGGU	Cleavage
22	1081	1102	UCUUCCCAAL	: ..::::.:::: :::::.::	GAGGUGGGU	Cleavage
22	1155	1176	UCUUCCCAAL	: ..::::.:::: :::::.::	GAGGUGGGU	Cleavage
22	516	537	UCUUCCCUAC	: : :: :.:::::.::::::	GAUUUGAGG	Cleavage
22	516	537	UCUUCCCUAC	: : :: :.:::::.::::::	GAUUUGAGG	Cleavage
22	78	99	UCUUCCCAAL	: .:: :.::::::::::.:.	UGCGUGUGU	Cleavage
22	864	885	UCUUCCCUAC	:: ::::::: :::::::.	AAGAUUGGA	Cleavage
22	864	885	UCUUCCCUAC	:: ::::::: :::::::.	AAGAUUGGA	Cleavage
22	571	592	UCUUCCCAAL	:: :::::.::..:::::: :	GGCAUGGGU	Cleavage
22	811	832	UCUUCCCAAL	:: :::::.:::::::: :::	GGUAUGGGU	Cleavage
22	781	802	UCUUCCCAAL	: .. :::.:::::::::.::.	GAGGAGGGU	Cleavage
22	781	802	UCUUCCCAAL	: .. :::.:::::::::.::.	GAGGAGGGU	Cleavage
22	781	802	UCUUCCCAAL	: .. :::.:::::::::.::.	GAGGAGGGU	Cleavage
22	781	802	UCUUCCCAAL	: .. :::.:::::::::.::.	GAGGAGGGU	Cleavage
22	781	802	UCUUCCCAAL	: .. :::.:::::::::.::.	GAGGAGGGU	Cleavage
22	781	802	UCUUCCCAAL	: .. :::.:::::::::.::.	GAGGAGGGU	Cleavage
22	781	802	UCUUCCCAAL	: .. :::.:::::::::.::.	GAGGAGGGU	Cleavage
22	517	538	UCUUCCCAAL	:: ::::::::::: :: ::::	GGUAUGGGC	Cleavage
22	746	767	UCUUCCCAAL	:: :::::.:: :::: ::::	GGCAUGGGU	Translation
22	709	730	UCUUCCCUAC	:: ::::::::: :.:: ::::	GGGAUGGGA	Translation
22	709	730	UCUUCCCUAC	:: ::::::::: :.:: ::::	GGGAUGGGA	Translation
22	1008	1029	UCUUCCCUAC	.::: .::::.:::::	GACGUGGAG	Cleavage
22	1008	1029	UCUUCCCUAC	.::: .::::.:::::	GACGUGGAG	Cleavage
22	513	534	UCUUCCCAAL	:.:::::.: .:::::::::	AGGAUGGGU	Cleavage
22	613	634	UCUUCCCAAL	:.:::::.: .:::::::::	AGGAUGGGU	Cleavage

22	1221	1242	UCUUCCCAAU	:: :: : :::::::::::::	AUAAGGGUC	Cleavage
22	493	514	UCUUCCCAAU	::.:::::::::::::	CCUACUGGU	Cleavage
22	138	159	UCUUCCCUAC	::::::::::::: :::	UGGCAGGGA	Cleavage
22	138	159	UCUUCCCUAC	::::::::::::: :::	UGGCAGGGA	Cleavage
22	126	147	UCUUCCCUAC	.::: :::::::: ::.::	GAGGUGGAA	Cleavage
22	126	147	UCUUCCCUAC	.::: :::::::: ::.::	GAGGUGGAA	Cleavage
22	2611	2632	UCUUCCCUAC	: :::: : :::::::::::	GCUAUGUCA	Cleavage
22	2611	2632	UCUUCCCUAC	: :::: : :::::::::::	GCUAUGUCA	Cleavage
22	487	508	UCUUCCCAAU	:. ::::: :::::::.:::	UUAGCGGGC	Cleavage
22	661	682	UCUUCCCUAC	:: ::::: :::::::::::	GGAAUGGGC	Cleavage
22	661	682	UCUUCCCUAC	:: ::::: :::::::::::	GGAAUGGGC	Cleavage
22	844	865	UCUUCCCUAC	:: ::::::: ::.::::.::	UGUUUGGGA	Translation
22	844	865	UCUUCCCUAC	:: ::::::: ::.::::.::	UGUUUGGGA	Translation
22	508	529	UCUUCCCUAC	:: :::::::: ::.::::: :	GGCAUGGGA	Translation
22	508	529	UCUUCCCUAC	:: :::::::: ::.::::: :	GGCAUGGGA	Translation
22	2091	2112	UCUUCCCAAU	::..: :::::: ::::::::.	GGGGUUGGC	Translation
22	550	571	UCUUCCCUAC	:: .: :::::::.:: ::::	GGGGUUGGA	Cleavage
22	550	571	UCUUCCCUAC	:: .: :::::::.:: ::::	GGGGUUGGA	Cleavage
22	550	571	UCUUCCCUAC	:: .: :::::::.:: ::::	GGGGUUGGA	Cleavage
22	550	571	UCUUCCCUAC	:: .: :::::::.:: ::::	GGGGUUGGA	Cleavage
22	1939	1960	UCUUCCCAAU	:.: ::::::.:: ::::::	AUAGUAGGC	Cleavage
22	113	134	UCUUCCCUAC	: :: :.:::::.::::::.	AUUUUGAGG	Cleavage
22	113	134	UCUUCCCUAC	: :: :.:::::.::::::.	AUUUUGAGG	Cleavage
22	113	134	UCUUCCCUAC	: :: :.:::::.::::::.	AUUUUGAGG	Cleavage
22	113	134	UCUUCCCUAC	: :: :.:::::.::::::.	AUUUUGAGG	Cleavage
22	750	771	UCUUCCCAAU	:: :::::.:: ::::: ::::	GGCAUGGGU	Translation
22	747	768	UCUUCCCAAU	:: :::::.:: ::::: ::::	GGCAUGGGU	Translation
22	802	823	UCUUCCCAAU	:: ::::: :::::::: :::	GGUAUGGGG	Cleavage
22	59	80	UCUUCCCUAC	::::: :::::::.:: .:::	UAUAUGGUA	Cleavage
22	59	80	UCUUCCCUAC	::::: :::::::.:: .:::	UAUAUGGUA	Cleavage
22	59	80	UCUUCCCUAC	::::: :::::::.:: .:::	UAUAUGGUA	Cleavage
22	59	80	UCUUCCCUAC	::::: :::::::.:: .:::	UAUAUGGUA	Cleavage
22	680	701	UCUUCCCAAU	::.:::::.::::: :: ::::	GGGAUGGGU	Cleavage
22	720	741	UCUUCCCAAU	::.:::::.::::: :: ::::	GGGAUGGGU	Cleavage
22	586	607	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	658	679	UCUUCCCUAC	:: :::::::: ::.:: ::::	GGAAUGGGA	Translation
22	658	679	UCUUCCCUAC	:: :::::::: ::.:: ::::	GGAAUGGGA	Translation
22	793	814	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	589	610	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	703	724	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	798	819	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	723	744	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	532	553	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	589	610	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	656	677	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	636	657	UCUUCCCAAU	:: :::::::::.:: :: ::::	GGCAUGGGC	Cleavage

22	589	610	UCUUCCCAAU	:: :::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	589	610	UCUUCCCAAU	:::::::.:: :: ::::	GCUAUGGGC	Cleavage
22	842	863	UCUUCCCAAU	:: :::::::.:: :: ::::	GGUAUGGGC	Cleavage
22	39	60	UCUUCCCAAU	::.:::::::.:: :: ::::	GGGAUGGGC	Cleavage
22	716	737	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	716	737	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	601	622	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	601	622	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	604	625	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	604	625	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	752	773	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	752	773	UCUUCCCUAC	:: ::::::: ::.:: ::::	GGAAUGGGA	Translation
22	211	232	UCUUCCCUAC	: :.::: : ::::::::::.	GUUGUGGAA	Cleavage
22	516	537	UCUUCCCUAC	: :.::: : ::::::::::.	GUUGUGGAA	Cleavage
22	211	232	UCUUCCCUAC	: :.::: : ::::::::::.	GUUGUGGAA	Cleavage
22	516	537	UCUUCCCUAC	: :.::: : ::::::::::.	GUUGUGGAA	Cleavage
22	1599	1620	UCUUCCCUAC	:: :: :.:::: :::::::	GGAAUUAGG	Cleavage
22	1681	1702	UCUUCCCUAC	:: :: :.:::: :::::::	GGAAUUAGG	Cleavage
22	1599	1620	UCUUCCCUAC	:: :: :.:::: :::::::	GGAAUUAGG	Cleavage
22	1681	1702	UCUUCCCUAC	:: :: :.:::: :::::::	GGAAUUAGG	Cleavage
22	757	778	UCUUCCCAAU	:::: ::: :::: :::::.::	GGAAGGGGA	Cleavage
22	757	778	UCUUCCCAAU	:::: ::: :::: :::::.::	GGAAGGGGA	Cleavage
22	647	668	UCUUCCCUAC	.:::::::: ::::.: :	AACGUGGGA	Cleavage
22	647	668	UCUUCCCUAC	.:::::::: ::::.: :	AACGUGGGA	Cleavage
22	414	435	UCUUCCCAAU	.:::::. :.:::: :::::	CAGAUGGGU	Cleavage
22	724	745	UCUUCCCAAU	.::::. :.:::: :::::	CAGAUGGGU	Cleavage
22	720	741	UCUUCCCAAU	.::::. :.:::: :::::	CAGAUGGGU	Cleavage
22	801	822	UCUUCCCAAU	.::::. :.:::: :::::	CAGAUGGGU	Cleavage
22	1183	1204	UCUUCCCAAU	.:::::.: : :::::::::.	UUGAUGGGU	Translation
22	2066	2087	UCUUCCCUAC	:.::: ::::::. :::::.	CUUGUGGAA	Cleavage
22	2066	2087	UCUUCCCUAC	:.::: ::::::. :::::.	CUUGUGGAA	Cleavage
22	804	825	UCUUCCCAAU	::..::::. :.:::::::.:	GGGGUGGGU	Cleavage
22	804	825	UCUUCCCAAU	::..::::. :.:::::::.:	GGGGUGGGU	Cleavage
22	505	526	UCUUCCCUAC	::: :::::::::: :.:	AUUAUUGGA	Cleavage
22	505	526	UCUUCCCUAC	::: :::::::::: :.:	AUUAUUGGA	Cleavage
22	83	104	UCUUCCCAAU	:::::: :::: ::::::	AAAAUGGGA	Cleavage
22	83	104	UCUUCCCAAU	:::::: :::: ::::::	AAAAUGGGA	Cleavage
22	83	104	UCUUCCCAAU	:::::: :::: ::::::	AAAAUGGGA	Cleavage
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation
22	1325	1346	UCUUCCCUAC	:::::: : ::.::::::.	CCGAUGGGA	Translation

22	667	688	UCUUCCCUAC	:: ::::: :: :: :::::::	GGAAUGGGC	Translation
22	667	688	UCUUCCCUAC	:: ::::: :: :: :::::::	GGAAUGGGC	Translation
22	326	347	UCUUCCCUAC	:: : ::: :::::.:: ::::	GGCAAGGGC	Cleavage
22	326	347	UCUUCCCUAC	:: : ::: :::::.:: ::::	GGCAAGGGC	Cleavage
22	791	812	UCUUCCCAAU	::.::::: ::::: :::.::	UGAGUGGGC	Cleavage
22	837	858	UCUUCCCUAC	:::::: :::::: :::::.	UGUAUGGUU	Cleavage
22	837	858	UCUUCCCUAC	:::::: :::::: :::::.	UGUAUGGUU	Cleavage
22	634	655	UCUUCCCAAU	:::::::::.::::.: :: ::::	GGAAUGGGU	Cleavage
22	666	687	UCUUCCCAAU	.::::.:::: ::::: :	AAUGUGGGU	Cleavage
22	1615	1636	UCUUCCCAAU	:: :::::.:::: :: .:::	GGCAUGGGU	Cleavage
22	619	640	UCUUCCCUAC	:: : ::::::::::: :.::	GGCAAAGGA	Cleavage
22	619	640	UCUUCCCUAC	:: : ::::::::::: :.::	GGCAAAGGA	Cleavage
22	265	287	UCUUCCCAAU	: .:::::. :::::::::::.:	GUGAUGGGU	Cleavage
22	312	333	UCUUCCCAAU	::.: :: ::..:::::::::	GGGAAAGGA	Cleavage
22	1781	1802	UCUUCCCAAU	::::: ::.::.:::: .:::	GGAAUAGGU	Cleavage
22	1891	1912	UCUUCCCUAC	::.::::: :::::::: ::.	CGUGUGGGA	Cleavage
22	1891	1912	UCUUCCCUAC	::.::::: :::::::: ::.	CGUGUGGGA	Cleavage
22	404	425	UCUUCCCUAC	::::::::: .:::::::.	ACCAUGGGA	Translation
22	479	500	UCUUCCCUAC	::::::::: .:::::::.	ACCAUGGGA	Translation
22	404	425	UCUUCCCUAC	::::::::: .:::::::.	ACCAUGGGA	Translation
22	479	500	UCUUCCCUAC	::::::::: .:::::::.	ACCAUGGGA	Translation
22	1415	1436	UCUUCCCAAU	:::.::.::::::::.:.	AAGCAGGGU	Cleavage
22	715	736	UCUUCCCUAC	: :.::: :: :::.::::::.	GAUGUGGAA	Cleavage
22	728	749	UCUUCCCUAC	: :.::: :: :::.::::::.	GAUGUGGAA	Cleavage
22	715	736	UCUUCCCUAC	: :.::: :: :::.::::::.	GAUGUGGAA	Cleavage
22	728	749	UCUUCCCUAC	: :.:::.:: :::.::::::.	GAUGUGGAA	Cleavage
22	811	832	UCUUCCCAAU	::.:::::: ::: : :::::::	GGGAUGGGG	Translation
22	811	832	UCUUCCCUAC	:: ::::.:: :.:::::::	GGGAUGGGG	Translation
22	811	832	UCUUCCCUAC	:: ::::.:: :.:::::::	GGGAUGGGG	Translation
22	1673	1694	UCUUCCCAAU	::.::::: :::::::: :: :	GGGAUGGGA	Cleavage
22	1698	1719	UCUUCCCAAU	::.::::: :::::::: :: :	GGGAUGGGA	Cleavage
22	1135	1156	UCUUCCCUAC	: :::::: ::::::: :.:.	UGAAUGGGA	Cleavage
22	1135	1156	UCUUCCCUAC	: :::::: ::::::: :.:.	UGAAUGGGA	Cleavage
22	596	617	UCUUCCCAAU	:: :::::::..:::: :: :	GGCAUGGGC	Cleavage
22	2364	2385	UCUUCCCAAU	:::::: ::.:::::::::	AAAAUGGGA	Cleavage
22	409	430	UCUUCCCAAU	: ::::: . :.:::::::::.	GCAAUGGCU	Cleavage
22	719	740	UCUUCCCAAU	: ::::: . :.:::::::::.	GCAAUGGCU	Cleavage
22	722	743	UCUUCCCAAU	: ::::: . :.:::::::::.	GCAAUGGCU	Cleavage
22	722	743	UCUUCCCAAU	: ::::: . :.:::::::::.	GCAAUGGCU	Cleavage
22	719	740	UCUUCCCAAU	: ::::: . :.:::::::::.	GCAAUGGCU	Cleavage
22	770	791	UCUUCCCAAU	: ::::: . :.:::::::::.	GCAAUGGCU	Cleavage
22	568	589	UCUUCCCAAU	:: ::::: ::: : :::::::	GGCAUGGGG	Translation
22	568	589	UCUUCCCUAC	:: :::::.:: :.:::::::	GGCAUGGGG	Translation
22	568	589	UCUUCCCUAC	:: :::::.:: :.:::::::	GGCAUGGGG	Translation
22	180	201	UCUUCCCAAU	: .::::::: ..: :::::::	GCGAUGGGC	Cleavage
22	159	180	UCUUCCCAAU	: .::::::: ..: :::::::	GCGAUGGGC	Cleavage

22	180	201	UCUUCCCAA	: .::::::: ..: :::::::GCGAUGGGC		Cleavage
22	618	639	UCUUCCCUAC	:: :::: ::::.::::: :	GGAAUGGCC	Cleavage
22	618	639	UCUUCCCUAC	:: :::: ::::.::::: :	GGAAUGGCC	Cleavage
22	817	838	UCUUCCCAA	::::::::.:::.: :: ::::	GGAAUGGGU	Cleavage
22	444	465	UCUUCCCUAC	:::: :::: :::::::::	AAUAUGAGA	Translation
22	444	465	UCUUCCCUAC	:::: :::: :::::::::	AAUAUGAGA	Translation
22	592	613	UCUUCCCAA	:: :::::.::.:: :: ::::	GGUAUGGGU	Cleavage
22	640	661	UCUUCCCAA	:: :::::.::.:: :: ::::	GGUAUGGGU	Cleavage
22	529	550	UCUUCCCAA	:: :::::.::.:: :: ::::	GGUAUGGGU	Cleavage
22	667	688	UCUUCCCUAC	:::::::: ::: :::: ::::	GGUAUGGGC	Translation
22	667	688	UCUUCCCUAC	:::::::: ::: :::: ::::	GGUAUGGGC	Translation
22	589	610	UCUUCCCAA	:: :::::.::.:: :: ::::	GGUAUGGGU	Cleavage
22	779	800	UCUUCCCAA	:: :::::.::.:: :: ::::	GGUAUGGGU	Cleavage
22	634	655	UCUUCCCAA	::::::::.:::.: :: ::::	GGAAUGGGU	Cleavage
22	640	661	UCUUCCCAA	:: :::::.:::.: :: ::::	GGCAUGGGU	Cleavage
22	823	844	UCUUCCCAA	..: ::.::..::::::: :	AUGGUUGGU	Cleavage
22	1538	1559	UCUUCCCAA	::.:::::::::::	AGCUCUGGU	Cleavage
22	651	672	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	651	672	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	64	85	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	64	85	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	615	636	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	615	636	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	916	937	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	916	937	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	651	672	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	651	672	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	635	656	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	635	656	UCUUCCCUAC	::::: ::::: :.:::::::	GGUAUUGGA	Translation
22	1429	1450	UCUUCCCUAC	:::: : :::::::::	UACAUGGAC	Cleavage
22	1429	1450	UCUUCCCUAC	:::: : :::::::::	UACAUGGAC	Cleavage
22	653	674	UCUUCCCAA	:::::::.: :: ::::::.:	CAAAUGGGU	Cleavage
22	963	984	UCUUCCCUAC	:: ::::::: :::::::::.	AGUUUGGGA	Translation
22	963	984	UCUUCCCUAC	:: ::::::: :::::::::.	AGUUUGGGA	Translation
22	932	953	UCUUCCCUAC	:: : :::: :::: :::::.::	GGCACGGGA	Cleavage
22	932	953	UCUUCCCUAC	:: : :::: :::: :::::.::	GGCACGGGA	Cleavage
22	591	612	UCUUCCCAA	: :::::.:::::::: ::	AGCAUGGGU	Cleavage
22	1313	1334	UCUUCCCAA	::: : ::.: ::::::.::	UUCAUGAGA	Cleavage
22	1335	1356	UCUUCCCAA	::: : ::.: ::::::.::	UUCAUGAGA	Cleavage
22	1014	1035	UCUUCCCUAC	:.::: . ::::.::::::.	AUUGUGGAG	Cleavage
22	1014	1035	UCUUCCCUAC	:.::: . ::::.::::::.	AUUGUGGAG	Cleavage
22	29	50	UCUUCCCUAC	::.:: :::::: .::::.:.	UGUGUGUGA	Cleavage
22	29	50	UCUUCCCUAC	::.:: :::::: .::::.:.	UGUGUGUGA	Cleavage
22	2018	2039	UCUUCCCAA	::.:::: : .::::::::.::	GGGAUGGAA	Cleavage
22	2000	2021	UCUUCCCUAC	:::::: ::: ::::::::.	CAUAUGGGU	Cleavage
22	2000	2021	UCUUCCCUAC	:::::: ::: ::::::::.	CAUAUGGGU	Cleavage

22	816	837	UCUUCCCAAL	::.:: : .:::.:::::: :	GGGAUCGCU	Cleavage
22	449	470	UCUUCCCAAL	::. ::::.: ::::::: ::	GGGUUGGGU	Cleavage
22	449	470	UCUUCCCAAL	::. ::::.: ::::::: ::	GGGUUGGGU	Cleavage
22	1711	1732	UCUUCCCUAC	:::::: :::::. ::.::	UUUAUGGGU	Cleavage
22	1711	1732	UCUUCCCUAC	:::::: :::::. ::.::	UUUAUGGGU	Cleavage
22	529	550	UCUUCCCAAL	:::: ::::::::::	CUACAGGC	Cleavage
22	525	546	UCUUCCCUAC	:::::: ::::.: :::::	AAUAUGGGC	Cleavage
22	525	546	UCUUCCCUAC	:::::: ::::.: :::::	AAUAUGGGC	Cleavage
22	843	864	UCUUCCCUAC	::: ::: .:::: :::::::.	GGUUUGGUG	Cleavage
22	843	864	UCUUCCCUAC	::: ::: .:::: :::::::.	GGUUUGGUG	Cleavage
22	822	843	UCUUCCCAAL	:::::::: ::.:: :: ::::	GGAAUGGGA	Cleavage
22	248	269	UCUUCCCUAC	:: .::: :::: :::: ::	GGAGUGGCA	Cleavage
22	248	269	UCUUCCCUAC	:: .::: :::: :::: ::	GGAGUGGCA	Cleavage
22	1667	1688	UCUUCCCAAL	:..::: .::..: :::::::	UGGGUGGAU	Cleavage
22	1756	1777	UCUUCCCAAL	:..::: .::..: :::::::	UGGGUGGAU	Cleavage
22	1759	1780	UCUUCCCAAL	:..::: .::..: :::::::	UGGGUGGAU	Cleavage
22	181	202	UCUUCCCAAL	: :::: .:::::: ::::.:	GAAAUGGAU	Cleavage
22	634	655	UCUUCCCUAC	:: ::::: :: ::.:: ::::	GGAAUGGGU	Translation
22	634	655	UCUUCCCUAC	:: ::::: :: ::.:: ::::	GGAAUGGGU	Translation
22	704	725	UCUUCCCAAL	:: :::::.::..:::: :: :	GGCAUGGGU	Cleavage
22	704	725	UCUUCCCAAL	:: :::::.::..:::: :: :	GGCAUGGGU	Cleavage
22	732	753	UCUUCCCUAC	:::::::: ::: :.::::: :	GGUAUGGGU	Translation
22	732	753	UCUUCCCUAC	:::::::: ::: :.::::: :	GGUAUGGGU	Translation
22	544	565	UCUUCCCUAC	:::.: :: :::::.:: ::::	GGUGUUGGU	Cleavage
22	544	565	UCUUCCCUAC	:::.: :: :::::.:: ::::	GGUGUUGGU	Cleavage
22	494	516	UCUUC-CCAA	.::::.:::.:::: ::::	CUUGUGGGU	Cleavage
22	750	772	UCUUC-CCAA	.::::.:::.:::: ::::	CUUGUGGGU	Cleavage
22	620	641	UCUUCCCAAL	:::. :::.::..:: ::::::	GGAGAGGGU	Cleavage
22	271	292	UCUUCCCUAC	::::::::::. :::.::	GGAUGGGGA	Cleavage
22	271	292	UCUUCCCUAC	::::::::::. :::.::	GGAUGGGGA	Cleavage
22	226	247	UCUUCCCUAC	:::: ::::::::::::	GGGGACGGA	Cleavage
22	226	247	UCUUCCCUAC	:::: ::::::::::::	GGGGACGGA	Cleavage
22	226	247	UCUUCCCUAC	:::: ::::::::::::	GGGGACGGA	Cleavage
22	226	247	UCUUCCCUAC	:::: ::::::::::::	GGGGACGGA	Cleavage
22	244	265	UCUUCCCAAL	:: ::: ::::::: : ::::.	GGUAUGAGC	Cleavage
22	673	694	UCUUCCCAAL	:::::::: ::.::::: :: :	GGAAUGGGA	Cleavage
22	646	667	UCUUCCCAAL	:::::::: ::.::::: :: :	GGAAUGGGA	Cleavage
22	566	587	UCUUCCCAAL	:: :::::.::..:::: :: :	GGCAUGGGU	Cleavage
22	286	306	UCUUCCCAAL	: ::::::.:::.: ::::::.	GAAAUGGGU	Cleavage
22	1001	1022	UCUUCCCAAL	:::::::.: : ::::::.::.	AAAAUGGGU	Translation
22	468	489	UCUUCCCUAC	: :::::: :::: :: :.:::	GUUAUGGGU	Cleavage
22	468	489	UCUUCCCUAC	: :::::: :::: :: :.:::	GUUAUGGGU	Cleavage
22	1083	1104	UCUUCCCAAL	:::: ::: :.::: ::::::	UGAAUUGGC	Cleavage
22	817	838	UCUUCCCUAC	:: ::::: :: ::.:: ::::	GGAAUGGGU	Translation
22	817	838	UCUUCCCUAC	:: ::::: :: ::.:: ::::	GGAAUGGGU	Translation
22	716	737	UCUUCCCUAC	:: ::::: ::: :.:: ::::	GGGAUGGGC	Translation

22	716	737	UCUUCCCUAC	:: :::: ::: :.:: ::::	GGGAUGGGC	Translation
22	1231	1252	UCUUCCCAAU	::::::: ::.:: :: ::::	GGAAUGGGA	Cleavage
22	1231	1252	UCUUCCCAAU	::::::: ::.:: :: ::::	GGAAUGGGA	Cleavage
22	634	655	UCUUCCCUAC	:: :::: :: ::.:: ::::	GGAAUGGGU	Translation
22	634	655	UCUUCCCUAC	:: :::: :: ::.:: ::::	GGAAUGGGU	Translation
22	640	661	UCUUCCCUAC	:: :::: :: ::.:: ::::	GGCAUGGGU	Translation
22	640	661	UCUUCCCUAC	:: :::: :: ::.:: ::::	GGCAUGGGU	Translation
22	238	259	UCUUCCCUAC	:: ::: :::: ::.:: ::::	GGAAUGCGA	Translation
22	238	259	UCUUCCCUAC	:: ::: :::: ::.:: ::::	GGAAUGCGA	Translation
22	1714	1735	UCUUCCCUAC	:: ::: :: :::::: :.::	GGGAUGAGA	Cleavage
22	1714	1735	UCUUCCCUAC	:: ::: :: :::::: :.::	GGGAUGAGA	Cleavage
22	318	339	UCUUCCCAAU	:..::::.: :::: ::.:.	AGGGUGGGU	Cleavage
22	394	415	UCUUCCCAAU	:..::::.: :::: ::.:.	AGGGUGGGU	Cleavage
22	394	415	UCUUCCCAAU	:..::::.: :::: ::.:.	AGGGUGGGU	Cleavage
22	394	415	UCUUCCCAAU	:..::::.: :::: ::.:.	AGGGUGGGU	Cleavage
22	334	355	UCUUCCCUAC	:: ::::. :: ::::::::.	CGUUUGGGG	Translation
22	334	355	UCUUCCCUAC	:: ::::. :: ::::::::.	CGUUUGGGG	Translation
22	838	859	UCUUCCCAAU	:::: :: :::: :: ::::	GGAAUCGGG	Cleavage
22	321	342	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	321	342	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	383	404	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	383	404	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	434	455	UCUUCCCUAC	:.:::::::::: :: ...:.	ACUGUGGGA	Cleavage
22	1054	1075	UCUUCCCUAC	:::. : : :::: ::::::::	GGUGAGAGU	Cleavage
22	1360	1381	UCUUCCCUAC	:::. : : :::: ::::::::	GGUGAGAGU	Cleavage
22	1452	1473	UCUUCCCUAC	:::. : : :::: ::::::::	GGUGAGAGU	Cleavage
22	1054	1075	UCUUCCCUAC	:::. : : :::: ::::::::	GGUGAGAGU	Cleavage
22	1360	1381	UCUUCCCUAC	:::. : : :::: ::::::::	GGUGAGAGU	Cleavage
22	1452	1473	UCUUCCCUAC	:::. : : :::: ::::::::	GGUGAGAGU	Cleavage
22	923	944	UCUUCCCAAU	:::.::: ::::.: :::::::	GGAGUGGUC	Cleavage
22	945	966	UCUUCCCAAU	:::.::: ::::.: :::::::	GGAGUGGUC	Cleavage
22	5224	5245	UCUUCCCAAU	: :.:: :.:::: : ::::	GAAGUGCGU	Cleavage
22	5224	5245	UCUUCCCAAU	: :.:: :.:::: : ::::	GAAGUGCGU	Cleavage
22	5220	5241	UCUUCCCAAU	: :.:: :.:::: : ::::	GAAGUGCGU	Cleavage
22	1887	1908	UCUUCCCAAU	.:::::::::: :::..	AAGAUGGGC	Cleavage
22	1887	1908	UCUUCCCAAU	.:::::::::: :::..	AAGAUGGGC	Cleavage
22	3331	3352	UCUUCCCAAU	.:::::::::: :::..	AAGAUGGGC	Cleavage
22	623	644	UCUUCCCAAU	::::::: . :::::: :.::	GGAAUGGUU	Cleavage
22	733	754	UCUUCCCAAU	:::: :::.::: :::: :::.	GGAAGGGGU	Translation

22	1265	1286	UCUUCCCAAU	:::: :::.::: :::: ::::.	GGAAGGGGU	Translation
22	1508	1528	UCUUCCCUAC	::::: ::: :::.::::.::	UGUAUGCGA	Cleavage
22	1508	1528	UCUUCCCUAC	::::: ::: :::.::::.::	UGUAUGCGA	Cleavage
22	11	30	UCUUCCCUAC	::::::: ::::::::: :::	GGUAUGG-A	Cleavage
22	11	30	UCUUCCCUAC	::::::: ::::::::: :::	GGUAUGG-A	Cleavage
22	519	540	UCUUCCCAAU	::..: :: ::::::::::	GGGGUUGGG	Cleavage
22	525	546	UCUUCCCUAC	::::::::::.: :.:	UUCAUGGGA	Cleavage
22	525	546	UCUUCCCUAC	::::::::::.: :.:	UUCAUGGGA	Cleavage
22	81	102	UCUUCCCAAU	::::::: : ..:::: ::::	UGAAUGGGG	Cleavage
22	46	67	UCUUCCCUAC	.::::::::::::::.	CUAGUGGGA	Cleavage
22	46	67	UCUUCCCUAC	.::::::::::::::.	CUAGUGGGA	Cleavage
22	81	102	UCUUCCCAAU	::.:::: :::: ::: .:::	UGAGUGGGG	Cleavage
22	845	866	UCUUCCCUAC	::.:::::::: :.: ::.:.	AGUGUGGGA	Translation
22	845	866	UCUUCCCUAC	::.:::::::: :.: ::.:.	AGUGUGGGA	Translation
22	419	440	UCUUCCCAAU	:::.: :: ::.:::: .:::	GGAGUUGGG	Cleavage
22	1622	1643	UCUUCCCAAU	::.: :::.:::.: ::::.:	GGGAAGGGU	Cleavage
22	1951	1974	UCUUCCCAAU	::::::: .::.: ::::::	GGAAUGGGA	Cleavage
22	716	737	UCUUCCCAAU	:.:::: :::.:::::.:	CCAGUGGGA	Cleavage
22	1608	1629	UCUUCCCUAC	:::: ::.:::: : ::.:::	AGUAUUGGG	Cleavage
22	643	664	UCUUCCCUAC	: .:::::::: :. ::..::	UGAGUGGGA	Translation
22	1537	1558	UCUUCCCUAC	:::: ::.:::: : ::.:::	AGUAUUGGG	Cleavage
22	688	709	UCUUCCCUAC	: .:::::::: :. ::..::	UGAGUGGGA	Translation
22	1608	1629	UCUUCCCUAC	:::: ::.:::: : ::.:::	AGUAUUGGG	Cleavage
22	643	664	UCUUCCCUAC	: .:::::::: :. ::..::	UGAGUGGGA	Translation
22	1537	1558	UCUUCCCUAC	:::: ::.:::: : ::.:::	AGUAUUGGG	Cleavage
22	688	709	UCUUCCCUAC	: .:::::::: :. ::..::	UGAGUGGGA	Translation
22	3093	3114	UCUUCCCAAU	:::.: :.:::. ::::::::	GGAGUUAGU	Cleavage
22	658	679	UCUUCCCAAU	:::::::: ::..: :: ::::	GGAAUGGGA	Cleavage
22	716	737	UCUUCCCAAU	:::::::: ::..: :: ::::	GGAAUGGGA	Cleavage
22	601	622	UCUUCCCAAU	::::::: ::..: :: ::::	GGAAUGGGA	Cleavage
22	604	625	UCUUCCCAAU	::::::: ::..: :: ::::	GGAAUGGGA	Cleavage
22	752	773	UCUUCCCAAU	::::::: ::..: :: ::::	GGAAUGGGA	Cleavage

Target_Desc.	Multiplicity	Target_Acc.	ID	locusName	Pfam
pacid=371636	1	Phvul.004G048000.1	Phvul.004G048000	Phvul.004G04	PF00931
pacid=371689	1	Phvul.001G224800.1	Phvul.001G224800	Phvul.001G22	PF01344,PF13
pacid=371689	1	Phvul.001G224800.2	Phvul.001G224800	Phvul.001G22	PF01344,PF13
pacid=371689	1	Phvul.001G224800.1	Phvul.001G224800	Phvul.001G22	PF01344,PF13
pacid=371689	1	Phvul.001G224800.2	Phvul.001G224800	Phvul.001G22	PF01344,PF13
pacid=371656	1	Phvul.007G201700.1	Phvul.007G201700	Phvul.007G20	PF01344,PF13
pacid=371656	1	Phvul.007G201700.1	Phvul.007G201700	Phvul.007G20	PF01344,PF13
pacid=371606	1	Phvul.008G061300.2	Phvul.008G061300	Phvul.008G06	PF13855,PF00
pacid=371606	1	Phvul.008G061300.1	Phvul.008G061300	Phvul.008G06	PF13855,PF00
pacid=371606	1	Phvul.008G061300.2	Phvul.008G061300	Phvul.008G06	PF13855,PF00
pacid=371606	1	Phvul.008G061300.1	Phvul.008G061300	Phvul.008G06	PF13855,PF00
pacid=371779	1	Phvul.002G079200.1	Phvul.002G079200	Phvul.002G07	PF05729,PF13
pacid=371683	1	Phvul.001G217600.1	Phvul.001G217600	Phvul.001G21	0
pacid=371775	1	Phvul.002G001500.1	Phvul.002G001500	Phvul.002G00	PF13919,PF00
pacid=371775	1	Phvul.002G001500.1	Phvul.002G001500	Phvul.002G00	PF13919,PF00
pacid=371469	1	Phvul.003G072500.1	Phvul.003G072500	Phvul.003G07	PF13676,PF00
pacid=371456	2	Phvul.003G244225.3	Phvul.003G244225	Phvul.003G24	0
pacid=371456	2	Phvul.003G244225.2	Phvul.003G244225	Phvul.003G24	0
pacid=371456	2	Phvul.003G244225.1	Phvul.003G244225	Phvul.003G24	0
pacid=371634	1	Phvul.004G137300.1	Phvul.004G137300	Phvul.004G13	PF13676,PF00
pacid=371543	1	Phvul.005G029400.1	Phvul.005G029400	Phvul.005G02	PF03145
pacid=371543	1	Phvul.005G029400.3	Phvul.005G029400	Phvul.005G02	PF03145
pacid=371543	1	Phvul.005G029400.2	Phvul.005G029400	Phvul.005G02	PF03145
pacid=371662	1	Phvul.007G210600.1	Phvul.007G210600	Phvul.007G21	PF03110
pacid=371662	1	Phvul.007G210600.1	Phvul.007G210600	Phvul.007G21	PF03110
pacid=371605	1	Phvul.008G055500.1	Phvul.008G055500	Phvul.008G05	PF00005
pacid=371577	1	Phvul.008G280900.1	Phvul.008G280900	Phvul.008G28	PF01594
pacid=371577	1	Phvul.008G280900.1	Phvul.008G280900	Phvul.008G28	PF01594
pacid=371428	1	Phvul.010G064700.1	Phvul.010G064700	Phvul.010G06	PF00931
pacid=371426	1	Phvul.010G136700.1	Phvul.010G136700	Phvul.010G13	PF07725,PF13
pacid=371549	1	Phvul.011G149100.7	Phvul.011G149100	Phvul.011G14	0
pacid=371549	1	Phvul.011G149100.6	Phvul.011G149100	Phvul.011G14	0
pacid=371549	1	Phvul.011G149100.5	Phvul.011G149100	Phvul.011G14	0
pacid=371549	1	Phvul.011G149100.2	Phvul.011G149100	Phvul.011G14	0
pacid=371549	1	Phvul.011G149100.1	Phvul.011G149100	Phvul.011G14	0
pacid=371549	1	Phvul.011G149100.4	Phvul.011G149100	Phvul.011G14	0
pacid=371549	1	Phvul.011G149100.3	Phvul.011G149100	Phvul.011G14	0
pacid=371569	1	Phvul.011G166100.1	Phvul.011G166100	Phvul.011G16	PF00931
pacid=371711	1	Phvul.001G128200.2	Phvul.001G128200	Phvul.001G12	PF07725,PF13
pacid=371696	1	Phvul.001G134000.1	Phvul.001G134000	Phvul.001G13	PF13855,PF00
pacid=371696	1	Phvul.001G134000.1	Phvul.001G134000	Phvul.001G13	PF13855,PF00
pacid=371708	1	Phvul.001G243900.1	Phvul.001G243900	Phvul.001G24	PF02861,PF07
pacid=371708	1	Phvul.001G243900.1	Phvul.001G243900	Phvul.001G24	PF02861,PF07
pacid=371772	1	Phvul.002G057300.2	Phvul.002G057300	Phvul.002G05	PF08458,PF05
pacid=371772	1	Phvul.002G057300.1	Phvul.002G057300	Phvul.002G05	PF08458,PF05

pacid=371769	1	Phvul.002G122200.1	Phvul.002G122200	Phvul.002G12	PF00067
pacid=371750	1	Phvul.002G187600.1	Phvul.002G187600	Phvul.002G18	0
pacid=371773	1	Phvul.002G261500.1	Phvul.002G261500	Phvul.002G26	PF00076
pacid=371773	1	Phvul.002G261500.1	Phvul.002G261500	Phvul.002G26	PF00076
pacid=371475	1	Phvul.003G101200.1	Phvul.003G101200	Phvul.003G10	PF04535
pacid=371475	1	Phvul.003G101200.1	Phvul.003G101200	Phvul.003G10	PF04535
pacid=371460	1	Phvul.003G202900.1	Phvul.003G202900	Phvul.003G20	PF02657,PF02
pacid=371460	1	Phvul.003G202900.1	Phvul.003G202900	Phvul.003G20	PF02657,PF02
pacid=371627	1	Phvul.004G026200.1	Phvul.004G026200	Phvul.004G02	PF00505,PF08
pacid=371631	1	Phvul.004G140400.1	Phvul.004G140400	Phvul.004G14	PF05729,PF13
pacid=371631	1	Phvul.004G140400.1	Phvul.004G140400	Phvul.004G14	PF05729,PF13
pacid=371524	1	Phvul.005G038200.1	Phvul.005G038200	Phvul.005G03	PF00590
pacid=371524	1	Phvul.005G038200.1	Phvul.005G038200	Phvul.005G03	PF00590
pacid=371534	1	Phvul.005G087100.1	Phvul.005G087100	Phvul.005G08	PF13855,PF00
pacid=371534	1	Phvul.005G087100.1	Phvul.005G087100	Phvul.005G08	PF13855,PF00
pacid=371730	1	Phvul.006G102700.1	Phvul.006G102700	Phvul.006G10	PF11721,PF00
pacid=371579	1	Phvul.008G072300.2	Phvul.008G072300	Phvul.008G07	PF00931
pacid=371579	1	Phvul.008G072300.1	Phvul.008G072300	Phvul.008G07	PF00931
pacid=371579	1	Phvul.008G072300.2	Phvul.008G072300	Phvul.008G07	PF00931
pacid=371579	1	Phvul.008G072300.1	Phvul.008G072300	Phvul.008G07	PF00931
pacid=371579	1	Phvul.008G202300.1	Phvul.008G202300	Phvul.008G20	PF04031
pacid=371595	1	Phvul.008G259600.2	Phvul.008G259600	Phvul.008G25	PF02705
pacid=371595	1	Phvul.008G259600.1	Phvul.008G259600	Phvul.008G25	PF02705
pacid=371595	1	Phvul.008G259600.2	Phvul.008G259600	Phvul.008G25	PF02705
pacid=371595	1	Phvul.008G259600.1	Phvul.008G259600	Phvul.008G25	PF02705
pacid=371424	1	Phvul.010G131650.1	Phvul.010G131650	Phvul.010G13	PF07725,PF13
pacid=371433	1	Phvul.010G132333.1	Phvul.010G132333	Phvul.010G13	PF07725
pacid=371436	1	Phvul.010G136800.1	Phvul.010G136800	Phvul.010G13	PF07725,PF13
pacid=371426	1	Phvul.010G151400.6	Phvul.010G151400	Phvul.010G15	PF16994
pacid=371426	1	Phvul.010G151400.4	Phvul.010G151400	Phvul.010G15	PF16994
pacid=371426	1	Phvul.010G151400.6	Phvul.010G151400	Phvul.010G15	PF16994
pacid=371426	1	Phvul.010G151400.4	Phvul.010G151400	Phvul.010G15	PF16994
pacid=371547	1	Phvul.011G140300.1	Phvul.011G140300	Phvul.011G14	PF07725,PF13
pacid=371561	1	Phvul.011G140400.1	Phvul.011G140400	Phvul.011G14	PF13676,PF13
pacid=371574	1	Phvul.011G151300.1	Phvul.011G151300	Phvul.011G15	PF00931
pacid=371561	1	Phvul.011G181700.1	Phvul.011G181700	Phvul.011G18	PF00931
pacid=371561	1	Phvul.011G181700.1	Phvul.011G181700	Phvul.011G18	PF00931
pacid=371570	1	Phvul.011G192400.1	Phvul.011G192400	Phvul.011G19	PF00931
pacid=371555	1	Phvul.011G192600.1	Phvul.011G192600	Phvul.011G19	PF13855,PF00
pacid=371558	1	Phvul.011G193100.1	Phvul.011G193100	Phvul.011G19	PF00931
pacid=371551	1	Phvul.011G193500.1	Phvul.011G193500	Phvul.011G19	PF13855,PF00
pacid=371558	1	Phvul.011G193600.1	Phvul.011G193600	Phvul.011G19	PF13855,PF00
pacid=371550	1	Phvul.011G194800.1	Phvul.011G194800	Phvul.011G19	PF00931
pacid=371546	1	Phvul.011G194900.1	Phvul.011G194900	Phvul.011G19	PF00931
pacid=371570	1	Phvul.011G195000.1	Phvul.011G195000	Phvul.011G19	PF00931
pacid=371563	1	Phvul.011G195200.1	Phvul.011G195200	Phvul.011G19	PF00931

pacid=371572	1	Phvul.011G195400.1	Phvul.011G195400	Phvul.011G19	PF00931
pacid=371554	1	Phvul.011G195500.1	Phvul.011G195500	Phvul.011G19	PF00931
pacid=371565	1	Phvul.011G196000.1	Phvul.011G196000	Phvul.011G19	PF13855,PF00
pacid=371571	1	Phvul.011G196066.1	Phvul.011G196066	Phvul.011G19	PF00931
pacid=371573	1	Phvul.011G200820.1	Phvul.011G200820	Phvul.011G20	PF00931
pacid=371573	1	Phvul.011G200820.1	Phvul.011G200820	Phvul.011G20	PF00931
pacid=371560	1	Phvul.011G202100.1	Phvul.011G202100	Phvul.011G20	PF00931
pacid=371560	1	Phvul.011G202100.1	Phvul.011G202100	Phvul.011G20	PF00931
pacid=371555	1	Phvul.011G202300.1	Phvul.011G202300	Phvul.011G20	PF00931
pacid=371555	1	Phvul.011G202300.1	Phvul.011G202300	Phvul.011G20	PF00931
pacid=371563	1	Phvul.011G203100.1	Phvul.011G203100	Phvul.011G20	PF00931
pacid=371563	1	Phvul.011G203100.1	Phvul.011G203100	Phvul.011G20	PF00931
pacid=371575	1	Phvul.L002337.2	Phvul.L002337	Phvul.L00233	PF00107,PF08
pacid=371575	1	Phvul.L002337.1	Phvul.L002337	Phvul.L00233	PF00107,PF08
pacid=371575	1	Phvul.L002337.2	Phvul.L002337	Phvul.L00233	PF00107,PF08
pacid=371575	1	Phvul.L002337.1	Phvul.L002337	Phvul.L00233	PF00107,PF08
pacid=371699	1	Phvul.001G015600.1	Phvul.001G015600	Phvul.001G01	PF01553
pacid=371699	1	Phvul.001G015600.2	Phvul.001G015600	Phvul.001G01	PF01553
pacid=371699	1	Phvul.001G015600.1	Phvul.001G015600	Phvul.001G01	PF01553
pacid=371699	1	Phvul.001G015600.2	Phvul.001G015600	Phvul.001G01	PF01553
pacid=371677	1	Phvul.001G085500.2	Phvul.001G085500	Phvul.001G08	PF00010
pacid=371677	1	Phvul.001G085500.1	Phvul.001G085500	Phvul.001G08	PF00010
pacid=371685	1	Phvul.001G232600.1	Phvul.001G232600	Phvul.001G23	PF03330,PF01
pacid=371685	1	Phvul.001G232600.1	Phvul.001G232600	Phvul.001G23	PF03330,PF01
pacid=371756	1	Phvul.002G041400.4	Phvul.002G041400	Phvul.002G04	PF04640
pacid=371756	1	Phvul.002G041400.1	Phvul.002G041400	Phvul.002G04	PF04640
pacid=371756	1	Phvul.002G041400.2	Phvul.002G041400	Phvul.002G04	PF04640
pacid=371756	1	Phvul.002G041400.3	Phvul.002G041400	Phvul.002G04	PF04640
pacid=371778	1	Phvul.002G298800.1	Phvul.002G298800	Phvul.002G29	PF01764
pacid=371450	1	Phvul.003G010900.1	Phvul.003G010900	Phvul.003G01	PF00503
pacid=371450	1	Phvul.003G010900.1	Phvul.003G010900	Phvul.003G01	PF00503
pacid=371453	1	Phvul.003G195800.2	Phvul.003G195800	Phvul.003G19	PF01535,PF13
pacid=371453	1	Phvul.003G195800.1	Phvul.003G195800	Phvul.003G19	PF01535,PF13
pacid=371455	1	Phvul.003G252400.1	Phvul.003G252400	Phvul.003G25	PF12171
pacid=371455	1	Phvul.003G252400.1	Phvul.003G252400	Phvul.003G25	PF12171
pacid=371465	1	Phvul.003G295800.4	Phvul.003G295800	Phvul.003G29	PF12624,PF09
pacid=371465	1	Phvul.003G295800.3	Phvul.003G295800	Phvul.003G29	PF12624,PF09
pacid=371465	1	Phvul.003G295800.2	Phvul.003G295800	Phvul.003G29	PF12624,PF09
pacid=371636	1	Phvul.004G032300.4	Phvul.004G032300	Phvul.004G03	PF14008,PF16
pacid=371636	1	Phvul.004G032300.2	Phvul.004G032300	Phvul.004G03	PF14008,PF16
pacid=371636	1	Phvul.004G032300.3	Phvul.004G032300	Phvul.004G03	PF14008,PF16
pacid=371636	1	Phvul.004G032300.1	Phvul.004G032300	Phvul.004G03	PF14008,PF16
pacid=371636	1	Phvul.004G032300.4	Phvul.004G032300	Phvul.004G03	PF14008,PF16
pacid=371636	1	Phvul.004G032300.2	Phvul.004G032300	Phvul.004G03	PF14008,PF16
pacid=371636	1	Phvul.004G032300.3	Phvul.004G032300	Phvul.004G03	PF14008,PF16
pacid=371636	1	Phvul.004G032300.1	Phvul.004G032300	Phvul.004G03	PF14008,PF16

pacid=371636	1	Phvul.004G048000.1	Phvul.004G048000	Phvul.004G04	PF00931
pacid=371636	1	Phvul.004G048000.1	Phvul.004G048000	Phvul.004G04	PF00931
pacid=371625	1	Phvul.004G106800.2	Phvul.004G106800	Phvul.004G10	PF01656
pacid=371625	1	Phvul.004G106800.2	Phvul.004G106800	Phvul.004G10	PF01656
pacid=371628	1	Phvul.004G133100.1	Phvul.004G133100	Phvul.004G13	PF12695
pacid=371545	1	Phvul.005G165800.1	Phvul.005G165800	Phvul.005G16	PF01535,PF12
pacid=371545	1	Phvul.005G165800.1	Phvul.005G165800	Phvul.005G16	PF01535,PF12
pacid=371714	1	Phvul.006G066800.1	Phvul.006G066800	Phvul.006G06	PF00931
pacid=371738	1	Phvul.006G086800.1	Phvul.006G086800	Phvul.006G08	PF03330,PF01
pacid=371723	1	Phvul.006G148800.1	Phvul.006G148800	Phvul.006G14	0
pacid=371734	1	Phvul.006G180900.1	Phvul.006G180900	Phvul.006G18	PF08100,PF00
pacid=371734	1	Phvul.006G180900.1	Phvul.006G180900	Phvul.006G18	PF08100,PF00
pacid=371673	1	Phvul.007G027400.1	Phvul.007G027400	Phvul.007G02	0
pacid=371669	1	Phvul.007G096800.1	Phvul.007G096800	Phvul.007G09	PF01656
pacid=371591	1	Phvul.008G158100.1	Phvul.008G158100	Phvul.008G15	PF08263,PF13
pacid=371493	1	Phvul.009G020000.1	Phvul.009G020000	Phvul.009G02	PF08241,PF08
pacid=371493	1	Phvul.009G020000.1	Phvul.009G020000	Phvul.009G02	PF08241,PF08
pacid=371498	1	Phvul.009G065500.1	Phvul.009G065500	Phvul.009G06	PF00170
pacid=371498	1	Phvul.009G065500.2	Phvul.009G065500	Phvul.009G06	PF00170
pacid=371498	1	Phvul.009G065500.1	Phvul.009G065500	Phvul.009G06	PF00170
pacid=371498	1	Phvul.009G065500.2	Phvul.009G065500	Phvul.009G06	PF00170
pacid=371487	1	Phvul.009G213300.1	Phvul.009G213300	Phvul.009G21	PF13812,PF01
pacid=371497	1	Phvul.009G226300.2	Phvul.009G226300	Phvul.009G22	PF14416,PF13
pacid=371497	1	Phvul.009G226300.1	Phvul.009G226300	Phvul.009G22	PF14416,PF13
pacid=371497	1	Phvul.009G226300.2	Phvul.009G226300	Phvul.009G22	PF14416,PF13
pacid=371497	1	Phvul.009G226300.1	Phvul.009G226300	Phvul.009G22	PF14416,PF13
pacid=371517	1	Phvul.009G233700.1	Phvul.009G233700	Phvul.009G23	PF00931
pacid=371517	1	Phvul.009G233700.1	Phvul.009G233700	Phvul.009G23	PF00931
pacid=371517	1	Phvul.009G233700.1	Phvul.009G233700	Phvul.009G23	PF00931
pacid=371439	1	Phvul.010G008700.2	Phvul.010G008700	Phvul.010G00	PF00931
pacid=371439	1	Phvul.010G008700.1	Phvul.010G008700	Phvul.010G00	PF00931
pacid=371428	1	Phvul.010G056500.1	Phvul.010G056500	Phvul.010G05	PF13041
pacid=371428	1	Phvul.010G056500.1	Phvul.010G056500	Phvul.010G05	PF13041
pacid=371423	1	Phvul.010G063100.1	Phvul.010G063100	Phvul.010G06	PF00931
pacid=371428	1	Phvul.010G070584.1	Phvul.010G070584	Phvul.010G07	PF00890,PF05
pacid=371439	1	Phvul.010G146900.6	Phvul.010G146900	Phvul.010G14	PF07766
pacid=371439	1	Phvul.010G146900.2	Phvul.010G146900	Phvul.010G14	PF07766
pacid=371439	1	Phvul.010G146900.3	Phvul.010G146900	Phvul.010G14	PF07766
pacid=371438	1	Phvul.010G146900.1	Phvul.010G146900	Phvul.010G14	PF07766
pacid=371438	1	Phvul.010G146900.4	Phvul.010G146900	Phvul.010G14	PF07766
pacid=371439	1	Phvul.010G146900.5	Phvul.010G146900	Phvul.010G14	PF07766
pacid=371563	1	Phvul.011G014500.2	Phvul.011G014500	Phvul.011G01	PF00931
pacid=371563	1	Phvul.011G014500.2	Phvul.011G014500	Phvul.011G01	PF00931
pacid=371563	1	Phvul.011G014500.2	Phvul.011G014500	Phvul.011G01	PF00931
pacid=371573	1	Phvul.011G082700.3	Phvul.011G082700	Phvul.011G08	0
pacid=371573	1	Phvul.011G082700.2	Phvul.011G082700	Phvul.011G08	0

pacid=371573	1	Phvul.011G082700.1	Phvul.011G082700	Phvul.011G08	0
pacid=371549	1	Phvul.011G149400.1	Phvul.011G149400	Phvul.011G14	PF00931
pacid=371549	1	Phvul.011G149400.1	Phvul.011G149400	Phvul.011G14	PF00931
pacid=371566	1	Phvul.011G181500.1	Phvul.011G181500	Phvul.011G18	PF00931
pacid=371546	1	Phvul.011G182900.1	Phvul.011G182900	Phvul.011G18	PF00407
pacid=371546	1	Phvul.011G182900.1	Phvul.011G182900	Phvul.011G18	PF00407
pacid=371551	1	Phvul.011G191600.1	Phvul.011G191600	Phvul.011G19	PF13191,PF13
pacid=371571	1	Phvul.011G191800.1	Phvul.011G191800	Phvul.011G19	PF00931
pacid=371553	1	Phvul.011G192200.1	Phvul.011G192200	Phvul.011G19	PF00931
pacid=371553	1	Phvul.011G192900.1	Phvul.011G192900	Phvul.011G19	PF00931
pacid=371553	1	Phvul.011G192900.1	Phvul.011G192900	Phvul.011G19	PF00931
pacid=371552	1	Phvul.011G195751.1	Phvul.011G195751	Phvul.011G19	PF00931
pacid=371555	1	Phvul.011G198400.1	Phvul.011G198400	Phvul.011G19	PF13855,PF00
pacid=371548	1	Phvul.011G201000.1	Phvul.011G201000	Phvul.011G20	PF00931
pacid=371569	1	Phvul.011G201101.1	Phvul.011G201101	Phvul.011G20	PF00931
pacid=371680	1	Phvul.001G027100.1	Phvul.001G027100	Phvul.001G02	PF00646
pacid=371711	1	Phvul.001G123000.2	Phvul.001G123000	Phvul.001G12	PF01055
pacid=371712	1	Phvul.001G132516.1	Phvul.001G132516	Phvul.001G13	PF00931
pacid=371712	1	Phvul.001G132516.1	Phvul.001G132516	Phvul.001G13	PF00931
pacid=371694	1	Phvul.001G132701.1	Phvul.001G132701	Phvul.001G13	PF13855,PF00
pacid=371694	1	Phvul.001G132701.1	Phvul.001G132701	Phvul.001G13	PF13855,PF00
pacid=371700	1	Phvul.001G132800.1	Phvul.001G132800	Phvul.001G13	PF13855,PF00
pacid=371700	1	Phvul.001G132800.1	Phvul.001G132800	Phvul.001G13	PF13855,PF00
pacid=371678	1	Phvul.001G132864.1	Phvul.001G132864	Phvul.001G13	PF13855,PF00
pacid=371678	1	Phvul.001G132864.1	Phvul.001G132864	Phvul.001G13	PF13855,PF00
pacid=371687	1	Phvul.001G133100.1	Phvul.001G133100	Phvul.001G13	PF13855,PF00
pacid=371687	1	Phvul.001G133100.1	Phvul.001G133100	Phvul.001G13	PF13855,PF00
pacid=371684	1	Phvul.001G133101.1	Phvul.001G133101	Phvul.001G13	PF13855,PF00
pacid=371684	1	Phvul.001G133101.1	Phvul.001G133101	Phvul.001G13	PF13855,PF00
pacid=371712	1	Phvul.001G185400.1	Phvul.001G185400	Phvul.001G18	PF08263,PF00
pacid=371712	1	Phvul.001G185400.1	Phvul.001G185400	Phvul.001G18	PF08263,PF00
pacid=371700	1	Phvul.001G217800.1	Phvul.001G217800	Phvul.001G21	PF07885
pacid=371778	1	Phvul.002G063500.1	Phvul.002G063500	Phvul.002G06	PF00295
pacid=371778	1	Phvul.002G063500.1	Phvul.002G063500	Phvul.002G06	PF00295
pacid=371754	1	Phvul.002G104200.1	Phvul.002G104200	Phvul.002G10	PF00614,PF00
pacid=371754	1	Phvul.002G104200.1	Phvul.002G104200	Phvul.002G10	PF00614,PF00
pacid=371780	1	Phvul.002G279500.1	Phvul.002G279500	Phvul.002G27	PF03470,PF03
pacid=371464	2	Phvul.003G050200.2	Phvul.003G050200	Phvul.003G05	0
pacid=371464	2	Phvul.003G050200.1	Phvul.003G050200	Phvul.003G05	0
pacid=371478	1	Phvul.003G076900.1	Phvul.003G076900	Phvul.003G07	PF00067
pacid=371478	1	Phvul.003G076900.1	Phvul.003G076900	Phvul.003G07	PF00067
pacid=371447	1	Phvul.003G104900.1	Phvul.003G104900	Phvul.003G10	PF00403
pacid=371447	1	Phvul.003G104900.1	Phvul.003G104900	Phvul.003G10	PF00403
pacid=371471	1	Phvul.003G157600.1	Phvul.003G157600	Phvul.003G15	PF05182
pacid=371466	1	Phvul.003G158700.1	Phvul.003G158700	Phvul.003G15	PF07714,PF00
pacid=371466	1	Phvul.003G158700.1	Phvul.003G158700	Phvul.003G15	PF07714,PF00

pacid=371463	1	Phvul.003G162300.1	Phvul.003G162300	Phvul.003G16	PF12854,PF14
pacid=371483	1	Phvul.003G209600.2	Phvul.003G209600	Phvul.003G20	PF07521,PF00
pacid=371483	1	Phvul.003G209600.1	Phvul.003G209600	Phvul.003G20	PF07521,PF00
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pacid=371483	1	Phvul.003G288300.1	Phvul.003G288300	Phvul.003G28	PF00069
pacid=371628	1	Phvul.004G011400.1	Phvul.004G011400	Phvul.004G01	PF13921
pacid=371621	1	Phvul.004G064300.1	Phvul.004G064300	Phvul.004G06	PF00415
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pacid=371634	1	Phvul.004G131300.1	Phvul.004G131300	Phvul.004G13	PF01535,PF12
pacid=371542	1	Phvul.005G031200.1	Phvul.005G031200	Phvul.005G03	PF00931
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pacid=371542	1	Phvul.005G071300.1	Phvul.005G071300	Phvul.005G07	PF00304
pacid=371723	1	Phvul.006G057000.1	Phvul.006G057000	Phvul.006G05	PF00076
pacid=371721	1	Phvul.006G057100.5	Phvul.006G057100	Phvul.006G05	PF00076
pacid=371721	1	Phvul.006G057100.4	Phvul.006G057100	Phvul.006G05	PF00076
pacid=371716	1	Phvul.006G057700.2	Phvul.006G057700	Phvul.006G05	PF02146
pacid=371714	1	Phvul.006G066800.1	Phvul.006G066800	Phvul.006G06	PF00931
pacid=371714	1	Phvul.006G066800.1	Phvul.006G066800	Phvul.006G06	PF00931
pacid=371653	1	Phvul.007G086300.2	Phvul.007G086300	Phvul.007G08	PF00931
pacid=371653	1	Phvul.007G086300.1	Phvul.007G086300	Phvul.007G08	PF00931
pacid=371596	1	Phvul.008G014700.1	Phvul.008G014700	Phvul.008G01	PF00931
pacid=371596	1	Phvul.008G014700.1	Phvul.008G014700	Phvul.008G01	PF00931
pacid=371582	1	Phvul.008G072032.1	Phvul.008G072032	Phvul.008G07	PF13855,PF00
pacid=371582	1	Phvul.008G072032.1	Phvul.008G072032	Phvul.008G07	PF13855,PF00
pacid=371605	1	Phvul.008G168300.2	Phvul.008G168300	Phvul.008G16	0
pacid=371604	1	Phvul.008G168300.1	Phvul.008G168300	Phvul.008G16	0
pacid=371505	1	Phvul.009G039200.1	Phvul.009G039200	Phvul.009G03	PF00892
pacid=371497	1	Phvul.009G079700.1	Phvul.009G079700	Phvul.009G07	PF00433,PF07
pacid=371497	1	Phvul.009G079700.1	Phvul.009G079700	Phvul.009G07	PF00433,PF07
pacid=371486	1	Phvul.009G180800.1	Phvul.009G180800	Phvul.009G18	PF08477
pacid=371486	1	Phvul.009G180800.2	Phvul.009G180800	Phvul.009G18	PF08477
pacid=371486	1	Phvul.009G180800.1	Phvul.009G180800	Phvul.009G18	PF08477
pacid=371486	1	Phvul.009G180800.2	Phvul.009G180800	Phvul.009G18	PF08477
pacid=371520	1	Phvul.009G249500.1	Phvul.009G249500	Phvul.009G24	PF03242
pacid=371428	1	Phvul.010G025000.1	Phvul.010G025000	Phvul.010G02	PF13676,PF00
pacid=371440	1	Phvul.010G025700.1	Phvul.010G025700	Phvul.010G02	PF13676,PF00
pacid=371426	1	Phvul.010G063700.2	Phvul.010G063700	Phvul.010G06	PF00931
pacid=371437	1	Phvul.010G101700.1	Phvul.010G101700	Phvul.010G10	0
pacid=371429	1	Phvul.010G141400.1	Phvul.010G141400	Phvul.010G14	PF02701
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pacid=371432	1	Phvul.010G149500.1	Phvul.010G149500	Phvul.010G14	PF13307,PF06
pacid=371571	1	Phvul.011G015000.1	Phvul.011G015000	Phvul.011G01	PF03514
pacid=371566	1	Phvul.011G181500.1	Phvul.011G181500	Phvul.011G18	PF00931
pacid=371566	1	Phvul.011G181500.1	Phvul.011G181500	Phvul.011G18	PF00931
pacid=371548	1	Phvul.011G198000.1	Phvul.011G198000	Phvul.011G19	PF00931

pacid=371548	1	Phvul.011G198000.1	Phvul.011G198000	Phvul.011G19	PF00931
pacid=371547	1	Phvul.011G200880.2	Phvul.011G200880	Phvul.011G20	PF00931
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pacid=371569	1	Phvul.011G201101.1	Phvul.011G201101	Phvul.011G20	PF00931
pacid=371569	1	Phvul.011G201101.1	Phvul.011G201101	Phvul.011G20	PF00931
pacid=371566	1	Phvul.011G202366.1	Phvul.011G202366	Phvul.011G20	PF13191
pacid=371566	1	Phvul.011G202366.1	Phvul.011G202366	Phvul.011G20	PF13191
pacid=371639	1	Phvul.L004500.1	Phvul.L004500	Phvul.L00450	PF00332
pacid=371639	1	Phvul.L004500.1	Phvul.L004500	Phvul.L00450	PF00332
pacid=371683	1	Phvul.001G183400.2	Phvul.001G183400	Phvul.001G18	PF04640
pacid=371683	1	Phvul.001G183400.3	Phvul.001G183400	Phvul.001G18	PF04640
pacid=371683	1	Phvul.001G183400.4	Phvul.001G183400	Phvul.001G18	PF04640
pacid=371683	1	Phvul.001G183400.1	Phvul.001G183400	Phvul.001G18	PF04640
pacid=371768	1	Phvul.002G089800.1	Phvul.002G089800	Phvul.002G08	PF08536
pacid=371768	1	Phvul.002G089800.1	Phvul.002G089800	Phvul.002G08	PF08536
pacid=371777	1	Phvul.002G171400.1	Phvul.002G171400	Phvul.002G17	PF13676,PF13
pacid=371778	1	Phvul.002G244900.1	Phvul.002G244900	Phvul.002G24	PF01925
pacid=371778	1	Phvul.002G244900.1	Phvul.002G244900	Phvul.002G24	PF01925
pacid=371757	1	Phvul.002G245000.5	Phvul.002G245000	Phvul.002G24	PF01925
pacid=371757	1	Phvul.002G245000.4	Phvul.002G245000	Phvul.002G24	PF01925
pacid=371757	1	Phvul.002G245000.3	Phvul.002G245000	Phvul.002G24	PF01925
pacid=371757	1	Phvul.002G245000.1	Phvul.002G245000	Phvul.002G24	PF01925
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pacid=371757	1	Phvul.002G245000.3	Phvul.002G245000	Phvul.002G24	PF01925
pacid=371757	1	Phvul.002G245000.1	Phvul.002G245000	Phvul.002G24	PF01925
pacid=371757	1	Phvul.002G245000.2	Phvul.002G245000	Phvul.002G24	PF01925
pacid=371449	1	Phvul.003G002200.5	Phvul.003G002200	Phvul.003G00	PF00612,PF00
pacid=371449	1	Phvul.003G002200.4	Phvul.003G002200	Phvul.003G00	PF00612,PF00
pacid=371449	1	Phvul.003G002200.3	Phvul.003G002200	Phvul.003G00	PF00612,PF00
pacid=371449	1	Phvul.003G002200.5	Phvul.003G002200	Phvul.003G00	PF00612,PF00
pacid=371449	1	Phvul.003G002200.4	Phvul.003G002200	Phvul.003G00	PF00612,PF00
pacid=371449	1	Phvul.003G002200.3	Phvul.003G002200	Phvul.003G00	PF00612,PF00
pacid=371464	2	Phvul.003G050200.2	Phvul.003G050200	Phvul.003G05	0
pacid=371464	2	Phvul.003G050200.1	Phvul.003G050200	Phvul.003G05	0
pacid=371456	2	Phvul.003G244225.3	Phvul.003G244225	Phvul.003G24	0
pacid=371456	2	Phvul.003G244225.2	Phvul.003G244225	Phvul.003G24	0
pacid=371456	2	Phvul.003G244225.1	Phvul.003G244225	Phvul.003G24	0
pacid=371459	1	Phvul.003G282200.3	Phvul.003G282200	Phvul.003G28	PF00856,PF05
pacid=371459	1	Phvul.003G282200.2	Phvul.003G282200	Phvul.003G28	PF00856,PF05
pacid=371464	1	Phvul.003G282250.1	Phvul.003G282250	Phvul.003G28	PF01535,PF13
pacid=371615	1	Phvul.004G011100.1	Phvul.004G011100	Phvul.004G01	PF03726,PF00
pacid=371618	1	Phvul.004G086300.2	Phvul.004G086300	Phvul.004G08	PF00069

pacid=371618	1	Phvul.004G086300.1	Phvul.004G086300	Phvul.004G08	PF00069
pacid=371544	1	Phvul.005G041300.1	Phvul.005G041300	Phvul.005G04	PF13041,PF01
pacid=371544	1	Phvul.005G041300.1	Phvul.005G041300	Phvul.005G04	PF13041,PF01
pacid=371528	1	Phvul.005G069700.1	Phvul.005G069700	Phvul.005G06	0
pacid=371528	1	Phvul.005G069700.1	Phvul.005G069700	Phvul.005G06	0
pacid=371525	1	Phvul.005G072000.1	Phvul.005G072000	Phvul.005G07	PF04765
pacid=371724	1	Phvul.006G027500.1	Phvul.006G027500	Phvul.006G02	PF00400
pacid=371724	1	Phvul.006G027500.1	Phvul.006G027500	Phvul.006G02	PF00400
pacid=371735	1	Phvul.006G100600.1	Phvul.006G100600	Phvul.006G10	PF06026
pacid=371715	1	Phvul.006G126400.1	Phvul.006G126400	Phvul.006G12	0
pacid=371715	1	Phvul.006G126400.1	Phvul.006G126400	Phvul.006G12	0
pacid=371718	1	Phvul.006G170700.1	Phvul.006G170700	Phvul.006G17	PF12796,PF13
pacid=371615	1	Phvul.008G107400.1	Phvul.008G107400	Phvul.008G10	PF01535,PF12
pacid=371615	1	Phvul.008G107400.1	Phvul.008G107400	Phvul.008G10	PF01535,PF12
pacid=371598	1	Phvul.008G206300.1	Phvul.008G206300	Phvul.008G20	PF05383
pacid=371492	1	Phvul.009G103100.1	Phvul.009G103100	Phvul.009G10	PF13855,PF08
pacid=371436	1	Phvul.010G008500.1	Phvul.010G008500	Phvul.010G00	PF05340
pacid=371429	1	Phvul.010G013500.1	Phvul.010G013500	Phvul.010G01	PF02701
pacid=371430	2	Phvul.010G044000.3	Phvul.010G044000	Phvul.010G04	PF02493
pacid=371430	2	Phvul.010G044000.3	Phvul.010G044000	Phvul.010G04	PF02493
pacid=371430	2	Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04	PF02493
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pacid=371430	2	Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04	PF02493
pacid=371430	2	Phvul.010G044000.2	Phvul.010G044000	Phvul.010G04	PF02493
pacid=371432	1	Phvul.010G145600.1	Phvul.010G145600	Phvul.010G14	PF14510,PF08
pacid=371561	1	Phvul.011G181700.1	Phvul.011G181700	Phvul.011G18	PF00931
pacid=371573	1	Phvul.011G200820.1	Phvul.011G200820	Phvul.011G20	PF00931
pacid=371560	1	Phvul.011G202100.1	Phvul.011G202100	Phvul.011G20	PF00931
pacid=371555	1	Phvul.011G202300.1	Phvul.011G202300	Phvul.011G20	PF00931
pacid=371563	1	Phvul.011G203100.1	Phvul.011G203100	Phvul.011G20	PF00931

Panther	KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
PTHR23155,P	0	0	0	GO:0043531	AT4G27220.1	0
PTHR23244,P	0	0	0	GO:0005515	AT1G74150.1	0
PTHR23244,P	0	0	0	GO:0005515	AT1G74150.1	0
PTHR23244,P	0	0	0	GO:0005515	AT1G74150.1	0
PTHR23244,P	0	0	0	GO:0005515	AT1G74150.1	0
PTHR23244,P	KOG4693	0	0	GO:0005515	AT1G74150.1	0
PTHR23244,P	KOG4693	0	0	GO:0005515	AT1G74150.1	0
PTHR23155,P	0	0	K13459	GO:0005515,(	AT5G63020.1	0
PTHR23155,P	0	0	K13459	GO:0005515,(	AT5G63020.1	0
PTHR23155,P	0	0	K13459	GO:0005515,(	AT5G63020.1	0
PTHR23155,P	0	0	K13459	GO:0005515,(	AT5G63020.1	0
PTHR11017,P	KOG4658	0	0	GO:0007165,(	AT1G27170.1	0
PTHR24078,P	0	0	0	0	AT1G75250.1	ATRL6,RL6,RSI
PTHR10071,P	0	0	0	GO:0043565,(	AT4G17570.3	GATA26
PTHR10071,P	0	0	0	GO:0043565,(	AT4G17570.3	GATA26
PTHR11017,P	KOG4658	0	0	GO:0007165,(	AT1G27170.1	0
PTHR32093,P	0	0	0	0	AT3G50370.1	0
PTHR32093,P	0	0	0	0	AT3G50370.1	0
PTHR32093,P	0	0	0	0	AT3G50370.1	0
PTHR11017,P	KOG4658	0	0	GO:0007165,(	AT5G36930.2	0
PTHR10315,P	KOG3002	6.3.2.19	K04506	GO:0007275,(	AT3G61790.1	0
PTHR10315,P	KOG3002	6.3.2.19	K04506	GO:0007275,(	AT3G61790.1	0
PTHR10315,P	KOG3002	6.3.2.19	K04506	GO:0007275,(	AT3G61790.1	0
PTHR31251,P	0	0	0	GO:0005634,(	AT2G47070.1	SPL1
PTHR31251,P	0	0	0	GO:0005634,(	AT2G47070.1	SPL1
PTHR24220,P	0	3.6.3.25		0 GO:0016887,(	AT1G65410.1	ATNAP11,NAP
PTHR21716,P	KOG2365	0	0	0	AT5G55960.1	0
PTHR21716,P	KOG2365	0	0	0	AT5G55960.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR11017,P	0	0	0	GO:0007165,(	AT5G17680.1	0
PTHR14221,P	0	0	0	0	AT5G54200.1	0
PTHR14221,P	0	0	0	0	AT5G54200.1	0
PTHR14221,P	0	0	0	0	AT5G54200.1	0
PTHR14221,P	0	0	0	0	AT5G54200.1	0
PTHR14221,P	0	0	0	0	AT5G54200.1	0
PTHR14221,P	0	0	0	0	AT5G54200.1	0
PTHR14221,P	0	0	0	0	AT5G54200.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR11017,P	KOG0472	0	0	0	AT5G17680.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR11638,P	KOG1051	0	0	GO:0019538,(	AT2G40130.2	0
PTHR11638,P	KOG1051	0	0	GO:0019538,(	AT2G40130.2	0
PTHR31351,P	0	0	0	0	AT4G17350.1	0
PTHR31351,P	0	0	0	0	AT4G17350.1	0

PTHR24286,P	KOG0157	1.14.13.93	0	GO:0055114,(	AT4G19230.1	CYP707A1
PTHR36320,P	0	0	0	0	AT1G30880.1	0
PTHR24012,P	KOG4209	0	K14396	GO:0003676	AT5G10350.1	0
PTHR24012,P	KOG4209	0	K14396	GO:0003676	AT5G10350.1	0
PTHR11615,P	0	0	0	0	AT4G15630.1	0
PTHR11615,P	0	0	0	0	AT4G15630.1	0
PTHR30573,P	0	2.5.1.72	K03517	GO:0051539,(	AT5G50210.1	OLD5,QS,SUF
PTHR30573,P	0	2.5.1.72	K03517	GO:0051539,(	AT5G50210.1	OLD5,QS,SUF
PTHR13711,P	0	0	K09272	0	AT3G28730.1	ATHMG,HMG,
PTHR11017,P	0	0	0	GO:0007165,(	AT5G17680.1	0
PTHR11017,P	0	0	0	GO:0007165,(	AT5G17680.1	0
PTHR21091,P	KOG1527	0	0	GO:0008168,(	AT5G40850.1	UPM1
PTHR21091,P	KOG1527	0	0	GO:0008168,(	AT5G40850.1	UPM1
PTHR23155,P	KOG4658	0	K13459	GO:0005515,(	AT4G27220.1	0
PTHR23155,P	KOG4658	0	K13459	GO:0005515,(	AT4G27220.1	0
PTHR27003,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT3G04690.1	ANX1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT1G63350.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT1G63350.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT1G63350.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT1G63350.1	0
PTHR15002	KOG2425	0	K16912	0	AT5G12220.1	0
PTHR30540,P	0	0	0	GO:0071805,(	AT2G30070.1	ATKT1,ATKT1
PTHR30540,P	0	0	0	GO:0071805,(	AT2G30070.1	ATKT1,ATKT1
PTHR30540,P	0	0	0	GO:0071805,(	AT2G30070.1	ATKT1,ATKT1
PTHR30540,P	0	0	0	GO:0071805,(	AT2G30070.1	ATKT1,ATKT1
PTHR11017,P	KOG4658	0	0	GO:0007165,(	AT5G41750.1	0
PTHR11017,P	KOG0617	0	0	0	AT5G41750.2	0
PTHR11017,P	KOG4658	0	0	GO:0007165,(	AT5G17680.1	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR12526,P	KOG0853	0	0	0	AT3G15940.2	0
PTHR11017,P	KOG4658	0	0	GO:0007165,(	AT5G17680.1	0
PTHR11017,P	KOG4658	0	0	GO:0007165,(	AT5G17680.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0

PTHR23155,P	0	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658		0	0	GO:0005515,	AT3G14470.1	0
PTHR23155,P	0	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658		0	0	GO:0043531	AT3G14460.1	0
PTHR11695,P	KOG0022	1.1.1.1		0	GO:0055114,	AT5G42250.1	0
PTHR11695,P	KOG0022	1.1.1.1		0	GO:0055114,	AT5G42250.1	0
PTHR11695,P	KOG0022	1.1.1.1		0	GO:0055114,	AT5G42250.1	0
PTHR11695,P	KOG0022	1.1.1.1		0	GO:0055114,	AT5G42250.1	0
PTHR23063,P	KOG4666	2.3.1.25	K13510		GO:0016746,	AT1G80950.1	0
PTHR23063,P	KOG4666	2.3.1.25	K13510		GO:0016746,	AT1G80950.1	0
PTHR23063,P	KOG4666	2.3.1.25	K13510		GO:0016746,	AT1G80950.1	0
PTHR23063,P	KOG4666	2.3.1.25	K13510		GO:0016746,	AT1G80950.1	0
PTHR31945,P	0	0	0	GO:0046983	AT3G26744.1	ATICE1,ICE1,S
PTHR31945,P	0	0	0	GO:0046983	AT3G26744.1	ATICE1,ICE1,S
PTHR31867,P	0	0	0	0	AT2G39700.1	ATEXP4,ATEX
PTHR31867,P	0	0	0	0	AT2G39700.1	ATEXP4,ATEX
PTHR31065,P	0	0	0	0	AT1G32700.1	0
PTHR31065,P	0	0	0	0	AT1G32700.1	0
PTHR31065,P	0	0	0	0	AT1G32700.1	0
PTHR31065,P	0	0	0	0	AT1G32700.1	0
PTHR31479,P	0	0	0	GO:0006629	AT4G10955.1	0
PTHR10218,P	KOG0082		0	0	GO:0031683,	AT2G23460.1	ATXLG1,XLG1
PTHR10218,P	KOG0082		0	0	GO:0031683,	AT2G23460.1	ATXLG1,XLG1
PTHR24015,P	0	0	0	0	AT1G74850.1	PTAC2
PTHR24015,P	0	0	0	0	AT1G74850.1	PTAC2
PTHR10593,P	0	0	0	0	AT5G66730.1	0
PTHR10593,P	0	0	0	0	AT5G66730.1	0
PTHR13190,P	KOG2993	0	K17906	GO:0006914	AT3G19190.1	ATATG2,ATG2
PTHR13190,P	KOG2993	0	K17906	GO:0006914	AT3G19190.1	ATATG2,ATG2
PTHR13190,P	KOG2993	0	K17906	GO:0006914	AT3G19190.1	ATATG2,ATG2
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP
PTHR22953,P	KOG1378	3.6.1.7,3.1.3.2	0	GO:0016787	AT4G13700.1	ATPAP23,PAP

PTHR23155,P	0	0	0	GO:0043531	AT4G27220.1	0
PTHR23155,P	0	0	0	GO:0043531	AT4G27220.1	0
PTHR13696,P	KOG3022	0	K03609	0	AT5G24020.1	ARC11,ATMIN
PTHR13696,P	KOG3022	0	K03609	0	AT5G24020.1	ARC11,ATMIN
PTHR23024,P	KOG1515	3.1.1.1	0	0	AT5G23530.1	AtCXE18,CXE1
PTHR24015,P	0	0	0	0	AT3G49730.1	0
PTHR24015,P	0	0	0	0	AT3G49730.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR31867,P	0	0	0	0	AT3G03220.1	ATEXP13,ATE
0	0	0	0	0	0	0
PTHR11746,P	KOG3178	0	0	GO:0046983,(	AT4G35160.1	0
PTHR11746,P	KOG3178	0	0	GO:0046983,(	AT4G35160.1	0
0	0	0	0	0	AT1G68500.1	0
PTHR10803	KOG2825	3.6.3.16	K01551	GO:0016887,(	AT3G10350.1	0
PTHR27008,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT5G35390.1	0
PTHR10108,P	KOG1269	2.1.1.143,2.1.	K08242	GO:0008168,(	AT1G20330.1	CVP1,FRL1,SM
PTHR10108,P	KOG1269	2.1.1.143,2.1.	K08242	GO:0008168,(	AT1G20330.1	CVP1,FRL1,SM
PTHR22952,P	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A
PTHR22952,P	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A
PTHR22952,P	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A
PTHR22952,P	0	0	K14432	GO:0043565,(	AT1G45249.1	ABF2,AREB1,A
PTHR24015,P	0	0	K17964	0	AT1G19290.1	0
PTHR13533,P	0	0	0	0	AT5G20680.1	TBL16
PTHR13533,P	0	0	0	0	AT5G20680.1	TBL16
PTHR13533,P	0	0	0	0	AT5G20680.1	TBL16
PTHR13533,P	0	0	0	0	AT5G20680.1	TBL16
PTHR23155,P	KOG4658	0	0	GO:0043531	AT1G50180.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT1G50180.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT1G50180.1	0
PTHR11017,P	0	0	0	GO:0043531	AT5G36930.2	0
PTHR11017,P	0	0	0	GO:0043531	AT5G36930.2	0
PTHR24015,P	0	0	0	0	AT2G17670.1	0
PTHR24015,P	0	0	0	0	AT2G17670.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR10668,P	KOG1238	1.1.3.20	K17756	GO:0055114,(	AT3G23410.1	ATFAO3,FAO3
PTHR14009,P	0	0	0	0	AT3G11560.2	0
PTHR14009,P	0	0	0	0	AT3G11560.2	0
PTHR14009,P	0	0	0	0	AT3G11560.2	0
PTHR14009,P	0	0	0	0	AT3G11560.2	0
PTHR14009,P	0	0	0	0	AT3G11560.2	0
PTHR14009,P	0	0	0	0	AT3G11560.2	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G46530.1	RPP13
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G46530.1	RPP13
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G46530.1	RPP13
PTHR33477,P	0	0	0	0	AT5G60760.1	0
PTHR33477,P	0	0	0	0	AT5G60760.1	0

PTHR33477,P	0	0	0	0	AT5G60760.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT4G26090.1	RPS2
PTHR23155,P	KOG4658	0	0	GO:0043531	AT4G26090.1	RPS2
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR31907,P	0	0	0	GO:0009607,(	AT1G70890.1	MLP43
PTHR31907,P	0	0	0	GO:0009607,(	AT1G70890.1	MLP43
PTHR23155,P	KOG4658	0	0	GO:0005515	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	0	0	0	GO:0043531	AT3G14470.1	0
PTHR32133,P	0	0	0	GO:0005515	AT5G43190.1	0
PTHR22762,P	0	3.2.1.20	0	GO:0005975,(	AT5G63840.1	PSL5,RSW3
PTHR23155,P	0	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	0	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG0617	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG0617	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0005515,(	AT3G14470.1	0
PTHR27008,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G36570.1	0
PTHR27008,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G36570.1	0
PTHR11003,P	0	0	K05389	0	AT4G01840.1	ATKCO5,ATTP
PTHR31375,P	0	3.2.1.15	K01213	GO:0005975,(	AT3G26610.1	0
PTHR31375,P	0	3.2.1.15	K01213	GO:0005975,(	AT3G26610.1	0
PTHR18896,P	0	3.1.4.4	K01115	GO:0003824,(	AT4G35790.2	ATPLDDELTA,I
PTHR18896,P	0	3.1.4.4	K01115	GO:0003824,(	AT4G35790.2	ATPLDDELTA,I
PTHR21596,P	0	0	0	GO:0031047	AT5G23570.1	ATSGS3,SGS3
PTHR37076,P	0	0	0	0	0	0
PTHR37076,P	0	0	0	0	0	0
PTHR24298,P	KOG0156	0	0	GO:0055114,(	AT1G11600.1	CYP77B1
PTHR24298,P	KOG0156	0	0	GO:0055114,(	AT1G11600.1	CYP77B1
PTHR22814,P	KOG1603	0	0	GO:0046872,(	AT5G27690.1	0
PTHR22814,P	KOG1603	0	0	GO:0046872,(	AT5G27690.1	0
PTHR36884	0	0	0	0	AT5G58040.1	ATFIP1[V],ATF
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT4G23180.1	CRK10,RLK4
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT4G23180.1	CRK10,RLK4

PTHR24015,P	0	0	0	0	AT1G08070.1	OTP82
PTHR11203,P	KOG1137	3.5.2.6	0	GO:0046872,(	AT5G63420.1	emb2746
PTHR11203,P	KOG1137	3.5.2.6	0	GO:0046872,(	AT5G63420.1	emb2746
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10520.1	RBK1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G10520.1	RBK1
PTHR10641,P	0	0	0	0	AT3G27785.1	ATMYB118,M
PTHR22870,P	KOG1427	0	0	0	AT5G16040.1	0
PTHR22870,P	KOG1427	0	0	0	AT5G16040.1	0
PTHR24015,P	0	0	0	0	AT1G12775.1	0
PTHR24015,P	0	0	0	0	AT1G12775.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR33147	0	0	0	0	AT2G02130.1	LCR68,PDF2.3
PTHR33147	0	0	0	0	AT2G02130.1	LCR68,PDF2.3
PTHR24012,P	0	0	K14398	GO:0003676	AT5G55670.1	0
PTHR24012,P	0	0	K14398	GO:0003676	AT5G55670.1	0
PTHR24012,P	0	0	K14398	GO:0003676	AT5G55670.1	0
PTHR11085,P	KOG1905	0	K11416	GO:0070403	AT5G55760.1	SRT1
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G46530.1	RPP13
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G46530.1	RPP13
PTHR23155,P	0	0	0	GO:0005515,(	AT4G27190.1	0
PTHR23155,P	0	0	0	GO:0005515,(	AT4G27190.1	0
PTHR34112,P	0	0	0	0	AT1G36990.1	0
PTHR34112,P	0	0	0	0	AT1G36990.1	0
PTHR31218,P	0	0	0	GO:0016021,(	AT1G09380.1	0
PTHR24356,P	0	2.7.11.1	0	GO:0006468,(	AT4G33080.2	0
PTHR24356,P	0	2.7.11.1	0	GO:0006468,(	AT4G33080.2	0
PTHR24072,P	KOG0393	3.6.5.2	K04392	GO:0007264,(	AT3G48040.1	ARAC8,ATRAC
PTHR24072,P	KOG0393	3.6.5.2	K04392	GO:0007264,(	AT3G48040.1	ARAC8,ATRAC
PTHR24072,P	KOG0393	3.6.5.2	K04392	GO:0007264,(	AT3G48040.1	ARAC8,ATRAC
PTHR24072,P	KOG0393	3.6.5.2	K04392	GO:0007264,(	AT3G48040.1	ARAC8,ATRAC
PTHR33509,P	0	0	0	GO:0006950	AT4G15910.1	ATDI21,DI21
PTHR11017,P	0	0	0	GO:0007165,(	AT5G36930.2	0
PTHR11017,P	0	0	0	GO:0007165,(	AT5G36930.2	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR31016,P	0	0	0	0	AT2G30530.1	0
PTHR31992,P	0	0	0	GO:0006355,(	AT1G51700.1	ADOF1,DOF1
PTHR11472,P	0	3.6.4.13	K11273	GO:0016818,(	AT1G79890.1	0
PTHR11472,P	0	3.6.4.13	K11273	GO:0016818,(	AT1G79890.1	0
PTHR31636,P	0	0	0	0	AT1G50420.1	SCL-3,SCL3
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0

PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	0	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	0	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	0	0	0	0	AT3G14470.1	0
PTHR23155,P	0	0	0	0	AT3G14470.1	0
PTHR32227,P	0	3.2.1.39	0	GO:0005975,(	AT1G32860.1	0
PTHR32227,P	0	3.2.1.39	0	GO:0005975,(	AT1G32860.1	0
PTHR31065,P	0	0	0	0	AT2G27930.1	0
PTHR31065,P	0	0	0	0	AT2G27930.1	0
PTHR31065,P	0	0	0	0	AT2G27930.1	0
PTHR31065,P	0	0	0	0	AT2G27930.1	0
PTHR31745,P	0	0	0	0	AT1G14410.1	ATWHY1,PTA(
PTHR31745,P	0	0	0	0	AT1G14410.1	ATWHY1,PTA(
PTHR11017,P	KOG0617	0	0	GO:0007165,(	AT5G17680.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR14255,P	0	0	0	GO:0016021	AT2G25737.1	0
PTHR13140,P	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1
PTHR13140,P	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1
PTHR13140,P	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1
PTHR13140,P	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1
PTHR13140,P	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1
PTHR13140,P	0	3.6.4.1	0	GO:0005515,(	AT3G19960.1	ATM1
PTHR37076,P	0	0	0	0	0	0
PTHR37076,P	0	0	0	0	0	0
PTHR32093,P	0	0	0	0	AT3G50370.1	0
PTHR32093,P	0	0	0	0	AT3G50370.1	0
PTHR32093,P	0	0	0	0	AT3G50370.1	0
PTHR22884,P	KOG1082	2.1.1.43	K11420	GO:0005515,(	AT4G13460.1	SDG22,SET22,
PTHR22884,P	KOG1082	2.1.1.43	K11420	GO:0005515,(	AT4G13460.1	SDG22,SET22,
PTHR24015,P	0	0	0	0	AT2G03380.1	0
PTHR11252,P	0	2.7.7.8	K00962	GO:0006396,(	AT5G14580.1	0
PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,(	AT1G71830.1	ATSERK1,SERK

PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT1G71830.1	ATSERK1,SERK
PTHR24015,P	0	0	0	0	AT1G03510.1	0
PTHR24015,P	0	0	0	0	AT1G03510.1	0
PTHR23198,P	0	0	K14297	0	AT1G10390.2	0
PTHR23198,P	0	0	K14297	0	AT1G10390.2	0
PTHR12956,P	0	0	0	0	AT1G53040.1	0
PTHR22838,P	0	0	0	GO:0005515	AT5G08560.1	0
PTHR22838,P	0	0	0	GO:0005515	AT5G08560.1	0
PTHR11934,P	KOG3075	5.3.1.6	K01807	GO:0009052,	AT3G04790.1	0
PTHR31656,P	0	2.4.1.10	0	0	AT3G19430.1	0
PTHR31656,P	0	2.4.1.10	0	0	AT3G19430.1	0
PTHR24177,P	KOG4412	2.7.11.1	0	0	AT3G18670.1	0
PTHR24015,P	0	0	0	0	AT3G09060.1	0
PTHR24015,P	0	0	0	0	AT3G09060.1	0
PTHR22792,P	KOG2590	0	K18757	0	AT5G21160.3	0
PTHR27008,P	KOG1187	2.7.11.1	0	GO:0005515,	AT5G35390.1	0
PTHR31659,P	0	0	0	0	AT3G09070.1	0
PTHR31992,P	0	0	0	GO:0006355,	AT3G55370.2	OBP3
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR23084,P	0	2.7.1.68	0	0	AT4G17080.1	0
PTHR19241,P	0	3.6.3.25	0	GO:0016887,	AT1G59870.1	ABCG36,ATAB
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14470.1	0
PTHR23155,P	KOG4658	0	0	GO:0043531	AT3G14460.1	0

arabi-defline	ID	Annot_defline	IDENTIFIER
NB-ARC domain-containing disease resistance pro	Phvul.004G04	PTHR23155//I	Phvul.004G04
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G22	PTHR23244//I	Phvul.001G22
Galactose oxidase/kelch repeat superfamily protei	Phvul.007G20	PTHR23244//I	Phvul.007G20
Galactose oxidase/kelch repeat superfamily protei	Phvul.007G20	PTHR23244//I	Phvul.007G20
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:SI	Phvul.008G06
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:SI	Phvul.008G06
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:SI	Phvul.008G06
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G06	PTHR23155:SI	Phvul.008G06
transmembrane receptors;ATP binding	Phvul.002G07	PTHR11017:SI	Phvul.002G07
RAD-like 6	Phvul.001G21	PTHR24078:SI	Phvul.001G21
GATA transcription factor 26	Phvul.002G00	PTHR10071:SI	Phvul.002G00
GATA transcription factor 26	Phvul.002G00	PTHR10071:SI	Phvul.002G00
transmembrane receptors;ATP binding	Phvul.003G07	PTHR11017:SI	Phvul.003G07
0	0	0	Phvul.003G24
0	0	0	Phvul.003G24
0	0	0	Phvul.003G24
Disease resistance protein (TIR-NBS-LRR class) fam	Phvul.004G13	PTHR11017//I	Phvul.004G13
Protein with RING/U-box and TRAF-like domains	Phvul.005G02	PTHR10315//I	Phvul.005G02
Protein with RING/U-box and TRAF-like domains	Phvul.005G02	PTHR10315//I	Phvul.005G02
Protein with RING/U-box and TRAF-like domains	Phvul.005G02	PTHR10315//I	Phvul.005G02
squamosa promoter binding protein-like 1	Phvul.007G21	PTHR31251:SI	Phvul.007G21
squamosa promoter binding protein-like 1	Phvul.007G21	PTHR31251:SI	Phvul.007G21
non-intrinsic ABC protein 11	Phvul.008G05	PTHR24220:SI	Phvul.008G05
0	Phvul.008G28	PTHR21716 -	Phvul.008G28
0	Phvul.008G28	PTHR21716 -	Phvul.008G28
NB-ARC domain-containing disease resistance pro	Phvul.010G06	PTHR23155//I	Phvul.010G06
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.010G13	PTHR11017//I	Phvul.010G13
Transducin/WD40 repeat-like superfamily protein	Phvul.011G14	PTHR14221:SI	Phvul.011G14
Transducin/WD40 repeat-like superfamily protein	Phvul.011G14	PTHR14221:SI	Phvul.011G14
Transducin/WD40 repeat-like superfamily protein	Phvul.011G14	PTHR14221:SI	Phvul.011G14
Transducin/WD40 repeat-like superfamily protein	Phvul.011G14	PTHR14221:SI	Phvul.011G14
Transducin/WD40 repeat-like superfamily protein	Phvul.011G14	PTHR14221:SI	Phvul.011G14
Transducin/WD40 repeat-like superfamily protein	Phvul.011G14	PTHR14221:SI	Phvul.011G14
Transducin/WD40 repeat-like superfamily protein	Phvul.011G14	PTHR14221:SI	Phvul.011G14
NB-ARC domain-containing disease resistance pro	Phvul.011G16	PTHR23155//I	Phvul.011G16
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.001G12	PF07725//PF1	Phvul.001G12
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
Double Clp-N motif-containing P-loop nucleoside t	Phvul.001G24	PTHR11638:SI	Phvul.001G24
Double Clp-N motif-containing P-loop nucleoside t	Phvul.001G24	PTHR11638:SI	Phvul.001G24
Plant protein of unknown function (DUF828) with	Phvul.002G05	PF05703 - Au	Phvul.002G05
Plant protein of unknown function (DUF828) with	Phvul.002G05	PF05703 - Au	Phvul.002G05

cytochrome P450, family 707, subfamily A, polype	Phvul.002G12	PTHR24286:S	Phvul.002G12
0	0	0	Phvul.002G18
RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.002G26	K14396 - poly	Phvul.002G26
RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.002G26	K14396 - poly	Phvul.002G26
Uncharacterised protein family (UPF0497)	Phvul.003G10	PTHR11615//	Phvul.003G10
Uncharacterised protein family (UPF0497)	Phvul.003G10	PTHR11615//	Phvul.003G10
quinolinate synthase	Phvul.003G20	K03517 - quin	Phvul.003G20
quinolinate synthase	Phvul.003G20	K03517 - quin	Phvul.003G20
high mobility group	Phvul.004G02	K09272 - stru	Phvul.004G02
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.004G14	PF05729//PF1	Phvul.004G14
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.004G14	PF05729//PF1	Phvul.004G14
urophorphyrin methylase 1	Phvul.005G03	PTHR21091:S	Phvul.005G03
urophorphyrin methylase 1	Phvul.005G03	PTHR21091:S	Phvul.005G03
NB-ARC domain-containing disease resistance pro	Phvul.005G08	PTHR23155:S	Phvul.005G08
NB-ARC domain-containing disease resistance pro	Phvul.005G08	PTHR23155:S	Phvul.005G08
Malectin/receptor-like protein kinase family prote	Phvul.006G10	PTHR27003:S	Phvul.006G10
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) fam	Phvul.008G07	PTHR23155//	Phvul.008G07
las1-like family protein	Phvul.008G20	K16912 - ribo	Phvul.008G20
potassium transporter 1	Phvul.008G25	PTHR30540:S	Phvul.008G25
potassium transporter 1	Phvul.008G25	PTHR30540:S	Phvul.008G25
potassium transporter 1	Phvul.008G25	PTHR30540:S	Phvul.008G25
potassium transporter 1	Phvul.008G25	PTHR30540:S	Phvul.008G25
Disease resistance protein (TIR-NBS-LRR class) fa	Phvul.010G13	PF00931//PF	Phvul.010G13
Disease resistance protein (TIR-NBS-LRR class) fa	Phvul.010G13	PF07725 - Leu	Phvul.010G13
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.010G13	PTHR11017//	Phvul.010G13
UDP-Glycosyltransferase superfamily protein	Phvul.010G15	PTHR12526//	Phvul.010G15
UDP-Glycosyltransferase superfamily protein	Phvul.010G15	PTHR12526//	Phvul.010G15
UDP-Glycosyltransferase superfamily protein	Phvul.010G15	PTHR12526//	Phvul.010G15
UDP-Glycosyltransferase superfamily protein	Phvul.010G15	PTHR12526//	Phvul.010G15
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.011G14	PF00931//PF	Phvul.011G14
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.011G14	PF00931//PF1	Phvul.011G14
NB-ARC domain-containing disease resistance pro	Phvul.011G15	PTHR23155//	Phvul.011G15
NB-ARC domain-containing disease resistance pro	Phvul.011G18	PTHR23155//	Phvul.011G18
NB-ARC domain-containing disease resistance pro	Phvul.011G18	PTHR23155//	Phvul.011G18
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PF00931//PF1	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PF00931//PF1	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PF00931//PF1	Phvul.011G19
LRR and NB-ARC domains-containing disease resis	Phvul.011G19	PTHR23155//	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//	Phvul.011G19
LRR and NB-ARC domains-containing disease resis	Phvul.011G19	PTHR23155//	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//	Phvul.011G19

LRR and NB-ARC domains-containing disease resis	Phvul.011G19	PTHR23155//	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PF00931//PF1	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//	Phvul.011G20
Zinc-binding alcohol dehydrogenase family protei	Phvul.L00233	PTHR11695:S	Phvul.L00233
Zinc-binding alcohol dehydrogenase family protei	Phvul.L00233	PTHR11695:S	Phvul.L00233
Zinc-binding alcohol dehydrogenase family protei	Phvul.L00233	PTHR11695:S	Phvul.L00233
Zinc-binding alcohol dehydrogenase family protei	Phvul.L00233	PTHR11695:S	Phvul.L00233
Phospholipid/glycerol acyltransferase family prot	Phvul.001G01	K13510 - lyso	Phvul.001G01
Phospholipid/glycerol acyltransferase family prot	Phvul.001G01	K13510 - lyso	Phvul.001G01
Phospholipid/glycerol acyltransferase family prot	Phvul.001G01	K13510 - lyso	Phvul.001G01
Phospholipid/glycerol acyltransferase family prot	Phvul.001G01	K13510 - lyso	Phvul.001G01
basic helix-loop-helix (bHLH) DNA-binding superfa	Phvul.001G08	PTHR31945:S	Phvul.001G08
basic helix-loop-helix (bHLH) DNA-binding superfa	Phvul.001G08	PTHR31945:S	Phvul.001G08
expansin A4	Phvul.001G23	PTHR31867:S	Phvul.001G23
expansin A4	Phvul.001G23	PTHR31867:S	Phvul.001G23
PLATZ transcription factor family protein	Phvul.002G04	PF04640 - PLA	Phvul.002G04
PLATZ transcription factor family protein	Phvul.002G04	PF04640 - PLA	Phvul.002G04
PLATZ transcription factor family protein	Phvul.002G04	PF04640 - PLA	Phvul.002G04
PLATZ transcription factor family protein	Phvul.002G04	PF04640 - PLA	Phvul.002G04
alpha/beta-Hydrolases superfamily protein	Phvul.002G29	PTHR31479:S	Phvul.002G29
extra-large G-protein 1	Phvul.003G01	PTHR10218:S	Phvul.003G01
extra-large G-protein 1	Phvul.003G01	PTHR10218:S	Phvul.003G01
plastid transcriptionally active 2	Phvul.003G19	PF01535//PF1	Phvul.003G19
plastid transcriptionally active 2	Phvul.003G19	PF01535//PF1	Phvul.003G19
C2H2-like zinc finger protein	Phvul.003G25	PTHR10593:S	Phvul.003G25
C2H2-like zinc finger protein	Phvul.003G25	PTHR10593:S	Phvul.003G25
autophagy 2	Phvul.003G29	K17906 - auto	Phvul.003G29
autophagy 2	Phvul.003G29	K17906 - auto	Phvul.003G29
autophagy 2	Phvul.003G29	K17906 - auto	Phvul.003G29
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03
purple acid phosphatase 23	Phvul.004G03	3.1.3.2//3.1.3	Phvul.004G03

NB-ARC domain-containing disease resistance pro	Phvul.004G04	PTHR23155//I	Phvul.004G04
NB-ARC domain-containing disease resistance pro	Phvul.004G04	PTHR23155//I	Phvul.004G04
septum site-determining protein (MIND)	Phvul.004G10	K03609 - sept	Phvul.004G10
septum site-determining protein (MIND)	Phvul.004G10	K03609 - sept	Phvul.004G10
carboxyesterase 18	Phvul.004G13	PTHR23024//I	Phvul.004G13
Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.005G16	PF01535//PF1	Phvul.005G16
Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.005G16	PF01535//PF1	Phvul.005G16
NB-ARC domain-containing disease resistance pro	Phvul.006G06	PTHR23155//I	Phvul.006G06
expansin A13	Phvul.006G08	PTHR31867:SI	Phvul.006G08
0	0	0	Phvul.006G14
O-methyltransferase family protein	Phvul.006G18	PTHR11746//I	Phvul.006G18
O-methyltransferase family protein	Phvul.006G18	PTHR11746//I	Phvul.006G18
0	0	0	Phvul.007G02
P-loop containing nucleoside triphosphate hydrol	Phvul.007G09	3.6.3.16 - Ars	Phvul.007G09
Leucine-rich repeat protein kinase family protein	Phvul.008G15	PF07714//PF0	Phvul.008G15
sterol methyltransferase 2	Phvul.009G02	2.1.1.142 - Cy	Phvul.009G02
sterol methyltransferase 2	Phvul.009G02	2.1.1.142 - Cy	Phvul.009G02
abscisic acid responsive elements-binding factor 2	Phvul.009G06	PTHR22952//I	Phvul.009G06
abscisic acid responsive elements-binding factor 2	Phvul.009G06	PTHR22952//I	Phvul.009G06
abscisic acid responsive elements-binding factor 2	Phvul.009G06	PTHR22952//I	Phvul.009G06
abscisic acid responsive elements-binding factor 2	Phvul.009G06	PTHR22952//I	Phvul.009G06
Pentatricopeptide repeat (PPR) superfamily protei	Phvul.009G21	K17964 - leuci	Phvul.009G21
TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22	PF14416 - PM	Phvul.009G22
TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22	PF14416 - PM	Phvul.009G22
TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22	PF14416 - PM	Phvul.009G22
TRICHOME BIREFRINGENCE-LIKE 16	Phvul.009G22	PF14416 - PM	Phvul.009G22
NB-ARC domain-containing disease resistance pro	Phvul.009G23	PTHR23155:SI	Phvul.009G23
NB-ARC domain-containing disease resistance pro	Phvul.009G23	PTHR23155:SI	Phvul.009G23
NB-ARC domain-containing disease resistance pro	Phvul.009G23	PTHR23155:SI	Phvul.009G23
Disease resistance protein (TIR-NBS-LRR class) fam	Phvul.010G00	PF00931//PF1	Phvul.010G00
Disease resistance protein (TIR-NBS-LRR class) fam	Phvul.010G00	PF00931//PF1	Phvul.010G00
Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.010G05	PF13041 - PPF	Phvul.010G05
Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.010G05	PF13041 - PPF	Phvul.010G05
LRR and NB-ARC domains-containing disease resis	Phvul.010G06	PTHR23155//I	Phvul.010G06
fatty alcohol oxidase 3	Phvul.010G07	K17756 - long	Phvul.010G07
LETM1-like protein	Phvul.010G14	PTHR14009//I	Phvul.010G14
LETM1-like protein	Phvul.010G14	PTHR14009//I	Phvul.010G14
LETM1-like protein	Phvul.010G14	PTHR14009//I	Phvul.010G14
LETM1-like protein	Phvul.010G14	PTHR14009//I	Phvul.010G14
LETM1-like protein	Phvul.010G14	PTHR14009//I	Phvul.010G14
LETM1-like protein	Phvul.010G14	PTHR14009//I	Phvul.010G14
NB-ARC domain-containing disease resistance pro	Phvul.011G01	PTHR23155:SI	Phvul.011G01
NB-ARC domain-containing disease resistance pro	Phvul.011G01	PTHR23155:SI	Phvul.011G01
NB-ARC domain-containing disease resistance pro	Phvul.011G01	PTHR23155:SI	Phvul.011G01
P-loop containing nucleoside triphosphate hydrol	Phvul.011G08	PTHR33477:SI	Phvul.011G08
P-loop containing nucleoside triphosphate hydrol	Phvul.011G08	PTHR33477:SI	Phvul.011G08

P-loop containing nucleoside triphosphate hydrol	Phvul.011G08	PTHR33477:SI	Phvul.011G08
NB-ARC domain-containing disease resistance pro	Phvul.011G14	PTHR23155//I	Phvul.011G14
NB-ARC domain-containing disease resistance pro	Phvul.011G14	PTHR23155//I	Phvul.011G14
NB-ARC domain-containing disease resistance pro	Phvul.011G18	PTHR23155//I	Phvul.011G18
MLP-like protein 43	Phvul.011G18	PF00407 - Pat	Phvul.011G18
MLP-like protein 43	Phvul.011G18	PF00407 - Pat	Phvul.011G18
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PF13191//PF1	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//I	Phvul.011G19
LRR and NB-ARC domains-containing disease resis	Phvul.011G19	PTHR23155//I	Phvul.011G19
LRR and NB-ARC domains-containing disease resis	Phvul.011G19	PTHR23155//I	Phvul.011G19
LRR and NB-ARC domains-containing disease resis	Phvul.011G19	PTHR23155//I	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//I	Phvul.011G19
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PF00931//PF1	Phvul.011G19
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//I	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//I	Phvul.011G20
Galactose oxidase/kelch repeat superfamily protei	Phvul.001G02	PF00646 - F-b	Phvul.001G02
Glycosyl hydrolases family 31 protein	Phvul.001G12	PTHR22762//I	Phvul.001G12
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
NB-ARC domain-containing disease resistance pro	Phvul.001G13	PTHR23155//I	Phvul.001G13
Leucine-rich repeat protein kinase family protein	Phvul.001G18	PF00069//PFC	Phvul.001G18
Leucine-rich repeat protein kinase family protein	Phvul.001G18	PF00069//PFC	Phvul.001G18
Ca2+ activated outward rectifying K+ channel 5	Phvul.001G21	PTHR11003:SI	Phvul.001G21
Pectin lyase-like superfamily protein	Phvul.002G06	PTHR31375:SI	Phvul.002G06
Pectin lyase-like superfamily protein	Phvul.002G06	PTHR31375:SI	Phvul.002G06
phospholipase D delta	Phvul.002G10	PTHR18896:SI	Phvul.002G10
phospholipase D delta	Phvul.002G10	PTHR18896:SI	Phvul.002G10
XS domain-containing protein / XS zinc finger dom	Phvul.002G27	PTHR21596:SI	Phvul.002G27
	0	0	0 Phvul.003G05
	0	0	0 Phvul.003G05
cytochrome P450, family 77, subfamily B, polypep	Phvul.003G07	PTHR24298:SI	Phvul.003G07
cytochrome P450, family 77, subfamily B, polypep	Phvul.003G07	PTHR24298:SI	Phvul.003G07
Heavy metal transport/detoxification superfamily	Phvul.003G10	PTHR22814//I	Phvul.003G10
Heavy metal transport/detoxification superfamily	Phvul.003G10	PTHR22814//I	Phvul.003G10
homolog of yeast FIP1 [V]	Phvul.003G15	PF05182 - Fip	Phvul.003G15
cysteine-rich RLK (RECEPTOR-like protein kinase) 1	Phvul.003G15	PF00704//PFC	Phvul.003G15
cysteine-rich RLK (RECEPTOR-like protein kinase) 1	Phvul.003G15	PF00704//PFC	Phvul.003G15

Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.003G16	PF01535//PF1	Phvul.003G16
RNA-metabolising metallo-beta-lactamase family	Phvul.003G20	3.5.2.6 - Beta-	Phvul.003G20
RNA-metabolising metallo-beta-lactamase family	Phvul.003G20	3.5.2.6 - Beta-	Phvul.003G20
ROP binding protein kinases 1	Phvul.003G28	PTHR27001:S	Phvul.003G28
ROP binding protein kinases 1	Phvul.003G28	PTHR27001:S	Phvul.003G28
myb domain protein 118	Phvul.004G01	PTHR10641:S	Phvul.004G01
Regulator of chromosome condensation (RCC1) fa	Phvul.004G06	PTHR22870//	Phvul.004G06
Regulator of chromosome condensation (RCC1) fa	Phvul.004G06	PTHR22870//	Phvul.004G06
Pentatricopeptide repeat (PPR) superfamily protei	Phvul.004G13	PTHR24015:S	Phvul.004G13
Pentatricopeptide repeat (PPR) superfamily protei	Phvul.004G13	PTHR24015:S	Phvul.004G13
LRR and NB-ARC domains-containing disease resis	Phvul.005G03	PTHR23155//	Phvul.005G03
low-molecular-weight cysteine-rich 68	Phvul.005G07	PF00304 - Ga	Phvul.005G07
low-molecular-weight cysteine-rich 68	Phvul.005G07	PF00304 - Ga	Phvul.005G07
RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.006G05	K14398 - clea	Phvul.006G05
RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.006G05	K14398 - clea	Phvul.006G05
RNA-binding (RRM/RBD/RNP motifs) family protei	Phvul.006G05	K14398 - clea	Phvul.006G05
sirtuin 1	Phvul.006G05	K11416 - mon	Phvul.006G05
NB-ARC domain-containing disease resistance pro	Phvul.006G06	PTHR23155//	Phvul.006G06
NB-ARC domain-containing disease resistance pro	Phvul.006G06	PTHR23155//	Phvul.006G06
LRR and NB-ARC domains-containing disease resis	Phvul.007G08	PTHR23155//	Phvul.007G08
LRR and NB-ARC domains-containing disease resis	Phvul.007G08	PTHR23155//	Phvul.007G08
NB-ARC domain-containing disease resistance pro	Phvul.008G01	PTHR23155:S	Phvul.008G01
NB-ARC domain-containing disease resistance pro	Phvul.008G01	PTHR23155:S	Phvul.008G01
NB-ARC domain-containing disease resistance pro	Phvul.008G07	PTHR23155//	Phvul.008G07
NB-ARC domain-containing disease resistance pro	Phvul.008G07	PTHR23155//	Phvul.008G07
0	0	0	Phvul.008G16
0	0	0	Phvul.008G16
nodulin MtN21 /EamA-like transporter family prot	Phvul.009G03	PF00892 - Ea	Phvul.009G03
AGC (cAMP-dependent, cGMP-dependent and pr	Phvul.009G07	PTHR24356:S	Phvul.009G07
AGC (cAMP-dependent, cGMP-dependent and pr	Phvul.009G07	PTHR24356:S	Phvul.009G07
RHO-related protein from plants 10	Phvul.009G18	PTHR24072:S	Phvul.009G18
RHO-related protein from plants 10	Phvul.009G18	PTHR24072:S	Phvul.009G18
RHO-related protein from plants 10	Phvul.009G18	PTHR24072:S	Phvul.009G18
RHO-related protein from plants 10	Phvul.009G18	PTHR24072:S	Phvul.009G18
drought-induced 21	Phvul.009G24	PTHR33509:S	Phvul.009G24
Disease resistance protein (TIR-NBS-LRR class) fa	Phvul.010G02	PF00931//PF1	Phvul.010G02
Disease resistance protein (TIR-NBS-LRR class) fa	Phvul.010G02	PF00931//PF1	Phvul.010G02
LRR and NB-ARC domains-containing disease resis	Phvul.010G06	PTHR23155//	Phvul.010G06
0	0	0	Phvul.010G10
DOF zinc finger protein 1	Phvul.010G14	PF02701 - Dof	Phvul.010G14
RAD3-like DNA-binding helicase protein	Phvul.010G14	K11273 - chro	Phvul.010G14
RAD3-like DNA-binding helicase protein	Phvul.010G14	K11273 - chro	Phvul.010G14
scarecrow-like 3	Phvul.011G01	PF03514 - GR	Phvul.011G01
NB-ARC domain-containing disease resistance pro	Phvul.011G18	PTHR23155//	Phvul.011G18
NB-ARC domain-containing disease resistance pro	Phvul.011G18	PTHR23155//	Phvul.011G18
NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//	Phvul.011G19

NB-ARC domain-containing disease resistance pro	Phvul.011G19	PTHR23155//I	Phvul.011G19
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//I	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//I	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//I	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//I	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//I	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//I	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PF13191 - AA/	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PF13191 - AA/	Phvul.011G20
Glycosyl hydrolase superfamily protein	Phvul.L00450(	PTHR32227:SI	Phvul.L00450(
Glycosyl hydrolase superfamily protein	Phvul.L00450(	PTHR32227:SI	Phvul.L00450(
PLATZ transcription factor family protein	Phvul.001G18	PTHR31065:SI	Phvul.001G18
PLATZ transcription factor family protein	Phvul.001G18	PTHR31065:SI	Phvul.001G18
PLATZ transcription factor family protein	Phvul.001G18	PTHR31065:SI	Phvul.001G18
PLATZ transcription factor family protein	Phvul.001G18	PTHR31065:SI	Phvul.001G18
ssDNA-binding transcriptional regulator	Phvul.002G08	PTHR31745:SI	Phvul.002G08
ssDNA-binding transcriptional regulator	Phvul.002G08	PTHR31745:SI	Phvul.002G08
disease resistance protein (TIR-NBS-LRR class), pu	Phvul.002G17	PF00931//PF1	Phvul.002G17
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
Sulfite exporter TauE/SafE family protein	Phvul.002G24	PTHR14255//I	Phvul.002G24
myosin 1	Phvul.003G00	PTHR13140:SI	Phvul.003G00
myosin 1	Phvul.003G00	PTHR13140:SI	Phvul.003G00
myosin 1	Phvul.003G00	PTHR13140:SI	Phvul.003G00
myosin 1	Phvul.003G00	PTHR13140:SI	Phvul.003G00
myosin 1	Phvul.003G00	PTHR13140:SI	Phvul.003G00
myosin 1	Phvul.003G00	PTHR13140:SI	Phvul.003G00
0	0	0	Phvul.003G05
0	0	0	Phvul.003G05
0	0	0	Phvul.003G24
0	0	0	Phvul.003G24
0	0	0	Phvul.003G24
SU(VAR)3-9 homolog 9	Phvul.003G28	PTHR22884:SI	Phvul.003G28
SU(VAR)3-9 homolog 9	Phvul.003G28	PTHR22884:SI	Phvul.003G28
Pentatricopeptide repeat (PPR) superfamily protei	Phvul.003G28	PF01535//PF1	Phvul.003G28
polyribonucleotide nucleotidyltransferase, putativ	Phvul.004G01	2.7.7.8 - Polyr	Phvul.004G01
somatic embryogenesis receptor-like kinase 1	Phvul.004G08	K13418 - som	Phvul.004G08

somatic embryogenesis receptor-like kinase 1	Phvul.004G08	K13418 - som	Phvul.004G08
Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.005G04	PF01535//PF1	Phvul.005G04
Tetratricopeptide repeat (TPR)-like superfamily pr	Phvul.005G04	PF01535//PF1	Phvul.005G04
Nucleoporin autopeptidase	Phvul.005G06	K14297 - nucl	Phvul.005G06
Nucleoporin autopeptidase	Phvul.005G06	K14297 - nucl	Phvul.005G06
Protein of unknown function (DUF616)	Phvul.005G07	PTHR12956//	Phvul.005G07
transducin family protein / WD-40 repeat family p	Phvul.006G02	PTHR22838:S	Phvul.006G02
transducin family protein / WD-40 repeat family p	Phvul.006G02	PTHR22838:S	Phvul.006G02
Ribose 5-phosphate isomerase, type A protein	Phvul.006G10	PTHR11934:S	Phvul.006G10
late embryogenesis abundant protein-related / LE	Phvul.006G12	2.4.1.10 - Lev	Phvul.006G12
late embryogenesis abundant protein-related / LE	Phvul.006G12	2.4.1.10 - Lev	Phvul.006G12
Ankyrin repeat family protein	Phvul.006G17	PF12796//PF1	Phvul.006G17
Pentatricopeptide repeat (PPR) superfamily protei	Phvul.008G10	PF01535//PF1	Phvul.008G10
Pentatricopeptide repeat (PPR) superfamily protei	Phvul.008G10	PF01535//PF1	Phvul.008G10
LA RNA-binding protein	Phvul.008G20	PTHR22792:S	Phvul.008G20
Leucine-rich repeat protein kinase family protein	Phvul.009G10	PF07714//PF	Phvul.009G10
Protein of unknown function (DUF740)	Phvul.010G00	PF05340 - Pro	Phvul.010G00
OBF-binding protein 3	Phvul.010G01	PF02701 - Dof	Phvul.010G01
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
Histone H3 K4-specific methyltransferase SET7/9 f	Phvul.010G04	PTHR23084:S	Phvul.010G04
ABC-2 and Plant PDR ABC-type transporter family	Phvul.010G14	PTHR19241:S	Phvul.010G14
NB-ARC domain-containing disease resistance pro	Phvul.011G18	PTHR23155//	Phvul.011G18
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//	Phvul.011G20
NB-ARC domain-containing disease resistance pro	Phvul.011G20	PTHR23155//	Phvul.011G20
LRR and NB-ARC domains-containing disease resis	Phvul.011G20	PTHR23155//	Phvul.011G20

NAME	DESCRIPTION
not assigned.a	(original description: pacid=37163660 transcript=Phvul.004G048000.1 locus=Phvul.0
not assigned.a	(original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.0
not assigned.a	(original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.0
not assigned.a	(original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.0
not assigned.a	(original description: pacid=37168996 transcript=Phvul.001G224800.2 locus=Phvul.0
not assigned.a	(original description: pacid=37165645 transcript=Phvul.007G201700.1 locus=Phvul.0
not assigned.a	(original description: pacid=37165645 transcript=Phvul.007G201700.1 locus=Phvul.0
not assigned.a	(original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37160667 transcript=Phvul.008G061300.2 locus=Phvul.0
External stimu	effector receptor (NLR) (original description: pacid=37177951 transcript=Phvul.002G
RNA biosynth	transcription factor (MYB-related) (original description: pacid=37168368 transcript=P
RNA biosynth	transcription factor (GATA) (original description: pacid=37177588 transcript=Phvul.0
RNA biosynth	transcription factor (GATA) (original description: pacid=37177588 transcript=Phvul.0
External stimu	effector receptor (NLR) (original description: pacid=37146968 transcript=Phvul.003G
not assigned.r	no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
not assigned.r	no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
not assigned.r	no hits & (original description: pacid=37145696 transcript=Phvul.003G244225.3 locu
External stimu	effector receptor (NLR) (original description: pacid=37163438 transcript=Phvul.004G
Protein home	SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029
Protein home	SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029
Protein home	SINA-class E3 ligase (original description: pacid=37154353 transcript=Phvul.005G029
RNA biosynth	transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007
RNA biosynth	transcription factor (SBP) (original description: pacid=37166230 transcript=Phvul.007
Lipid metaboli	ATPase component TGD3 of TGD lipid importer complex (original description: pacid=
not assigned.r	no hits & (original description: pacid=37157769 transcript=Phvul.008G280900.1 locu
not assigned.r	no hits & (original description: pacid=37157769 transcript=Phvul.008G280900.1 locu
not assigned.a	(original description: pacid=37142899 transcript=Phvul.010G064700.1 locus=Phvul.0
External stimu	effector receptor (NLR) (original description: pacid=37142699 transcript=Phvul.010G
not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
not assigned.r	no hits & (original description: pacid=37154984 transcript=Phvul.011G149100.7 locu
not assigned.a	(original description: pacid=37156909 transcript=Phvul.011G166100.1 locus=Phvul.0
not assigned.a	(original description: pacid=37171124 transcript=Phvul.001G128200.2 locus=Phvul.0
not assigned.a	(original description: pacid=37169603 transcript=Phvul.001G134000.1 locus=Phvul.0
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Phytohormon	SMXL strigolactone signal transducer (original description: pacid=37170890 transcrip
Phytohormon	SMXL strigolactone signal transducer (original description: pacid=37170890 transcrip
not assigned.r	no hits & (original description: pacid=37177208 transcript=Phvul.002G057300.2 locu
not assigned.r	no hits & (original description: pacid=37177208 transcript=Phvul.002G057300.2 locu

Phytohormon	abscisic acid hydroxylase (original description: pacid=37176949 transcript=Phvul.002
not assigned.n	no hits & (original description: pacid=37175068 transcript=Phvul.002G187600.1 locu
RNA processin	poly(A) RNA polymerase regulatory protein (original description: pacid=37177379 tra
RNA processin	poly(A) RNA polymerase regulatory protein (original description: pacid=37177379 tra
not assigned.a	(original description: pacid=37147525 transcript=Phvul.003G101200.1 locus=Phvul.0
not assigned.a	(original description: pacid=37147525 transcript=Phvul.003G101200.1 locus=Phvul.0
Coenzyme me	component SUF-E2/-E3 of plastidial SUF system assembly phase (original description
Coenzyme me	component SUF-E2/-E3 of plastidial SUF system assembly phase (original description
Chromatin org	component SSRP of FACT histone chaperone complex (original description: pacid=37
External stimu	effector receptor (NLR) (original description: pacid=37163195 transcript=Phvul.004G
External stimu	effector receptor (NLR) (original description: pacid=37163195 transcript=Phvul.004G
Coenzyme me	uroporphyrinogen III methyltransferase (original description: pacid=37152438 transc
Coenzyme me	uroporphyrinogen III methyltransferase (original description: pacid=37152438 transc
not assigned.a	(original description: pacid=37153472 transcript=Phvul.005G087100.1 locus=Phvul.0
not assigned.a	(original description: pacid=37153472 transcript=Phvul.005G087100.1 locus=Phvul.0
Protein modif	protein kinase (CrlRLK1) (original description: pacid=37173044 transcript=Phvul.006
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
Protein biosyn	LAS1 pre-rRNA cleavage factor involved in ITS2 rRNA removal (original description: pa
Solute transpo	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
Solute transpo	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
Solute transpo	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
Solute transpo	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37159589 tr
External stimu	effector receptor (NLR) (original description: pacid=37142428 transcript=Phvul.010G
not assigned.a	(original description: pacid=37143313 transcript=Phvul.010G132333.3 locus=Phvul.0
External stimu	effector receptor (NLR) (original description: pacid=37143628 transcript=Phvul.010G
not assigned.n	no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
not assigned.n	no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
not assigned.n	no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
not assigned.n	no hits & (original description: pacid=37142610 transcript=Phvul.010G151400.6 locu
External stimu	effector receptor (NLR) (original description: pacid=37154763 transcript=Phvul.011G
External stimu	effector receptor (NLR) (original description: pacid=37156164 transcript=Phvul.011G
not assigned.a	(original description: pacid=37157447 transcript=Phvul.011G151300.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37157092 transcript=Phvul.011G192400.1 locus=Phvul.0
not assigned.a	(original description: pacid=37155577 transcript=Phvul.011G192600.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37155134 transcript=Phvul.011G193500.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37156343 transcript=Phvul.011G195200.1 locus=Phvul.0

not assigned.a	(original description: pacid=37157211 transcript=Phvul.011G195400.2 locus=Phvul.0
not assigned.a	(original description: pacid=37155487 transcript=Phvul.011G195500.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37157155 transcript=Phvul.011G196066.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37155566 transcript=Phvul.011G202300.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37156337 transcript=Phvul.011G203100.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002
not assigned.a	(original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002
not assigned.a	(original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002
not assigned.a	(original description: pacid=37157542 transcript=Phvul.L002337.2 locus=Phvul.L002
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not assigned.a	(original description: pacid=37169910 transcript=Phvul.001G015600.3 locus=Phvul.0
not assigned.a	(original description: pacid=37169910 transcript=Phvul.001G015600.3 locus=Phvul.0
External stimu	transcription factor (ICE1|2) (original description: pacid=37167713 transcript=Phvul.0
External stimu	transcription factor (ICE1|2) (original description: pacid=37167713 transcript=Phvul.0
Cell wall organ	alpha-class expansin (original description: pacid=37168526 transcript=Phvul.001G23
Cell wall organ	alpha-class expansin (original description: pacid=37168526 transcript=Phvul.001G23
RNA biosynthe	transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
RNA biosynthe	transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
RNA biosynthe	transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
RNA biosynthe	transcription factor (PLATZ) (original description: pacid=37175648 transcript=Phvul.0
not assigned.a	(original description: pacid=37177875 transcript=Phvul.002G298800.1 locus=Phvul.0
External stimu	G-alpha component XLG of non-canonical heterotrimeric G-protein complex (original
External stimu	G-alpha component XLG of non-canonical heterotrimeric G-protein complex (original
RNA biosynthe	PAP2/TAC2 cofactor of plastid-encoded RNA polymerase (original description: pacid=
RNA biosynthe	PAP2/TAC2 cofactor of plastid-encoded RNA polymerase (original description: pacid=
RNA biosynthe	C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript
RNA biosynthe	C2H2 zinc finger transcription factor (original description: pacid=37145501 transcript
Protein homeo	component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origin
Protein homeo	component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origin
Protein homeo	component ATG2 of autophagosome ATG9-2-18 membrane shuttling complex (origin
not assigned.a	(original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.0
not assigned.a	(original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.0
not assigned.a	(original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.0
not assigned.a	(original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.0
not assigned.a	(original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.0
not assigned.a	(original description: pacid=37163670 transcript=Phvul.004G032300.4 locus=Phvul.0
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Cell cycle orga	MinD plastid division FtsZ assembly factor (original description: pacid=37162532 tran
Cell cycle orga	MinD plastid division FtsZ assembly factor (original description: pacid=37162532 tran
not assigned.a	(original description: pacid=37162837 transcript=Phvul.004G133100.1 locus=Phvul.0
not assigned.a	(original description: pacid=37154568 transcript=Phvul.005G165800.1 locus=Phvul.0
not assigned.a	(original description: pacid=37154568 transcript=Phvul.005G165800.1 locus=Phvul.0
not assigned.a	(original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.0
Cell wall orga	alpha-class expansin (original description: pacid=37173891 transcript=Phvul.006G08
not assigned.r	no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
Enzyme classi	Trans-resveratrol di-O-methyltransferase OS=Vitis vinifera (sp|b6vjs4|romt_vitvi : 34
Enzyme classi	Trans-resveratrol di-O-methyltransferase OS=Vitis vinifera (sp|b6vjs4|romt_vitvi : 34
not assigned.r	no hits & (original description: pacid=37167355 transcript=Phvul.007G027400.1 locu
Enzyme classi	ATPase ARSA1 OS=Chlamydomonas reinhardtii (sp|a8jgb0|asna1_chlre : 369.0) & En
Protein modif	protein kinase (LRR-III) (original description: pacid=37159143 transcript=Phvul.008G
Lipid metaboli	sterol C-24 methyltransferase (original description: pacid=37149363 transcript=Phvu
Lipid metaboli	sterol C-24 methyltransferase (original description: pacid=37149363 transcript=Phvu
RNA biosynth	transcription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
RNA biosynth	transcription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
RNA biosynth	transcription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
RNA biosynth	transcription factor (bZIP) (original description: pacid=37149873 transcript=Phvul.00
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not assigned.a	(original description: pacid=37149744 transcript=Phvul.009G226300.2 locus=Phvul.0
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not assigned.r	no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
not assigned.r	no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
not assigned.r	no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
not assigned.r	no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
not assigned.r	no hits & (original description: pacid=37143904 transcript=Phvul.010G146900.7 locu
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not assigned.	(original description: pacid=37155164 transcript=Phvul.011G191600.1 locus=Phvul.
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not assigned.	(original description: pacid=37155563 transcript=Phvul.011G198400.1 locus=Phvul.
not assigned.	(original description: pacid=37154846 transcript=Phvul.011G201000.1 locus=Phvul.
not assigned.	(original description: pacid=37156971 transcript=Phvul.011G201101.1 locus=Phvul.
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not assigned.	(original description: pacid=37171258 transcript=Phvul.001G132516.1 locus=Phvul.
not assigned.	(original description: pacid=37169452 transcript=Phvul.001G132701.1 locus=Phvul.
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not assigned.	(original description: pacid=37170073 transcript=Phvul.001G132800.1 locus=Phvul.
not assigned.	(original description: pacid=37170073 transcript=Phvul.001G132800.1 locus=Phvul.
not assigned.	(original description: pacid=37167899 transcript=Phvul.001G132864.1 locus=Phvul.
not assigned.	(original description: pacid=37167899 transcript=Phvul.001G132864.1 locus=Phvul.
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not assigned.	(original description: pacid=37168771 transcript=Phvul.001G133100.1 locus=Phvul.
not assigned.	(original description: pacid=37168444 transcript=Phvul.001G133101.1 locus=Phvul.
not assigned.	(original description: pacid=37168444 transcript=Phvul.001G133101.1 locus=Phvul.
Protein modif	protein kinase (LRR-III) (original description: pacid=37171243 transcript=Phvul.001G
Protein modif	protein kinase (LRR-III) (original description: pacid=37171243 transcript=Phvul.001G
Solute transp	voltage-gated potassium cation channel (TPK/KCO) (original description: pacid=3717
Cell wall orga	polygalacturonase (PGX1) (original description: pacid=37177802 transcript=Phvul.00
Cell wall orga	polygalacturonase (PGX1) (original description: pacid=37177802 transcript=Phvul.00
Lipid metaboli	phospholipase D (PLD-delta) (original description: pacid=37175497 transcript=Phvul.
Lipid metaboli	phospholipase D (PLD-delta) (original description: pacid=37175497 transcript=Phvul.
Chromatin org	SGS3 stabilization factor of DNA methylation pathway (original description: pacid=37
not assigned.	no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 loc
not assigned.	no hits & (original description: pacid=37146447 transcript=Phvul.003G050200.2 loc
Enzyme classi	Cytochrome P450 77A1 (Fragment) OS=Solanum melongena (sp|p37123|c77a1_sol
Enzyme classi	Cytochrome P450 77A1 (Fragment) OS=Solanum melongena (sp|p37123|c77a1_sol
not assigned.	(original description: pacid=37144721 transcript=Phvul.003G104900.1 locus=Phvul.
not assigned.	(original description: pacid=37144721 transcript=Phvul.003G104900.1 locus=Phvul.
RNA processi	component Fip1 of Cleavage and Polyadenylation Specificity Factor (CPSF) complex (
Protein modif	protein kinase (SD-1) (original description: pacid=37146603 transcript=Phvul.003G15
Protein modif	protein kinase (SD-1) (original description: pacid=37146603 transcript=Phvul.003G15

RNA processi	RNA editing factor (OTP82) (original description: pacid=37146356 transcript=Phvul.0
RNA processi	exo-/endoribonuclease (RNase J) (original description: pacid=37148378 transcript=Ph
RNA processi	exo-/endoribonuclease (RNase J) (original description: pacid=37148378 transcript=Ph
Multi-process	GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37148383 tr
Multi-process	GTPase interactive protein kinase (RBK/RRK) (original description: pacid=37148383 tr
RNA biosynth	transcription factor (MYB) (original description: pacid=37162815 transcript=Phvul.00
not assigned.a	(original description: pacid=37162157 transcript=Phvul.004G064300.1 locus=Phvul.0
not assigned.a	(original description: pacid=37162157 transcript=Phvul.004G064300.1 locus=Phvul.0
not assigned.a	(original description: pacid=37163473 transcript=Phvul.004G131300.1 locus=Phvul.0
not assigned.a	(original description: pacid=37163473 transcript=Phvul.004G131300.1 locus=Phvul.0
not assigned.a	(original description: pacid=37154207 transcript=Phvul.005G031200.1 locus=Phvul.0
External stimu	defensin (PDF1) (original description: pacid=37154287 transcript=Phvul.005G071300
External stimu	defensin (PDF1) (original description: pacid=37154287 transcript=Phvul.005G071300
RNA processi	component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description
RNA processi	component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description
RNA processi	component CPFS6/CFIm68 of Cleavage Factor I (CF-Im) complex (original description
Chromatin org	histone deacetylase (SRT) (original description: pacid=37171603 transcript=Phvul.00
not assigned.a	(original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.0
not assigned.a	(original description: pacid=37171447 transcript=Phvul.006G066800.1 locus=Phvul.0
not assigned.a	(original description: pacid=37165347 transcript=Phvul.007G086300.2 locus=Phvul.0
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External stimu	effector receptor (NLR) (original description: pacid=37177710 transcript=Phvul.002G
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Solute transpo	transport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
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Solute transpo	transport protein (TSUP) (original description: pacid=37175732 transcript=Phvul.002
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Cytoskeleton	class VIII myosin microfilament-based motor protein (original description: pacid=371
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Cytoskeleton	class VIII myosin microfilament-based motor protein (original description: pacid=371
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Chromatin org	SUVH2/9 methyl-DNA-binding factor of DNA methylation pathway (original descripti
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Carbohydrate	ribose 5-phosphate isomerase (original description: pacid=37173541 transcript=Phvu
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not assigned.n	no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
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not assigned.n	no hits & (original description: pacid=37143088 transcript=Phvul.010G044000.3 locu
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01G015600 ID=Phvul.001G015600.3.v2.1 annot-version=v2.1) & Lysophospholipid acyltransferase
001G085500.2 locus=Phvul.001G085500 ID=Phvul.001G085500.2.v2.1 annot-version=v2.1) &
001G085500.2 locus=Phvul.001G085500 ID=Phvul.001G085500.2.v2.1 annot-version=v2.1) &
2600.1 locus=Phvul.001G232600 ID=Phvul.001G232600.1.v2.1 annot-version=v2.1) &
2600.1 locus=Phvul.001G232600 ID=Phvul.001G232600.1.v2.1 annot-version=v2.1) &
02G041400.4 locus=Phvul.002G041400 ID=Phvul.002G041400.4.v2.1 annot-version=v2.1) &
02G041400.4 locus=Phvul.002G041400 ID=Phvul.002G041400.4.v2.1 annot-version=v2.1) &
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02G298800 ID=Phvul.002G298800.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At4g10955
l description: pacid=37145098 transcript=Phvul.003G010900.1 locus=Phvul.003G010900 ID=Phvul.
l description: pacid=37145098 transcript=Phvul.003G010900.1 locus=Phvul.003G010900 ID=Phvul.
=37145330 transcript=Phvul.003G195800.2 locus=Phvul.003G195800 ID=Phvul.003G195800.2.v2.1
=37145330 transcript=Phvul.003G195800.2 locus=Phvul.003G195800 ID=Phvul.003G195800.2.v2.1
t=Phvul.003G252400.1 locus=Phvul.003G252400 ID=Phvul.003G252400.1.v2.1 annot-version=v2.1)
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nal description: pacid=37146502 transcript=Phvul.003G295800.4 locus=Phvul.003G295800 ID=Phvu
nal description: pacid=37146502 transcript=Phvul.003G295800.4 locus=Phvul.003G295800 ID=Phvu
nal description: pacid=37146502 transcript=Phvul.003G295800.4 locus=Phvul.003G295800 ID=Phvu
04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
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04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A
04G032300 ID=Phvul.004G032300.4.v2.1 annot-version=v2.1) & Purple acid phosphatase 23 OS=A

04G048000 ID=Phvul.004G048000.1.v2.1 annot-version=v2.1) & Probable disease resistance prote

04G048000 ID=Phvul.004G048000.1.v2.1 annot-version=v2.1) & Probable disease resistance prote

script=Phvul.004G106800.2 locus=Phvul.004G106800 ID=Phvul.004G106800.2.v2.1 annot-version=

script=Phvul.004G106800.2 locus=Phvul.004G106800 ID=Phvul.004G106800.2.v2.1 annot-version=

04G133100 ID=Phvul.004G133100.1.v2.1 annot-version=v2.1) & Probable carboxylesterase 18 OS=

05G165800 ID=Phvul.005G165800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

05G165800 ID=Phvul.005G165800.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

6800.1 locus=Phvul.006G086800 ID=Phvul.006G086800.1.v2.1 annot-version=v2.1) &

s=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)

46.0) & Enzyme classification.EC_2 transferases.EC_2.1 transferase transferring one-carbon group(5

46.0) & Enzyme classification.EC_2 transferases.EC_2.1 transferase transferring one-carbon group(5

s=Phvul.007G027400 ID=Phvul.007G027400.1.v2.1 annot-version=v2.1)

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158100.1 locus=Phvul.008G158100 ID=Phvul.008G158100.1.v2.1 annot-version=v2.1) &

l.009G020000.1 locus=Phvul.009G020000 ID=Phvul.009G020000.1.v2.1 annot-version=v2.1) &

l.009G020000.1 locus=Phvul.009G020000 ID=Phvul.009G020000.1.v2.1 annot-version=v2.1) &

9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &

9G065500.2 locus=Phvul.009G065500 ID=Phvul.009G065500.2.v2.1 annot-version=v2.1) &

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09G213300 ID=Phvul.009G213300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repea

09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik

09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik

09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik

09G226300 ID=Phvul.009G226300.2.v2.1 annot-version=v2.1) & Protein trichome birefringence-lik

09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-

09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-

09G233700 ID=Phvul.009G233700.1.v2.1 annot-version=v2.1) & Probable disease resistance RPP8-

10G008700 ID=Phvul.010G008700.2.v2.1 annot-version=v2.1) & TMV resistance protein N OS=Nic

10G008700 ID=Phvul.010G008700.2.v2.1 annot-version=v2.1) & TMV resistance protein N OS=Nic

10G056500 ID=Phvul.010G056500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

10G056500 ID=Phvul.010G056500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

10G063100 ID=Phvul.010G063100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

10G070584 ID=Phvul.010G070584.1.v2.1 annot-version=v2.1) & Long-chain-alcohol oxidase FAO1

s=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)

s=Phvul.010G146900 ID=Phvul.010G146900.7.v2.1 annot-version=v2.1)

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11G014500 ID=Phvul.011G014500.2.v2.1 annot-version=v2.1) & Disease resistance protein RPP13

11G014500 ID=Phvul.011G014500.2.v2.1 annot-version=v2.1) & Disease resistance protein RPP13

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11G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing

11G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing

11G082700 ID=Phvul.011G082700.3.v2.1 annot-version=v2.1) & P-loop NTPase domain-containing
11G149400 ID=Phvul.011G149400.1.v2.1 annot-version=v2.1) & Disease resistance protein At4g27
11G149400 ID=Phvul.011G149400.1.v2.1 annot-version=v2.1) & Disease resistance protein At4g27
11G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
s=Phvul.011G182900 ID=Phvul.011G182900.1.v2.1 annot-version=v2.1)
s=Phvul.011G182900 ID=Phvul.011G182900.1.v2.1 annot-version=v2.1)
11G191600 ID=Phvul.011G191600.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G191800 ID=Phvul.011G191800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G192200 ID=Phvul.011G192200.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G192900 ID=Phvul.011G192900.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G192900 ID=Phvul.011G192900.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G195751 ID=Phvul.011G195751.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G198400 ID=Phvul.011G198400.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G201000 ID=Phvul.011G201000.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G201101 ID=Phvul.011G201101.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
01G027100 ID=Phvul.001G027100.1.v2.1 annot-version=v2.1) & F-box/kelch-repeat protein At5g4
01G123000 ID=Phvul.001G123000.2.v2.1 annot-version=v2.1) & Alpha-glucosidase OS=Spinacia ol
01G132516 ID=Phvul.001G132516.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G132516 ID=Phvul.001G132516.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G132701 ID=Phvul.001G132701.1.v2.1 annot-version=v2.1) & Disease resistance protein RGA2 (
01G132701 ID=Phvul.001G132701.1.v2.1 annot-version=v2.1) & Disease resistance protein RGA2 (
01G132800 ID=Phvul.001G132800.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G132800 ID=Phvul.001G132800.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G132864 ID=Phvul.001G132864.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G132864 ID=Phvul.001G132864.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G133100 ID=Phvul.001G133100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G133100 ID=Phvul.001G133100.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G133101 ID=Phvul.001G133101.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
01G133101 ID=Phvul.001G133101.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
185400.1 locus=Phvul.001G185400 ID=Phvul.001G185400.1.v2.1 annot-version=v2.1) &
185400.1 locus=Phvul.001G185400 ID=Phvul.001G185400.1.v2.1 annot-version=v2.1) &
0086 transcript=Phvul.001G217800.1 locus=Phvul.001G217800 ID=Phvul.001G217800.1.v2.1 annot
2G063500.1 locus=Phvul.002G063500 ID=Phvul.002G063500.1.v2.1 annot-version=v2.1) &
2G063500.1 locus=Phvul.002G063500 ID=Phvul.002G063500.1.v2.1 annot-version=v2.1) &
002G104200.1 locus=Phvul.002G104200 ID=Phvul.002G104200.1.v2.1 annot-version=v2.1) &
002G104200.1 locus=Phvul.002G104200 ID=Phvul.002G104200.1.v2.1 annot-version=v2.1) &
178074 transcript=Phvul.002G279500.1 locus=Phvul.002G279500 ID=Phvul.002G279500.1.v2.1 an
s=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)
s=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)
ne : 391.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired
ne : 391.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired
03G104900 ID=Phvul.003G104900.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenyl
03G104900 ID=Phvul.003G104900.1.v2.1 annot-version=v2.1) & Heavy metal-associated isoprenyl
original description: pacid=37147165 transcript=Phvul.003G157600.1 locus=Phvul.003G157600 ID=
8700.1 locus=Phvul.003G158700 ID=Phvul.003G158700.1.v2.1 annot-version=v2.1) &
8700.1 locus=Phvul.003G158700 ID=Phvul.003G158700.1.v2.1 annot-version=v2.1) &

03G162300.1 locus=Phvul.003G162300 ID=Phvul.003G162300.1.v2.1 annot-version=v2.1) &
hvul.003G209600.2 locus=Phvul.003G209600 ID=Phvul.003G209600.2.v2.1 annot-version=v2.1) &
hvul.003G209600.2 locus=Phvul.003G209600 ID=Phvul.003G209600.2.v2.1 annot-version=v2.1) &
ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versi
ranscript=Phvul.003G288300.1 locus=Phvul.003G288300 ID=Phvul.003G288300.1.v2.1 annot-versi
4G011400.1 locus=Phvul.004G011400 ID=Phvul.004G011400.1.v2.1 annot-version=v2.1) &
04G064300 ID=Phvul.004G064300.1.v2.1 annot-version=v2.1) & Ultraviolet-B receptor UVR8 OS=A
04G064300 ID=Phvul.004G064300.1.v2.1 annot-version=v2.1) & Ultraviolet-B receptor UVR8 OS=A
04G131300 ID=Phvul.004G131300.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
04G131300 ID=Phvul.004G131300.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
05G031200 ID=Phvul.005G031200.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
.1 locus=Phvul.005G071300 ID=Phvul.005G071300.1.v2.1 annot-version=v2.1) &
.1 locus=Phvul.005G071300 ID=Phvul.005G071300.1.v2.1 annot-version=v2.1) &
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: pacid=37172194 transcript=Phvul.006G057100.5 locus=Phvul.006G057100 ID=Phvul.006G057100
: pacid=37172194 transcript=Phvul.006G057100.5 locus=Phvul.006G057100 ID=Phvul.006G057100
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06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
06G066800 ID=Phvul.006G066800.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
07G086300 ID=Phvul.007G086300.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
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08G014700 ID=Phvul.008G014700.1.v2.1 annot-version=v2.1) & Disease resistance protein RPP13
08G072032 ID=Phvul.008G072032.1.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072032 ID=Phvul.008G072032.1.v2.1 annot-version=v2.1) & Probable disease resistance prote
s=Phvul.008G168300 ID=Phvul.008G168300.2.v2.1 annot-version=v2.1)
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l.009G079700.1 locus=Phvul.009G079700 ID=Phvul.009G079700.1.v2.1 annot-version=v2.1) &
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800.2 locus=Phvul.009G180800 ID=Phvul.009G180800.2.v2.1 annot-version=v2.1) &
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10G063700 ID=Phvul.010G063700.2.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
s=Phvul.010G101700 ID=Phvul.010G101700.1.v2.1 annot-version=v2.1)
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11G015000.1 locus=Phvul.011G015000 ID=Phvul.011G015000.1.v2.1 annot-version=v2.1) &
11G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G181500 ID=Phvul.011G181500.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
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11G202366 ID=Phvul.011G202366.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
11G202366 ID=Phvul.011G202366.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13
ath : 469.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 354.6) (original des
ath : 469.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 354.6) (original des
01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
01G183400.4 locus=Phvul.001G183400 ID=Phvul.001G183400.4.v2.1 annot-version=v2.1) &
script=Phvul.002G089800.1 locus=Phvul.002G089800 ID=Phvul.002G089800.1.v2.1 annot-version=
script=Phvul.002G089800.1 locus=Phvul.002G089800 ID=Phvul.002G089800.1.v2.1 annot-version=
171400.1 locus=Phvul.002G171400 ID=Phvul.002G171400.1.v2.1 annot-version=v2.1) &
G244900.1 locus=Phvul.002G244900 ID=Phvul.002G244900.1.v2.1 annot-version=v2.1) &
G244900.1 locus=Phvul.002G244900 ID=Phvul.002G244900.1.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
G245000.5 locus=Phvul.002G245000 ID=Phvul.002G245000.5.v2.1 annot-version=v2.1) &
.44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 ann
.44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 ann
.44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 ann
.44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 ann
.44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 ann
.44970 transcript=Phvul.003G002200.5 locus=Phvul.003G002200 ID=Phvul.003G002200.5.v2.1 ann
s=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)
s=Phvul.003G050200 ID=Phvul.003G050200.2.v2.1 annot-version=v2.1)
s=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
s=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
s=Phvul.003G244225 ID=Phvul.003G244225.3.v2.1 annot-version=v2.1)
on: pacid=37145910 transcript=Phvul.003G282200.3 locus=Phvul.003G282200 ID=Phvul.003G2822
on: pacid=37145910 transcript=Phvul.003G282200.3 locus=Phvul.003G282200 ID=Phvul.003G2822
03G282250 ID=Phvul.003G282250.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
t=Phvul.004G011100.1 locus=Phvul.004G011100 ID=Phvul.004G011100.1.v2.1 annot-version=v2.1)
86300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-version=v2.1) &

86300.2 locus=Phvul.004G086300 ID=Phvul.004G086300.2.v2.1 annot-version=v2.1) &

05G041300 ID=Phvul.005G041300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repea

05G041300 ID=Phvul.005G041300.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repea

05G069700 ID=Phvul.005G069700.1.v2.1 annot-version=v2.1) & Nuclear pore complex protein NU

05G069700 ID=Phvul.005G069700.1.v2.1 annot-version=v2.1) & Nuclear pore complex protein NU

s=Phvul.005G072000 ID=Phvul.005G072000.1.v2.1 annot-version=v2.1)

06G027500 ID=Phvul.006G027500.1.v2.1 annot-version=v2.1) & WD repeat-containing protein 26

06G027500 ID=Phvul.006G027500.1.v2.1 annot-version=v2.1) & WD repeat-containing protein 26

l.006G100600.1 locus=Phvul.006G100600 ID=Phvul.006G100600.1.v2.1 annot-version=v2.1) &

s=Phvul.006G126400 ID=Phvul.006G126400.1.v2.1 annot-version=v2.1)

s=Phvul.006G126400 ID=Phvul.006G126400.1.v2.1 annot-version=v2.1)

s=Phvul.006G170700 ID=Phvul.006G170700.1.v2.1 annot-version=v2.1)

08G107400 ID=Phvul.008G107400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

08G107400 ID=Phvul.008G107400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

cript=Phvul.008G206300.1 locus=Phvul.008G206300 ID=Phvul.008G206300.1.v2.1 annot-version=v

103100.1 locus=Phvul.009G103100 ID=Phvul.009G103100.1.v2.1 annot-version=v2.1) &

10G008500 ID=Phvul.010G008500.1.v2.1 annot-version=v2.1) & no description available(sp|q9ss8

0G013500.1 locus=Phvul.010G013500 ID=Phvul.010G013500.1.v2.1 annot-version=v2.1) &

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

s=Phvul.010G044000 ID=Phvul.010G044000.3.v2.1 annot-version=v2.1)

010G145600.1 locus=Phvul.010G145600 ID=Phvul.010G145600.1.v2.1 annot-version=v2.1) &

11G181700 ID=Phvul.011G181700.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

11G200820 ID=Phvul.011G200820.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

11G202100 ID=Phvul.011G202100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

11G202300 ID=Phvul.011G202300.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

11G203100 ID=Phvul.011G203100.1.v2.1 annot-version=v2.1) & Putative disease resistance RPP13

in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 137.0)
7|gpa3_orysj : 136.0)
7|gpa3_orysj : 136.0)
7|gpa3_orysj : 136.0)
7|gpa3_orysj : 136.0)
ing protein 5 OS=Arabidopsis thaliana (sp|q8rwd9|acbp5_arath : 133.0)
ing protein 5 OS=Arabidopsis thaliana (sp|q8rwd9|acbp5_arath : 133.0)
in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)
in At5g63020 OS=Arabidopsis thaliana (sp|q8rxs5|drl40_arath : 433.0)

annot-version=v2.1) &

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 265.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 458.0)
otiana glutinosa (sp|q40392|tmvrn_nicgu : 238.0)
in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 413.0)
in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 413.0)
) &
) &

=v2.1) &

=v2.1) &

max (sp|c6tbd0|cspl6_soybn : 249.0)

max (sp|c6tbd0|cspl6_soybn : 249.0)

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

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

not-version=v2.1) &

2.1) &

2.1) &

in At4g10780 OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 303.0)

in At4g10780 OS=Arabidopsis thaliana (sp|o82484|drl23_arath : 303.0)

in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 160.0)

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

n=v2.1) &

n=v2.1) &

n=v2.1) &

n=v2.1) &

OS=Arabidopsis thaliana (sp|f4i594|rlm1a_arath : 191.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 503.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 474.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 513.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 538.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 543.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 501.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 555.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 536.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 549.0)

3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 360.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 543.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 357.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 565.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 565.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 479.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 479.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 519.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 519.0)
thaliana (sp|q9fh04|adhl7_arath : 523.0)
thaliana (sp|q9fh04|adhl7_arath : 523.0)
thaliana (sp|q9fh04|adhl7_arath : 523.0)
thaliana (sp|q9fh04|adhl7_arath : 523.0)
LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)
LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)
LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)
LPEAT1 OS=Arabidopsis thaliana (sp|q8l7r3|lpct1_arath : 452.0)

OS=Arabidopsis thaliana (sp|q680c0|gdl62_arath : 442.0)
003G010900.1.v2.1 annot-version=v2.1) &
003G010900.1.v2.1 annot-version=v2.1) &
annot-version=v2.1) &
annot-version=v2.1) &
&
&
l.003G295800.4.v2.1 annot-version=v2.1) &
l.003G295800.4.v2.1 annot-version=v2.1) &
l.003G295800.4.v2.1 annot-version=v2.1) &
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)
rabidopsis thaliana (sp|q6tph1|ppa23_arath : 715.0)

in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 137.0)
in At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 137.0)
=v2.1) &
=v2.1) &
=Arabidopsis thaliana (sp|q9lt10|cxe18_arath : 385.0)
ing protein At3g49730 OS=Arabidopsis thaliana (sp|p0c8a0|pp275_arath : 692.0)
ing protein At3g49730 OS=Arabidopsis thaliana (sp|p0c8a0|pp275_arath : 692.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 446.0)

0.2.1 : 182.1) (original description: pacid=37173441 transcript=Phvul.006G180900.1 locus=Phvul.0
0.2.1 : 182.1) (original description: pacid=37173441 transcript=Phvul.006G180900.1 locus=Phvul.0

inal description: pacid=37166954 transcript=Phvul.007G096800.1 locus=Phvul.007G096800 ID=Ph

t-containing protein At1g19290 OS=Arabidopsis thaliana (sp|q9ln69|ppr50_arath : 769.0)
e 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
e 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
e 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
e 16 OS=Arabidopsis thaliana (sp|f4k5l5|tbl16_arath : 573.0)
-like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2_arath : 498.0)
-like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2_arath : 498.0)
-like protein 2 OS=Arabidopsis thaliana (sp|p0c8s1|rp8l2_arath : 498.0)
otiana glutinosa (sp|q40392|tmvrn_nicgu : 371.0)
otiana glutinosa (sp|q40392|tmvrn_nicgu : 371.0)
ing protein At2g17670 OS=Arabidopsis thaliana (sp|q84j71|pp161_arath : 496.0)
ing protein At2g17670 OS=Arabidopsis thaliana (sp|q84j71|pp161_arath : 496.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 612.0)
OS=Lotus japonicus (sp|b5wwz8|fao1_lotja : 932.0)

OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 310.0)
OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 310.0)
OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 310.0)
protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1_arath : 804.0)
protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1_arath : 804.0)

protein LPA1 homolog 1 OS=Arabidopsis thaliana (sp|q9fjh9|lpah1_arath : 804.0)
7190 OS=Arabidopsis thaliana (sp|q9t048|drl27_arath : 177.0)
7190 OS=Arabidopsis thaliana (sp|q9t048|drl27_arath : 177.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 540.0)

3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 542.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 545.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 525.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 424.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 424.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 443.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 558.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 333.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 159.0)
3190 OS=Arabidopsis thaliana (sp|q9fhs6|fk119_arath : 285.0)
eracea (sp|o04893|aglu_spiol : 80.9)
in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 306.0)
in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 306.0)
OS=Solanum bulbocastanum (sp|q7xbq9|rga2_solbu : 325.0)
OS=Solanum bulbocastanum (sp|q7xbq9|rga2_solbu : 325.0)
in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 332.0)
in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 332.0)
in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 367.0)
in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 367.0)
in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 389.0)
in RGA3 OS=Solanum bulbocastanum (sp|q7xa40|rga3_solbu : 389.0)
in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 379.0)
in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 379.0)

t-version=v2.1) &

not-version=v2.1) &

donor with incorporation or reduction of molecular oxygen(50.1.13 : 208.0) (original description: p
donor with incorporation or reduction of molecular oxygen(50.1.13 : 208.0) (original description: p
ated plant protein 36 OS=Arabidopsis thaliana (sp|q84j88|hip36_arath : 102.0)
ated plant protein 36 OS=Arabidopsis thaliana (sp|q84j88|hip36_arath : 102.0)
Phvul.003G157600.1.v2.1 annot-version=v2.1) &

on=v2.1) &
on=v2.1) &

Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 171.0)
Arabidopsis thaliana (sp|q9fn03|uvr8_arath : 171.0)
ing protein At1g12300, mitochondrial OS=Arabidopsis thaliana (sp|q0wkv3|ppr36_arath : 382.0)
ing protein At1g12300, mitochondrial OS=Arabidopsis thaliana (sp|q0wkv3|ppr36_arath : 382.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 617.0)

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

3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 446.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 446.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 597.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 597.0)
OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 306.0)
OS=Arabidopsis thaliana (sp|q9m667|rpp13_arath : 306.0)
ein At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 171.0)
ein At4g27220 OS=Arabidopsis thaliana (sp|o81825|drl28_arath : 171.0)

3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 528.0)

helicase 1 homolog OS=Oryza sativa subsp. japonica (sp|a0a0p0v4r0|rtel1_orysj : 203.0)
helicase 1 homolog OS=Oryza sativa subsp. japonica (sp|a0a0p0v4r0|rtel1_orysj : 203.0)

3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 540.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 540.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 559.0)

-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 559.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 489.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 489.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 333.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 333.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 159.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 159.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 203.0)
-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 203.0)
scription: pacid=37163915 transcript=Phvul.L004500.1 locus=Phvul.L004500 ID=Phvul.L004500.1.v2
scription: pacid=37163915 transcript=Phvul.L004500.1 locus=Phvul.L004500 ID=Phvul.L004500.1.v2

v2.1) &
v2.1) &

ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &
ot-version=v2.1) &

00.3.v2.1 annot-version=v2.1) &
00.3.v2.1 annot-version=v2.1) &
ing protein At2g03380, mitochondrial OS=Arabidopsis thaliana (sp|q9zq74|pp146_arath : 626.0)
&

t-containing protein At1g03510 OS=Arabidopsis thaliana (sp|q9lr72|ppr7_arath : 388.0)
t-containing protein At1g03510 OS=Arabidopsis thaliana (sp|q9lr72|ppr7_arath : 388.0)
P98A OS=Arabidopsis thaliana (sp|q8ry25|nu98a_arath : 109.0)
P98A OS=Arabidopsis thaliana (sp|q8ry25|nu98a_arath : 109.0)

homolog OS=Arabidopsis thaliana (sp|q9fnn2|wdr26_arath : 697.0)
homolog OS=Arabidopsis thaliana (sp|q9fnn2|wdr26_arath : 697.0)

ing protein At3g09060 OS=Arabidopsis thaliana (sp|q9ss81|pp221_arath : 736.0)
ing protein At3g09060 OS=Arabidopsis thaliana (sp|q9ss81|pp221_arath : 736.0)
2.1) &

0|ops_arath : 167.0)

3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 541.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 565.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 479.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 483.0)
3-like protein 1 OS=Arabidopsis thaliana (sp|q9lrr4|r13l1_arath : 519.0)

06G180900 ID=Phvul.006G180900.1.v2.1 annot-version=v2.1) &

06G180900 ID=Phvul.006G180900.1.v2.1 annot-version=v2.1) &

vul.007G096800.1.v2.1 annot-version=v2.1) &

acid=37147806 transcript=Phvul.003G076900.1 locus=Phvul.003G076900 ID=Phvul.003G076900.1.

acid=37147806 transcript=Phvul.003G076900.1 locus=Phvul.003G076900 ID=Phvul.003G076900.1.

.1 annot-version=v2.1) &

.1 annot-version=v2.1) &

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

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

miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
ccgaccuuagcu	Phvul.005G179400.1	2.5	-1	1	21
ccgaccuuagcu	Phvul.001G025900.1	3	-1	1	21
ccgaccuuagcu	Phvul.002G321900.1	3	-1	1	21
ccgaccuuagcu	Phvul.005G110300.3	3	-1	1	21
ccgaccuuagcu	Phvul.005G110300.2	3	-1	1	21
ccgaccuuagcu	Phvul.005G110300.1	3	-1	1	21
ccgaccuuagcu	Phvul.009G128800.1	3	-1	1	21
ccgaccuuagcu	Phvul.002G220500.1	3.5	-1	1	21
ccgaccuuagcu	Phvul.006G047700.1	3.5	-1	1	21
ccgaccuuagcu	Phvul.006G059900.1	3.5	-1	1	21
ccgaccuuagcu	Phvul.002G133400.1	4	-1	1	21
ccgaccuuagcu	Phvul.002G302600.1	4	-1	1	21
ccgaccuuagcu	Phvul.003G263400.1	4	-1	1	21
ccgaccuuagcu	Phvul.005G100500.1	4	-1	1	21
ccgaccuuagcu	Phvul.006G017100.1	4	-1	1	21
ccgaccuuagcu	Phvul.006G199400.1	4	-1	1	21
ccgaccuuagcu	Phvul.008G070100.1	4	-1	1	21
ccgaccuuagcu	Phvul.001G119000.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.001G259300.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.002G003000.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.002G278800.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.003G138382.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.003G155500.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.003G185100.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.006G015900.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.006G015900.2	4.5	-1	1	21
ccgaccuuagcu	Phvul.006G086100.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.006G117700.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.006G125600.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.006G142200.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.007G042700.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.011G012400.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.011G024700.1	4.5	-1	1	21
ccgaccuuagcu	Phvul.001G016500.2	5	-1	1	21
ccgaccuuagcu	Phvul.001G016500.1	5	-1	1	21
ccgaccuuagcu	Phvul.001G023100.1	5	-1	1	21
ccgaccuuagcu	Phvul.002G208300.1	5	-1	1	21
ccgaccuuagcu	Phvul.002G267600.2	5	-1	1	21
ccgaccuuagcu	Phvul.002G267600.1	5	-1	1	21
ccgaccuuagcu	Phvul.003G011400.1	5	-1	1	21
ccgaccuuagcu	Phvul.003G031500.1	5	-1	1	21
ccgaccuuagcu	Phvul.003G216800.1	5	-1	1	21
ccgaccuuagcu	Phvul.004G041500.2	5	-1	1	21
ccgaccuuagcu	Phvul.004G041500.1	5	-1	1	21
ccgaccuuagcu	Phvul.004G106700.1	5	-1	1	21

ccgaccuuagcu	Phvul.004G170800.1	5	-1	1	21
ccgaccuuagcu	Phvul.005G003300.2	5	-1	1	21
ccgaccuuagcu	Phvul.005G003300.1	5	-1	1	21
ccgaccuuagcu	Phvul.005G084000.1	5	-1	1	21
ccgaccuuagcu	Phvul.005G160700.1	5	-1	1	21
ccgaccuuagcu	Phvul.006G004580.1	5	-1	1	21
ccgaccuuagcu	Phvul.006G135500.1	5	-1	1	21
ccgaccuuagcu	Phvul.007G080800.2	5	-1	1	21
ccgaccuuagcu	Phvul.008G080100.2	5	-1	1	21
ccgaccuuagcu	Phvul.008G080100.1	5	-1	1	21
ccgaccuuagcu	Phvul.008G131301.1	5	-1	1	21
ccgaccuuagcu	Phvul.008G191200.2	5	-1	1	21
ccgaccuuagcu	Phvul.008G191200.1	5	-1	1	21
ccgaccuuagcu	Phvul.008G240000.1	5	-1	1	21
ccgaccuuagcu	Phvul.008G240300.1	5	-1	1	21
ccgaccuuagcu	Phvul.008G240500.1	5	-1	1	21
ccgaccuuagcu	Phvul.009G183600.4	5	-1	1	21
ccgaccuuagcu	Phvul.009G183600.1	5	-1	1	21
ccgaccuuagcu	Phvul.009G183600.3	5	-1	1	21
ccgaccuuagcu	Phvul.009G183600.2	5	-1	1	21
ccgaccuuagcu	Phvul.009G194700.1	5	-1	1	21
ccgaccuuagcu	Phvul.009G194700.2	5	-1	1	21
ccgaccuuagcu	Phvul.010G069638.1	5	-1	1	21
ccgaccuuagcu	Phvul.010G112500.1	5	-1	1	21
ccgaccuuagcu	Phvul.011G077600.1	5	-1	1	21
ccgaccuuagcu	Phvul.011G158600.1	5	-1	1	21

Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
468	488	CCGACCUUAG	.:::. ::::::::::.::	GUUCAAUCG	Cleavage	pacid=371539
1494	1514	CCGACCUUAG	: ::: ::::::::::::. :	CUCCAUCUG	Cleavage	pacid=371692
493	513	CCGACCUUAG	..:::: :::::::::.::	AUUUAACUG	Cleavage	pacid=371769
865	885	CCGACCUUAG	: :::: :.: ::::::::	CUCCAACAGG	Translation	pacid=371530
966	986	CCGACCUUAG	: :::: :.: ::::::::	CUCCAACAGG	Translation	pacid=371530
1033	1053	CCGACCUUAG	: :::: :.: ::::::::	CUCCAACAGG	Translation	pacid=371529
491	511	CCGACCUUAG	..:::: :::::::::.::	AUUUAACUG	Cleavage	pacid=371499
1612	1632	CCGACCUUAG	:.::::::::.::.: :.::	GAUCAACUG	Cleavage	pacid=371751
1828	1848	CCGACCUUAG	::.:::.:.:.::::.::	CUACAGCUG	Cleavage	pacid=371722
2179	2199	CCGACCUUAG	::.:::.:.:.::::.::	CUACAGCUG	Cleavage	pacid=371732
632	652	CCGACCUUAG	...: :::.::::.::::	AGUUACCUG	Cleavage	pacid=371771
503	523	CCGACCUUAG	::. :. ::::.::::.::	GACUCAUAG	Cleavage	pacid=371771
550	570	CCGACCUUAG	:::.: :::::.::: .::	GCCCAGCGG	Cleavage	pacid=371470
1367	1386	CCGACCUUAG	..::: ::::::::::.:	AGUCAA-UGA	Cleavage	pacid=371535
1847	1867	CCGACCUUAG	.:::. :::.::: ::::	ACUCAAUGG	Cleavage	pacid=371741
2302	2322	CCGACCUUAG	:.:::.::: .::::::::	AAUCAAUUG	Translation	pacid=371712
604	624	CCGACCUUAG	: ::::.: :::: :::.::	CUCCAAUUU	Cleavage	pacid=371602
750	770	CCGACCUUAG	:::: ::.:.:..:::.::	GACCACAUG	Cleavage	pacid=371700
1493	1513	CCGACCUUAG	.::::. .:.:::::.::	GGCCAAUGA	Cleavage	pacid=371679
11011	11031	CCGACCUUAG	.::::::::.::.:: .::	UCUUAAUUG	Cleavage	pacid=371751
155	174	CCGACCUUAG	::::::::.:.:: ::::	UCCCAACUG	Cleavage	pacid=371783
328	348	CCGACCUUAG	::::::::: :: .:::	AGGCAACUG	Cleavage	pacid=371474
1579	1599	CCGACCUUAG	.::.::.: .:::::::.:	UACUAAUUU	Cleavage	pacid=371481
868	888	CCGACCUUAG	:..:.::.::::::: :	ACCUGAUUG	Cleavage	pacid=371455
1196	1216	CCGACCUUAG	:::::::: :.::::.:	GGGCAACUG	Translation	pacid=371726
1210	1230	CCGACCUUAG	:::::::: :.::::.:	GGGCAACUG	Translation	pacid=371726
1859	1879	CCGACCUUAG	::.: ::.::::::::	UUUGAAUUA	Cleavage	pacid=371717
1058	1078	CCGACCUUAG	.:::::::.::.:::. :	UUAUAACUG	Cleavage	pacid=371736
927	947	CCGACCUUAG	::.: : ::::.::::.:	AACUAUCAG	Cleavage	pacid=371722
419	439	CCGACCUUAG	: .:::.: :::: :::.::	CCUCAAUUCA	Cleavage	pacid=371720
822	842	CCGACCUUAG	:::.:: :.:.:.::::.:	AACCGACGG	Cleavage	pacid=371652
1225	1245	CCGACCUUAG	:: :::::: ::::::::	CAAAAACUGA	Translation	pacid=371546
313	333	CCGACCUUAG	:....: .::::::::.::	ACCUGGUUU	Cleavage	pacid=371566
1535	1555	CCGACCUUAG	:::::: . .:..:::::	GACCAACUU	Translation	pacid=371687
1672	1692	CCGACCUUAG	:::::: . .:..:::::	GACCAACUU	Translation	pacid=371687
440	460	CCGACCUUAG	...::::::.:.::.: :.:	UGUCAACUG	Cleavage	pacid=371701
1441	1461	CCGACCUUAG	: ..::::: :..:::.::	AAAUGACUG	Translation	pacid=371780
1929	1949	CCGACCUUAG	.:. :::: :::.::::.:	UAUGAACUG	Cleavage	pacid=371771
1933	1953	CCGACCUUAG	.:. :::: :::.::::.:	UAUGAACUG	Cleavage	pacid=371771
2267	2288	CCGACCUUAG	.:::::. :: ::::::::.::	UACCAAUGG	Translation	pacid=371482
993	1013	CCGACCUUAG	::::.::::.::. ::. :	AACCAAUUG	Cleavage	pacid=371476
1219	1239	CCGACCUUAG	.:. ::.::::.:.: ::.::	UAUAAAUUG	Cleavage	pacid=371459
698	718	CCGACCUUAG	:: :::.::::::::	CUGCAUCUG	Cleavage	pacid=371627
698	718	CCGACCUUAG	:: :::.::::::::	CUGCAUCUG	Cleavage	pacid=371627
378	398	CCGACCUUAG	..::::. :.:.:..:::.:	UGCCAAUGG	Cleavage	pacid=371634

1561	1581	CCGACCUUAG	.:::::. :::. :.::::	UACCAAUGG	Cleavage	pacid=371635
1676	1696	CCGACCUUAG	...:::: ::.::: ::.::	AGUUAACUC	Cleavage	pacid=371543
1787	1807	CCGACCUUAG	...:::: ::.::: ::.::	AGUUAACUC	Cleavage	pacid=371543
2606	2626	CCGACCUUAG	:: ::.:::: ::::: :.::	CAGCAGCUG	Translation	pacid=371531
2602	2622	CCGACCUUAG	::..:.::: : :::::.::	AACUGAUUG	Translation	pacid=371527
530	550	CCGACCUUAG	:::.: . ::::::: :.::	CACUAUUAG	Cleavage	pacid=371742
1265	1285	CCGACCUUAG	::...:. :::.:::::.:	CAUUGAUGG	Cleavage	pacid=371716
1827	1847	CCGACCUUAG	::.::::::::::::	AGGGAAUUG	Cleavage	pacid=371676
2286	2306	CCGACCUUAG	:: : .::::: :::::::	CAGCUGCUG	Translation	pacid=371612
2271	2291	CCGACCUUAG	:: : .::::: :::::::	CAGCUGCUG	Translation	pacid=371612
517	537	CCGACCUUAG	.:::: .:::::: .:::: :	UACCAUUUG	Cleavage	pacid=371609
1062	1082	CCGACCUUAG	.:.:::::::::::. :	GGGAGAUUG	Cleavage	pacid=371596
1156	1176	CCGACCUUAG	.:.:::::::::::. :	GGGAGAUUG	Cleavage	pacid=371596
238	258	CCGACCUUAG	:.::: ::.:.:..::: ::	AAUCAAGUG	Cleavage	pacid=371605
517	537	CCGACCUUAG	:.::: ::.:.:..::: ::	GAUCAAGUG	Cleavage	pacid=371608
685	705	CCGACCUUAG	:.::: ::.:.:..::: ::	GAUCAAGUG	Cleavage	pacid=371577
75	95	CCGACCUUAG	.:.. ::::::.:.:: :.::	UAUUUACUG	Cleavage	pacid=371493
75	95	CCGACCUUAG	.:.. ::::::.:.:: :.::	UAUUUACUG	Cleavage	pacid=371493
75	95	CCGACCUUAG	.:.. ::::::.:.:: :.::	UAUUUACUG	Cleavage	pacid=371493
75	95	CCGACCUUAG	.:.. ::::::.:.:: :.::	UAUUUACUG	Cleavage	pacid=371493
1382	1402	CCGACCUUAG	.:::::. :::::::::.:	UACUAAUCU	Cleavage	pacid=371491
1526	1546	CCGACCUUAG	.:::.::. :::::::::.:	UACUAAUCU	Cleavage	pacid=371491
600	620	CCGACCUUAG	:.:::. :.:.::::: :.::	GAUCAAUGG	Cleavage	pacid=371437
64	85	CCGACCUUAG	..:::: :: :::::::::.:	UGCCAAGCU	Cleavage	pacid=371438
2178	2198	CCGACCUUAG	:: .::: ::::::::::	CAGUAACAA	Cleavage	pacid=371546
702	722	CCGACCUUAG	::::: . ::: :.::::.::	CACCACUAGA	Translation	pacid=371558

Multiplicity	Target_Acc.	ID	locusName	Pfam
1	Phvul.005G179400.1	Phvul.005G179400	Phvul.005G179400	PF01257
1	Phvul.001G025900.1	Phvul.001G025900	Phvul.001G025900	PF04788
1	Phvul.002G321900.1	Phvul.002G321900	Phvul.002G321900	PF01920
1	Phvul.005G110300.3	Phvul.005G110300	Phvul.005G110300	PF08276,PF00
1	Phvul.005G110300.2	Phvul.005G110300	Phvul.005G110300	PF08276,PF00
1	Phvul.005G110300.1	Phvul.005G110300	Phvul.005G110300	PF08276,PF00
1	Phvul.009G128800.1	Phvul.009G128800	Phvul.009G128800	PF01920
1	Phvul.002G220500.1	Phvul.002G220500	Phvul.002G220500	PF08276,PF00
1	Phvul.006G047700.1	Phvul.006G047700	Phvul.006G047700	PF14432,PF13
1	Phvul.006G059900.1	Phvul.006G059900	Phvul.006G059900	PF14432,PF01
1	Phvul.002G133400.1	Phvul.002G133400	Phvul.002G133400	PF13855,PF00
1	Phvul.002G302600.1	Phvul.002G302600	Phvul.002G302600	PF08263,PF13
1	Phvul.003G263400.1	Phvul.003G263400	Phvul.003G263400	PF00314
1	Phvul.005G100500.1	Phvul.005G100500	Phvul.005G100500	PF00226,PF01
1	Phvul.006G017100.1	Phvul.006G017100	Phvul.006G017100	PF01477,PF00
1	Phvul.006G199400.1	Phvul.006G199400	Phvul.006G199400	PF00439,PF17
1	Phvul.008G070100.1	Phvul.008G070100	Phvul.008G070100	PF08449
1	Phvul.001G119000.1	Phvul.001G119000	Phvul.001G119000	PF07690
1	Phvul.001G259300.1	Phvul.001G259300	Phvul.001G259300	PF08418,PF04
1	Phvul.002G003000.1	Phvul.002G003000	Phvul.002G003000	PF00169,PF12
1	Phvul.002G278800.1	Phvul.002G278800	Phvul.002G278800	0
1	Phvul.003G138382.1	Phvul.003G138382	Phvul.003G138382	PF02309
1	Phvul.003G155500.1	Phvul.003G155500	Phvul.003G155500	PF02881,PF00
1	Phvul.003G185100.1	Phvul.003G185100	Phvul.003G185100	PF12171,PF00
1	Phvul.006G015900.1	Phvul.006G015900	Phvul.006G015900	PF00646
1	Phvul.006G015900.2	Phvul.006G015900	Phvul.006G015900	PF00646
1	Phvul.006G086100.1	Phvul.006G086100	Phvul.006G086100	PF13193,PF00
1	Phvul.006G117700.1	Phvul.006G117700	Phvul.006G117700	PF00583
1	Phvul.006G125600.1	Phvul.006G125600	Phvul.006G125600	PF08031,PF01
1	Phvul.006G142200.1	Phvul.006G142200	Phvul.006G142200	PF04526
1	Phvul.007G042700.1	Phvul.007G042700	Phvul.007G042700	PF12854,PF13
1	Phvul.011G012400.1	Phvul.011G012400	Phvul.011G012400	PF14226
1	Phvul.011G024700.1	Phvul.011G024700	Phvul.011G024700	PF02365
1	Phvul.001G016500.2	Phvul.001G016500	Phvul.001G016500	PF07974,PF01
1	Phvul.001G016500.1	Phvul.001G016500	Phvul.001G016500	PF07974,PF01
1	Phvul.001G023100.1	Phvul.001G023100	Phvul.001G023100	PF13920
1	Phvul.002G208300.1	Phvul.002G208300	Phvul.002G208300	PF01535,PF13
1	Phvul.002G267600.2	Phvul.002G267600	Phvul.002G267600	PF00443
1	Phvul.002G267600.1	Phvul.002G267600	Phvul.002G267600	PF00443
1	Phvul.003G011400.1	Phvul.003G011400	Phvul.003G011400	PF00787,PF08
1	Phvul.003G031500.1	Phvul.003G031500	Phvul.003G031500	PF10497,PF02
1	Phvul.003G216800.1	Phvul.003G216800	Phvul.003G216800	PF08449
1	Phvul.004G041500.2	Phvul.004G041500	Phvul.004G041500	PF02005
1	Phvul.004G041500.1	Phvul.004G041500	Phvul.004G041500	PF02005
1	Phvul.004G106700.1	Phvul.004G106700	Phvul.004G106700	PF11947

1	Phvul.004G170800.1	Phvul.004G170800	Phvul.004G170800	PF00390,PF03
1	Phvul.005G003300.2	Phvul.005G003300	Phvul.005G003300	PF07714,PF00
1	Phvul.005G003300.1	Phvul.005G003300	Phvul.005G003300	PF07714,PF00
1	Phvul.005G084000.1	Phvul.005G084000	Phvul.005G084000	0
1	Phvul.005G160700.1	Phvul.005G160700	Phvul.005G160700	PF00069
1	Phvul.006G004580.1	Phvul.006G004580	Phvul.006G004580	PF08263
1	Phvul.006G135500.1	Phvul.006G135500	Phvul.006G135500	PF05691
1	Phvul.007G080800.2	Phvul.007G080800	Phvul.007G080800	PF03033
1	Phvul.008G080100.2	Phvul.008G080100	Phvul.008G080100	PF00651,PF03
1	Phvul.008G080100.1	Phvul.008G080100	Phvul.008G080100	PF00651,PF03
1	Phvul.008G131301.1	Phvul.008G131301	Phvul.008G131301	PF00498
1	Phvul.008G191200.2	Phvul.008G191200	Phvul.008G191200	0
1	Phvul.008G191200.1	Phvul.008G191200	Phvul.008G191200	0
1	Phvul.008G240000.1	Phvul.008G240000	Phvul.008G240000	PF03080
1	Phvul.008G240300.1	Phvul.008G240300	Phvul.008G240300	PF14365,PF03
1	Phvul.008G240500.1	Phvul.008G240500	Phvul.008G240500	PF14365,PF03
1	Phvul.009G183600.4	Phvul.009G183600	Phvul.009G183600	PF00010
1	Phvul.009G183600.1	Phvul.009G183600	Phvul.009G183600	PF00010
1	Phvul.009G183600.3	Phvul.009G183600	Phvul.009G183600	PF00010
1	Phvul.009G183600.2	Phvul.009G183600	Phvul.009G183600	PF00010
1	Phvul.009G194700.1	Phvul.009G194700	Phvul.009G194700	PF02881,PF00
1	Phvul.009G194700.2	Phvul.009G194700	Phvul.009G194700	PF02881,PF00
1	Phvul.010G069638.1	Phvul.010G069638	Phvul.010G069638	PF00225
1	Phvul.010G112500.1	Phvul.010G112500	Phvul.010G112500	PF10604
1	Phvul.011G077600.1	Phvul.011G077600	Phvul.011G077600	PF02837,PF02
1	Phvul.011G158600.1	Phvul.011G158600	Phvul.011G158600	PF02485

Panther	KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
PTHR10371,P	KOG3196	1.6.99.3,1.6.5	K03943	0	AT4G02580.1	0
PTHR31300,P	0	0	0	0	AT3G19540.1	0
PTHR21431,P	KOG3478	0	K04798	GO:0051082,(	AT1G29990.1	PFD6
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G19130.1	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G19130.1	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT2G19130.1	0
PTHR21431,P	0	0	K04798	GO:0051082,(	AT1G29990.1	PFD6
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0048544,(	AT4G21390.1	B120
PTHR24015,P	0	0	0	0	AT4G02750.1	0
PTHR24015,P	0	0	0	0	AT4G02750.1	0
PTHR23155,P	KOG4658	0	K13457	GO:0005515,(	AT3G07040.1	RPM1,RPS3
PTHR27008,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT5G35390.1	0
PTHR31048,P	0	0	0	0	AT4G38660.1	0
PTHR24078,P	KOG0714	0	K09510	0	AT2G20560.1	0
PTHR11771,P	0	1.13.11.12	K00454	GO:0005515,(	AT3G45140.1	ATLOX2,LOX2
PTHR22880,P	KOG1474	0	0	GO:0005515	AT5G65630.1	GTE7
PTHR10778,P	KOG1582	0	K15277	GO:0055085	AT4G23010.3	ATUTR2,UTR2
PTHR11654,P	0	0	K14638	GO:0055085,(	AT1G68570.1	0
PTHR23061,P	KOG1625	2.7.7.7	K02321	GO:0006260,(	AT1G67630.1	POLA2
PTHR16166,P	KOG1809	0	0	0	AT4G17140.3	0
0	0	0	0	0	0	0
PTHR31734,P	0	0	K14484	GO:0006355,(	AT1G04240.1	IAA3,SHY2
PTHR11564,P	0	0	K13431	GO:0006614,(	AT4G30600.1	0
PTHR24078,P	0	0	K09506	0	AT1G74250.1	0
PTHR31482,P	0	0	0	GO:0005515	AT2G32560.1	0
PTHR31482,P	0	0	0	GO:0005515	AT2G32560.1	0
PTHR24095,P	0	0	0	GO:0008152,(	AT1G65890.1	AAE12
PTHR23091,P	0	2.3.1.88	0	GO:0008080	AT2G23060.1	0
PTHR32448,P	KOG1231	1.3.3.8	0	GO:0055114,(	AT4G20840.1	0
PTHR23130,P	0	0	0	0	AT5G47530.1	0
PTHR24015,P	0	0	0	0	AT5G02860.1	0
PTHR10209,P	0	0	0	0	AT4G13400.1	0
PTHR31989,P	0	0	0	GO:0006355,(	AT2G17040.1	anac036,NAC(
PTHR10942,P	KOG2556	3.4.24.36	0	GO:0016020,(	AT5G42620.2	0
PTHR10942,P	KOG2556	3.4.24.36	0	GO:0016020,(	AT5G42620.2	0
PTHR10044,P	KOG1100	0	K19042	0	AT1G45976.1	SBP1
PTHR24015,P	0	0	0	0	AT5G18390.1	0
PTHR24006,P	0	3.4.19.12	0	GO:0036459,(	AT4G39370.1	UBP27
PTHR24006,P	0	3.4.19.12	0	GO:0036459,(	AT4G39370.1	UBP27
PTHR22999,P	0	0	K17925	GO:0035091	AT2G15900.1	0
PTHR12549,P	0	0	K15601	0	AT1G62310.1	0
PTHR11132,P	KOG1441	0	0	GO:0055085	AT1G12500.1	0
PTHR10631	0	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
PTHR10631	0	2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
PTHR34575,P	0	0	0	0	AT5G52780.1	0

PTHR23406,P	0	1.1.1.40	K00029	GO:0055114,(	AT1G79750.1	ATNADP-ME4
PTHR24351,P	0	2.7.11.1	0	GO:0006468,(	AT3G52890.1	KIPK
PTHR24351,P	0	2.7.11.1	0	GO:0006468,(	AT3G52890.1	KIPK
PTHR31008,P	0	0	0	0	AT4G27430.1	CIP7
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT3G13690.1	0
PTHR27004,P	0	0	0	0	AT4G13880.1	AtRLP48,RLP4
PTHR31268,P	0	0	0	0	AT3G57520.1	AtSIP2,SIP2
PTHR11926,P	0	2.4.1.173	0	GO:0030259,(	AT1G43620.2	TT15,UGT80B
PTHR32370,P	0	0	0	GO:0005515	AT3G08570.1	0
PTHR32370,P	0	0	0	GO:0005515	AT3G08570.1	0
PTHR21712,P	0	0	0	GO:0005515	AT3G07220.1	0
0	0	0	0	0	0	0
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PTHR31589,P	0	0	0	0	AT4G23350.1	0
PTHR31589,P	0	0	0	0	AT5G56530.1	0
PTHR31589,P	0	0	0	0	AT4G23380.1	0
PTHR12565,P	0	0	0	GO:0046983	AT1G59640.2	BPE,BPEp,BPE
PTHR12565,P	0	0	0	GO:0046983	AT1G59640.2	BPE,BPEp,BPE
PTHR12565,P	0	0	0	GO:0046983	AT1G59640.2	BPE,BPEp,BPE
PTHR12565,P	0	0	0	GO:0046983	AT1G59640.2	BPE,BPEp,BPE
PTHR11564,P	0	0	K13431	GO:0006614,(	AT4G30600.1	0
PTHR11564,P	0	0	K13431	GO:0006614,(	AT4G30600.1	0
PTHR24115,P	KOG0242,KO(	3.6.4.4	0	GO:0008017,(	AT4G14330.1	0
PTHR31213,P	0	0	K14496	0	AT1G01360.1	PYL9,RCAR1
PTHR23421,P	0	3.2.1.23	0	GO:0005975,(	AT2G28470.1	BGAL8
PTHR19297,P	KOG0799	0	0	GO:0016020,(	AT3G15350.1	0

arabi-defline	ID	Annot_define
NADH-ubiquinone oxidoreductase 24 kDa subunit, putative	Phvul.005G17	K03943 - NAD
Protein of unknown function (DUF620)	Phvul.001G02	PTHR31300:S
prefoldin 6	Phvul.002G32	K04798 - pref
S-locus lectin protein kinase family protein	Phvul.005G11	PF00069//PF
S-locus lectin protein kinase family protein	Phvul.005G11	PF00069//PF
S-locus lectin protein kinase family protein	Phvul.005G11	PF00069//PF
prefoldin 6	Phvul.009G12	K04798 - pref
S-locus lectin protein kinase family protein	Phvul.002G22	PF00954//PF
Tetratricopeptide repeat (TPR)-like superfamily protein	Phvul.006G04	PF01535//PF1
Tetratricopeptide repeat (TPR)-like superfamily protein	Phvul.006G05	PF01535//PF1
NB-ARC domain-containing disease resistance protein	Phvul.002G13	PTHR23155//
Leucine-rich repeat protein kinase family protein	Phvul.002G30	PTHR27008:S
Pathogenesis-related thaumatin superfamily protein	Phvul.003G26	PTHR31048:S
DNAJ heat shock family protein	Phvul.005G10	PTHR24078:S
lipoxygenase 2	Phvul.006G01	PTHR11771:S
global transcription factor group E7	Phvul.006G19	PTHR22880//
UDP-galactose transporter 2	Phvul.008G07	K15277 - solu
Major facilitator superfamily protein	Phvul.001G11	PTHR11654//
DNA polymerase alpha 2	Phvul.001G25	K02321 - DNA
pleckstrin homology (PH) domain-containing protein	Phvul.002G00	PTHR16166:S
0	0	0
AUX/IAA transcriptional regulator family protein	Phvul.003G13	PTHR31734:S
signal recognition particle receptor alpha subunit family prot	Phvul.003G15	K13431 - sign
DNAJ heat shock N-terminal domain-containing protein	Phvul.003G18	K09506 - DnaJ
F-box family protein	Phvul.006G01	PF00646 - F-b
F-box family protein	Phvul.006G01	PF00646 - F-b
acyl activating enzyme 12	Phvul.006G08	PF00501//PF1
Acyl-CoA N-acyltransferases (NAT) superfamily protein	Phvul.006G11	PTHR23091:S
FAD-binding Berberine family protein	Phvul.006G12	PTHR32448:S
Auxin-responsive family protein	Phvul.006G14	PTHR23130:S
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.007G04	PF12854//PF1
2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase super	Phvul.011G01	PTHR10209:S
NAC domain containing protein 36	Phvul.011G02	PTHR31989:S
metalloendopeptidases;zinc ion binding	Phvul.001G01	3.4.24.36 - Lei
metalloendopeptidases;zinc ion binding	Phvul.001G01	3.4.24.36 - Lei
S-ribonuclease binding protein 1	Phvul.001G02	PTHR10044:S
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.002G20	PF01535//PF1
ubiquitin-specific protease 27	Phvul.002G26	K11851 - ubiq
ubiquitin-specific protease 27	Phvul.002G26	K11851 - ubiq
Phox-associated domain;Phox-like;Sorting nexin, C-terminal	Phvul.003G01	K17925 - sorti
transcription factor jumonji (jmjC) domain-containing protei	Phvul.003G03	K15601 - lysin
Nucleotide-sugar transporter family protein	Phvul.003G21	PTHR11132//
N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tR
N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tR
Protein of unknown function (DUF3464)	Phvul.004G10	PF11947 - Pro

NADP-malic enzyme 4	Phvul.004G17	PTHR23406:S
KCBP-interacting protein kinase	Phvul.005G00	PTHR24351//
KCBP-interacting protein kinase	Phvul.005G00	PTHR24351//
COP1-interacting protein 7	Phvul.005G08	PTHR31008:S
Protein kinase protein with adenine nucleotide alpha hydrol	Phvul.005G16	PTHR27001:S
receptor like protein 48	Phvul.006G00	PF08263 - Leu
seed imbibition 2	Phvul.006G13	PF05691 - Raf
UDP-Glycosyltransferase superfamily protein	Phvul.007G08	PTHR11926:S
Phototropic-responsive NPH3 family protein	Phvul.008G08	PF00651//PF
Phototropic-responsive NPH3 family protein	Phvul.008G08	PF00651//PF
SMAD/FHA domain-containing protein	Phvul.008G13	PF00498 - FH
0	0	0
0	0	0
Protein of Unknown Function (DUF239)	Phvul.008G24	PF03080 - Do
Protein of Unknown Function (DUF239)	Phvul.008G24	PF14365 - Do
Protein of Unknown Function (DUF239)	Phvul.008G24	PF14365 - Do
BIG PETAL P	Phvul.009G18	PTHR12565//
BIG PETAL P	Phvul.009G18	PTHR12565//
BIG PETAL P	Phvul.009G18	PTHR12565//
BIG PETAL P	Phvul.009G18	PTHR12565//
signal recognition particle receptor alpha subunit family prot	Phvul.009G19	K13431 - sign
signal recognition particle receptor alpha subunit family prot	Phvul.009G19	K13431 - sign
P-loop containing nucleoside triphosphate hydrolases superf	Phvul.010G06	PTHR24115:S
regulatory component of ABA receptor 1	Phvul.010G11	PTHR31213:S
beta-galactosidase 8	Phvul.011G07	PF01301//PF
Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferas	Phvul.011G15	PTHR19297:S

IDENTIFIER	NAME	DESCRIPTION
Phvul.005G17	Cellular respir	component NQO2 of NADH dehydrogenase electron input (module N)
Phvul.001G02	Multi-process	GTPase effector (BDR) (original description: pacid=37169232 transcript
Phvul.002G32	Cytoskeleton (	component PFD6 of Prefoldin co-chaperone complex (original descript
Phvul.005G11	Enzyme classi	G-type lectin S-receptor-like serine/threonine-protein kinase At2g191
Phvul.005G11	Enzyme classi	G-type lectin S-receptor-like serine/threonine-protein kinase At2g191
Phvul.005G11	Enzyme classi	G-type lectin S-receptor-like serine/threonine-protein kinase At2g191
Phvul.009G12	Cytoskeleton (	component PFD6 of Prefoldin co-chaperone complex (original descript
Phvul.002G22	Protein modif	protein kinase (SD-1) (original description: pacid=37175156 transcript=
Phvul.006G04	not assigned.a	(original description: pacid=37172255 transcript=Phvul.006G047700.1
Phvul.006G05	not assigned.a	(original description: pacid=37173205 transcript=Phvul.006G059900.1
Phvul.002G13	not assigned.a	(original description: pacid=37177101 transcript=Phvul.002G133400.1
Phvul.002G30	Protein modif	protein kinase (LRR-III) (original description: pacid=37177113 transcrip
Phvul.003G26	not assigned.a	(original description: pacid=37147040 transcript=Phvul.003G263400.1
Phvul.005G10	not assigned.a	(original description: pacid=37153534 transcript=Phvul.005G100500.1
Phvul.006G01	Phytohormon	13-lipoxygenase (original description: pacid=37174172 transcript=Phvu
Phvul.006G19	RNA biosynth	transcriptional co-activator (BET/GTE) (original description: pacid=371
Phvul.008G07	Solute transp	nucleotide sugar transporter (UTR1|5) (original description: pacid=371
Phvul.001G11	Solute transp	anion transporter (NRT1/PTR) (original description: pacid=37170064 tr
Phvul.001G25	Cell cycle orga	replication fork tethering component POLA2 of DNA polymerase alpha
Phvul.002G00	not assigned.n	no hits & (original description: pacid=37175146 transcript=Phvul.002G
Phvul.002G27	not assigned.n	no hits & (original description: pacid=37178371 transcript=Phvul.002G
Phvul.003G13	not assigned.a	(original description: pacid=37147466 transcript=Phvul.003G138382.1
Phvul.003G15	Protein transl	component SR-alpha of SRP (signal recognition particle) receptor comp
Phvul.003G18	Protein home	co-chaperone (Jjj1) (original description: pacid=37145570 transcript=P
Phvul.006G01	Protein home	component FBX of SCF E3 ubiquitin ligase complex (original descriptior
Phvul.006G01	Protein home	component FBX of SCF E3 ubiquitin ligase complex (original descriptior
Phvul.006G08	not assigned.a	(original description: pacid=37171712 transcript=Phvul.006G086100.1
Phvul.006G11	not assigned.a	(original description: pacid=37173640 transcript=Phvul.006G117700.1
Phvul.006G12	Enzyme classi	Berberine bridge enzyme-like 21 OS=Arabidopsis thaliana (sp|q9svg3|
Phvul.006G14	not assigned.a	(original description: pacid=37172040 transcript=Phvul.006G142200.1
Phvul.007G04	RNA processin	plastidial mRNA processing factor (PPR10) (original description: pacid=
Phvul.011G01	not assigned.n	no hits & (original description: pacid=37154680 transcript=Phvul.011G
Phvul.011G02	RNA biosynth	transcription factor (NAC) (original description: pacid=37156658 transc
Phvul.001G01	Protein home	Leishmanolysin-type protease (original description: pacid=37168734 tr
Phvul.001G01	Protein home	Leishmanolysin-type protease (original description: pacid=37168734 tr
Phvul.001G02	not assigned.a	(original description: pacid=37170145 transcript=Phvul.001G023100.1
Phvul.002G20	not assigned.a	(original description: pacid=37178018 transcript=Phvul.002G208300.1
Phvul.002G26	Protein home	deubiquitinase (UBP27) (original description: pacid=37177124 transcri
Phvul.002G26	Protein home	deubiquitinase (UBP27) (original description: pacid=37177124 transcri
Phvul.003G01	not assigned.n	no hits & (original description: pacid=37148267 transcript=Phvul.003G
Phvul.003G03	RNA biosynth	transcription factor (JUMONJI) (original description: pacid=37147655 t
Phvul.003G21	not assigned.a	(original description: pacid=37145919 transcript=Phvul.003G216800.1
Phvul.004G04	RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid
Phvul.004G04	RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid
Phvul.004G10	Photosynthesi	PAM68 protein involved in PS-II assembly (original description: pacid=

Phvul.004G17	Lipid metaboli	cytosolic NADP-dependent malic enzyme (original description: pacid=3
Phvul.005G00	Protein modif	protein kinase (AGC-VIII) (original description: pacid=37154375 transcr
Phvul.005G00	Protein modif	protein kinase (AGC-VIII) (original description: pacid=37154375 transcr
Phvul.005G08	not assigned.	(original description: pacid=37153134 transcript=Phvul.005G084000.1
Phvul.005G16	Protein modif	protein kinase (PERK-related) (original description: pacid=37152765 tr
Phvul.006G00	not assigned.	(original description: pacid=37174231 transcript=Phvul.006G004580.1
Phvul.006G13	not assigned.	(original description: pacid=37171646 transcript=Phvul.006G135500.1
Phvul.007G08	Lipid metaboli	UDP-glucose:sterol glucosyltransferase (original description: pacid=37
Phvul.008G08	not assigned.	(original description: pacid=37161262 transcript=Phvul.008G080100.2
Phvul.008G08	not assigned.	(original description: pacid=37161262 transcript=Phvul.008G080100.2
Phvul.008G13	not assigned.	(original description: pacid=37160906 transcript=Phvul.008G131301.1
Phvul.008G19	not assigned.	no hits & (original description: pacid=37159620 transcript=Phvul.008
Phvul.008G19	not assigned.	no hits & (original description: pacid=37159620 transcript=Phvul.008
Phvul.008G24	not assigned.	no hits & (original description: pacid=37160578 transcript=Phvul.008
Phvul.008G24	not assigned.	no hits & (original description: pacid=37160890 transcript=Phvul.008
Phvul.008G24	not assigned.	no hits & (original description: pacid=37157759 transcript=Phvul.008
Phvul.009G18	External stim	transcriptional regulator (CIB) (original description: pacid=37149341 tr
Phvul.009G18	External stim	transcriptional regulator (CIB) (original description: pacid=37149341 tr
Phvul.009G18	External stim	transcriptional regulator (CIB) (original description: pacid=37149341 tr
Phvul.009G18	External stim	transcriptional regulator (CIB) (original description: pacid=37149341 tr
Phvul.009G19	Protein transl	component SR-alpha of SRP (signal recognition particle) receptor com
Phvul.009G19	Protein transl	component SR-alpha of SRP (signal recognition particle) receptor com
Phvul.010G06	Cytoskeleton	motor protein (Kinesin-10) (original description: pacid=37143788 trans
Phvul.010G11	Phytohormon	receptor component PYL/RCAR of cytoplasm-localized abscisic acid rec
Phvul.011G07	Cell wall orga	beta-galactosidase (BGAL) (original description: pacid=37154665 trans
Phvul.011G15	not assigned.	(original description: pacid=37155876 transcript=Phvul.011G158600.1

(original description: pacid=37153994 transcript=Phvul.005G179400.1 locus=Phvul.005G179400 ID

t=Phvul.001G025900.1 locus=Phvul.001G025900 ID=Phvul.001G025900.1.v2.1 annot-version=v2.1)

ion: pacid=37176929 transcript=Phvul.002G321900.1 locus=Phvul.002G321900 ID=Phvul.002G321

30 OS=Arabidopsis thaliana (sp|o64477|y2913_arath : 511.0) & Enzyme classification.EC_2 transfer

30 OS=Arabidopsis thaliana (sp|o64477|y2913_arath : 511.0) & Enzyme classification.EC_2 transfer

30 OS=Arabidopsis thaliana (sp|o64477|y2913_arath : 511.0) & Enzyme classification.EC_2 transfer

ion: pacid=37149943 transcript=Phvul.009G128800.1 locus=Phvul.009G128800 ID=Phvul.009G128

=Phvul.002G220500.1 locus=Phvul.002G220500 ID=Phvul.002G220500.1.v2.1 annot-version=v2.1) &

locus=Phvul.006G047700 ID=Phvul.006G047700.1.v2.1 annot-version=v2.1) & Pentatricopeptide r

locus=Phvul.006G059900 ID=Phvul.006G059900.1.v2.1 annot-version=v2.1) & Pentatricopeptide r

locus=Phvul.002G133400 ID=Phvul.002G133400.1.v2.1 annot-version=v2.1) & Disease resistance p

t=Phvul.002G302600.1 locus=Phvul.002G302600 ID=Phvul.002G302600.1.v2.1 annot-version=v2.1)

locus=Phvul.003G263400 ID=Phvul.003G263400.1.v2.1 annot-version=v2.1) & Thaumatin-like prot

locus=Phvul.005G100500 ID=Phvul.005G100500.1.v2.1 annot-version=v2.1) & DnaJ protein ERDJ3

ul.006G017100.1 locus=Phvul.006G017100 ID=Phvul.006G017100.1.v2.1 annot-version=v2.1) &

71293 transcript=Phvul.006G199400.1 locus=Phvul.006G199400 ID=Phvul.006G199400.1.v2.1 annc

60296 transcript=Phvul.008G070100.1 locus=Phvul.008G070100 ID=Phvul.008G070100.1.v2.1 ann

anscript=Phvul.001G119000.1 locus=Phvul.001G119000 ID=Phvul.001G119000.1.v2.1 annot-versio

complex (original description: pacid=37167920 transcript=Phvul.001G259300.1 locus=Phvul.001G2

003000.1 locus=Phvul.002G003000 ID=Phvul.002G003000.1.v2.1 annot-version=v2.1)

278800.1 locus=Phvul.002G278800 ID=Phvul.002G278800.1.v2.1 annot-version=v2.1)

locus=Phvul.003G138382 ID=Phvul.003G138382.1.v2.1 annot-version=v2.1) & Auxin-induced prot

plex (original description: pacid=37148117 transcript=Phvul.003G155500.1 locus=Phvul.003G15550

hvul.003G185100.1 locus=Phvul.003G185100 ID=Phvul.003G185100.1.v2.1 annot-version=v2.1) &

: pacid=37172683 transcript=Phvul.006G015900.2 locus=Phvul.006G015900 ID=Phvul.006G01590

: pacid=37172683 transcript=Phvul.006G015900.2 locus=Phvul.006G015900 ID=Phvul.006G01590

locus=Phvul.006G086100 ID=Phvul.006G086100.1.v2.1 annot-version=v2.1) & Probable acyl-activa

locus=Phvul.006G117700 ID=Phvul.006G117700.1.v2.1 annot-version=v2.1) & Probable N-acetyltr

bbe21_arath : 580.0) & Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting c

locus=Phvul.006G142200 ID=Phvul.006G142200.1.v2.1 annot-version=v2.1) & Cytochrome b561 a

37165270 transcript=Phvul.007G042700.1 locus=Phvul.007G042700 ID=Phvul.007G042700.1.v2.1 a

012400.1 locus=Phvul.011G012400 ID=Phvul.011G012400.1.v2.1 annot-version=v2.1)

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ranscript=Phvul.001G016500.2 locus=Phvul.001G016500 ID=Phvul.001G016500.2.v2.1 annot-versio

locus=Phvul.001G023100 ID=Phvul.001G023100.1.v2.1 annot-version=v2.1) & Probable BOI-relate

locus=Phvul.002G208300 ID=Phvul.002G208300.1.v2.1 annot-version=v2.1) & Pentatricopeptide r

pt=Phvul.002G267600.2 locus=Phvul.002G267600 ID=Phvul.002G267600.2.v2.1 annot-version=v2.1

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ranscript=Phvul.003G031500.1 locus=Phvul.003G031500 ID=Phvul.003G031500.1.v2.1 annot-versic

locus=Phvul.003G216800 ID=Phvul.003G216800.1.v2.1 annot-version=v2.1) & Probable sugar pho

=37162701 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1

=37162701 transcript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1

37163415 transcript=Phvul.004G106700.1 locus=Phvul.004G106700 ID=Phvul.004G106700.1.v2.1 a

37163561 transcript=Phvul.004G170800.1 locus=Phvul.004G170800 ID=Phvul.004G170800.1.v2.1 a
ript=Phvul.005G003300.2 locus=Phvul.005G003300 ID=Phvul.005G003300.2.v2.1 annot-version=v2.
ript=Phvul.005G003300.2 locus=Phvul.005G003300 ID=Phvul.005G003300.2.v2.1 annot-version=v2.
1 locus=Phvul.005G084000 ID=Phvul.005G084000.1.v2.1 annot-version=v2.1) & COP1-interacting pr
anscript=Phvul.005G160700.1 locus=Phvul.005G160700 ID=Phvul.005G160700.1.v2.1 annot-versio
1 locus=Phvul.006G004580 ID=Phvul.006G004580.1.v2.1 annot-version=v2.1) & Receptor-like prote
1 locus=Phvul.006G135500 ID=Phvul.006G135500.1.v2.1 annot-version=v2.1) & Probable galactinol-
167623 transcript=Phvul.007G080800.2 locus=Phvul.007G080800 ID=Phvul.007G080800.2.v2.1 ann
2 locus=Phvul.008G080100 ID=Phvul.008G080100.2.v2.1 annot-version=v2.1) & BTB/POZ domain-c
2 locus=Phvul.008G080100 ID=Phvul.008G080100.2.v2.1 annot-version=v2.1) & BTB/POZ domain-c
1 locus=Phvul.008G131301 ID=Phvul.008G131301.1.v2.1 annot-version=v2.1) & FHA domain-contai
G191200.2 locus=Phvul.008G191200 ID=Phvul.008G191200.2.v2.1 annot-version=v2.1)
G191200.2 locus=Phvul.008G191200 ID=Phvul.008G191200.2.v2.1 annot-version=v2.1)
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ranscript=Phvul.009G183600.4 locus=Phvul.009G183600 ID=Phvul.009G183600.4.v2.1 annot-versio
ranscript=Phvul.009G183600.4 locus=Phvul.009G183600 ID=Phvul.009G183600.4.v2.1 annot-versio
ranscript=Phvul.009G183600.4 locus=Phvul.009G183600 ID=Phvul.009G183600.4.v2.1 annot-versio
plex (original description: pacid=37149160 transcript=Phvul.009G194700.2 locus=Phvul.009G19470
plex (original description: pacid=37149160 transcript=Phvul.009G194700.2 locus=Phvul.009G19470
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ceptor complex (original description: pacid=37143807 transcript=Phvul.010G112500.1 locus=Phvul.
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1 locus=Phvul.011G158600 ID=Phvul.011G158600.1.v2.1 annot-version=v2.1) & Beta-glucuronosyltr

=Phvul.005G179400.1.v2.1 annot-version=v2.1) &
&
900.1.v2.1 annot-version=v2.1) &
ases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript
ases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript
ases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 114.9) (original descript
800.1.v2.1 annot-version=v2.1) &
&
epeat-containing protein At4g02750 OS=Arabidopsis thaliana (sp|q9sy02|pp301_arath : 429.0)
epeat-containing protein At4g02750 OS=Arabidopsis thaliana (sp|q9sy02|pp301_arath : 469.0)
protein RPM1 OS=Arabidopsis thaliana (sp|q39214|rpm1_arath : 432.0)
) &
tein 1 OS=Arabidopsis thaliana (sp|a0a1p8b554|thlp1_arath : 285.0)
B OS=Arabidopsis thaliana (sp|q9lzk5|dnj19_arath : 137.0)

t-version=v2.1) &
ot-version=v2.1) &
n=v2.1) &
259300 ID=Phvul.001G259300.1.v2.1 annot-version=v2.1) &

ein 22B OS=Vigna radiata var. radiata (sp|p32294|ax22b_vigrr : 291.0)
0 ID=Phvul.003G155500.1.v2.1 annot-version=v2.1) &

.2.v2.1 annot-version=v2.1) &
.2.v2.1 annot-version=v2.1) &
ating enzyme 12, peroxisomal OS=Arabidopsis thaliana (sp|q9ss00|aae12_arath : 670.0)
ansferase HLS1-like OS=Arabidopsis thaliana (sp|o64815|hls1l_arath : 254.0)
n CH-OH group of donor(50.1.1 : 461.0) (original description: pacid=37172282 transcript=Phvul.00
nd DOMON domain-containing protein At5g47530 OS=Arabidopsis thaliana (sp|q9fgk4|b561j_arat
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2.1) &
n=v2.1) &
n=v2.1) &
d E3 ubiquitin-protein ligase 3 OS=Arabidopsis thaliana (sp|q9ldd1|brg3_arath : 117.0)
epeat-containing protein At5g18390, mitochondrial OS=Arabidopsis thaliana (sp|q94jx6|pp391_ar
1) &
1) &

on=v2.1) &
sphate/phosphate translocator At1g12500 OS=Arabidopsis thaliana (sp|q9ldh3|pt112_arath : 462.
annot-version=v2.1) &
annot-version=v2.1) &
nnot-version=v2.1) &

nnot-version=v2.1) &
.1) &
.1) &
rotein 7 OS=Arabidopsis thaliana (sp|o80386|cip7_arath : 505.0)
n=v2.1) &
in EIX2 OS=Solanum lycopersicum (sp|q6jn46|eix2_sollc : 120.0)
--sucrose galactosyltransferase 2 OS=Arabidopsis thaliana (sp|q94a08|rfs2_arath : 732.0)
ıot-version=v2.1) &
ontaining protein At3g08570 OS=Arabidopsis thaliana (sp|q9c9z7|y3857_arath : 661.0)
ontaining protein At3g08570 OS=Arabidopsis thaliana (sp|q9c9z7|y3857_arath : 661.0)
ning protein FHA2 OS=Arabidopsis thaliana (sp|q9sfv2|fha2_arath : 431.0)

n=v2.1) &
n=v2.1) &
n=v2.1) &
n=v2.1) &
0 ID=Phvul.009G194700.2.v2.1 annot-version=v2.1) &
0 ID=Phvul.009G194700.2.v2.1 annot-version=v2.1) &
v2.1) &
010G112500 ID=Phvul.010G112500.1.v2.1 annot-version=v2.1) &
2.1) &
ransferase GlcAT14A OS=Arabidopsis thaliana (sp|q9fld7|gt14a_arath : 462.0)

:ion: pacid=37153001 transcript=Phvul.005G110300.3 locus=Phvul.005G110300 ID=Phvul.005G1103

:ion: pacid=37153001 transcript=Phvul.005G110300.3 locus=Phvul.005G110300 ID=Phvul.005G1103

:ion: pacid=37153001 transcript=Phvul.005G110300.3 locus=Phvul.005G110300 ID=Phvul.005G1103

6G125600.1 locus=Phvul.006G125600 ID=Phvul.006G125600.1.v2.1 annot-version=v2.1) &

:h : 147.0)

ath : 590.0)

.0)

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

miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
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gauccccggcaa	Phvul.005G120700.1	3	-1	1	20
gauccccggcaa	Phvul.005G120700.2	3	-1	1	20
gauccccggcaa	Phvul.006G001600.1	3	-1	1	20
gauccccggcaa	Phvul.007G023000.1	3.5	-1	1	20
gauccccggcaa	Phvul.008G271000.1	3.5	-1	1	20
gauccccggcaa	Phvul.001G240600.1	4	-1	1	20
gauccccggcaa	Phvul.003G220500.1	4	-1	1	20
gauccccggcaa	Phvul.003G237300.1	4	-1	1	20
gauccccggcaa	Phvul.003G285700.1	4	-1	1	20
gauccccggcaa	Phvul.004G086300.2	4	-1	1	20
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gauccccggcaa	Phvul.006G068400.1	4	-1	1	20
gauccccggcaa	Phvul.006G130200.1	4	-1	1	20
gauccccggcaa	Phvul.007G268300.1	4	-1	1	20
gauccccggcaa	Phvul.008G036200.1	4	-1	1	20
gauccccggcaa	Phvul.008G290700.1	4	-1	1	20
gauccccggcaa	Phvul.009G144300.1	4	-1	1	20
gauccccggcaa	Phvul.001G028400.1	4.5	-1	1	20
gauccccggcaa	Phvul.001G071200.1	4.5	-1	1	20
gauccccggcaa	Phvul.001G146900.1	4.5	-1	1	20
gauccccggcaa	Phvul.001G147001.1	4.5	-1	1	20
gauccccggcaa	Phvul.001G147001.2	4.5	-1	1	20
gauccccggcaa	Phvul.002G006700.1	4.5	-1	1	20
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gauccccggcaa	Phvul.002G092900.2	4.5	-1	1	20
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gauccccggcaa	Phvul.002G274500.1	4.5	-1	1	20
gauccccggcaa	Phvul.002G315300.1	4.5	-1	1	20
gauccccggcaa	Phvul.003G076700.2	4.5	-1	1	20
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gauccccggcaa	Phvul.003G099100.3	4.5	-1	1	20
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gauccccggcaa	Phvul.004G037600.3	4.5	-1	1	20
gauccccggcaa	Phvul.004G037600.2	4.5	-1	1	20
gauccccggcaa	Phvul.004G049200.1	4.5	-1	1	20
gauccccggcaa	Phvul.004G110200.2	4.5	-1	1	20
gauccccggcaa	Phvul.004G171500.6	4.5	-1	1	20
gauccccggcaa	Phvul.004G171500.2	4.5	-1	1	20
gauccccggcaa	Phvul.004G171500.3	4.5	-1	1	20
gauccccggcaa	Phvul.004G171500.1	4.5	-1	1	20
gauccccggcaa	Phvul.004G171500.5	4.5	-1	1	20
gauccccggcaa	Phvul.004G171500.4	4.5	-1	1	20
gauccccggcaa	Phvul.005G022300.1	4.5	-1	1	20

gaucccggcaa	Phvul.005G159600.1	4.5	-1	1	20
gaucccggcaa	Phvul.006G049100.1	4.5	-1	1	20
gaucccggcaa	Phvul.006G068100.1	4.5	-1	1	20
gaucccggcaa	Phvul.006G087700.1	4.5	-1	1	20
gaucccggcaa	Phvul.007G208400.1	4.5	-1	1	20
gaucccggcaa	Phvul.008G042900.1	4.5	-1	1	20
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gaucccggcaa	Phvul.009G157200.1	4.5	-1	1	20
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gaucccggcaa	Phvul.010G082300.1	4.5	-1	1	20
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gaucccggcaa	Phvul.001G025101.1	5	-1	1	20
gaucccggcaa	Phvul.001G183700.1	5	-1	1	20
gaucccggcaa	Phvul.001G209500.2	5	-1	1	20
gaucccggcaa	Phvul.001G209900.2	5	-1	1	20
gaucccggcaa	Phvul.001G250100.2	5	-1	1	20
gaucccggcaa	Phvul.001G250100.1	5	-1	1	20
gaucccggcaa	Phvul.002G063100.1	5	-1	1	20
gaucccggcaa	Phvul.002G111100.1	5	-1	1	20
gaucccggcaa	Phvul.002G132600.2	5	-1	1	20
gaucccggcaa	Phvul.002G132600.1	5	-1	1	20
gaucccggcaa	Phvul.002G188300.1	5	-1	1	20
gaucccggcaa	Phvul.002G252700.1	5	-1	1	20
gaucccggcaa	Phvul.002G324600.1	5	-1	1	20
gaucccggcaa	Phvul.003G043600.2	5	-1	1	20
gaucccggcaa	Phvul.003G064900.1	5	-1	1	20
gaucccggcaa	Phvul.003G076900.1	5	-1	1	20
gaucccggcaa	Phvul.003G192900.1	5	-1	1	20
gaucccggcaa	Phvul.003G192900.2	5	-1	1	20
gaucccggcaa	Phvul.004G017600.1	5	-1	1	20
gaucccggcaa	Phvul.005G035400.1	5	-1	1	20
gaucccggcaa	Phvul.005G080800.2	5	-1	1	20
gaucccggcaa	Phvul.005G080800.1	5	-1	1	20
gaucccggcaa	Phvul.005G095300.1	5	-1	1	20
gaucccggcaa	Phvul.005G176600.1	5	-1	1	20
gaucccggcaa	Phvul.006G034100.1	5	-1	1	20
gaucccggcaa	Phvul.007G196100.2	5	-1	1	20
gaucccggcaa	Phvul.007G196100.1	5	-1	1	20
gaucccggcaa	Phvul.007G268300.1	5	-1	1	20
gaucccggcaa	Phvul.008G015300.3	5	-1	1	20
gaucccggcaa	Phvul.008G015300.4	5	-1	1	20
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gaucccggcaa	Phvul.008G015300.5	5	-1	1	20
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gaucccggcaa	Phvul.008G203314.1	5	-1	1	20
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gaucccggcaa	Phvul.009G128500.4	5	-1	1	20
gaucccggcaa	Phvul.009G255500.1	5	-1	1	20
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gaucccggcaa	Phvul.010G032000.1	5	-1	1	20
gaucccggcaa	Phvul.011G062200.1	5	-1	1	20
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Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
1053	1072	GAUCCCCGGC	::::: ::::.:::: ::	GGGCGCGGU	Cleavage	pacid=371628
222	241	GAUCCCCGGC	::::::::::::: : ::	CGGCGCCGU	Cleavage	pacid=371525
367	386	GAUCCCCGGC	::::::::::::: : ::	CGGCGCCGU	Cleavage	pacid=371525
716	735	GAUCCCCGGC	::::: :::: :::::::.	CGGCGCAGU	Cleavage	pacid=371718
559	578	GAUCCCCGGC	:::::::::::.:: :: :	CGGCGCCGU	Cleavage	pacid=371640
1667	1686	GAUCCCCGGC	:::::::: :.:::::.:	AGGCGCCGU	Translation	pacid=371600
945	964	GAUCCCCGGC	::::::.:::::.:: : ::	UGGCGCUGU	Cleavage	pacid=371707
623	642	GAUCCCCGGC	::::::: ::::::: ::	CGGCGCCGA	Cleavage	pacid=371463
619	638	GAUCCCCGGC	::::: .:::::::: :::	UGGCGGUGU	Cleavage	pacid=371472
1454	1473	GAUCCCCGGC	:::.:::::::::.:: :.:	UGGUGCCGU	Cleavage	pacid=371474
1131	1150	GAUCCCCGGC	:: ::.::::..::::::.	UGAGGCUGU	Cleavage	pacid=371618
1663	1682	GAUCCCCGGC	:: ::.::::..::::::.	UGAGGCUGU	Cleavage	pacid=371618
238	257	GAUCCCCGGC	::.:.::: :::::::: :	CGGUGUCGU	Translation	pacid=371737
1177	1196	GAUCCCCGGC	::. :.:::::.::::.:	CGGUUCUGU	Cleavage	pacid=371732
560	579	GAUCCCCGGC	:::::: ::::::::::	CCGCGCCGCC	Translation	pacid=371658
316	335	GAUCCCCGGC	::.::::::::..: ::::	CGGUGCCGU	Cleavage	pacid=371600
221	240	GAUCCCCGGC	:::: :::::::::: ::	AGGCGGCGU	Cleavage	pacid=371609
681	700	GAUCCCCGGC	:::::: ::::::::::	GGGCGCCUC	Cleavage	pacid=371502
596	615	GAUCCCCGGC	:: ::.::::::.: ::::	AGGAGCUGU	Cleavage	pacid=371709
702	721	GAUCCCCGGC	::.:::::::..:::: :	GGGUGCUGU	Cleavage	pacid=371698
1160	1179	GAUCCCCGGC	: :. :.::::.::::::	UUGUUCUGU	Cleavage	pacid=371680
816	835	GAUCCCCGGC	: :. ::::::::::::	UUGUUCUGU	Cleavage	pacid=371704
928	947	GAUCCCCGGC	: :. :.::::.:::::	UUGUUCUGU	Cleavage	pacid=371704
1011	1030	GAUCCCCGGC	::::.: ::::.:::: ::	UGGUGAAGU	Cleavage	pacid=371753
680	699	GAUCCCCGGC	:::.:::::.::::: :	CUCCGCUGU	Cleavage	pacid=371755
5389	5408	GAUCCCCGGC	: :::::::::::: :::	AUGAGCCGU	Cleavage	pacid=371766
5401	5420	GAUCCCCGGC	: :::::::::::: :::	AUGAGCCGU	Cleavage	pacid=371766
710	729	GAUCCCCGGC	::: :::::::. :::: :	GGGCACCGU	Cleavage	pacid=371760
1178	1197	GAUCCCCGGC	::: :..::::..: :::::	UGGGGUUGU	Cleavage	pacid=371744
247	266	GAUCCCCGGC	::::: .::::::: ::::	UGGCGAUGU	Cleavage	pacid=371472
247	266	GAUCCCCGGC	::::: .::::::: ::::	UGGCGAUGU	Cleavage	pacid=371472
2013	2032	GAUCCCCGGC	::::: ::::.:: :::.:	AGGCGCAGU	Cleavage	pacid=371449
2411	2430	GAUCCCCGGC	::::: ::::.:: :::.:	AGGCGCAGU	Cleavage	pacid=371449
2449	2468	GAUCCCCGGC	::::: ::::.:: :::.:	AGGCGCAGU	Cleavage	pacid=371449
1246	1265	GAUCCCCGGC	::: : .:::::::: :::.	UGGGGAUGU	Cleavage	pacid=371632
1246	1265	GAUCCCCGGC	::: : .:::::::: :::.	UGGGGAUGU	Cleavage	pacid=371632
1075	1094	GAUCCCCGGC	:: .: .::::..::::::.	UGUUGGUGU	Cleavage	pacid=371636
705	724	GAUCCCCGGC	::::: :: ::.:::: ::	GGGCGCGGU	Translation	pacid=371636
463	482	GAUCCCCGGC	:::.::.::::..:: :::	UGGUGCUGU	Cleavage	pacid=371623
472	491	GAUCCCCGGC	:::.::.::::..:: :::	UGGUGCUGU	Cleavage	pacid=371623
463	482	GAUCCCCGGC	:::.::.::::..:: :::	UGGUGCUGU	Cleavage	pacid=371623
472	491	GAUCCCCGGC	:::.::.::::..:: :::	UGGUGCUGU	Cleavage	pacid=371623
463	482	GAUCCCCGGC	:::.::.::::..:: :::	UGGUGCUGU	Cleavage	pacid=371623
472	491	GAUCCCCGGC	:::.::.::::..:: :::	UGGUGCUGU	Cleavage	pacid=371623
998	1017	GAUCCCCGGC	::.:..::::.: :::.:.	GGGUGUUGU	Cleavage	pacid=371537

513	532	GAUCCCCGGC	::.: : :::: :::::::	AGGUGGCCU	Cleavage	pacid=371545
1225	1244	GAUCCCCGGC	:::.::::::::..: ::::	UGGUGCCGU	Cleavage	pacid=371719
511	530	GAUCCCCGGC	::.:..::::. ::::.:.	GGGUGUUGU	Cleavage	pacid=371741
861	880	GAUCCCCGGC	:: ::.:::::.:::: :	GGGGGCUGU	Cleavage	pacid=371738
576	595	GAUCCCCGGC	::: : :::::::::::	CGGCACAGU	Cleavage	pacid=371665
432	451	GAUCCCCGGC	: :.:::::.::::::.	UCCCACUGU	Cleavage	pacid=371596
773	792	GAUCCCCGGC	:.::.:::::. :::.::	AAGUGCUGU	Cleavage	pacid=371580
1132	1151	GAUCCCCGGC	:.::.:::::. :::.::	AAGUGCUGU	Cleavage	pacid=371580
516	535	GAUCCCCGGC	:::.:. :::::: :::::	UGGUGUAGU	Cleavage	pacid=371605
1341	1360	GAUCCCCGGC	:::. :.:::: :::::::	UGGUUCUGU	Cleavage	pacid=371499
1368	1387	GAUCCCCGGC	:::. :.:::: :::::::	UGGUUCUGU	Cleavage	pacid=371499
154	173	GAUCCCCGGC	:::.:. :::::: :::::	UGGUGUAGU	Cleavage	pacid=371422
1652	1671	GAUCCCCGGC	:::: ::::::: :::::.	UGGCACCGU	Cleavage	pacid=371438
597	616	GAUCCCCGGC	:: :::.:: ::::: ::::	UGUCGCUGU	Translation	pacid=371439
2765	2784	GAUCCCCGGC	: .::.:::::: :::::	GGCUGCUGU	Cleavage	pacid=371573
276	295	GAUCCCCGGC	::.: :::::.:::::.	AGGUGGCGU	Cleavage	pacid=371681
871	890	GAUCCCCGGC	::::: ::::: .: ::.::	UGGCGGCGU	Cleavage	pacid=371692
1254	1273	GAUCCCCGGC	::.::::::::..:: :. :	GGGUGCCGU	Cleavage	pacid=371677
1156	1175	GAUCCCCGGC	::::: :::::. :::::	UGGCGAAGU	Cleavage	pacid=371689
48	67	GAUCCCCGGC	::: ::.::::.::: : ::	UGGAGCUGU	Cleavage	pacid=371707
57	76	GAUCCCCGGC	::: ::.::::.::: : ::	UGGAGCUGU	Cleavage	pacid=371707
707	726	GAUCCCCGGC	::::: ::::::::::	CUGCGCCAA	Cleavage	pacid=371743
1118	1137	GAUCCCCGGC	::::::: :::.: ::::.	ACGCGCCGU	Translation	pacid=371761
1742	1761	GAUCCCCGGC	::.::.:::::.: :::. :	AGGUGCUGU	Cleavage	pacid=371787
1708	1727	GAUCCCCGGC	::.::.:::::.: :::. :	AGGUGCUGU	Cleavage	pacid=371787
624	643	GAUCCCCGGC	:: : :.:: :::::::::	UGUCACUGU	Translation	pacid=371749
896	915	GAUCCCCGGC	::.::.::: .:::::. :	CGGUGCUGU	Translation	pacid=371746
1576	1595	GAUCCCCGGC	:: .:..:::::..:::: ::	UGUUGUUGU	Cleavage	pacid=371755
89	108	GAUCCCCGGC	:::.: .::::: : :::::	UGGUGAUGU	Cleavage	pacid=371474
900	919	GAUCCCCGGC	:::::.:::: .:::::	GGGCGCUGU	Cleavage	pacid=371461
1207	1227	GAUCC-CCGG	::::. ::::.::: :::::	CGGCGUGGU	Cleavage	pacid=371478
81	100	GAUCCCCGGC	::.:::::..:::: ::	UCUCGUCGU	Cleavage	pacid=371457
81	100	GAUCCCCGGC	::.:::::..:::: ::	UCUCGUCGU	Cleavage	pacid=371457
3869	3888	GAUCCCCGGC	: :.:..::: ..:::::::	UCGUGUUGU	Translation	pacid=371629
842	861	GAUCCCCGGC	:::::.:::: .:: :.:.	AGGCGCUGU	Cleavage	pacid=371525
860	879	GAUCCCCGGC	:::. :.:::::.:: :.:.	UGGUUCUGU	Cleavage	pacid=371543
863	882	GAUCCCCGGC	:::. :.:::::.:: :.:.	UGGUUCUGU	Cleavage	pacid=371543
542	561	GAUCCCCGGC	:::. ..: :::.::::::.	UGGUCUUGA	Cleavage	pacid=371545
1260	1279	GAUCCCCGGC	: .:.::::::.:::::	AGUUGUCGU	Cleavage	pacid=371526
472	491	GAUCCCCGGC	:::.:..: :::. ::::::	UGGUGUUGG	Cleavage	pacid=371721
1295	1314	GAUCCCCGGC	:::.:::: :::::: :.:	UGGUGCCGG	Cleavage	pacid=371642
1580	1599	GAUCCCCGGC	:::.:::: :::::: :.:	UGGUGCCGG	Cleavage	pacid=371642
293	312	GAUCCCCGGC	::: :.::::. : :::::	CGGCACUGU	Cleavage	pacid=371658
876	895	GAUCCCCGGC	:: .::.:::::. :::::	UGAUGCUGU	Cleavage	pacid=371611
876	895	GAUCCCCGGC	:: .::.:::::. :::::	UGAUGCUGU	Cleavage	pacid=371611
875	894	GAUCCCCGGC	:: .::.:::::. :::::	UGAUGCUGU	Cleavage	pacid=371611

876	895	GAUCCCCGGC	:: .::.:::::. :::::	UGAUGCUGU	Cleavage	pacid=371611
875	894	GAUCCCCGGC	:: .::.:::::. :::::	UGAUGCUGU	Cleavage	pacid=371611
242	261	GAUCCCCGGC	: :: :.:: :::::::::	UUGCUCUGU	Translation	pacid=371607
558	577	GAUCCCCGGC	::::: .: :::.:::: ::	UGGCGGUGC	Cleavage	pacid=371595
558	577	GAUCCCCGGC	::::: .: :::.:::: ::	UGGCGGUGC	Cleavage	pacid=371595
3937	3956	GAUCCCCGGC	::::.:::: : :::.::	GAGCGCUGU	Cleavage	pacid=371594
3937	3956	GAUCCCCGGC	::::.:::: : :::.::	GAGCGCUGU	Cleavage	pacid=371594
1330	1349	GAUCCCCGGC	::: :..:::: .::::::	UGGAGUUGU	Cleavage	pacid=371598
1154	1173	GAUCCCCGGC	::.:..::::.: :: :::	AGGUGUUGU	Cleavage	pacid=371589
709	728	GAUCCCCGGC	:::.: .:::::.:: :::	UGGUGGUGU	Cleavage	pacid=371614
388	407	GAUCCCCGGC	:::: .: :::::: :.::	UGGCCUCCU	Cleavage	pacid=371499
1505	1524	GAUCCCCGGC	:::: :.::::::.::: ::	UGGCUCUGU	Cleavage	pacid=371492
1517	1536	GAUCCCCGGC	:::: :.::::::.::: ::	UGGCUCUGU	Cleavage	pacid=371492
1544	1563	GAUCCCCGGC	:::: :.::::::.::: ::	UGGCUCUGU	Cleavage	pacid=371492
1767	1786	GAUCCCCGGC	:::: :.::::::.::: ::	UGGCUCUGU	Cleavage	pacid=371493
741	760	GAUCCCCGGC	::: ::.::: ::: ::::.	UGGAGCUGU	Translation	pacid=371491
843	862	GAUCCCCGGC	::: ::.::: ::: ::::.	UGGAGCUGU	Translation	pacid=371491
2180	2199	GAUCCCCGGC	::.:..:::::. : ::::	GGGUGUUGU	Cleavage	pacid=371428
752	771	GAUCCCCGGC	::.::.::::::: : :	CGGUGCUGU	Cleavage	pacid=371564
382	401	GAUCCCCGGC	:.:::::::::::::.	CCAACCUGU	Cleavage	pacid=371553
382	401	GAUCCCCGGC	:.:::::::::::::.	CCAACCUGU	Cleavage	pacid=371553

Multiplicity	Target_Acc.	ID	locusName	Pfam
1	Phvul.004G110400.1	Phvul.004G110400	Phvul.004G110400	PF00168
1	Phvul.005G120700.1	Phvul.005G120700	Phvul.005G120700	PF00069
1	Phvul.005G120700.2	Phvul.005G120700	Phvul.005G120700	PF00069
1	Phvul.006G001600.1	Phvul.006G001600	Phvul.006G001600	PF00012
1	Phvul.007G023000.1	Phvul.007G023000	Phvul.007G023000	PF01814
1	Phvul.008G271000.1	Phvul.008G271000	Phvul.008G271000	PF07983,PF00
1	Phvul.001G240600.1	Phvul.001G240600	Phvul.001G240600	PF00168
1	Phvul.003G220500.1	Phvul.003G220500	Phvul.003G220500	PF01095
1	Phvul.003G237300.1	Phvul.003G237300	Phvul.003G237300	PF05922,PF02
1	Phvul.003G285700.1	Phvul.003G285700	Phvul.003G285700	PF00010,PF14
1	Phvul.004G086300.2	Phvul.004G086300	Phvul.004G086300	PF00069
1	Phvul.004G086300.1	Phvul.004G086300	Phvul.004G086300	PF00069
1	Phvul.006G068400.1	Phvul.006G068400	Phvul.006G068400	PF13540,PF00
1	Phvul.006G130200.1	Phvul.006G130200	Phvul.006G130200	PF04146
2	Phvul.007G268300.1	Phvul.007G268300	Phvul.007G268300	0
1	Phvul.008G036200.1	Phvul.008G036200	Phvul.008G036200	PF00520
1	Phvul.008G290700.1	Phvul.008G290700	Phvul.008G290700	PF05678
1	Phvul.009G144300.1	Phvul.009G144300	Phvul.009G144300	PF03479
1	Phvul.001G028400.1	Phvul.001G028400	Phvul.001G028400	PF03081
1	Phvul.001G071200.1	Phvul.001G071200	Phvul.001G071200	PF00069
1	Phvul.001G146900.1	Phvul.001G146900	Phvul.001G146900	PF00069
1	Phvul.001G147001.1	Phvul.001G147001	Phvul.001G147001	PF07714
1	Phvul.001G147001.2	Phvul.001G147001	Phvul.001G147001	PF07714
1	Phvul.002G006700.1	Phvul.002G006700	Phvul.002G006700	PF03479
1	Phvul.002G059000.1	Phvul.002G059000	Phvul.002G059000	0
1	Phvul.002G092900.2	Phvul.002G092900	Phvul.002G092900	PF00118,PF01
1	Phvul.002G092900.1	Phvul.002G092900	Phvul.002G092900	PF00118,PF01
1	Phvul.002G274500.1	Phvul.002G274500	Phvul.002G274500	PF01764
1	Phvul.002G315300.1	Phvul.002G315300	Phvul.002G315300	PF03456,PF00
1	Phvul.003G076700.2	Phvul.003G076700	Phvul.003G076700	PF00232
1	Phvul.003G076700.1	Phvul.003G076700	Phvul.003G076700	PF00232
1	Phvul.003G099100.1	Phvul.003G099100	Phvul.003G099100	PF01156
1	Phvul.003G099100.3	Phvul.003G099100	Phvul.003G099100	PF01156
1	Phvul.003G099100.2	Phvul.003G099100	Phvul.003G099100	PF01156
1	Phvul.004G037600.3	Phvul.004G037600	Phvul.004G037600	PF00560,PF00
1	Phvul.004G037600.2	Phvul.004G037600	Phvul.004G037600	PF00560,PF00
1	Phvul.004G049200.1	Phvul.004G049200	Phvul.004G049200	PF03639
1	Phvul.004G110200.2	Phvul.004G110200	Phvul.004G110200	PF00168
1	Phvul.004G171500.6	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.2	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.3	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.1	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.5	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.004G171500.4	Phvul.004G171500	Phvul.004G171500	PF00132
1	Phvul.005G022300.1	Phvul.005G022300	Phvul.005G022300	PF03151

1	Phvul.005G159600.1	Phvul.005G159600	Phvul.005G159600	PF05879
1	Phvul.006G049100.1	Phvul.006G049100	Phvul.006G049100	PF12327,PF00
1	Phvul.006G068100.1	Phvul.006G068100	Phvul.006G068100	PF01713,PF08
1	Phvul.006G087700.1	Phvul.006G087700	Phvul.006G087700	PF00069,PF00
1	Phvul.007G208400.1	Phvul.007G208400	Phvul.007G208400	PF00249
1	Phvul.008G042900.1	Phvul.008G042900	Phvul.008G042900	PF13360
1	Phvul.008G124000.2	Phvul.008G124000	Phvul.008G124000	PF12452
1	Phvul.008G124000.1	Phvul.008G124000	Phvul.008G124000	PF12452
1	Phvul.008G233100.1	Phvul.008G233100	Phvul.008G233100	PF01841,PF10
1	Phvul.009G157200.2	Phvul.009G157200	Phvul.009G157200	PF02493,PF01
1	Phvul.009G157200.1	Phvul.009G157200	Phvul.009G157200	PF02493,PF01
1	Phvul.010G024866.1	Phvul.010G024866	Phvul.010G024866	PF10404,PF10
1	Phvul.010G082300.1	Phvul.010G082300	Phvul.010G082300	PF01073
1	Phvul.010G119800.1	Phvul.010G119800	Phvul.010G119800	PF03168
1	Phvul.011G029450.1	Phvul.011G029450	Phvul.011G029450	PF04818,PF00
1	Phvul.001G025101.1	Phvul.001G025101	Phvul.001G025101	PF03629
1	Phvul.001G183700.1	Phvul.001G183700	Phvul.001G183700	PF03465,PF03
1	Phvul.001G209500.2	Phvul.001G209500	Phvul.001G209500	PF00759
1	Phvul.001G209900.2	Phvul.001G209900	Phvul.001G209900	PF01966,PF04
1	Phvul.001G250100.2	Phvul.001G250100	Phvul.001G250100	PF00168,PF00
1	Phvul.001G250100.1	Phvul.001G250100	Phvul.001G250100	PF00168,PF00
1	Phvul.002G063100.1	Phvul.002G063100	Phvul.002G063100	PF01095
1	Phvul.002G111100.1	Phvul.002G111100	Phvul.002G111100	PF08263,PF07
1	Phvul.002G132600.2	Phvul.002G132600	Phvul.002G132600	0
1	Phvul.002G132600.1	Phvul.002G132600	Phvul.002G132600	0
1	Phvul.002G188300.1	Phvul.002G188300	Phvul.002G188300	PF00646
1	Phvul.002G252700.1	Phvul.002G252700	Phvul.002G252700	PF00400
1	Phvul.002G324600.1	Phvul.002G324600	Phvul.002G324600	PF08263,PF13
1	Phvul.003G043600.2	Phvul.003G043600	Phvul.003G043600	PF00232
1	Phvul.003G064900.1	Phvul.003G064900	Phvul.003G064900	PF01384
1	Phvul.003G076900.1	Phvul.003G076900	Phvul.003G076900	PF00067
1	Phvul.003G192900.1	Phvul.003G192900	Phvul.003G192900	PF02183,PF00
1	Phvul.003G192900.2	Phvul.003G192900	Phvul.003G192900	PF02183,PF00
1	Phvul.004G017600.1	Phvul.004G017600	Phvul.004G017600	PF15612,PF01
1	Phvul.005G035400.1	Phvul.005G035400	Phvul.005G035400	PF08799,PF02
1	Phvul.005G080800.2	Phvul.005G080800	Phvul.005G080800	PF09507
1	Phvul.005G080800.1	Phvul.005G080800	Phvul.005G080800	PF09507
1	Phvul.005G095300.1	Phvul.005G095300	Phvul.005G095300	PF00311
1	Phvul.005G176600.1	Phvul.005G176600	Phvul.005G176600	PF13041
1	Phvul.006G034100.1	Phvul.006G034100	Phvul.006G034100	PF01501
1	Phvul.007G196100.2	Phvul.007G196100	Phvul.007G196100	0
1	Phvul.007G196100.1	Phvul.007G196100	Phvul.007G196100	0
2	Phvul.007G268300.1	Phvul.007G268300	Phvul.007G268300	0
1	Phvul.008G015300.3	Phvul.008G015300	Phvul.008G015300	0
1	Phvul.008G015300.4	Phvul.008G015300	Phvul.008G015300	0
1	Phvul.008G015300.2	Phvul.008G015300	Phvul.008G015300	0

1	Phvul.008G015300.5	Phvul.008G015300	Phvul.008G015300	0
1	Phvul.008G015300.1	Phvul.008G015300	Phvul.008G015300	0
1	Phvul.008G050200.1	Phvul.008G050200	Phvul.008G050200	0
1	Phvul.008G092200.2	Phvul.008G092200	Phvul.008G092200	0
1	Phvul.008G092200.3	Phvul.008G092200	Phvul.008G092200	0
1	Phvul.008G106950.2	Phvul.008G106950	Phvul.008G106950	PF02207
1	Phvul.008G106950.1	Phvul.008G106950	Phvul.008G106950	PF02207
1	Phvul.008G114300.1	Phvul.008G114300	Phvul.008G114300	PF05920,PF07
1	Phvul.008G130400.1	Phvul.008G130400	Phvul.008G130400	PF10510
1	Phvul.008G203314.1	Phvul.008G203314	Phvul.008G203314	PF02298
1	Phvul.009G108800.1	Phvul.009G108800	Phvul.009G108800	PF00230
1	Phvul.009G128500.2	Phvul.009G128500	Phvul.009G128500	PF01490
1	Phvul.009G128500.3	Phvul.009G128500	Phvul.009G128500	PF01490
1	Phvul.009G128500.1	Phvul.009G128500	Phvul.009G128500	PF01490
1	Phvul.009G128500.4	Phvul.009G128500	Phvul.009G128500	PF01490
1	Phvul.009G255500.1	Phvul.009G255500	Phvul.009G255500	0
1	Phvul.009G255500.2	Phvul.009G255500	Phvul.009G255500	0
1	Phvul.010G032000.1	Phvul.010G032000	Phvul.010G032000	PF01453,PF00
1	Phvul.011G062200.1	Phvul.011G062200	Phvul.011G062200	PF00806,PF07
1	Phvul.011G175000.2	Phvul.011G175000	Phvul.011G175000	PF08276,PF07
1	Phvul.011G175000.1	Phvul.011G175000	Phvul.011G175000	PF08276,PF07

Panther	KOG	KEGG	KOG	GO	Best-hit-arabi
PTHR32246,P	0	0	0	GO:0005515	AT5G23950.1
PTHR24362,P	0	2.7.11.1	0	GO:0006468,	AT3G44200.1
PTHR24362,P	0	2.7.11.1	0	GO:0006468,	AT3G44200.1
PTHR19375,P	0	0	K09486	0	AT4G16660.1
PTHR35739,P	0	0	0	0	AT3G54290.1
PTHR32227,P	0	3.2.1.39	0	GO:0005975,	AT5G55180.1
PTHR32246,P	0	0	0	GO:0005515	AT1G07310.1
PTHR31321,P	0	3.1.1.11	0	GO:0042545,	AT5G47500.1
PTHR10795,P	0	3.4.14.10	0	GO:0006508,	AT5G67360.1
PTHR11514,P	0	0	K13422	GO:0046983	AT1G32640.1
PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT1G71830.1
PTHR27001,P	KOG1187	2.7.11.1,2.7.1	0	GO:0006468,	AT1G71830.1
PTHR27003,P	KOG1187	2.7.11.1	0	GO:0006468,	AT3G55950.1
PTHR12357,P	KOG1902	0	K14404	0	AT1G30460.1
PTHR36351,P	0	0	0	0	0
PTHR10217,P	0	0	K05391	GO:0055085,	AT5G15410.2
PTHR33179,P	0	0	0	0	AT3G22160.1
PTHR31100,P	0	0	0	0	AT5G49700.1
PTHR12542,P	0	0	K07195	GO:0006887,	AT4G31540.1
PTHR27006,P	KOG1187	2.7.11.1	0	GO:0006468,	AT1G11050.1
PTHR27006,P	KOG1187	2.7.11.1	0	GO:0006468,	AT2G48010.1
PTHR27006,P	KOG1187	2.7.11.1	0	GO:0006468,	AT2G48010.1
PTHR27006,P	KOG1187	2.7.11.1	0	GO:0006468,	AT2G48010.1
PTHR31500,P	0	0	0	0	AT4G17950.1
PTHR34043,P	0	3.1.1.32,3.1.1	0	0	AT1G10740.3
PTHR11353,P	0	2.7.1.150	K00921	GO:0005524,	AT1G71010.1
PTHR11353,P	0	2.7.1.150	K00921	GO:0005524,	AT1G71010.1
PTHR21493,P	0	3.1.1.1	0	GO:0006629	AT3G52430.1
PTHR22844,P	KOG3569	0	0	GO:0005515	AT1G49040.1
PTHR10353,P	0	3.2.1.21	0	GO:0005975,	AT1G61820.1
PTHR10353,P	0	3.2.1.21	0	GO:0005975,	AT1G61820.1
PTHR12304,P	KOG2938	0	0	0	AT5G18860.1
PTHR12304,P	KOG2938	0	0	0	AT5G18860.1
PTHR12304,P	KOG2938	0	0	0	AT5G18860.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,	AT3G02130.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0005515,	AT3G02130.1
PTHR31983	0	3.2.1.39	K01180	GO:0052862,	AT5G15870.1
PTHR32246,P	0	0	0	GO:0005515	AT5G23950.1
PTHR23416,P	0	2.3.1.129	0	0	AT4G29540.2
PTHR23416,P	0	2.3.1.129	0	0	AT4G29540.2
PTHR23416,P	0	2.3.1.129	0	0	AT4G29540.2
PTHR23416,P	0	2.3.1.129	0	0	AT4G29540.2
PTHR23416,P	0	2.3.1.129	0	0	AT4G29540.2
PTHR23416,P	0	2.3.1.129	0	0	AT4G29540.2
PTHR11132,P	KOG1441	0	K15283	0	AT5G17630.1

PTHR11649,P	0	0	0	0	AT1G72960.1
PTHR30314,P	0	3.6.5.6	K03531	GO:0003924	AT5G55280.1
PTHR13308,P	KOG2401	0	0	0	AT5G58720.1
PTHR27007,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT3G53380.1
PTHR10641,P	KOG0048	0	K09422	0	AT4G01680.1
PTHR32303,P	0	1.1.2.6	0	0	0
PTHR36807,P	0	0	0	0	AT5G48830.1
PTHR36807,P	0	0	0	0	AT5G48830.1
PTHR12135,P	KOG2179	0	K10838	GO:0003677,(	AT5G16630.1
PTHR23086,P	0	2.7.1.68	K00889	GO:0046488,(	AT1G21980.1
PTHR23086,P	0	2.7.1.68	K00889	GO:0046488,(	AT1G21980.1
PTHR12135,P	KOG2179	0	K10838	GO:0003677,(	AT5G16630.1
PTHR10366,P	KOG1371	5.1.3.6	K08679	GO:0055114,(	AT4G00110.1
PTHR31415,P	0	0	0	0	AT4G01410.1
PTHR12550,P	0	0	0	0	AT5G08230.1
PTHR31988	0	3.1.1.73	0	0	AT4G34215.1
PTHR10853	KOG2869	0	K06965	GO:0071025,(	AT4G27650.1
PTHR22298,P	0	3.2.1.4	0	GO:0005975,(	AT4G02290.1
PTHR21262,P	0	2.7.6.5	0	GO:0015969	AT4G02260.2
PTHR23315,P	KOG2160,KO(	0	0	GO:0005515	AT2G22125.1
PTHR23315,P	KOG2160,KO(	0	0	GO:0005515	AT2G22125.1
PTHR31321,P	0	3.1.1.11	0	GO:0042545,(	AT5G47500.1
PTHR27000,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT4G36180.1
PTHR37891,P	0	0	0	0	0
PTHR37891,P	0	0	0	0	0
PTHR32133,P	0	0	0	GO:0005515	AT1G30950.1
PTHR22844,P	KOG0645	2.7.11.7	0	GO:0005515	AT1G24530.1
PTHR27001,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT1G66150.1
PTHR10353,P	0	3.2.1.21	K01188	GO:0005975,(	AT1G26560.1
PTHR11101	KOG2493	0	K14640	GO:0016020,(	AT3G26570.2
PTHR24298,P	KOG0156	0	0	GO:0055114,(	AT1G11600.1
PTHR24326,P	0	0	0	GO:0043565,(	AT3G01470.1
PTHR24326,P	0	0	0	GO:0043565,(	AT3G01470.1
PTHR14140,P	0	2.3.1.48	0	GO:0005634,(	AT3G01460.1
PTHR13007,P	KOG2808	0	K12817	GO:0008380,(	AT1G03140.1
PTHR17598	0	0	K03504	GO:0006260,(	AT1G78650.1
PTHR17598	0	0	K03504	GO:0006260,(	AT1G78650.1
PTHR30523,P	0	4.1.1.31	K01595	GO:0015977,(	AT2G42600.2
PTHR24015,P	0	0	0	0	AT1G52620.1
PTHR32116,P	0	2.4.1.43	K13648	GO:0016757,(	AT3G58790.1
PTHR10593,P	0	0	0	0	AT3G50700.1
PTHR10593,P	0	0	0	0	AT3G50700.1
PTHR36351,P	0	0	0	0	0
PTHR10159,P	0	3.1.3.48	0	0	AT3G55270.1
PTHR10159,P	0	3.1.3.48	0	0	AT3G55270.1
PTHR10159,P	0	3.1.3.48	0	0	AT3G55270.1

PTHR10159,P	0	3.1.3.48	0	0	AT3G55270.1
PTHR10159,P	0	3.1.3.48	0	0	AT3G55270.1
PTHR12655,P	KOG2763	3.1.2.2,3.1.2.	K17361	0	AT5G48370.1
PTHR20938,P	0	0	K13141	0	AT3G08800.1
PTHR20938,P	0	0	K13141	0	AT3G08800.1
PTHR21497,P	KOG1139	3.4.17.20	0	GO:0008270	AT5G02310.1
PTHR21497,P	KOG1139	3.4.17.20	0	GO:0008270	AT5G02310.1
PTHR11850,P	KOG0773	0	0	GO:0006355,(	AT5G02030.1
PTHR21072	KOG2459	0	K05291	GO:0042765,(	AT3G07180.1
PTHR33021,P	0	0	0	GO:0009055	AT1G08500.1
PTHR19139	KOG0223	0	K09873	GO:0016020,(	AT2G25810.1
PTHR22950,P	KOG1303	0	0	0	AT1G77380.1
PTHR22950,P	KOG1303	0	0	0	AT1G77380.1
PTHR22950,P	KOG1303	0	0	0	AT1G77380.1
PTHR22950,P	KOG1303	0	0	0	AT1G77380.1
0	0	0	0	0	0
0	0	0	0	0	0
PTHR27002,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G60900.1
PTHR12537,P	0	0	K17943	GO:0003723	AT2G29190.2
PTHR27002,P	0	2.7.11.1	0	GO:0006468,(	AT1G67520.1
PTHR27002,P	0	2.7.11.1	0	GO:0006468,(	AT1G67520.1

arabi-symbol	arabi-defline	ID
0	Calcium-dependent lipid-binding (CaLB domain) family	Phvul.004G11
ATNEK6,IBO1,NEK6	NIMA (never in mitosis, gene A)-related 6	Phvul.005G12
ATNEK6,IBO1,NEK6	NIMA (never in mitosis, gene A)-related 6	Phvul.005G12
0	heat shock protein 70 (Hsp 70) family protein	Phvul.006G00
0	0	Phvul.007G02
0	O-Glycosyl hydrolases family 17 protein	Phvul.008G27
0	Calcium-dependent lipid-binding (CaLB domain) family	Phvul.001G24
0	Pectin lyase-like superfamily protein	Phvul.003G22
ARA12	Subtilase family protein	Phvul.003G23
ATMYC2,JAI1,JIN1,M	Basic helix-loop-helix (bHLH) DNA-binding family protei	Phvul.003G28
ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1	Phvul.004G08
ATSERK1,SERK1	somatic embryogenesis receptor-like kinase 1	Phvul.004G08
ATCRR3,CCR3	CRINKLY4 related 3	Phvul.006G06
ATCPSF30,CPSF30	cleavage and polyadenylation specificity factor 30	Phvul.006G13
0	0	Phvul.007G26
ATCNGC2,CNGC2,DN	Cyclic nucleotide-regulated ion channel family protein	Phvul.008G03
0	VQ motif-containing protein	Phvul.008G29
0	Predicted AT-hook DNA-binding family protein	Phvul.009G14
ATEXO70G1,EXO70G	exocyst subunit exo70 family protein G1	Phvul.001G02
0	Protein kinase superfamily protein	Phvul.001G07
RKF3	receptor-like kinase in in flowers 3	Phvul.001G14
RKF3	receptor-like kinase in in flowers 3	Phvul.001G14
RKF3	receptor-like kinase in in flowers 3	Phvul.001G14
0	AT hook motif DNA-binding family protein	Phvul.002G00
0	alpha/beta-Hydrolases superfamily protein	Phvul.002G05
FAB1C	FORMS APLOID AND BINUCLEATE CELLS 1C	Phvul.002G09
FAB1C	FORMS APLOID AND BINUCLEATE CELLS 1C	Phvul.002G09
ATPAD4,PAD4	alpha/beta-Hydrolases superfamily protein	Phvul.002G27
SCD1	stomatal cytokinesis defective / SCD1 protein (SCD1)	Phvul.002G31
BGLU46	beta glucosidase 46	Phvul.003G07
BGLU46	beta glucosidase 46	Phvul.003G07
0	inosine-uridine preferring nucleoside hydrolase family	Phvul.003G09
0	inosine-uridine preferring nucleoside hydrolase family	Phvul.003G09
0	inosine-uridine preferring nucleoside hydrolase family	Phvul.003G09
RPK2,TOAD2	receptor-like protein kinase 2	Phvul.004G03
RPK2,TOAD2	receptor-like protein kinase 2	Phvul.004G03
0	glycosyl hydrolase family 81 protein	Phvul.004G04
0	Calcium-dependent lipid-binding (CaLB domain) family	Phvul.004G11
0	bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
0	bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
0	bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
0	bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
0	bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
0	bacterial transferase hexapeptide repeat-containing pr	Phvul.004G17
0	Nucleotide/sugar transporter family protein	Phvul.005G02

0	Root hair defective 3 GTP-binding protein (RHD3)	Phvul.005G15
ATFTSZ1-1,CPFTSZ,FT	homolog of bacterial cytokinesis Z-ring protein FTSZ 1-	Phvul.006G04
0	smr (Small MutS Related) domain-containing protein	Phvul.006G06
0	Concanavalin A-like lectin protein kinase family protein	Phvul.006G08
AtMYB55,MYB55	myb domain protein 55	Phvul.007G20
0	0	Phvul.008G04
0	0	Phvul.008G12
0	0	Phvul.008G12
ATRAD4,RAD4	DNA repair protein Rad4 family	Phvul.008G23
ATPIP5K1,ATPIPK1,PI	phosphatidylinositol-4-phosphate 5-kinase 1	Phvul.009G15
ATPIP5K1,ATPIPK1,PI	phosphatidylinositol-4-phosphate 5-kinase 1	Phvul.009G15
ATRAD4,RAD4	DNA repair protein Rad4 family	Phvul.010G02
GAE3	UDP-D-glucuronate 4-epimerase 3	Phvul.010G08
0	Late embryogenesis abundant (LEA) hydroxyproline-ric	Phvul.010G11
0	Tudor/PWWP/MBT domain-containing protein	Phvul.011G02
0	Domain of unknown function (DUF303)	Phvul.001G02
PEL1	Eukaryotic release factor 1 (eRF1) family protein	Phvul.001G18
AtGH9B13,GH9B13	glycosyl hydrolase 9B13	Phvul.001G20
AT-RSH1,ATRSH1,RSH	RELA/SPOT homolog 1	Phvul.001G20
CSI1	binding	Phvul.001G25
CSI1	binding	Phvul.001G25
0	Pectin lyase-like superfamily protein	Phvul.002G06
0	Leucine-rich receptor-like protein kinase family protein	Phvul.002G11
0	0	0
0	0	0
UFO	F-box family protein	Phvul.002G18
0	Transducin/WD40 repeat-like superfamily protein	Phvul.002G25
TMK1	transmembrane kinase 1	Phvul.002G32
BGLU40	beta glucosidase 40	Phvul.003G04
ORF02,PHT2;1	phosphate transporter 2;1	Phvul.003G06
CYP77B1	cytochrome P450, family 77, subfamily B, polypeptide	Phvul.003G07
ATHB-1,ATHB1,HAT5,	homeobox 1	Phvul.003G19
ATHB-1,ATHB1,HAT5,	homeobox 1	Phvul.003G19
ATMBD9,MBD9	methyl-CPG-binding domain 9	Phvul.004G01
0	splicing factor Prp18 family protein	Phvul.005G03
POLD3	DNA-directed DNA polymerases	Phvul.005G08
POLD3	DNA-directed DNA polymerases	Phvul.005G08
ATPPC2,PPC2	phosphoenolpyruvate carboxylase 2	Phvul.005G09
0	Pentatricopeptide repeat (PPR) superfamily protein	Phvul.005G17
GAUT15	galacturonosyltransferase 15	Phvul.006G03
AtIDD2,IDD2	indeterminate(ID)-domain 2	Phvul.007G19
AtIDD2,IDD2	indeterminate(ID)-domain 2	Phvul.007G19
0	0	Phvul.007G26
ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01

ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
ATMKP1,MKP1	mitogen-activated protein kinase phosphatase 1	Phvul.008G01
0	Thioesterase/thiol ester dehydrase-isomerase superfar	Phvul.008G05
0	ARM repeat superfamily protein	Phvul.008G09
0	ARM repeat superfamily protein	Phvul.008G09
PRT6	proteolysis 6	Phvul.008G10
PRT6	proteolysis 6	Phvul.008G10
BLH9,BLR,HB-6,LSN,P	POX (plant homeobox) family protein	Phvul.008G11
0	GPI transamidase component PIG-S-related	Phvul.008G13
AtENODL18,ENODL1	early nodulin-like protein 18	Phvul.008G20
TIP4;1	tonoplast intrinsic protein 4;1	Phvul.009G10
AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
AAP3,ATAAP3	amino acid permease 3	Phvul.009G12
0	0	0
0	0	0
RLK1	receptor-like protein kinase 1	Phvul.010G03
APUM2,PUM2	pumilio 2	Phvul.011G06
0	lectin protein kinase family protein	Phvul.011G17
0	lectin protein kinase family protein	Phvul.011G17

Annot_deflin	IDENTIFIER	NAME	DESCRIPTION
PF00168 - C2	Phvul.004G11	not assigned.	no hits & (original description: pacid=37162836 transcri
PTHR24362:S	Phvul.005G12	Protein modif	protein kinase (NEK) (original description: pacid=371525
PTHR24362:S	Phvul.005G12	Protein modif	protein kinase (NEK) (original description: pacid=371525
K09486 - hyp	Phvul.006G00	Protein home	nucleotide exchange factor (Grp170) (original descriptio
PF01814 - He	Phvul.007G02	not assigned.	no hits & (original description: pacid=37164059 transcri
PTHR32227:S	Phvul.008G27	Enzyme classi	Glucan endo-1,3-beta-glucosidase 12 OS=Arabidopsis th
PTHR32246:S	Phvul.001G24	not assigned.	no hits & (original description: pacid=37170768 transcri
PTHR31321:S	Phvul.003G22	Cell wall orga	pectin methylesterase (original description: pacid=3714
PTHR10795//	Phvul.003G23	Protein home	protease (SBT1) (original description: pacid=37147285 tr
K13422 - tran	Phvul.003G28	RNA biosynth	transcription factor (bHLH) (original description: pacid=3
K13418 - som	Phvul.004G08	Protein modif	protein kinase (LRR-II) (original description: pacid=37161
K13418 - som	Phvul.004G08	Protein modif	protein kinase (LRR-II) (original description: pacid=37161
PF00069//PF1	Phvul.006G06	Protein modif	protein kinase (Crinkly-like) (original description: pacid=
PTHR12357:S	Phvul.006G13	RNA processi	component CPSF30/Yth1 of Cleavage and Polyadenylati
PTHR36351:S	Phvul.007G26	not assigned.	no hits & (original description: pacid=37165888 transcri
PTHR10217:S	Phvul.008G03	External stim	temperature sensor protein (CNGC2) (original descriptio
PTHR33179:S	Phvul.008G29	not assigned.	no hits & (original description: pacid=37160918 transcri
PTHR31100:S	Phvul.009G14	not assigned.a	(original description: pacid=37150218 transcript=Phvul.
PTHR12542//	Phvul.001G02	Vesicle traffic	component EXO70 of Exocyst complex (original descripti
2.7.11.1 - Non	Phvul.001G07	Protein modif	protein kinase (RKF3) (original description: pacid=37169
PTHR27006:S	Phvul.001G14	Protein modif	protein kinase (RKF3) (original description: pacid=37168
PTHR27006:S	Phvul.001G14	Enzyme classi	Probable LRR receptor-like serine/threonine-protein kin
PTHR27006:S	Phvul.001G14	Enzyme classi	Probable LRR receptor-like serine/threonine-protein kin
PTHR31500:S	Phvul.002G00	not assigned.a	(original description: pacid=37175392 transcript=Phvul.
3.1.1.3//3.1.1	Phvul.002G05	not assigned.	no hits & (original description: pacid=37175506 transcri
PTHR11353:S	Phvul.002G09	Multi-process	phosphatidylinositol 3-phosphate 5-kinase (FAB1) (origi
PTHR11353:S	Phvul.002G09	Multi-process	phosphatidylinositol 3-phosphate 5-kinase (FAB1) (origi
PTHR21493//	Phvul.002G27	External stim	PAD4 effector-triggered immunity co-regulator (original
PTHR22844:S	Phvul.002G31	Vesicle traffic	SCD1 component of post-Golgi trafficking SCD complex (
PTHR10353:S	Phvul.003G07	Enzyme classi	Beta-glucosidase 46 OS=Arabidopsis thaliana (sp|o8069
PTHR10353:S	Phvul.003G07	Enzyme classi	Beta-glucosidase 46 OS=Arabidopsis thaliana (sp|o8069
PTHR12304:S	Phvul.003G09	Nucleotide m	nucleoside hydrolase (original description: pacid=37144
PTHR12304:S	Phvul.003G09	Nucleotide m	nucleoside hydrolase (original description: pacid=37144
PTHR12304:S	Phvul.003G09	Nucleotide m	nucleoside hydrolase (original description: pacid=37144
PTHR27000:S	Phvul.004G03	Protein modif	protein kinase (LRR-XV) (original description: pacid=3716
PTHR27000:S	Phvul.004G03	Protein modif	protein kinase (LRR-XV) (original description: pacid=3716
K01180 - end	Phvul.004G04	not assigned.	no hits & (original description: pacid=37163654 transcri
PF00168 - C2	Phvul.004G11	not assigned.	no hits & (original description: pacid=37163692 transcri
2.3.1.129 - Ac	Phvul.004G17	Lipid metabol	UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
2.3.1.129 - Ac	Phvul.004G17	Lipid metabol	UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
2.3.1.129 - Ac	Phvul.004G17	Lipid metabol	UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
2.3.1.129 - Ac	Phvul.004G17	Lipid metabol	UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
2.3.1.129 - Ac	Phvul.004G17	Lipid metabol	UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
2.3.1.129 - Ac	Phvul.004G17	Lipid metabol	UDP-N-acetylglucosamine O-acyltransferase (LpxA) (orig
PTHR11132:S	Phvul.005G02	Solute transp	phosphometabolite transporter (TPT|PPT|GPT|XPT) (ori

PTHR11649:S	Phvul.005G15	Cell cycle orga	ER tubulae formation factor (RHD3/RL) (original descript
PTHR30314:S	Phvul.006G04	Cell cycle orga	component FtsZ1 of plastid division FtsZ prokaryotic-tub
KOG2401 - Pr	Phvul.006G06	not assigned.a	(original description: pacid=37174192 transcript=Phvul.
PTHR27007:S	Phvul.006G08	Protein modif	protein kinase (L-lectin) (original description: pacid=3717
PTHR10641:S	Phvul.007G20	RNA biosynth	transcription factor (MYB) (original description: pacid=37
1.1.2.6 - Polyv	Phvul.008G04	not assigned.n	no hits & (original description: pacid=37159669 transcri
PF12452 - Pro	Phvul.008G12	not assigned.n	no hits & (original description: pacid=37158036 transcri
PF12452 - Pro	Phvul.008G12	not assigned.n	no hits & (original description: pacid=37158036 transcri
K10838 - xero	Phvul.008G23	DNA damage	DNA repair protein (XPC) (original description: pacid=37
PTHR23086:S	Phvul.009G15	Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (origi
PTHR23086:S	Phvul.009G15	Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (origi
K10838 - xero	Phvul.010G02	DNA damage	DNA repair protein (XPC) (original description: pacid=37
PTHR10366:S	Phvul.010G08	Carbohydrate	UDP-D-glucuronic acid 4-epimerase (original description
PF03168 - Lat	Phvul.010G11	not assigned.a	(original description: pacid=37143932 transcript=Phvul.
PTHR12550:S	Phvul.011G02	RNA biosynth	transcription factor (HUA2) (original description: pacid=3
3.1.1.73 - Fer	Phvul.001G02	not assigned.a	(original description: pacid=37168114 transcript=Phvul.
K06965 - prot	Phvul.001G18	Protein biosyr	component DOM34 of DOM34-HBS1 aberrant mRNA de
PTHR22298:S	Phvul.001G20	not assigned.a	(original description: pacid=37167724 transcript=Phvul.
PTHR21262:S	Phvul.001G20	not assigned.a	(original description: pacid=37168990 transcript=Phvul.
KOG2160//KC	Phvul.001G25	Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (origi
KOG2160//KC	Phvul.001G25	Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (origi
PTHR31321:S	Phvul.002G06	Cell wall orgar	pectin methylesterase (original description: pacid=3717
PTHR27000:S	Phvul.002G11	Protein modif	protein kinase (LRR-VII) (original description: pacid=3717
0	Phvul.002G13	not assigned.n	no hits & (original description: pacid=37178726 transcri
0	Phvul.002G13	not assigned.n	no hits & (original description: pacid=37178726 transcri
PTHR32133:S	Phvul.002G18	Protein home	component UFO of SCF E3 ubiquitin ligase complex (orig
PTHR22844:S	Phvul.002G25	not assigned.a	(original description: pacid=37174658 transcript=Phvul.
PTHR27001:S	Phvul.002G32	Protein modif	protein kinase (LRR-IX) (original description: pacid=3717
PTHR10353:S	Phvul.003G04	Enzyme classi	Beta-glucosidase 40 OS=Arabidopsis thaliana (sp|q9fze0
K14640 - solu	Phvul.003G06	Solute transp	phosphate transporter (PHT2) (original description: paci
PTHR24298:S	Phvul.003G07	Enzyme classi	Cytochrome P450 77A1 (Fragment) OS=Solanum melong
KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription factor (HD-ZIP I/II) (original description: pa
KOG0483 - Tr	Phvul.003G19	RNA biosynth	transcription factor (HD-ZIP I/II) (original description: pa
PTHR14140:S	Phvul.004G01	not assigned.a	(original description: pacid=37162939 transcript=Phvul.
K12817 - pre-	Phvul.005G03	not assigned.n	no hits & (original description: pacid=37152518 transcri
K03504 - DNA	Phvul.005G08	Cell cycle orga	component POLD3 of DNA polymerase delta complex (o
K03504 - DNA	Phvul.005G08	Cell cycle orga	component POLD3 of DNA polymerase delta complex (o
K01595 - phos	Phvul.005G09	Photosynthesi	PEP carboxylase (original description: pacid=37154500 t
PF13041 - PPF	Phvul.005G17	not assigned.a	(original description: pacid=37152686 transcript=Phvul.
PTHR32116:S	Phvul.006G03	not assigned.a	(original description: pacid=37172111 transcript=Phvul.
PTHR10593:S	Phvul.007G19	RNA biosynth	C2H2 zinc finger transcription factor (original descriptio
PTHR10593:S	Phvul.007G19	RNA biosynth	C2H2 zinc finger transcription factor (original descriptio
PTHR36351:S	Phvul.007G26	not assigned.n	no hits & (original description: pacid=37165888 transcri
PTHR10159:S	Phvul.008G01	not assigned.a	(original description: pacid=37161122 transcript=Phvul.
PTHR10159:S	Phvul.008G01	not assigned.a	(original description: pacid=37161122 transcript=Phvul.
PTHR10159:S	Phvul.008G01	not assigned.a	(original description: pacid=37161122 transcript=Phvul.

PTHR10159:SI	Phvul.008G01	not assigned.a	(original description: pacid=37161122 transcript=Phvul.0
PTHR10159:SI	Phvul.008G01	not assigned.a	(original description: pacid=37161122 transcript=Phvul.0
3.1.2.2//3.1.2	Phvul.008G05	not assigned.n	no hits & (original description: pacid=37160794 transcri
K13141 - integ	Phvul.008G09	Protein transl	SIEL plasmodesmata intercellular trafficking regulator pr
K13141 - integ	Phvul.008G09	Protein transl	SIEL plasmodesmata intercellular trafficking regulator pr
3.4.17.20 - Ca	Phvul.008G10	Protein home	type-I-residues E3 ubiquitin ligase (PRT6) (original descri
3.4.17.20 - Ca	Phvul.008G10	Protein home	type-I-residues E3 ubiquitin ligase (PRT6) (original descri
PTHR11850:SI	Phvul.008G11	RNA biosynth	transcription factor (BEL) (original description: pacid=371
K05291 - phos	Phvul.008G13	Protein modif	component PIG-S of GPI transamidase complex (original
PTHR33021:SI	Phvul.008G20	not assigned.n	no hits & (original description: pacid=37161432 transcri
K09873 - aqua	Phvul.009G10	Solute transpo	tonoplast intrinsic protein (TIP) (original description: pac
PTHR22950:SI	Phvul.009G12	Solute transpo	amino acid transporter (AAP) (original description: pacid
PTHR22950:SI	Phvul.009G12	Solute transpo	amino acid transporter (AAP) (original description: pacid
PTHR22950:SI	Phvul.009G12	Solute transpo	amino acid transporter (AAP) (original description: pacid
PTHR22950:SI	Phvul.009G12	Solute transpo	amino acid transporter (AAP) (original description: pacid
0	Phvul.009G25	not assigned.n	no hits & (original description: pacid=37149126 transcri
0	Phvul.009G25	not assigned.n	no hits & (original description: pacid=37149126 transcri
PF00069//PFC	Phvul.010G03	Enzyme classi	G-type lectin S-receptor-like serine/threonine-protein kin
PTHR12537:SI	Phvul.011G06	not assigned.a	(original description: pacid=37156482 transcript=Phvul.0
PF01453//PFC	Phvul.011G17	Enzyme classi	G-type lectin S-receptor-like serine/threonine-protein kin
PF01453//PFC	Phvul.011G17	Enzyme classi	G-type lectin S-receptor-like serine/threonine-protein kin

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865 transcript=Phvul.001G071200.1 locus=Phvul.001G071200 ID=Phvul.001G071200.1.v2.1 annot-
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ase RKF3 OS=Arabidopsis thaliana (sp|p93050|rkf3_arath : 454.0) & Enzyme classification.EC_2 tra
002G006700.1 locus=Phvul.002G006700 ID=Phvul.002G006700.1.v2.1 annot-version=v2.1) & AT-hc
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0|bgl46_arath : 462.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 272.9) (
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inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
inal description: pacid=37162324 transcript=Phvul.004G171500.6 locus=Phvul.004G171500 ID=Phv
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inal description: pacid=37149983 transcript=Phvul.009G157200.2 locus=Phvul.009G157200 ID=Phv
142287 transcript=Phvul.010G024866.1 locus=Phvul.010G024866 ID=Phvul.010G024866.1.v2.1 ann
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001G209500.2 locus=Phvul.001G209500 ID=Phvul.001G209500.2.v2.1 annot-version=v2.1) & Endo
001G209900.2 locus=Phvul.001G209900 ID=Phvul.001G209900.2.v2.1 annot-version=v2.1) & Putat
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inal description: pacid=37170740 transcript=Phvul.001G250100.2 locus=Phvul.001G250100 ID=Phv
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|bgl40_arath : 657.0) & Enzyme classification.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 409.7) (
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cid=37145774 transcript=Phvul.003G192900.2 locus=Phvul.003G192900 ID=Phvul.003G192900.2.v
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riginal description: pacid=37154337 transcript=Phvul.005G080800.2 locus=Phvul.005G080800 ID=P
ranscript=Phvul.005G095300.1 locus=Phvul.005G095300 ID=Phvul.005G095300.1.v2.1 annot-versi
005G176600.1 locus=Phvul.005G176600 ID=Phvul.005G176600.1.v2.1 annot-version=v2.1) & Penta
006G034100.1 locus=Phvul.006G034100 ID=Phvul.006G034100.1.v2.1 annot-version=v2.1) & Proba
: pacid=37164279 transcript=Phvul.007G196100.2 locus=Phvul.007G196100 ID=Phvul.007G19610
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008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote
008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote

008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote
008G015300.5 locus=Phvul.008G015300 ID=Phvul.008G015300.5.v2.1 annot-version=v2.1) & Prote
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rotein (original description: pacid=37159576 transcript=Phvul.008G092200.3 locus=Phvul.008G0922
iption: pacid=37159444 transcript=Phvul.008G106950.2 locus=Phvul.008G106950 ID=Phvul.008G10
iption: pacid=37159444 transcript=Phvul.008G106950.2 locus=Phvul.008G106950 ID=Phvul.008G10
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nase RLK1 OS=Arabidopsis thaliana (sp|q39202|rlk1_arath : 652.0) & Enzyme classification.EC_2 tra
011G062200.1 locus=Phvul.011G062200 ID=Phvul.011G062200.1.v2.1 annot-version=v2.1) & Pumil
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nase At1g67520 OS=Arabidopsis thaliana (sp|o64793|y1675_arath : 249.0) & Enzyme classification

1)
ersion=v2.1) &
ersion=v2.1) &
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1)
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400.1.v2.1 annot-version=v2.1) &
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version=v2.1) &
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nsferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 109.2) (original des
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l.002G092900.2.v2.1 annot-version=v2.1) &
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original description: pacid=37147256 transcript=Phvul.003G076700.2 locus=Phvul.003G076700 ID=
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t-version=v2.1) &
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vul.004G171500.6.v2.1 annot-version=v2.1) &
vul.004G171500.6.v2.1 annot-version=v2.1) &
vul.004G171500.6.v2.1 annot-version=v2.1) &
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vul.005G022300.1.v2.1 annot-version=v2.1) &

600.1.v2.1 annot-version=v2.1) &
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domain-containing protein At5g58720 OS=Arabidopsis thaliana (sp|o65573|y5872_arath : 334.0)
ot-version=v2.1) &
nnot-version=v2.1) &
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1)
not-version=v2.1) &
ul.009G157200.2.v2.1 annot-version=v2.1) &
ul.009G157200.2.v2.1 annot-version=v2.1) &
not-version=v2.1) &
.1.v2.1 annot-version=v2.1) &
L/HIN1-like protein 12 OS=Arabidopsis thaliana (sp|q9sj54|nhl12_arath : 94.7)
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able carbohydrate esterase At4g34215 OS=Arabidopsis thaliana (sp|q8l9j9|caes_arath : 216.0)
l.001G183700 ID=Phvul.001G183700.1.v2.1 annot-version=v2.1) &
glucanase 17 OS=Arabidopsis thaliana (sp|o81416|gun17_arath : 701.0)
ive GTP diphosphokinase RSH1, chloroplastic OS=Arabidopsis thaliana (sp|p0dkg8|rsh1l_arath : 11
ul.001G250100.2.v2.1 annot-version=v2.1) &
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-version=v2.1) &
t-version=v2.1) &
1)
1)
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t-version=v2.1) &
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1 annot-version=v2.1) &
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2.1 annot-version=v2.1) &
2.1 annot-version=v2.1) &
yl-CpG-binding domain-containing protein 9 OS=Arabidopsis thaliana (sp|q9sgh2|mbd9_arath : 15
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hvul.005G080800.2.v2.1 annot-version=v2.1) &
hvul.005G080800.2.v2.1 annot-version=v2.1) &
n=v2.1) &
tricopeptide repeat-containing protein At1g52620 OS=Arabidopsis thaliana (sp|q9ssr4|ppr77_arat
able galacturonosyltransferase 15 OS=Arabidopsis thaliana (sp|q8l4b0|gautf_arath : 590.0)
.2.v2.1 annot-version=v2.1) &
.2.v2.1 annot-version=v2.1) &
1)
in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)

in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
in-tyrosine-phosphatase MKP1 OS=Arabidopsis thaliana (sp|q9c5s1|mkp1_arath : 348.0)
1)
200 ID=Phvul.008G092200.3.v2.1 annot-version=v2.1) &
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6950.2.v2.1 annot-version=v2.1) &
6950.2.v2.1 annot-version=v2.1) &
ot-version=v2.1) &
08G130400.1.v2.1 annot-version=v2.1) &
1)
2.1 annot-version=v2.1) &
annot-version=v2.1) &
annot-version=v2.1) &
annot-version=v2.1) &
annot-version=v2.1) &
1)
1)
ansferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 103.4) (original de
lio homolog 2 OS=Arabidopsis thaliana (sp|q9zw06|pum2_arath : 992.0)
.EC_2 transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 57.7) (orig
.EC_2 transferases.EC_2.7 transferase transferring phosphorus-containing group(50.2.7 : 57.7) (orig

l.008G271000 ID=Phvul.008G271000.1.v2.1 annot-version=v2.1) &

scription: pacid=37170420 transcript=Phvul.001G147001.2 locus=Phvul.001G147001 ID=Phvul.001G

scription: pacid=37170420 transcript=Phvul.001G147001.2 locus=Phvul.001G147001 ID=Phvul.001G

=Phvul.003G076700.2.v2.1 annot-version=v2.1) &

=Phvul.003G076700.2.v2.1 annot-version=v2.1) &

83.0)

Phvul.003G043600.2.v2.1 annot-version=v2.1) &

!08.0) (original description: pacid=37147806 transcript=Phvul.003G076900.1 locus=Phvul.003G0769

65.0)

th : 801.0)

escription: pacid=37142844 transcript=Phvul.010G032000.1 locus=Phvul.010G032000 ID=Phvul.010

ginal description: pacid=37155309 transcript=Phvul.011G175000.2 locus=Phvul.011G175000 ID=Ph

ginal description: pacid=37155309 transcript=Phvul.011G175000.2 locus=Phvul.011G175000 ID=Ph

147001.2.v2.1 annot-version=v2.1) &

147001.2.v2.1 annot-version=v2.1) &

900 ID=Phvul.003G076900.1.v2.1 annot-version=v2.1) &

G032000.1.v2.1 annot-version=v2.1) &

vul.011G175000.2.v2.1 annot-version=v2.1) &

vul.011G175000.2.v2.1 annot-version=v2.1) &

Id	H42_1	H42_2	H42_3	X42_1	X42_2
cfa-miR-31	13	0	2	17	3
cpo-miR-31-5p	13	0	2	17	3
dno-miR-31-5p	13	0	2	17	3
ocu-miR-31-5p	13	0	2	17	3
aly-miR164a-5p	477	598	177	50	83
aly-miR164b-5p	477	598	177	50	83
aof-miR164	477	598	177	50	83
ata-miR164b-5p	477	598	177	50	83
ata-miR164c-5p	477	598	177	50	83
ath-miR164a	477	598	177	50	83
ath-miR164b-5p	477	598	177	50	83
atr-miR164a	477	598	177	50	83
atr-miR164b	477	598	177	50	83
bdi-miR164a-5p	477	598	177	50	83
bdi-miR164b	477	598	177	50	83
bdi-miR164e	477	598	177	50	83
bna-miR164a	477	598	177	50	83
bra-miR164a	477	598	177	50	83
cas-miR164	477	598	177	50	83
cme-miR164c	477	598	177	50	83
cme-miR164d	477	598	177	50	83
cpa-miR164a	477	598	177	50	83
cpa-miR164b	477	598	177	50	83
cpa-miR164c	477	598	177	50	83
csi-miR164a-5p	477	598	177	50	83
csi-miR164b-5p	477	598	177	50	83
csi-miR164c-5p	477	598	177	50	83
csi-miR164d-5p	477	598	177	50	83
ctr-miR164	477	598	177	50	83
fve-miR164a-5p	477	598	177	50	83
fve-miR164b	477	598	177	50	83
ghr-miR164	477	598	177	50	83
gma-miR164a	477	598	177	50	83
gma-miR164e	477	598	177	50	83
gma-miR164f	477	598	177	50	83
gma-miR164g	477	598	177	50	83
gma-miR164h	477	598	177	50	83
gma-miR164i	477	598	177	50	83
gma-miR164j	477	598	177	50	83
gma-miR164k	477	598	177	50	83
lus-miR164a	477	598	177	50	83
lus-miR164b	477	598	177	50	83

lus-miR164c	477	598	177	50	83
lus-miR164d	477	598	177	50	83
lus-miR164e	477	598	177	50	83
mdm-miR164b	477	598	177	50	83
mdm-miR164c	477	598	177	50	83
mdm-miR164d	477	598	177	50	83
mdm-miR164e	477	598	177	50	83
mdm-miR164f	477	598	177	50	83
mes-miR164a	477	598	177	50	83
mes-miR164b	477	598	177	50	83
mes-miR164c	477	598	177	50	83
mtr-miR164a	477	598	177	50	83
mtr-miR164b	477	598	177	50	83
mtr-miR164c	477	598	177	50	83
nta-miR164a	477	598	177	50	83
nta-miR164b	477	598	177	50	83
osa-miR164a	477	598	177	50	83
osa-miR164b	477	598	177	50	83
osa-miR164f	477	598	177	50	83
ppe-miR164a	477	598	177	50	83
ppe-miR164b	477	598	177	50	83
ppe-miR164c	477	598	177	50	83
ptc-miR164a	477	598	177	50	83
ptc-miR164b	477	598	177	50	83
ptc-miR164c	477	598	177	50	83
ptc-miR164d	477	598	177	50	83
ptc-miR164e	477	598	177	50	83
rco-miR164a	477	598	177	50	83
rco-miR164b	477	598	177	50	83
rco-miR164c	477	598	177	50	83
sbi-miR164a	477	598	177	50	83
sbi-miR164d	477	598	177	50	83
sbi-miR164e	477	598	177	50	83
sly-miR164a-5p	477	598	177	50	83
sly-miR164b-5p	477	598	177	50	83
ssl-miR164a	477	598	177	50	83
ssl-miR164b	477	598	177	50	83
tae-miR164	477	598	177	50	83
tcc-miR164a	477	598	177	50	83
tcc-miR164b	477	598	177	50	83
vvi-miR164a	477	598	177	50	83
vvi-miR164c	477	598	177	50	83
vvi-miR164d	477	598	177	50	83

zma-miR164a-5p	477	598	177	50	83
zma-miR164b-5p	477	598	177	50	83
zma-miR164c-5p	477	598	177	50	83
zma-miR164d-5p	477	598	177	50	83
zma-miR164g-5p	477	598	177	50	83
bra-miR164e-5p	482	598	180	50	83
bta-miR-451	86	276	3131	81	55
cja-miR-451	86	276	3131	81	55
cpo-miR-451-5p	86	276	3131	81	55
dno-miR-451-5p	86	276	3131	81	55
gga-miR-451	86	276	3131	81	55
oan-miR-451	86	276	3131	81	55
ocu-miR-451-5p	86	276	3131	81	55
oha-miR-451-??	86	276	3131	81	55
tgu-miR-451	86	276	3131	81	55
aca-miR-451-5p	33	261	1822	29	15
cfa-miR-451	33	261	1822	29	15
cgr-miR-451a	33	261	1822	29	15
dre-miR-451	33	261	1822	29	15
hsa-miR-451a	33	261	1822	29	15
mml-miR-451	33	261	1822	29	15
mmu-miR-451a	33	261	1822	29	15
ppy-miR-451	33	261	1822	29	15
ptr-miR-451	33	261	1822	29	15
rno-miR-451-5p	33	261	1822	29	15
ssc-miR-451	33	261	1822	29	15
xtr-miR-451	33	261	1822	29	15
ebv-miR-BART8-3p	0	0	1	0	0
ebv-miR-BART1-3p	0	0	1	0	0
ebv-miR-BART1-5p	0	0	1	0	0
ebv-miR-BART17-5p	0	0	0	0	0
ebv-miR-BART6-3p	0	0	0	0	0
ebv-miR-BART17-3p	0	0	0	0	0
ebv-miR-BART6-5p	0	0	1	0	0
ebv-miR-BART7-5p	0	0	0	0	0
ebv-miR-BART19-3p	0	0	0	0	0
ebv-miR-BART14-5p	0	0	0	0	0
ebv-miR-BART2-5p	0	0	1	0	0
ebv-miR-BART5-5p	0	0	1	0	0
ebv-miR-BART9-3p	0	0	2	0	0
ebv-miR-BART22	0	0	5	0	0
rlcv-miR-rL1-6-3p	0	0	11	0	0
ebv-miR-BART10-3p	0	0	2	0	0

ebv-miR-BART7-3p	0	0	2	0	0
ebv-miR-BART11-5p	0	0	2	0	0
ebv-miR-BART8-5p	0	0	3	0	0
efu-miR-192	3	5	9	5	2
cfa-miR-192	0	2	3	2	1
chi-miR-192-5p	0	2	3	2	1
cpo-miR-192-5p	0	2	3	2	1
eca-miR-192	0	2	3	2	1
ggo-miR-192	0	2	3	2	1
hsa-miR-192-5p	0	2	3	2	1
mml-miR-192-5p	0	2	3	2	1
mmu-miR-192-5p	0	2	3	2	1
nle-miR-192	0	2	3	2	1
oan-miR-192-5p	0	2	3	2	1
oga-miR-192	0	2	3	2	1
ppa-miR-192	0	2	3	2	1
ppy-miR-192	0	2	3	2	1
ptr-miR-192	0	2	3	2	1
rno-miR-192-5p	0	2	3	2	1
ssc-miR-192	0	2	3	2	1
tch-miR-192-5p	0	2	3	2	1
bta-miR-192	3	5	5	4	2
cgr-miR-192	2	4	4	3	2
oar-miR-127	5	2	39	5	6
age-miR-127	5	2	39	5	6
bta-miR-127	5	2	39	5	6
cfa-miR-127	5	2	39	5	6
cgr-miR-127	5	2	39	5	6
cpo-miR-127-3p	5	2	39	5	6
dma-miR-127	5	2	39	5	6
dno-miR-127-3p	5	2	39	5	6
eca-miR-127	5	2	39	5	6
hsa-miR-127-3p	5	2	39	5	6
lla-miR-127	5	2	39	5	6
mml-miR-127-3p	5	2	39	5	6
mmu-miR-127-3p	5	2	39	5	6
mne-miR-127	5	2	39	5	6
nle-miR-127	5	2	39	5	6
ocu-miR-127-3p	5	2	39	5	6
oga-miR-127	5	2	39	5	6
pal-miR-127-3p	5	2	39	5	6
pha-miR-127	5	2	39	5	6
ppa-miR-127	5	2	39	5	6

ppy-miR-127	5	2	39	5	6
ptr-miR-127	5	2	39	5	6
rno-miR-127-3p	5	2	39	5	6
sbo-miR-127	5	2	39	5	6
sla-miR-127	5	2	39	5	6
ssc-miR-127	5	2	39	5	6
tch-miR-127-3p	5	2	39	5	6
efu-miR-127	5	2	40	5	6
ola-miR-7	14	28	15	9	6
aae-miR-7	14	28	15	9	6
abu-miR-7	14	28	15	9	6
aca-miR-7-5p	14	28	15	9	6
aga-miR-7	14	28	15	9	6
ame-miR-7-5p	14	28	15	9	6
ami-miR-7a-5p	14	28	15	9	6
bbe-miR-7-5p	14	28	15	9	6
bfl-miR-7	14	28	15	9	6
bmo-miR-7-5p	14	28	15	9	6
cfa-miR-7	14	28	15	9	6
cgr-miR-7a	14	28	15	9	6
cqu-miR-7	14	28	15	9	6
csa-miR-7	14	28	15	9	6
dan-miR-7	14	28	15	9	6
der-miR-7	14	28	15	9	6
dgr-miR-7	14	28	15	9	6
dme-miR-7-5p	14	28	15	9	6
dmo-miR-7	14	28	15	9	6
dpe-miR-7	14	28	15	9	6
dps-miR-7	14	28	15	9	6
dpu-miR-7	14	28	15	9	6
dre-miR-7a	14	28	15	9	6
dse-miR-7	14	28	15	9	6
dsi-miR-7	14	28	15	9	6
dwi-miR-7	14	28	15	9	6
dya-miR-7	14	28	15	9	6
eca-miR-7	14	28	15	9	6
gmo-miR-7c-5p	14	28	15	9	6
ipu-miR-7a	14	28	15	9	6
isc-miR-7	14	28	15	9	6
lva-miR-7-5p	14	28	15	9	6
mml-miR-7	14	28	15	9	6
mmu-miR-7a-5p	14	28	15	9	6
mze-miR-7b	14	28	15	9	6

nbr-miR-7	14	28	15	9	6
nlo-miR-7	14	28	15	9	6
nvi-miR-7	14	28	15	9	6
oan-miR-7-5p	14	28	15	9	6
oni-miR-7	14	28	15	9	6
pma-miR-7a-5p	14	28	15	9	6
pmi-miR-7-5p	14	28	15	9	6
pny-miR-7	14	28	15	9	6
ptr-miR-7	14	28	15	9	6
rno-miR-7a-5p	14	28	15	9	6
sko-miR-7-5p	14	28	15	9	6
spu-miR-7	14	28	15	9	6
ssa-miR-7a-5p	14	28	15	9	6
tgu-miR-7-5p	14	28	15	9	6
tni-miR-7	14	28	15	9	6
bta-miR-411a	6	1	21	8	2
cfa-miR-411	6	1	21	8	2
ggo-miR-411	6	1	21	8	2
oar-miR-411a-5p	6	1	21	8	2
cja-miR-411	6	1	14	6	1
cpo-miR-411-5p	6	1	14	6	1
dno-miR-411-5p	6	1	14	6	1
eca-miR-411	6	1	14	6	1
hsa-miR-411-5p	6	1	14	6	1
mml-miR-411-5p	6	1	14	6	1
mmr-miR-411a	6	1	14	6	1
mmu-miR-411-5p	6	1	14	6	1
ocu-miR-411-5p	6	1	14	6	1
oga-miR-411a	6	1	14	6	1
pha-miR-411a	6	1	14	6	1
ppa-miR-411a	6	1	14	6	1
ppy-miR-411	6	1	14	6	1
ptr-miR-411	6	1	14	6	1
rno-miR-411-5p	6	1	14	6	1
tch-miR-411-5p	6	1	14	6	1
aca-miR-10a-5p	8	5	15	4	5
age-miR-10a	8	5	15	4	5
ami-miR-10a-5p	8	5	15	4	5
bfl-miR-10a-5p	8	5	15	4	5
bta-miR-10a	8	5	15	4	5
cli-miR-10a-5p	8	5	15	4	5
dno-miR-10a-5p	8	5	15	4	5
eca-miR-10a	8	5	15	4	5

ggo-miR-10a	8	5	15	4	5
hsa-miR-10a-5p	8	5	15	4	5
mdo-miR-10a-5p	8	5	15	4	5
mml-miR-10a-5p	8	5	15	4	5
mmu-miR-10a-5p	8	5	15	4	5
oha-miR-10a-5p	8	5	15	4	5
pbv-miR-10a-5p	8	5	15	4	5
ppa-miR-10a	8	5	15	4	5
ppy-miR-10a	8	5	15	4	5
ptr-miR-10a	8	5	15	4	5
rno-miR-10a-5p	8	5	15	4	5
sko-miR-10	8	5	15	4	5
sla-miR-10a	8	5	15	4	5
xtr-miR-10a	8	5	15	4	5
xla-miR-10a-5p	8	5	16	4	5
api-miR-7	97	187	35	103	49
bdo-miR-7	97	187	35	103	49
bta-miR-7	97	187	35	103	49
ccr-miR-7a	97	187	35	103	49
chi-miR-7-5p	97	187	35	103	49
cja-miR-7	97	187	35	103	49
cli-miR-7a-5p	97	187	35	103	49
cpo-miR-7-5p	97	187	35	103	49
dno-miR-7-5p	97	187	35	103	49
dqu-miR-7-5p	97	187	35	103	49
dvi-miR-7-5p	97	187	35	103	49
efu-miR-7a	97	187	35	103	49
efu-miR-7b	97	187	35	103	49
efu-miR-7c	97	187	35	103	49
gmo-miR-7a-5p	97	187	35	103	49
hsa-miR-7-5p	97	187	35	103	49
lgi-miR-7	97	187	35	103	49
mse-miR-7	97	187	35	103	49
mze-miR-7a	97	187	35	103	49
ocu-miR-7a-5p	97	187	35	103	49
oha-miR-7-5p	97	187	35	103	49
pal-miR-7b-5p	97	187	35	103	49
pbv-miR-7-5p	97	187	35	103	49
pca-miR-7-5p	97	187	35	103	49
ssc-miR-7-5p	97	187	35	103	49
tca-miR-7-5p	97	187	35	103	49
tcf-miR-7	97	187	35	103	49
tch-miR-7-5p	97	187	35	103	49

tur-miR-7-5p	97	187	35	103	49
abu-let-7a	261	217	212	242	138
aca-let-7a-5p	261	217	212	242	138
ami-let-7a-5p	261	217	212	242	138
asu-let-7-5p	261	217	212	242	138
bbe-let-7a-5p	261	217	212	242	138
bfl-let-7a-5p	261	217	212	242	138
bma-let-7	261	217	212	242	138
bta-let-7a-5p	261	217	212	242	138
cbn-let-7	261	217	212	242	138
cbr-let-7	261	217	212	242	138
ccr-let-7a	261	217	212	242	138
cel-let-7-5p	261	217	212	242	138
cfa-let-7a	261	217	212	242	138
cgr-let-7a	261	217	212	242	138
chi-let-7a-5p	261	217	212	242	138
cja-let-7a	261	217	212	242	138
cli-let-7a-5p	261	217	212	242	138
cpi-let-7a-5p	261	217	212	242	138
cpo-let-7a-5p	261	217	212	242	138
crm-let-7	261	217	212	242	138
dma-let-7a	261	217	212	242	138
dno-let-7a-5p	261	217	212	242	138
dre-let-7a	261	217	212	242	138
eca-let-7a	261	217	212	242	138
fru-let-7a	261	217	212	242	138
gga-let-7a-5p	261	217	212	242	138
gga-let-7j-5p	261	217	212	242	138
gmo-let-7a-5p	261	217	212	242	138
hpo-let-7-5p	261	217	212	242	138
hsa-let-7a-5p	261	217	212	242	138
ipu-let-7a	261	217	212	242	138
lgi-let-7	261	217	212	242	138
mdo-let-7a-5p	261	217	212	242	138
mml-let-7a-5p	261	217	212	242	138
mmr-let-7a	261	217	212	242	138
mmu-let-7a-5p	261	217	212	242	138
mze-let-7a	261	217	212	242	138
nbr-let-7a	261	217	212	242	138
nle-let-7a	261	217	212	242	138
oar-let-7a	261	217	212	242	138
ocu-let-7a-5p	261	217	212	242	138
oga-let-7a	261	217	212	242	138

oha-let-7a	261	217	212	242	138
oha-let-7a-5p	261	217	212	242	138
ola-let-7a	261	217	212	242	138
oni-let-7a	261	217	212	242	138
pal-let-7a-5p	261	217	212	242	138
pbv-let-7a-5p	261	217	212	242	138
pha-let-7a	261	217	212	242	138
pma-let-7a	261	217	212	242	138
pny-let-7a	261	217	212	242	138
ppa-let-7a	261	217	212	242	138
ppc-let-7	261	217	212	242	138
ppy-let-7a	261	217	212	242	138
pte-let-7-5p	261	217	212	242	138
ptr-let-7a	261	217	212	242	138
rno-let-7a-5p	261	217	212	242	138
sbo-let-7a	261	217	212	242	138
sko-let-7	261	217	212	242	138
ssa-let-7a-5p	261	217	212	242	138
ssc-let-7a	261	217	212	242	138
tgu-let-7a-5p	261	217	212	242	138
tni-let-7a	261	217	212	242	138
xla-let-7a-5p	261	217	212	242	138
xtr-let-7a	261	217	212	242	138
prd-let-7-5p	264	220	219	248	141
cgr-miR-196b	39	3	4	18	27
cja-miR-196b	39	3	4	18	27
eca-miR-196b	39	3	4	18	27
ggo-miR-196b	39	3	4	18	27
hsa-miR-196b-5p	39	3	4	18	27
mdo-miR-196a-5p	39	3	4	18	27
mml-miR-196b-5p	39	3	4	18	27
mmr-miR-196b	39	3	4	18	27
mmu-miR-196b-5p	39	3	4	18	27
nle-miR-196b	39	3	4	18	27
oga-miR-196b	39	3	4	18	27
pal-miR-196b-5p	39	3	4	18	27
ppy-miR-196b	39	3	4	18	27
ptr-miR-196b	39	3	4	18	27
rno-miR-196b-5p	39	3	4	18	27
ssc-miR-196b-5p	39	3	4	18	27
efu-miR-34a	69	10	99	57	33
ami-miR-34a-5p	69	10	99	57	33
cja-miR-34a	69	10	99	57	33

gga-miR-34a-5p	69	10	99	57	33
mdo-miR-34a-5p	69	10	99	57	33
oha-miR-34a-5p	69	10	99	57	33
tch-miR-34a-5p	69	10	99	57	33
xtr-miR-34a	69	10	99	57	33
bta-miR-196b	45	4	4	26	31
cfa-miR-196b	45	4	4	26	31
cpo-miR-196b-5p	45	4	4	26	31
dno-miR-196b-5p	45	4	4	26	31
ocu-miR-196b-5p	45	4	4	26	31
abu-let-7b	262	161	189	198	135
ami-let-7b-5p	262	161	189	198	135
bta-let-7b	262	161	189	198	135
ccr-let-7b	262	161	189	198	135
cfa-let-7b	262	161	189	198	135
cgr-let-7b	262	161	189	198	135
chi-let-7b-5p	262	161	189	198	135
cja-let-7b	262	161	189	198	135
cpi-let-7b-5p	262	161	189	198	135
cpo-let-7b-5p	262	161	189	198	135
dma-let-7b	262	161	189	198	135
dno-let-7b-5p	262	161	189	198	135
dre-let-7b	262	161	189	198	135
fru-let-7b	262	161	189	198	135
gga-let-7b	262	161	189	198	135
hsa-let-7b-5p	262	161	189	198	135
mdo-let-7b	262	161	189	198	135
mml-let-7b-5p	262	161	189	198	135
mmr-let-7b	262	161	189	198	135
mmu-let-7b-5p	262	161	189	198	135
mze-let-7b	262	161	189	198	135
nbr-let-7b	262	161	189	198	135
oan-let-7b-5p	262	161	189	198	135
ocu-let-7b-5p	262	161	189	198	135
oga-let-7b	262	161	189	198	135
oha-let-7b-5p	262	161	189	198	135
oni-let-7b	262	161	189	198	135
pbv-let-7b-5p	262	161	189	198	135
pha-let-7b	262	161	189	198	135
pny-let-7b	262	161	189	198	135
pol-let-7b-5p	262	161	189	198	135
ppa-let-7b	262	161	189	198	135
ppy-let-7b	262	161	189	198	135

ptr-let-7b	262	161	189	198	135
rno-let-7b-5p	262	161	189	198	135
sbo-let-7b	262	161	189	198	135
ssa-let-7b-5p	262	161	189	198	135
tgu-let-7b-5p	262	161	189	198	135
tni-let-7b	262	161	189	198	135
abu-miR-34	58	9	85	42	29
age-miR-34a	58	9	85	42	29
bta-miR-34a	58	9	85	42	29
ccr-miR-34	58	9	85	42	29
cfa-miR-34a	58	9	85	42	29
cgr-miR-34a	58	9	85	42	29
chi-miR-34a	58	9	85	42	29
cli-miR-34a-5p	58	9	85	42	29
cpi-miR-34a-5p	58	9	85	42	29
cpo-miR-34a-5p	58	9	85	42	29
dno-miR-34a-5p	58	9	85	42	29
dre-miR-34a	58	9	85	42	29
eca-miR-34a	58	9	85	42	29
ggo-miR-34a	58	9	85	42	29
gmo-miR-34-5p	58	9	85	42	29
hsa-miR-34a-5p	58	9	85	42	29
ipu-miR-34a	58	9	85	42	29
lla-miR-34a	58	9	85	42	29
mml-miR-34a-5p	58	9	85	42	29
mmr-miR-34a	58	9	85	42	29
mmu-miR-34a-5p	58	9	85	42	29
mne-miR-34a	58	9	85	42	29
mze-miR-34	58	9	85	42	29
nbr-miR-34	58	9	85	42	29
nle-miR-34a	58	9	85	42	29
ocu-miR-34a-5p	58	9	85	42	29
oga-miR-34a	58	9	85	42	29
oni-miR-34	58	9	85	42	29
pal-miR-34a-5p	58	9	85	42	29
pbv-miR-34a-5p	58	9	85	42	29
pny-miR-34	58	9	85	42	29
ppa-miR-34a	58	9	85	42	29
ppy-miR-34a	58	9	85	42	29
ptr-miR-34a	58	9	85	42	29
rno-miR-34a-5p	58	9	85	42	29
sla-miR-34a	58	9	85	42	29
ssc-miR-34a	58	9	85	42	29

tgu-miR-34a	58	9	85	42	29
cja-miR-222	28	20	33	32	14
cpi-miR-222a-3p	28	20	33	32	14
gmo-miR-222-3p	28	20	33	32	14
mmu-miR-222-3p	28	20	33	32	14
pal-miR-222-3p	28	20	33	32	14
xla-miR-222-3p	28	20	33	32	14
ccr-miR-100	31	0	40	10	8
cgr-miR-100-5p	31	0	40	10	8
chi-miR-100-5p	31	0	40	10	8
cpi-miR-100-5p	31	0	40	10	8
dma-miR-100	31	0	40	10	8
mdo-miR-100-5p	31	0	40	10	8
pmi-miR-100-5p	31	0	40	10	8
sbo-miR-100	31	0	40	10	8
sha-miR-100	31	0	40	10	8
tgu-miR-100-5p	31	0	40	10	8
hme-let-7	86	41	76	62	44
pca-let-7-5p	86	41	76	62	44
ame-let-7-5p	86	41	76	62	43
bdo-let-7	86	41	76	62	43
bmo-let-7-5p	86	41	76	62	43
cte-let-7	86	41	76	62	43
dan-let-7	86	41	76	62	43
der-let-7	86	41	76	62	43
dgr-let-7	86	41	76	62	43
dme-let-7-5p	86	41	76	62	43
dmo-let-7	86	41	76	62	43
dpe-let-7	86	41	76	62	43
dps-let-7	86	41	76	62	43
dqu-let-7-5p	86	41	76	62	43
dse-let-7	86	41	76	62	43
dsi-let-7	86	41	76	62	43
dvi-let-7	86	41	76	62	43
dwi-let-7	86	41	76	62	43
dya-let-7	86	41	76	62	43
ggo-let-7a	86	41	76	62	43
isc-let-7	86	41	76	62	43
ngi-let-7	86	41	76	62	43
nvi-let-7	86	41	76	62	43
ola-let-7a-5p	86	41	76	62	43
sha-let-7a	86	41	76	62	43
abu-miR-222	123	106	185	150	53

age-miR-222	123	106	185	150	53
ami-miR-222a-3p	123	106	185	150	53
cgr-miR-222-3p	123	106	185	150	53
chi-miR-222-3p	123	106	185	150	53
cli-miR-222a-3p	123	106	185	150	53
cpo-miR-222-3p	123	106	185	150	53
dma-miR-222	123	106	185	150	53
dno-miR-222-3p	123	106	185	150	53
dre-miR-222a-3p	123	106	185	150	53
fru-miR-222	123	106	185	150	53
gga-miR-222a	123	106	185	150	53
mdo-miR-222a	123	106	185	150	53
mmr-miR-222	123	106	185	150	53
mze-miR-222	123	106	185	150	53
nbr-miR-222	123	106	185	150	53
nle-miR-222	123	106	185	150	53
ocu-miR-222-3p	123	106	185	150	53
oga-miR-222	123	106	185	150	53
oha-miR-222a-3p	123	106	185	150	53
oni-miR-222	123	106	185	150	53
pbv-miR-222a-3p	123	106	185	150	53
pha-miR-222	123	106	185	150	53
pny-miR-222	123	106	185	150	53
ppa-miR-222	123	106	185	150	53
ssa-miR-222a-3p	123	106	185	150	53
ssc-miR-222	123	106	185	150	53
tgu-miR-222-3p	123	106	185	150	53
tni-miR-222	123	106	185	150	53
xtr-miR-222	123	106	185	150	53
efu-let-7f	201	112	115	183	125
aca-let-7f-5p	199	112	115	182	125
bta-let-7f	199	112	115	182	125
cfa-let-7f	199	112	115	182	125
cgr-let-7f	199	112	115	182	125
chi-let-7f-5p	199	112	115	182	125
cja-let-7f	199	112	115	182	125
cli-let-7f-5p	199	112	115	182	125
cpi-let-7f-5p	199	112	115	182	125
cpo-let-7f-5p	199	112	115	182	125
dma-let-7f	199	112	115	182	125
dno-let-7f-5p	199	112	115	182	125
dre-let-7f	199	112	115	182	125
eca-let-7f	199	112	115	182	125

gga-let-7f-5p	199	112	115	182	125
gmo-let-7f-5p	199	112	115	182	125
hsa-let-7f-5p	199	112	115	182	125
ipu-let-7f	199	112	115	182	125
mdo-let-7f-5p	199	112	115	182	125
mml-let-7f-5p	199	112	115	182	125
mmr-let-7f	199	112	115	182	125
mmu-let-7f-5p	199	112	115	182	125
nle-let-7f	199	112	115	182	125
oan-let-7f-5p	199	112	115	182	125
ocu-let-7f-5p	199	112	115	182	125
oga-let-7f	199	112	115	182	125
oha-let-7f-5p	199	112	115	182	125
oni-let-7f	199	112	115	182	125
pal-let-7f-5p	199	112	115	182	125
pbv-let-7f-5p	199	112	115	182	125
pha-let-7f	199	112	115	182	125
ppa-let-7f	199	112	115	182	125
ppy-let-7f	199	112	115	182	125
ptr-let-7f	199	112	115	182	125
rno-let-7f-5p	199	112	115	182	125
sbo-let-7f	199	112	115	182	125
ssc-let-7f-5p	199	112	115	182	125
tch-let-7f-5p	199	112	115	182	125
tgu-let-7f-5p	199	112	115	182	125
xla-let-7f-5p	199	112	115	182	125
xtr-let-7f	199	112	115	182	125
bfl-miR-100-5p	57	2	301	35	20
dpu-miR-100	57	2	301	35	20
hpo-miR-100-5p	57	2	301	35	20
isc-miR-100	57	2	301	35	20
abu-let-7i	305	162	122	253	165
aca-let-7i-5p	305	162	122	253	165
bta-let-7i	305	162	122	253	165
chi-let-7i-5p	305	162	122	253	165
cja-let-7i	305	162	122	253	165
cpi-let-7i-5p	305	162	122	253	165
cpo-let-7i-5p	305	162	122	253	165
dno-let-7i-5p	305	162	122	253	165
dre-let-7i	305	162	122	253	165
fru-let-7i	305	162	122	253	165
gmo-let-7i-5p	305	162	122	253	165
hsa-let-7i-5p	305	162	122	253	165

ipu-let-7i	305	162	122	253	165
mml-let-7i-5p	305	162	122	253	165
mmu-let-7i-5p	305	162	122	253	165
mze-let-7i	305	162	122	253	165
nbr-let-7i	305	162	122	253	165
nle-let-7i	305	162	122	253	165
oar-let-7i	305	162	122	253	165
ocu-let-7i-5p	305	162	122	253	165
oga-let-7i	305	162	122	253	165
oha-let-7i-5p	305	162	122	253	165
oni-let-7i	305	162	122	253	165
pal-let-7i-5p	305	162	122	253	165
pbv-let-7i-5p	305	162	122	253	165
pha-let-7i	305	162	122	253	165
pny-let-7i	305	162	122	253	165
ppa-let-7i	305	162	122	253	165
ppy-let-7i	305	162	122	253	165
ptr-let-7i	305	162	122	253	165
rno-let-7i-5p	305	162	122	253	165
ssa-let-7i-5p	305	162	122	253	165
tch-let-7i-5p	305	162	122	253	165
tgu-let-7i-5p	305	162	122	253	165
tni-let-7i	305	162	122	253	165
cli-let-7i-5p	309	162	123	256	165
asu-miR-100a-5p	57	3	311	35	20
prd-miR-100-5p	57	3	311	35	20
oha-miR-100-5p	47	2	288	32	16
aae-miR-100	47	2	288	31	16
abu-miR-100	47	2	288	31	16
aca-miR-100	47	2	288	31	16
aga-miR-100	47	2	288	31	16
age-miR-100	47	2	288	31	16
ame-miR-100-5p	47	2	288	31	16
ami-miR-100-5p	47	2	288	31	16
bbe-miR-100-5p	47	2	288	31	16
bma-miR-100b	47	2	288	31	16
bmo-miR-100	47	2	288	31	16
bta-miR-100	47	2	288	31	16
cja-miR-100	47	2	288	31	16
cli-miR-100-5p	47	2	288	31	16
cpo-miR-100-5p	47	2	288	31	16
cqu-miR-100-5p	47	2	288	31	16
dno-miR-100-5p	47	2	288	31	16

dre-miR-100-5p	47	2	288	31	16
eca-miR-100	47	2	288	31	16
fru-miR-100	47	2	288	31	16
gga-miR-100-5p	47	2	288	31	16
ggo-miR-100	47	2	288	31	16
gmo-miR-100a-5p	47	2	288	31	16
hsa-miR-100-5p	47	2	288	31	16
ipu-miR-100	47	2	288	31	16
lgi-miR-100	47	2	288	31	16
lla-miR-100	47	2	288	31	16
mml-miR-100-5p	47	2	288	31	16
mmr-miR-100	47	2	288	31	16
mmu-miR-100-5p	47	2	288	31	16
mse-miR-100	47	2	288	31	16
mze-miR-100	47	2	288	31	16
nbr-miR-100	47	2	288	31	16
nle-miR-100	47	2	288	31	16
nvi-miR-100	47	2	288	31	16
oan-miR-100-5p	47	2	288	31	16
ocu-miR-100-5p	47	2	288	31	16
oga-miR-100	47	2	288	31	16
oni-miR-100	47	2	288	31	16
pal-miR-100-5p	47	2	288	31	16
pbv-miR-100-5p	47	2	288	31	16
pha-miR-100	47	2	288	31	16
pma-miR-100a-5p	47	2	288	31	16
pny-miR-100	47	2	288	31	16
ppa-miR-100	47	2	288	31	16
ppy-miR-100	47	2	288	31	16
pte-miR-100b-5p	47	2	288	31	16
ptr-miR-100	47	2	288	31	16
rno-miR-100-5p	47	2	288	31	16
sko-miR-100	47	2	288	31	16
sla-miR-100	47	2	288	31	16
ssa-miR-100a-5p	47	2	288	31	16
ssc-miR-100	47	2	288	31	16
tcf-miR-100	47	2	288	31	16
tch-miR-100-5p	47	2	288	31	16
tni-miR-100	47	2	288	31	16
xla-miR-100-5p	47	2	288	31	16
xtr-miR-100	47	2	288	31	16
tca-miR-100-5p	47	2	290	31	16
ami-let-7f-5p	54	16	39	51	36

ggo-let-7f	54	16	39	51	36
oar-let-7f	54	16	39	51	36
cli-miR-199-3p	450	16	114	402	242
efu-miR-199	450	16	114	402	242
dre-miR-199-3p	426	15	111	375	227
oha-miR-199c-3p	426	15	111	375	227
ssc-miR-199b-3p	426	15	111	375	227
xtr-miR-199a-3p	426	15	111	375	227
xla-miR-199-3p	379	12	105	334	200
ami-miR-199-3p	379	12	105	334	200
bta-miR-199a-3p	379	12	105	334	200
cpi-miR-199-3p	379	12	105	334	200
cpo-miR-199-3p	379	12	105	334	200
dno-miR-199-3p	379	12	105	334	200
eca-miR-199a-3p	379	12	105	334	200
eca-miR-199b-3p	379	12	105	334	200
gmo-miR-199-3p	379	12	105	334	200
hsa-miR-199a-3p	379	12	105	334	200
hsa-miR-199b-3p	379	12	105	334	200
mml-miR-199a-3p	379	12	105	334	200
mmu-miR-199a-3p	379	12	105	334	200
mmu-miR-199b-3p	379	12	105	334	200
ocu-miR-199a-3p	379	12	105	334	200
oha-miR-199a-3p	379	12	105	334	200
ola-miR-199a-3p	379	12	105	334	200
pol-miR-199a-3p	379	12	105	334	200
ptr-miR-199a-3p	379	12	105	334	200
ptr-miR-199b	379	12	105	334	200
rno-miR-199a-3p	379	12	105	334	200
ssc-miR-199a-3p	379	12	105	334	200
abu-miR-199-3p	358	11	102	309	185
ccr-miR-199-3p	358	11	102	309	185
cfa-miR-199	358	11	102	309	185
cgr-miR-199a-3p	358	11	102	309	185
chi-miR-199a-3p	358	11	102	309	185
chi-miR-199b-3p	358	11	102	309	185
chi-miR-199c-3p	358	11	102	309	185
cja-miR-199	358	11	102	309	185
dma-miR-199	358	11	102	309	185
gmo-miR-199-4-3p	358	11	102	309	185
ipu-miR-199a-3p	358	11	102	309	185
mdo-miR-199b-3p	358	11	102	309	185
mmr-miR-199	358	11	102	309	185

mze-miR-199	358	11	102	309	185
nbr-miR-199	358	11	102	309	185
nle-miR-199a	358	11	102	309	185
nle-miR-199b	358	11	102	309	185
oan-miR-199-3p	358	11	102	309	185
oar-miR-199a-3p	358	11	102	309	185
oga-miR-199	358	11	102	309	185
oni-miR-199a	358	11	102	309	185
pal-miR-199-3p	358	11	102	309	185
pbv-miR-199-3p	358	11	102	309	185
pha-miR-199	358	11	102	309	185
pny-miR-199	358	11	102	309	185
ppa-miR-199b	358	11	102	309	185
sbo-miR-199	358	11	102	309	185
sha-miR-199a	358	11	102	309	185
ssa-miR-199a-3p	358	11	102	309	185
tch-miR-199a-3p	358	11	102	309	185
tch-miR-199b-3p	358	11	102	309	185
tgu-miR-199-3p	358	11	102	309	185
aae-miR-125-5p	75	5	62	39	22
abu-miR-125b	75	5	62	39	22
aca-miR-125b	75	5	62	39	22
aga-miR-125	75	5	62	39	22
age-miR-125b	75	5	62	39	22
ami-miR-125b-5p	75	5	62	39	22
bbe-miR-125a-5p	75	5	62	39	22
bdo-miR-125	75	5	62	39	22
bfl-miR-125a-5p	75	5	62	39	22
bta-miR-125b	75	5	62	39	22
ccr-miR-125b	75	5	62	39	22
cfa-miR-125b	75	5	62	39	22
cgr-miR-125b-5p	75	5	62	39	22
cja-miR-125	75	5	62	39	22
cja-miR-125b	75	5	62	39	22
cli-miR-125-5p	75	5	62	39	22
cpi-miR-125b-5p	75	5	62	39	22
cpo-miR-125b-5p	75	5	62	39	22
cqu-miR-125-5p	75	5	62	39	22
cte-miR-125	75	5	62	39	22
dan-miR-125	75	5	62	39	22
der-miR-125	75	5	62	39	22
dgr-miR-125	75	5	62	39	22
dma-miR-125b	75	5	62	39	22

dme-miR-125-5p	75	5	62	39	22
dmo-miR-125	75	5	62	39	22
dno-miR-125b-5p	75	5	62	39	22
dpe-miR-125	75	5	62	39	22
dps-miR-125	75	5	62	39	22
dqu-miR-125-5p	75	5	62	39	22
dre-miR-125b-5p	75	5	62	39	22
dse-miR-125	75	5	62	39	22
dsi-miR-125	75	5	62	39	22
dwi-miR-125	75	5	62	39	22
dya-miR-125	75	5	62	39	22
eca-miR-125b-5p	75	5	62	39	22
efu-miR-125b	75	5	62	39	22
fru-miR-125b	75	5	62	39	22
gga-miR-125b-5p	75	5	62	39	22
ggo-miR-125b	75	5	62	39	22
gmo-miR-125b-5p	75	5	62	39	22
hsa-miR-125b-5p	75	5	62	39	22
ipu-miR-125b	75	5	62	39	22
lca-miR-125b	75	5	62	39	22
lla-miR-125b	75	5	62	39	22
lva-miR-125-5p	75	5	62	39	22
mdo-miR-125b-5p	75	5	62	39	22
mml-miR-125b-5p	75	5	62	39	22
mmr-miR-125a	75	5	62	39	22
mmu-miR-125b-5p	75	5	62	39	22
mne-miR-125b	75	5	62	39	22
mze-miR-125b	75	5	62	39	22
nbr-miR-125b	75	5	62	39	22
nle-miR-125b	75	5	62	39	22
nlo-miR-125	75	5	62	39	22
nvi-miR-125	75	5	62	39	22
oan-miR-125-5p	75	5	62	39	22
ocu-miR-125b-5p	75	5	62	39	22
oga-miR-125b	75	5	62	39	22
oha-miR-125b-5p	75	5	62	39	22
ola-miR-125b	75	5	62	39	22
ola-miR-125c	75	5	62	39	22
oni-miR-125b	75	5	62	39	22
pal-miR-125b-5p	75	5	62	39	22
pbv-miR-125b-5p	75	5	62	39	22
pha-miR-125b	75	5	62	39	22
pma-miR-125-5p	75	5	62	39	22

pmi-miR-125-5p	75	5	62	39	22
pny-miR-125b	75	5	62	39	22
ppa-miR-125b	75	5	62	39	22
ppy-miR-125b	75	5	62	39	22
ptr-miR-125b	75	5	62	39	22
rno-miR-125b-5p	75	5	62	39	22
sha-miR-125a	75	5	62	39	22
sko-miR-125a	75	5	62	39	22
sla-miR-125b	75	5	62	39	22
spu-miR-125-5p	75	5	62	39	22
ssa-miR-125a-5p	75	5	62	39	22
ssc-miR-125b	75	5	62	39	22
tca-miR-125-5p	75	5	62	39	22
tcf-miR-125	75	5	62	39	22
tch-miR-125b-5p	75	5	62	39	22
tgu-miR-125-5p	75	5	62	39	22
tni-miR-125b	75	5	62	39	22
xla-miR-125b-5p	75	5	62	39	22
xtr-miR-125b	75	5	62	39	22
aca-let-7b-5p	66	35	74	42	30
ggo-let-7b	66	35	74	42	30
ipu-let-7b	66	35	74	42	30
oar-let-7b	66	35	74	42	30
ola-let-7b	66	35	74	42	30
cgr-miR-125a-5p	43	2	23	26	18
cpo-miR-125a-5p	43	2	23	26	18
eca-miR-125a-5p	43	2	23	26	18
hsa-miR-125a-5p	43	2	23	26	18
mml-miR-125a-5p	43	2	23	26	18
mmu-miR-125a-5p	43	2	23	26	18
oga-miR-125a	43	2	23	26	18
ppy-miR-125a-5p	43	2	23	26	18
rno-miR-125a-5p	43	2	23	26	18
sbo-miR-125a	43	2	23	26	18
efu-miR-99b	42	1	76	17	18
bta-miR-99b	42	1	76	17	18
cfa-miR-99b	42	1	76	17	18
chi-miR-99b-5p	42	1	76	17	18
cpo-miR-99b-5p	42	1	76	17	18
eca-miR-99b	42	1	76	17	18
hsa-miR-99b-5p	42	1	76	17	18
mml-miR-99b-5p	42	1	76	17	18
mmu-miR-99b-5p	42	1	76	17	18

oga-miR-99b	42	1	76	17	18
pal-miR-99b-5p	42	1	76	17	18
ptr-miR-99b	42	1	76	17	18
rno-miR-99b-5p	42	1	76	17	18
ssc-miR-99b	42	1	76	17	18
tch-miR-99b-5p	42	1	76	17	18
abu-miR-26a	615	49	348	440	277
aca-miR-26-3-5p	615	49	348	440	277
ami-miR-26-5p	615	49	348	440	277
bta-miR-26a	615	49	348	440	277
ccr-miR-26a	615	49	348	440	277
cfa-miR-26a	615	49	348	440	277
chi-miR-26a-5p	615	49	348	440	277
cja-miR-26a	615	49	348	440	277
cli-miR-26-5p	615	49	348	440	277
cpi-miR-26-5p	615	49	348	440	277
cpo-miR-26a-5p	615	49	348	440	277
dma-miR-26a	615	49	348	440	277
dno-miR-26a-5p	615	49	348	440	277
dre-miR-26a-5p	615	49	348	440	277
eca-miR-26a	615	49	348	440	277
fru-miR-26	615	49	348	440	277
gga-miR-26a-2-5p	615	49	348	440	277
ggo-miR-26a	615	49	348	440	277
gmo-miR-26a-5p	615	49	348	440	277
hsa-miR-26a-5p	615	49	348	440	277
ipu-miR-26a	615	49	348	440	277
lla-miR-26a	615	49	348	440	277
mml-miR-26a-5p	615	49	348	440	277
mmr-miR-26a	615	49	348	440	277
mmu-miR-26a-5p	615	49	348	440	277
mne-miR-26a	615	49	348	440	277
mze-miR-26a	615	49	348	440	277
nbr-miR-26a	615	49	348	440	277
nle-miR-26a	615	49	348	440	277
oan-miR-26-5p	615	49	348	440	277
oar-miR-26a	615	49	348	440	277
ocu-miR-26a-5p	615	49	348	440	277
oga-miR-26a	615	49	348	440	277
oha-miR-26-5p	615	49	348	440	277
oni-miR-26a	615	49	348	440	277
pal-miR-26a-5p	615	49	348	440	277
pbv-miR-26-5p	615	49	348	440	277

pha-miR-26a	615	49	348	440	277
pma-miR-26a-5p	615	49	348	440	277
pny-miR-26a	615	49	348	440	277
ppa-miR-26a	615	49	348	440	277
ppy-miR-26a	615	49	348	440	277
ptr-miR-26a	615	49	348	440	277
rno-miR-26a-5p	615	49	348	440	277
sbo-miR-26a	615	49	348	440	277
ssa-miR-26a-5p	615	49	348	440	277
ssc-miR-26a	615	49	348	440	277
tch-miR-26a-5p	615	49	348	440	277
tgu-miR-26-5p	615	49	348	440	277
tni-miR-26	615	49	348	440	277
xla-miR-26-5p	615	49	348	440	277
efu-miR-26a	618	49	351	447	278
efu-miR-26c	618	49	351	447	278
bta-miR-21-5p	2370	1990	2099	2260	1180
cpo-miR-21-5p	2370	1990	2099	2260	1180
dno-miR-21-5p	2370	1990	2099	2260	1180
ocu-miR-21-5p	2370	1990	2099	2260	1180
sha-miR-21	2370	1990	2099	2260	1180
ami-miR-21-5p	2354	1975	2085	2242	1167
chi-miR-21-5p	2354	1975	2085	2242	1167
dma-miR-21	2354	1975	2085	2242	1167
mmr-miR-21	2354	1975	2085	2242	1167
nle-miR-21	2354	1975	2085	2242	1167
oar-miR-21	2354	1975	2085	2242	1167
oga-miR-21	2354	1975	2085	2242	1167
pbv-miR-21-5p	2354	1975	2085	2242	1167
pha-miR-21	2354	1975	2085	2242	1167
sbo-miR-21	2354	1975	2085	2242	1167
aca-miR-181a	530	24	204	364	281
ami-miR-181a-5p	530	24	204	364	281
cgr-miR-181a-5p	530	24	204	364	281
cja-miR-181a	530	24	204	364	281
cpi-miR-181a-5p	530	24	204	364	281
dma-miR-181a	530	24	204	364	281
dre-miR-181a-5p	530	24	204	364	281
eca-miR-181a	530	24	204	364	281
fru-miR-181a-5p	530	24	204	364	281
gga-miR-181a-5p	530	24	204	364	281
ggo-miR-181a-5p	530	24	204	364	281
gmo-miR-181a-5p	530	24	204	364	281

hsa-miR-181a-5p	530	24	204	364	281
lla-miR-181a-5p	530	24	204	364	281
mdo-miR-181a-5p	530	24	204	364	281
mml-miR-181a-5p	530	24	204	364	281
mmu-miR-181a-5p	530	24	204	364	281
mne-miR-181a-5p	530	24	204	364	281
nle-miR-181a	530	24	204	364	281
oan-miR-181a-5p	530	24	204	364	281
oar-miR-181a	530	24	204	364	281
oga-miR-181a	530	24	204	364	281
pha-miR-181a	530	24	204	364	281
pma-miR-181a-5p	530	24	204	364	281
ppa-miR-181a-5p	530	24	204	364	281
ppy-miR-181a-5p	530	24	204	364	281
ptr-miR-181a-5p	530	24	204	364	281
rno-miR-181a-5p	530	24	204	364	281
sla-miR-181a	530	24	204	364	281
ssa-miR-181a-5p	530	24	204	364	281
tch-miR-181a-5p	530	24	204	364	281
tgu-miR-181a-5p	530	24	204	364	281
tni-miR-181a-5p	530	24	204	364	281
xtr-miR-181a-5p	530	24	204	364	281
gma-miR169k	4455	4521	1104	4737	10493
gma-miR169l-5p	4455	4521	1104	4737	10493
mes-miR169l	4455	4521	1104	4737	10493
mes-miR169m	4455	4521	1104	4737	10493
bta-miR-181a	573	27	235	389	301
cli-miR-181a-5p	573	27	235	389	301
cpo-miR-181a-5p	573	27	235	389	301
dno-miR-181a-5p	573	27	235	389	301
ocu-miR-181a-5p	573	27	235	389	301
oha-miR-181a-5p	573	27	235	389	301
pal-miR-181a-5p	573	27	235	389	301
pbv-miR-181a-5p	573	27	235	389	301
ssc-miR-181a	573	27	235	389	301
ami-let-7i-5p	41	17	46	40	27
ccr-let-7i	41	17	46	40	27
gga-let-7i	41	17	46	40	27
ggo-let-7i	41	17	46	40	27
mdo-let-7i-5p	41	17	46	40	27
sha-let-7i	41	17	46	40	27
xla-let-7i-5p	41	17	46	40	27
xtr-let-7i	41	17	46	40	27

bta-miR-26b	46	28	38	40	14
cfa-miR-26b	46	28	38	40	14
cgr-miR-26b-5p	46	28	38	40	14
chi-miR-26b-5p	46	28	38	40	14
cja-miR-26b	46	28	38	40	14
cpo-miR-26b-5p	46	28	38	40	14
dma-miR-26b	46	28	38	40	14
dno-miR-26b-5p	46	28	38	40	14
mmr-miR-26b	46	28	38	40	14
ocu-miR-26b-5p	46	28	38	40	14
pal-miR-26b-5p	46	28	38	40	14
pha-miR-26b	46	28	38	40	14
ppa-miR-26b	46	28	38	40	14
ssc-miR-26b-5p	46	28	38	40	14
tch-miR-26b-5p	46	28	38	40	14
efu-miR-26b	47	30	39	41	14
cfa-miR-24	507	314	364	538	238
cgr-miR-24-3p	507	314	364	538	238
ipu-miR-24	507	314	364	538	238
oga-miR-24	507	314	364	538	238
oha-miR-24-3p	507	314	364	538	238
abu-miR-24b-3p	505	314	364	538	237
aca-miR-24-3p	505	314	364	538	237
ami-miR-24-3p	505	314	364	538	237
bta-miR-24-3p	505	314	364	538	237
ccr-miR-24	505	314	364	538	237
cja-miR-24	505	314	364	538	237
cpo-miR-24-3p	505	314	364	538	237
dno-miR-24a-3p	505	314	364	538	237
dre-miR-24	505	314	364	538	237
eca-miR-24	505	314	364	538	237
fru-miR-24-3p	505	314	364	538	237
gga-miR-24-3p	505	314	364	538	237
ggo-miR-24	505	314	364	538	237
hsa-miR-24-3p	505	314	364	538	237
mml-miR-24-3p	505	314	364	538	237
mmu-miR-24-3p	505	314	364	538	237
mne-miR-24-3p	505	314	364	538	237
nbr-miR-24a	505	314	364	538	237
oan-miR-24-3p	505	314	364	538	237
ocu-miR-24-3p	505	314	364	538	237
ola-miR-24a	505	314	364	538	237
oni-miR-24a	505	314	364	538	237

pbv-miR-24-3p	505	314	364	538	237
pma-miR-24	505	314	364	538	237
pny-miR-24a	505	314	364	538	237
ppa-miR-24-3p	505	314	364	538	237
ppy-miR-24-3p	505	314	364	538	237
ptr-miR-24	505	314	364	538	237
rno-miR-24-3p	505	314	364	538	237
ssc-miR-24-3p	505	314	364	538	237
tgu-miR-24-3p	505	314	364	538	237
tni-miR-24	505	314	364	538	237
xla-miR-24a-3p	505	314	364	538	237
xtr-miR-24a-3p	505	314	364	538	237
abu-miR-181c	64	15	28	42	45
chi-miR-181b-5p	64	15	28	42	45
eca-miR-181b	64	15	28	42	45
hsa-miR-181b-5p	64	15	28	42	45
mdo-miR-181b-5p	64	15	28	42	45
oha-miR-181b-5p	64	15	28	42	45
ppy-miR-181b	64	15	28	42	45
ptr-miR-181b	64	15	28	42	45
rno-miR-181b-5p	64	15	28	42	45
tch-miR-181b-5p	64	15	28	42	45
pde-miR159	342	153	44	381	330
ssa-miR-23b-3p	153	17	36	119	64
bta-miR-10174-3p	155	17	35	118	64
oga-miR-23b	155	17	35	118	64
tch-miR-23b-3p	155	17	35	118	64
cpi-miR-93-5p	11	10	75	9	5
sha-miR-93	11	10	75	9	5
gga-let-7g-5p	33	17	56	30	20
ggo-let-7g	33	17	56	30	20
mdo-let-7g-5p	33	17	56	30	20
oar-let-7g	33	17	56	30	20
sha-let-7g	33	17	56	30	20
cli-miR-23b-3p	155	18	35	119	63
efu-miR-23b	156	17	36	118	65
aca-let-7g	99	80	152	91	48
ami-let-7g-5p	99	80	152	91	48
bta-let-7g	99	80	152	91	48
cfa-let-7g	99	80	152	91	48
cgr-let-7g-5p	99	80	152	91	48
chi-let-7g-5p	99	80	152	91	48
cja-let-7g	99	80	152	91	48

cli-let-7g-5p	99	80	152	91	48
cpi-let-7g-5p	99	80	152	91	48
cpo-let-7g-5p	99	80	152	91	48
dma-let-7g	99	80	152	91	48
dno-let-7g-5p	99	80	152	91	48
eca-let-7g	99	80	152	91	48
hsa-let-7g-5p	99	80	152	91	48
mml-let-7g-5p	99	80	152	91	48
mmr-let-7g	99	80	152	91	48
mmu-let-7g-5p	99	80	152	91	48
nle-let-7g	99	80	152	91	48
oan-let-7g-5p	99	80	152	91	48
ocu-let-7g-5p	99	80	152	91	48
oga-let-7g	99	80	152	91	48
oha-let-7g-5p	99	80	152	91	48
pal-let-7g-5p	99	80	152	91	48
pbv-let-7g-5p	99	80	152	91	48
pha-let-7g	99	80	152	91	48
ppa-let-7g	99	80	152	91	48
ppy-let-7g	99	80	152	91	48
ptr-let-7g	99	80	152	91	48
rno-let-7g-5p	99	80	152	91	48
ssc-let-7g	99	80	152	91	48
tch-let-7g-5p	99	80	152	91	48
tgu-let-7g-5p	99	80	152	91	48
ami-miR-23b-3p	153	17	35	116	63
bta-miR-23b-3p	153	17	35	116	63
cpo-miR-23b-3p	153	17	35	116	63
dno-miR-23b-3p	153	17	35	116	63
dre-miR-23b-3p	153	17	35	116	63
hsa-miR-23b-3p	153	17	35	116	63
ocu-miR-23b-3p	153	17	35	116	63
oha-miR-23b-3p	153	17	35	116	63
ola-miR-23b	153	17	35	116	63
pbv-miR-23b-3p	153	17	35	116	63
pma-miR-23b	153	17	35	116	63
ppa-miR-23b	153	17	35	116	63
ppy-miR-23b	153	17	35	116	63
ptr-miR-23b	153	17	35	116	63
aca-miR-23a-3p	403	112	128	342	207
age-miR-23a	403	112	128	342	207
ccr-miR-23a	403	112	128	342	207
cgr-miR-23a-3p	403	112	128	342	207

chi-miR-23a	403	112	128	342	207
cpi-miR-23a-3p	403	112	128	342	207
eca-miR-23a	403	112	128	342	207
ggo-miR-23a	403	112	128	342	207
hsa-miR-23a-3p	403	112	128	342	207
ipu-miR-23a	403	112	128	342	207
lca-miR-23a	403	112	128	342	207
mml-miR-23a-3p	403	112	128	342	207
mmu-miR-23a-3p	403	112	128	342	207
mne-miR-23a	403	112	128	342	207
pbv-miR-23a-3p	403	112	128	342	207
pha-miR-23a	403	112	128	342	207
pny-miR-23a	403	112	128	342	207
ppa-miR-23a	403	112	128	342	207
ppy-miR-23a	403	112	128	342	207
ptr-miR-23a	403	112	128	342	207
rno-miR-23a-3p	403	112	128	342	207
sla-miR-23a	403	112	128	342	207
ssa-miR-23a-3p	403	112	128	342	207
ssc-miR-23a	403	112	128	342	207
xla-miR-23a	403	112	128	342	207
xtr-miR-23a	403	112	128	342	207
bta-miR-93	14	16	76	13	8
cpo-miR-151-5p	38	45	24	48	27
dno-miR-151-5p	38	45	24	48	27
ami-miR-181b-5p	95	27	50	66	59
bta-miR-181b	95	27	50	66	59
cli-miR-181b-5p	95	27	50	66	59
cpi-miR-181b-5p	95	27	50	66	59
cpo-miR-181b-5p	95	27	50	66	59
dno-miR-181b-5p	95	27	50	66	59
efu-miR-181e	95	27	50	66	59
ggo-miR-181b	95	27	50	66	59
gmo-miR-181b-5p	95	27	50	66	59
hhi-miR-181b	95	27	50	66	59
lla-miR-181b	95	27	50	66	59
mml-miR-181b-5p	95	27	50	66	59
mmu-miR-181b-5p	95	27	50	66	59
mne-miR-181b	95	27	50	66	59
ocu-miR-181b-5p	95	27	50	66	59
ola-miR-181b-5p	95	27	50	66	59
pal-miR-181b-5p	95	27	50	66	59
ppa-miR-181b	95	27	50	66	59

ssc-miR-181b	95	27	50	66	59
tgu-miR-181b-5p	95	27	50	66	59
abu-miR-221	34	21	39	23	11
ami-miR-221-3p	34	21	39	23	11
cgr-miR-221-3p	34	21	39	23	11
cpo-miR-221-3p	34	21	39	23	11
dma-miR-221	34	21	39	23	11
dno-miR-221-3p	34	21	39	23	11
dre-miR-221-3p	34	21	39	23	11
eca-miR-221	34	21	39	23	11
fru-miR-221	34	21	39	23	11
gga-miR-221-3p	34	21	39	23	11
ggo-miR-221	34	21	39	23	11
hsa-miR-221-3p	34	21	39	23	11
mdo-miR-221-3p	34	21	39	23	11
mml-miR-221-3p	34	21	39	23	11
mmr-miR-221	34	21	39	23	11
mmu-miR-221-3p	34	21	39	23	11
mze-miR-221	34	21	39	23	11
nbr-miR-221	34	21	39	23	11
nle-miR-221	34	21	39	23	11
ocu-miR-221-3p	34	21	39	23	11
oga-miR-221	34	21	39	23	11
oha-miR-221-3p	34	21	39	23	11
ola-miR-221	34	21	39	23	11
oni-miR-221	34	21	39	23	11
pha-miR-221	34	21	39	23	11
pny-miR-221	34	21	39	23	11
ppa-miR-221	34	21	39	23	11
ppy-miR-221	34	21	39	23	11
ptr-miR-221	34	21	39	23	11
rno-miR-221-3p	34	21	39	23	11
sbo-miR-221	34	21	39	23	11
tgu-miR-221-3p	34	21	39	23	11
tni-miR-221	34	21	39	23	11
xtr-miR-221	34	21	39	23	11
abu-miR-23b	106	6	23	67	42
aca-miR-23b-3p	106	6	23	67	42
ccr-miR-23b	106	6	23	67	42
cgr-miR-23b-3p	106	6	23	67	42
chi-miR-23b-3p	106	6	23	67	42
cja-miR-23b	106	6	23	67	42
cpi-miR-23b-3p	106	6	23	67	42

dma-miR-23b	106	6	23	67	42
eca-miR-23b	106	6	23	67	42
gga-miR-23b-3p	106	6	23	67	42
ipu-miR-23b	106	6	23	67	42
mdo-miR-23b-3p	106	6	23	67	42
mml-miR-23b-3p	106	6	23	67	42
mmr-miR-23b	106	6	23	67	42
mmu-miR-23b-3p	106	6	23	67	42
mze-miR-23b	106	6	23	67	42
nbr-miR-23b	106	6	23	67	42
nle-miR-23b	106	6	23	67	42
oni-miR-23b	106	6	23	67	42
pha-miR-23b	106	6	23	67	42
pma-miR-23a-3p	106	6	23	67	42
pny-miR-23b	106	6	23	67	42
rno-miR-23b-3p	106	6	23	67	42
tgu-miR-23-3p	106	6	23	67	42
xla-miR-23b-3p	106	6	23	67	42
xtr-miR-23b	106	6	23	67	42
efu-miR-23a	692	247	187	626	335
ami-miR-30d-5p	57	28	69	62	22
bta-miR-30d	57	28	69	62	22
cfa-miR-30d	57	28	69	62	22
cli-miR-30d-5p	57	28	69	62	22
cpo-miR-30d-5p	57	28	69	62	22
dno-miR-30d-5p	57	28	69	62	22
gmo-miR-30a-5p	57	28	69	62	22
nle-miR-30d	57	28	69	62	22
ocu-miR-30d-5p	57	28	69	62	22
oga-miR-30d	57	28	69	62	22
oha-miR-30d-5p	57	28	69	62	22
pal-miR-30d-5p	57	28	69	62	22
pbv-miR-30d-5p	57	28	69	62	22
pha-miR-30d	57	28	69	62	22
ssa-miR-30b-5p	57	28	69	62	22
ssc-miR-30d	57	28	69	62	22
tgu-miR-30d-5p	57	28	69	62	22
xla-miR-30d-5p	57	28	69	62	22
abu-miR-24a	90	32	44	67	41
chi-miR-24-3p	90	32	44	67	41
dma-miR-24	90	32	44	67	41
dre-miR-24b-3p	90	32	44	67	41
gmo-miR-24a-3p	90	32	44	67	41

ipu-miR-24b	90	32	44	67	41
mmr-miR-24	90	32	44	67	41
mze-miR-24a	90	32	44	67	41
nbr-miR-24c	90	32	44	67	41
nle-miR-24	90	32	44	67	41
oni-miR-24a-3	90	32	44	67	41
oni-miR-24a-4	90	32	44	67	41
oni-miR-24b-3p	90	32	44	67	41
pha-miR-24	90	32	44	67	41
pny-miR-24a-3	90	32	44	67	41
pny-miR-24a-4	90	32	44	67	41
ssa-miR-24a-3p	90	32	44	67	41
dre-miR-23b	138	9	32	97	54
fru-miR-23b	138	9	32	97	54
ggo-miR-23b	138	9	32	97	54
gmo-miR-23b-3p	138	9	32	97	54
pal-miR-23b-3p	138	9	32	97	54
ssc-miR-23b	138	9	32	97	54
tni-miR-23b	138	9	32	97	54
cpo-miR-23a-3p	672	228	184	607	324
dno-miR-23a-3p	672	228	184	607	324
bta-miR-423-3p	130	129	28	140	71
sbo-miR-423	130	129	28	140	71
dno-miR-24b-3p	91	32	44	67	42
efu-miR-92a	967	1113	98	1162	475
abu-miR-92a	967	1113	97	1161	475
aca-miR-92a	967	1113	97	1161	475
age-miR-92	967	1113	97	1161	475
ami-miR-92a-3p	967	1113	97	1161	475
bta-miR-92a	967	1113	97	1161	475
ccr-miR-92a	967	1113	97	1161	475
cfa-miR-92a	967	1113	97	1161	475
cgr-miR-92a-3p	967	1113	97	1161	475
chi-miR-92a-3p	967	1113	97	1161	475
chi-miR-92b	967	1113	97	1161	475
cja-miR-92a	967	1113	97	1161	475
cli-miR-92-3p	967	1113	97	1161	475
cpo-miR-92a-3p	967	1113	97	1161	475
dma-miR-92a	967	1113	97	1161	475
dno-miR-92a-3p	967	1113	97	1161	475
dre-miR-92a-3p	967	1113	97	1161	475
eca-miR-92a	967	1113	97	1161	475
fru-miR-92	967	1113	97	1161	475

ggo-miR-92	967	1113	97	1161	475
hsa-miR-92a-3p	967	1113	97	1161	475
ipu-miR-92a	967	1113	97	1161	475
lca-miR-92	967	1113	97	1161	475
lla-miR-92	967	1113	97	1161	475
mdo-miR-92a-3p	967	1113	97	1161	475
mml-miR-92a-3p	967	1113	97	1161	475
mmr-miR-92a	967	1113	97	1161	475
mmr-miR-92b	967	1113	97	1161	475
mne-miR-92	967	1113	97	1161	475
mze-miR-92a	967	1113	97	1161	475
nbr-miR-92a	967	1113	97	1161	475
nle-miR-92a	967	1113	97	1161	475
oan-miR-92a-3p	967	1113	97	1161	475
ocu-miR-92a-3p	967	1113	97	1161	475
oga-miR-92a	967	1113	97	1161	475
oha-miR-92a	967	1113	97	1161	475
oha-miR-92a-3p	967	1113	97	1161	475
oni-miR-92a	967	1113	97	1161	475
pal-miR-92a-3p	967	1113	97	1161	475
pbv-miR-92a-3p	967	1113	97	1161	475
pha-miR-92a	967	1113	97	1161	475
pny-miR-92	967	1113	97	1161	475
ppa-miR-92a	967	1113	97	1161	475
ppy-miR-92	967	1113	97	1161	475
ptr-miR-92	967	1113	97	1161	475
sbo-miR-92a	967	1113	97	1161	475
sla-miR-92	967	1113	97	1161	475
ssa-miR-92a-3p	967	1113	97	1161	475
ssc-miR-92a	967	1113	97	1161	475
tch-miR-92a-3p	967	1113	97	1161	475
tgu-miR-92-3p	967	1113	97	1161	475
tni-miR-92	967	1113	97	1161	475
xla-miR-92a-3p	967	1113	97	1161	475
abu-miR-23a	651	218	181	584	309
ami-miR-23a-3p	651	218	181	584	309
bta-miR-23a	651	218	181	584	309
cja-miR-23a	651	218	181	584	309
dre-miR-23a-3p	651	218	181	584	309
fru-miR-23a	651	218	181	584	309
gmo-miR-23a-3p	651	218	181	584	309
hhi-miR-23a	651	218	181	584	309
mze-miR-23a	651	218	181	584	309

nbr-miR-23a	651	218	181	584	309
oan-miR-23a-3p	651	218	181	584	309
oar-miR-23a	651	218	181	584	309
oga-miR-23a	651	218	181	584	309
oha-miR-23a-3p	651	218	181	584	309
ola-miR-23a	651	218	181	584	309
oni-miR-23a	651	218	181	584	309
pal-miR-23a-3p	651	218	181	584	309
tni-miR-23a	651	218	181	584	309
xla-miR-23a-3p	651	218	181	584	309
gma-miR396e	610	282	349	380	635
aau-miR396	610	282	348	380	635
aly-miR396a-5p	610	282	348	380	635
amg-miR396	610	282	348	380	635
aof-miR396b	610	282	348	380	635
aqc-miR396a	610	282	348	380	635
ata-miR396e-5p	610	282	348	380	635
ath-miR396a-5p	610	282	348	380	635
bcy-miR396a	610	282	348	380	635
bdi-miR396c-5p	610	282	348	380	635
bdi-miR396d-5p	610	282	348	380	635
bgy-miR396a	610	282	348	380	635
cas-miR396a	610	282	348	380	635
cme-miR396b	610	282	348	380	635
cpa-miR396	610	282	348	380	635
csi-miR396a-5p	610	282	348	380	635
csi-miR396b-5p	610	282	348	380	635
dpr-miR396	610	282	348	380	635
eun-miR396b-5p	610	282	348	380	635
fve-miR396a-5p	610	282	348	380	635
fve-miR396c-5p	610	282	348	380	635
fve-miR396d	610	282	348	380	635
ghr-miR396a	610	282	348	380	635
ghr-miR396b	610	282	348	380	635
gma-miR396a-5p	610	282	348	380	635
gma-miR396i-5p	610	282	348	380	635
hbr-miR396b	610	282	348	380	635
lja-miR396	610	282	348	380	635
lus-miR396a	610	282	348	380	635
lus-miR396c	610	282	348	380	635
mdm-miR396b	610	282	348	380	635
mes-miR396a	610	282	348	380	635
mes-miR396b	610	282	348	380	635

mtr-miR396b-5p	610	282	348	380	635
nta-miR396a	610	282	348	380	635
osa-miR396a-5p	610	282	348	380	635
osa-miR396b-5p	610	282	348	380	635
ptc-miR396a	610	282	348	380	635
ptc-miR396b	610	282	348	380	635
sbi-miR396a	610	282	348	380	635
sbi-miR396b	610	282	348	380	635
sly-miR396a-5p	610	282	348	380	635
sof-miR396	610	282	348	380	635
ssl-miR396	610	282	348	380	635
ssp-miR396	610	282	348	380	635
tcc-miR396a	610	282	348	380	635
tcc-miR396b	610	282	348	380	635
vvi-miR396c	610	282	348	380	635
vvi-miR396d	610	282	348	380	635
zma-miR396a-5p	610	282	348	380	635
zma-miR396b-5p	610	282	348	380	635
ami-miR-140-5p	150	17	4	108	74
ccr-miR-140-5p	150	17	4	108	74
cgr-miR-140-5p	150	17	4	108	74
chi-miR-140-5p	150	17	4	108	74
cli-miR-140-5p	150	17	4	108	74
cpi-miR-140-5p	150	17	4	108	74
cpo-miR-140-5p	150	17	4	108	74
dno-miR-140-5p	150	17	4	108	74
dre-miR-140-5p	150	17	4	108	74
eca-miR-140-5p	150	17	4	108	74
efu-miR-140	150	17	4	108	74
fru-miR-140	150	17	4	108	74
hsa-miR-140-5p	150	17	4	108	74
mdo-miR-140-5p	150	17	4	108	74
mml-miR-140-5p	150	17	4	108	74
mmu-miR-140-5p	150	17	4	108	74
ocu-miR-140-5p	150	17	4	108	74
oha-miR-140-5p	150	17	4	108	74
ola-miR-140-5p	150	17	4	108	74
pal-miR-140-5p	150	17	4	108	74
pma-miR-140	150	17	4	108	74
pol-miR-140-5p	150	17	4	108	74
ppy-miR-140-5p	150	17	4	108	74
rno-miR-140-5p	150	17	4	108	74
ssa-miR-140-5p	150	17	4	108	74

tgu-miR-140-5p	150	17	4	108	74
tni-miR-140	150	17	4	108	74
xla-miR-140-5p	152	18	4	110	74
cgr-miR-423-3p	123	121	27	134	63
chi-miR-423-3p	123	121	27	134	63
cja-miR-423-3p	123	121	27	134	63
cpo-miR-423-3p	123	121	27	134	63
dma-miR-423	123	121	27	134	63
dno-miR-423-3p	123	121	27	134	63
eca-miR-423-3p	123	121	27	134	63
hsa-miR-423-3p	123	121	27	134	63
mml-miR-423-3p	123	121	27	134	63
mmu-miR-423-3p	123	121	27	134	63
nle-miR-423	123	121	27	134	63
ocu-miR-423-3p	123	121	27	134	63
oga-miR-423	123	121	27	134	63
pal-miR-423-3p	123	121	27	134	63
ppa-miR-423	123	121	27	134	63
ppy-miR-423-3p	123	121	27	134	63
ptr-miR-423	123	121	27	134	63
rno-miR-423-3p	123	121	27	134	63
ssc-miR-423-3p	123	121	27	134	63
tch-miR-423-3p	123	121	27	134	63
ahy-miR408-3p	38	40	43	72	52
aly-miR408-3p	38	40	43	72	52
ath-miR408-3p	38	40	43	72	52
cas-miR408	38	40	43	72	52
cme-miR408	38	40	43	72	52
csi-miR408-3p	38	40	43	72	52
gma-miR408a-3p	38	40	43	72	52
gma-miR408b-3p	38	40	43	72	52
gma-miR408c-3p	38	40	43	72	52
lus-miR408a	38	40	43	72	52
mdm-miR408a	38	40	43	72	52
mes-miR408	38	40	43	72	52
mtr-miR408-3p	38	40	43	72	52
pta-miR408	38	40	43	72	52
ptc-miR408-3p	38	40	43	72	52
vun-miR408	38	40	43	72	52
vvi-miR408	38	40	43	72	52
dre-miR-27a-3p	526	304	354	521	256
ipu-miR-27a	526	304	354	521	256
ssa-miR-27a-3p	526	304	354	521	256

aly-miR396a-3p	127	102	90	94	201
ath-miR396a-3p	127	102	90	94	201
csi-miR396b-3p	127	102	90	94	201
eun-miR396a-3p	127	102	90	94	201
fve-miR396a-3p	127	102	90	94	201
fve-miR396c-3p	127	102	90	94	201
gma-miR396i-3p	127	102	90	94	201
mtr-miR396b-3p	127	102	90	94	201
sly-miR396a-3p	127	102	90	94	201
abu-miR-27a	466	289	340	482	226
aca-miR-27a-3p	466	289	340	482	226
ami-miR-27a-3p	466	289	340	482	226
ccr-miR-27a	466	289	340	482	226
cgr-miR-27a-3p	466	289	340	482	226
cja-miR-27a	466	289	340	482	226
cpi-miR-27a-3p	466	289	340	482	226
dno-miR-27a-3p	466	289	340	482	226
eca-miR-27a	466	289	340	482	226
hsa-miR-27a-3p	466	289	340	482	226
mdo-miR-27a-3p	466	289	340	482	226
mmu-miR-27a-3p	466	289	340	482	226
mze-miR-27a	466	289	340	482	226
nbr-miR-27a	466	289	340	482	226
oan-miR-27a-3p	466	289	340	482	226
oar-miR-27a	466	289	340	482	226
oni-miR-27a	466	289	340	482	226
pbv-miR-27a-3p	466	289	340	482	226
pny-miR-27a	466	289	340	482	226
rno-miR-27a-3p	466	289	340	482	226
sbo-miR-27a	466	289	340	482	226
ssc-miR-27a	466	289	340	482	226
xtr-miR-27a	466	289	340	482	226
age-miR-27a	466	290	340	483	226
ggo-miR-27a	466	290	340	483	226
lca-miR-27a	466	290	340	483	226
mml-miR-27a-3p	466	290	340	483	226
mne-miR-27a	466	290	340	483	226
oha-miR-27a-3p	466	290	340	483	226
ppa-miR-27a	466	290	340	483	226
ppy-miR-27a	466	290	340	483	226
ptr-miR-27a	466	290	340	483	226
sla-miR-27a	466	290	340	483	226
cpo-miR-27a-3p	178	92	314	181	109

tch-miR-27a-3p	178	92	314	181	109
efu-miR-93	52	85	87	71	35
ami-miR-93-5p	48	75	85	63	28
cfa-miR-93	48	75	85	63	28
cgr-miR-93-5p	48	75	85	63	28
chi-miR-93-5p	48	75	85	63	28
cja-miR-93	48	75	85	63	28
cpo-miR-93-5p	48	75	85	63	28
dma-miR-93	48	75	85	63	28
dno-miR-93-5p	48	75	85	63	28
eca-miR-93	48	75	85	63	28
hsa-miR-93-5p	48	75	85	63	28
mmu-miR-93-5p	48	75	85	63	28
nle-miR-93	48	75	85	63	28
ocu-miR-93-5p	48	75	85	63	28
oga-miR-93	48	75	85	63	28
pal-miR-93-5p	48	75	85	63	28
pha-miR-93	48	75	85	63	28
rno-miR-93-5p	48	75	85	63	28
tch-miR-93-5p	48	75	85	63	28
xla-miR-93-5p	48	75	85	63	28
ptc-miR6478	2152	3721	7602	2350	8982
pvu-miR482-5p	4383	5090	697	3076	6462
aca-miR-27b-3p	213	40	135	172	87
dre-miR-27b-3p	213	40	135	172	87
fru-miR-27b	213	40	135	172	87
oha-miR-27b-3p	213	40	135	172	87
tni-miR-27b	213	40	135	172	87
xla-miR-27b-3p	213	40	135	172	87
abu-miR-27b	171	33	131	134	76
bta-miR-27b	171	33	131	134	76
cfa-miR-27b	171	33	131	134	76
cgr-miR-27b-3p	171	33	131	134	76
chi-miR-27b-3p	171	33	131	134	76
cja-miR-27b	171	33	131	134	76
cli-miR-27b-3p	171	33	131	134	76
cpi-miR-27b-3p	171	33	131	134	76
cpo-miR-27b-3p	171	33	131	134	76
dno-miR-27b-3p	171	33	131	134	76
eca-miR-27b	171	33	131	134	76
gga-miR-27b-3p	171	33	131	134	76
ggo-miR-27b	171	33	131	134	76
hsa-miR-27b-3p	171	33	131	134	76

ipu-miR-27b	171	33	131	134	76
mdo-miR-27b-3p	171	33	131	134	76
mml-miR-27b-3p	171	33	131	134	76
mmr-miR-27b	171	33	131	134	76
mmu-miR-27b-3p	171	33	131	134	76
mze-miR-27b	171	33	131	134	76
nbr-miR-27b	171	33	131	134	76
oan-miR-27b-3p	171	33	131	134	76
ocu-miR-27b-3p	171	33	131	134	76
oni-miR-27b	171	33	131	134	76
pal-miR-27b-3p	171	33	131	134	76
pbv-miR-27b-3p	171	33	131	134	76
pma-miR-27b-3p	171	33	131	134	76
pny-miR-27b	171	33	131	134	76
ppa-miR-27b	171	33	131	134	76
ppy-miR-27b	171	33	131	134	76
ptr-miR-27b	171	33	131	134	76
rno-miR-27b-3p	171	33	131	134	76
sbo-miR-27b	171	33	131	134	76
sha-miR-27b	171	33	131	134	76
ssa-miR-27b-3p	171	33	131	134	76
ssc-miR-27b-3p	171	33	131	134	76
tch-miR-27b-3p	171	33	131	134	76
tgu-miR-27-3p	171	33	131	134	76
xtr-miR-27b	171	33	131	134	76
efu-miR-27b	217	42	137	172	87
ggo-let-7c	95	32	29	90	55
ola-let-7c	95	32	29	90	55
cpi-miR-24-3p	202	107	198	200	94
sbo-miR-24	202	107	198	200	94
bcy-miR156	497	289	178	259	317
bgy-miR156	497	289	178	259	317
ahy-miR156b-5p	497	289	177	259	317
aly-miR157a-5p	497	289	177	259	317
aly-miR157b-5p	497	289	177	259	317
aly-miR157c-5p	497	289	177	259	317
aof-miR156b	497	289	177	259	317
ath-miR157a-5p	497	289	177	259	317
ath-miR157b-5p	497	289	177	259	317
ath-miR157c-5p	497	289	177	259	317
atr-miR156a	497	289	177	259	317
atr-miR156c	497	289	177	259	317
bna-miR156b	497	289	177	259	317

bna-miR156c	497	289	177	259	317
bna-miR156g	497	289	177	259	317
bol-miR157a	497	289	177	259	317
bra-miR157a	497	289	177	259	317
cca-miR156c	497	289	177	259	317
cme-miR156b	497	289	177	259	317
cpa-miR156e	497	289	177	259	317
cpa-miR156f	497	289	177	259	317
fve-miR156f	497	289	177	259	317
fve-miR156g-5p	497	289	177	259	317
gma-miR156c	497	289	177	259	317
gma-miR156d	497	289	177	259	317
gma-miR156i	497	289	177	259	317
gma-miR156j	497	289	177	259	317
gma-miR156l	497	289	177	259	317
gma-miR156m	497	289	177	259	317
gra-miR157a	497	289	177	259	317
gra-miR157b	497	289	177	259	317
han-miR156c	497	289	177	259	317
lus-miR156b	497	289	177	259	317
lus-miR156c	497	289	177	259	317
lus-miR156e	497	289	177	259	317
lus-miR156f	497	289	177	259	317
lus-miR156h	497	289	177	259	317
lus-miR156i	497	289	177	259	317
mdm-miR156ab	497	289	177	259	317
mdm-miR156ac	497	289	177	259	317
mes-miR156h	497	289	177	259	317
mes-miR156i	497	289	177	259	317
mes-miR156j	497	289	177	259	317
mtr-miR156e	497	289	177	259	317
mtr-miR156f	497	289	177	259	317
mtr-miR156h-5p	497	289	177	259	317
ppe-miR156g	497	289	177	259	317
ppe-miR156h	497	289	177	259	317
ppe-miR156i	497	289	177	259	317
ptc-miR156g	497	289	177	259	317
ptc-miR156h	497	289	177	259	317
ptc-miR156i	497	289	177	259	317
ptc-miR156j	497	289	177	259	317
rco-miR156f	497	289	177	259	317
rco-miR156g	497	289	177	259	317
rco-miR156h	497	289	177	259	317

sly-miR156a	497	289	177	259	317
sly-miR156b	497	289	177	259	317
sly-miR156c	497	289	177	259	317
stu-miR156a	497	289	177	259	317
stu-miR156b	497	289	177	259	317
stu-miR156c	497	289	177	259	317
stu-miR156d-5p	497	289	177	259	317
tcc-miR156e	497	289	177	259	317
tcc-miR156f	497	289	177	259	317
vca-miR156b-5p	497	289	177	259	317
vun-miR156b	497	289	177	259	317
vvi-miR156f	497	289	177	259	317
vvi-miR156g	497	289	177	259	317
vvi-miR156i	497	289	177	259	317
pta-miR159a	214	147	5	235	134
osa-miR159c	221	151	6	236	138
aof-miR319b	4361	1697	3131	4130	2409
atr-miR319b	4361	1697	3131	4130	2409
atr-miR319d	4361	1697	3131	4130	2409
atr-miR319e	4361	1697	3131	4130	2409
cas-miR319c	4361	1697	3131	4130	2409
csi-miR159d	4361	1697	3131	4130	2409
fve-miR319	4361	1697	3131	4130	2409
tcc-miR319	4361	1697	3131	4130	2409
vvi-miR319e	4361	1697	3131	4130	2409
abu-let-7c	435	201	101	374	235
aca-let-7c-5p	435	201	101	374	235
ami-let-7c-5p	435	201	101	374	235
bta-let-7c	435	201	101	374	235
cfa-let-7c	435	201	101	374	235
chi-let-7c-5p	435	201	101	374	235
cja-let-7c	435	201	101	374	235
cli-let-7c-5p	435	201	101	374	235
cpi-let-7c-5p	435	201	101	374	235
cpo-let-7c-5p	435	201	101	374	235
dma-let-7c	435	201	101	374	235
dno-let-7c-5p	435	201	101	374	235
dre-let-7c-5p	435	201	101	374	235
eca-let-7c	435	201	101	374	235
gga-let-7c-5p	435	201	101	374	235
gmo-let-7c-5p	435	201	101	374	235
hhi-let-7c	435	201	101	374	235
hsa-let-7c-5p	435	201	101	374	235

ipu-let-7c	435	201	101	374	235
mml-let-7c-5p	435	201	101	374	235
mmr-let-7c	435	201	101	374	235
mmu-let-7c-5p	435	201	101	374	235
mze-let-7c	435	201	101	374	235
nbr-let-7c	435	201	101	374	235
nle-let-7c	435	201	101	374	235
oan-let-7c-5p	435	201	101	374	235
oar-let-7c	435	201	101	374	235
ocu-let-7c-5p	435	201	101	374	235
oga-let-7c	435	201	101	374	235
oha-let-7c-5p	435	201	101	374	235
oni-let-7c	435	201	101	374	235
pal-let-7c-5p	435	201	101	374	235
pbv-let-7c-5p	435	201	101	374	235
pha-let-7c	435	201	101	374	235
pny-let-7c	435	201	101	374	235
pol-let-7a-5p	435	201	101	374	235
ppa-let-7c	435	201	101	374	235
ppy-let-7c	435	201	101	374	235
ptr-let-7c	435	201	101	374	235
rno-let-7c-5p	435	201	101	374	235
ssa-let-7c-5p	435	201	101	374	235
ssc-let-7c	435	201	101	374	235
tcf-let-7-5p	435	201	101	374	235
tgu-let-7c-5p	435	201	101	374	235
xla-let-7c-5p	435	201	101	374	235
xtr-let-7c	435	201	101	374	235
efu-let-7c	448	209	111	385	247
abu-miR-143	115	4	328	51	30
aca-miR-143-3p	115	4	328	51	30
aja-miR-143	115	4	328	51	30
ami-miR-143-3p	115	4	328	51	30
bta-miR-143	115	4	328	51	30
cfa-miR-143	115	4	328	51	30
cgr-miR-143	115	4	328	51	30
chi-miR-143-3p	115	4	328	51	30
cli-miR-143-3p	115	4	328	51	30
cpi-miR-143-3p	115	4	328	51	30
cpo-miR-143-3p	115	4	328	51	30
dno-miR-143-3p	115	4	328	51	30
dre-miR-143	115	4	328	51	30
eca-miR-143	115	4	328	51	30

gga-miR-143-3p	115	4	328	51	30
hsa-miR-143-3p	115	4	328	51	30
ipu-miR-143	115	4	328	51	30
mdo-miR-143-3p	115	4	328	51	30
mml-miR-143-3p	115	4	328	51	30
mmu-miR-143-3p	115	4	328	51	30
nle-miR-143	115	4	328	51	30
oan-miR-143-3p	115	4	328	51	30
oar-miR-143	115	4	328	51	30
ocu-miR-143-3p	115	4	328	51	30
oga-miR-143	115	4	328	51	30
oni-miR-143	115	4	328	51	30
pal-miR-143-3p	115	4	328	51	30
pbv-miR-143-3p	115	4	328	51	30
pha-miR-143	115	4	328	51	30
ssa-miR-143-3p	115	4	328	51	30
ssc-miR-143-3p	115	4	328	51	30
tch-miR-143-3p	115	4	328	51	30
xla-miR-143-3p	115	4	328	51	30
xtr-miR-143	115	4	328	51	30
efu-miR-143	115	4	329	51	30
mes-miR319h	237	83	202	210	130
vun-miR319b	237	83	202	210	130
cme-miR319c	218	77	198	201	122
cme-miR319d	218	77	198	201	122
gma-miR319c	218	77	198	201	122
ptc-miR319e	218	77	198	201	122
ptc-miR319f	218	77	198	201	122
ptc-miR319g	218	77	198	201	122
ptc-miR319h	218	77	198	201	122
stu-miR319b	218	77	198	201	122
ipu-miR-99b	629	10	298	423	321
efu-miR-99a	615	9	287	415	310
gma-miR169n-5p	703	297	415	379	640
mtr-miR169c	703	297	415	379	640
oga-miR-99a	585	9	284	397	295
pbv-miR-99a-5p	585	9	284	397	295
pha-miR-99a	585	9	284	397	295
aca-miR-99a-5p	585	9	284	396	294
ami-miR-99a-5p	585	9	284	396	294
cli-miR-99-5p	585	9	284	396	294
cpi-miR-99a-5p	585	9	284	396	294
cpo-miR-99a-5p	585	9	284	396	294

dno-miR-99a-5p	585	9	284	396	294
dre-miR-99	585	9	284	396	294
eca-miR-99a	585	9	284	396	294
gga-miR-99a-5p	585	9	284	396	294
ggo-miR-99a	585	9	284	396	294
gmo-miR-99-5p	585	9	284	396	294
hsa-miR-99a-5p	585	9	284	396	294
ipu-miR-99a	585	9	284	396	294
lla-miR-99a	585	9	284	396	294
mml-miR-99a-5p	585	9	284	396	294
mmr-miR-99a	585	9	284	396	294
mmu-miR-99a-5p	585	9	284	396	294
mne-miR-99a	585	9	284	396	294
mze-miR-99b	585	9	284	396	294
nbr-miR-99b	585	9	284	396	294
ocu-miR-99a-5p	585	9	284	396	294
oha-miR-99a-5p	585	9	284	396	294
oni-miR-99b	585	9	284	396	294
pny-miR-99b	585	9	284	396	294
ppa-miR-99a	585	9	284	396	294
ppy-miR-99a	585	9	284	396	294
ptr-miR-99a	585	9	284	396	294
rno-miR-99a-5p	585	9	284	396	294
ssa-miR-99-5p	585	9	284	396	294
ssc-miR-99a-5p	585	9	284	396	294
tch-miR-99a-5p	585	9	284	396	294
xtr-miR-99	585	9	284	396	294
gma-miR171n	100	118	70	64	161
gma-miR171p	100	118	70	64	161
aly-miR319c-3p	246	84	228	218	126
aly-miR319d-3p	246	84	228	218	126
ath-miR319c	246	84	228	218	126
mes-miR319g	246	84	228	218	126
pvu-miR319c	246	84	228	218	126
rco-miR319d	246	84	228	218	126
sly-miR319c-3p	246	84	228	218	126
dma-miR-143	122	6	361	56	36
ggo-miR-143	122	6	361	56	36
lla-miR-143	122	6	361	56	36
oha-miR-143-3p	122	6	361	56	36
ppa-miR-143	122	6	361	56	36
ppy-miR-143	122	6	361	56	36
ptr-miR-143	122	6	361	56	36

rno-miR-143-3p	122	6	361	56	36
bta-miR-27a-3p	136	65	270	137	76
cfa-miR-27a	136	65	270	137	76
chi-miR-27a-3p	136	65	270	137	76
gmo-miR-27d-3p	136	65	270	137	76
oga-miR-27a	136	65	270	137	76
ola-miR-27a	136	65	270	137	76
pal-miR-27a-3p	136	65	270	137	76
xla-miR-27a-3p	136	65	270	137	76
cfa-miR-181a	163	6	105	105	85
ipu-miR-181a	163	6	105	105	85
mmr-miR-181a	163	6	105	105	85
oni-miR-181c	163	6	105	105	85
sbo-miR-181a	163	6	105	105	85
bta-miR-29a	105	39	119	96	50
ssc-miR-29a-3p	105	39	119	96	50
efu-miR-29a	109	41	122	97	52
age-miR-29a	65	23	96	58	29
ggo-miR-29a	65	23	96	58	29
lla-miR-29a	65	23	96	58	29
mml-miR-29a-3p	65	23	96	58	29
mne-miR-29a	65	23	96	58	29
ppa-miR-29a	65	23	96	58	29
ppy-miR-29a	65	23	96	58	29
ptr-miR-29a	65	23	96	58	29
sbo-miR-29a	65	23	96	58	29
sla-miR-29a	65	23	96	58	29
abu-miR-99b	366	1	184	239	176
bta-miR-99a-5p	366	1	184	239	176
ccr-miR-99	366	1	184	239	176
cfa-miR-99a	366	1	184	239	176
cgr-miR-99a-5p	366	1	184	239	176
chi-miR-99a-5p	366	1	184	239	176
cja-miR-99	366	1	184	239	176
nle-miR-99a	366	1	184	239	176
oan-miR-99-5p	366	1	184	239	176
pal-miR-99a-5p	366	1	184	239	176
sbo-miR-99a	366	1	184	239	176
tgu-miR-99-5p	366	1	184	239	176
xla-miR-99-5p	366	1	184	239	176
cpo-miR-652-3p	101	100	36	158	64
vca-miR396-5p	82	71	127	54	97
vvi-miR396b	82	71	127	54	97

bta-let-7d	116	139	52	122	61
cgr-let-7d-5p	116	139	52	122	61
chi-let-7d-5p	116	139	52	122	61
cja-let-7d	116	139	52	122	61
cli-let-7d-5p	116	139	52	122	61
cpi-let-7d-5p	116	139	52	122	61
cpo-let-7d-5p	116	139	52	122	61
dno-let-7d-5p	116	139	52	122	61
eca-let-7d	116	139	52	122	61
hsa-let-7d-5p	116	139	52	122	61
mml-let-7d	116	139	52	122	61
mmu-let-7d-5p	116	139	52	122	61
oan-let-7d-5p	116	139	52	122	61
ocu-let-7d-5p	116	139	52	122	61
oha-let-7d-5p	116	139	52	122	61
pbv-let-7d-5p	116	139	52	122	61
ppy-let-7d	116	139	52	122	61
ptr-let-7d	116	139	52	122	61
rno-let-7d-5p	116	139	52	122	61
ssc-let-7d-5p	116	139	52	122	61
tgu-let-7d-5p	116	139	52	122	61
efu-let-7d	119	140	55	124	63
pab-miR396a-5p	84	74	132	57	101
vvi-miR396a	84	74	132	57	101
pvu-miR159a.2	382	199	126	276	252
gma-miR319p	306	182	302	270	172
cfa-let-7d	75	62	14	75	34
cpo-miR-16b-5p	580	450	216	583	251
dno-miR-16b-5p	580	450	216	583	251
efu-miR-16	580	450	216	583	251
ocu-miR-16b-5p	580	450	216	583	251
ccr-miR-181a	114	4	73	73	54
xla-miR-181a-5p	114	4	73	73	54
ahy-miR159	1399117	1317402	284674	1510032	995210
aly-miR159a-3p	1399117	1317402	284674	1510032	995210
aof-miR159	1399117	1317402	284674	1510032	995210
ath-miR159a	1399117	1317402	284674	1510032	995210
atr-miR159	1399117	1317402	284674	1510032	995210
bna-miR159	1399117	1317402	284674	1510032	995210
bra-miR159a	1399117	1317402	284674	1510032	995210
cme-miR159a	1399117	1317402	284674	1510032	995210
cpa-miR159a	1399117	1317402	284674	1510032	995210
csi-miR159a-3p	1399117	1317402	284674	1510032	995210

fve-miR159a-3p	1399117	1317402	284674	1510032	995210
gma-miR159a-3p	1399117	1317402	284674	1510032	995210
gma-miR159e-3p	1399117	1317402	284674	1510032	995210
hbr-miR159a	1399117	1317402	284674	1510032	995210
htu-miR159a	1399117	1317402	284674	1510032	995210
mdm-miR159d	1399117	1317402	284674	1510032	995210
mdm-miR159e	1399117	1317402	284674	1510032	995210
mdm-miR159f	1399117	1317402	284674	1510032	995210
mes-miR159a-3p	1399117	1317402	284674	1510032	995210
mes-miR159b	1399117	1317402	284674	1510032	995210
mtr-miR159a	1399117	1317402	284674	1510032	995210
nta-miR159	1399117	1317402	284674	1510032	995210
ppe-miR159	1399117	1317402	284674	1510032	995210
ptc-miR159a	1399117	1317402	284674	1510032	995210
ptc-miR159b	1399117	1317402	284674	1510032	995210
pvu-miR159a.1	1399117	1317402	284674	1510032	995210
rco-miR159	1399117	1317402	284674	1510032	995210
sly-miR159	1399117	1317402	284674	1510032	995210
vca-miR159-3p	1399117	1317402	284674	1510032	995210
vvi-miR159c	1399117	1317402	284674	1510032	995210
osa-miR159f	21111	20133	10743	24199	16704
cgr-let-7d-3p	74	62	14	74	34
cpo-let-7d-3p	74	62	14	74	34
dno-let-7d-3p	74	62	14	74	34
hsa-let-7d-3p	74	62	14	74	34
mmu-let-7d-3p	74	62	14	74	34
ocu-let-7d-3p	74	62	14	74	34
rno-let-7d-3p	74	62	14	74	34
ssc-let-7d-3p	74	62	14	74	34
bdi-miR159b-3p.1	43621	42808	14189	43362	35789
far-miR159	43621	42808	14189	43362	35789
hvu-miR159a	43621	42808	14189	43362	35789
hvu-miR159b	43621	42808	14189	43362	35789
osa-miR159a.1	43621	42808	14189	43362	35789
osa-miR159b	43621	42808	14189	43362	35789
sbi-miR159a	43621	42808	14189	43362	35789
sof-miR159a	43621	42808	14189	43362	35789
sof-miR159b	43621	42808	14189	43362	35789
sof-miR159d	43621	42808	14189	43362	35789
ssp-miR159a	43621	42808	14189	43362	35789
tae-miR159a	43621	42808	14189	43362	35789
tae-miR159b	43621	42808	14189	43362	35789
zma-miR159a-3p	43621	42808	14189	43362	35789

zma-miR159b-3p	43621	42808	14189	43362	35789
zma-miR159f-3p	43621	42808	14189	43362	35789
zma-miR159j-3p	43621	42808	14189	43362	35789
zma-miR159k-3p	43621	42808	14189	43362	35789
cas-miR394	6054	4250	7309	3694	7125
ahy-miR394	6029	4235	7280	3673	7098
aly-miR394a-5p	6029	4235	7280	3673	7098
aly-miR394b-5p	6029	4235	7280	3673	7098
aof-miR394	6029	4235	7280	3673	7098
ata-miR394-5p	6029	4235	7280	3673	7098
ath-miR394a	6029	4235	7280	3673	7098
ath-miR394b-5p	6029	4235	7280	3673	7098
atr-miR394	6029	4235	7280	3673	7098
bdi-miR394	6029	4235	7280	3673	7098
bna-miR394a	6029	4235	7280	3673	7098
bna-miR394b	6029	4235	7280	3673	7098
cca-miR394	6029	4235	7280	3673	7098
cme-miR394a	6029	4235	7280	3673	7098
cme-miR394b	6029	4235	7280	3673	7098
cpa-miR394a	6029	4235	7280	3673	7098
cpa-miR394b	6029	4235	7280	3673	7098
csi-miR394a	6029	4235	7280	3673	7098
csi-miR394b-5p	6029	4235	7280	3673	7098
fve-miR394	6029	4235	7280	3673	7098
ghr-miR394a	6029	4235	7280	3673	7098
ghr-miR394b	6029	4235	7280	3673	7098
gma-miR394a-5p	6029	4235	7280	3673	7098
gma-miR394b-5p	6029	4235	7280	3673	7098
gma-miR394c-5p	6029	4235	7280	3673	7098
gma-miR394d	6029	4235	7280	3673	7098
gma-miR394e	6029	4235	7280	3673	7098
gma-miR394f	6029	4235	7280	3673	7098
gma-miR394g	6029	4235	7280	3673	7098
lus-miR394a	6029	4235	7280	3673	7098
lus-miR394b	6029	4235	7280	3673	7098
mdm-miR394a	6029	4235	7280	3673	7098
mdm-miR394b	6029	4235	7280	3673	7098
mes-miR394a	6029	4235	7280	3673	7098
mes-miR394b	6029	4235	7280	3673	7098
nta-miR394	6029	4235	7280	3673	7098
osa-miR394	6029	4235	7280	3673	7098
pab-miR394c	6029	4235	7280	3673	7098
ppe-miR394a	6029	4235	7280	3673	7098

ppe-miR394b	6029	4235	7280	3673	7098
ptc-miR394a-5p	6029	4235	7280	3673	7098
ptc-miR394b-5p	6029	4235	7280	3673	7098
sbi-miR394a	6029	4235	7280	3673	7098
sbi-miR394b	6029	4235	7280	3673	7098
sly-miR394-5p	6029	4235	7280	3673	7098
ssl-miR394	6029	4235	7280	3673	7098
stu-miR384-5p	6029	4235	7280	3673	7098
tcc-miR394a	6029	4235	7280	3673	7098
tcc-miR394b	6029	4235	7280	3673	7098
vvi-miR394b	6029	4235	7280	3673	7098
zma-miR394a-5p	6029	4235	7280	3673	7098
zma-miR394b-5p	6029	4235	7280	3673	7098
mes-miR394c	6040	4241	7286	3676	7110
vvi-miR394a	6040	4241	7286	3676	7110
vvi-miR394c	6040	4241	7286	3676	7110
lus-miR159b	43789	43024	14233	43434	35919
aly-miR159b-3p	51628	50239	15411	50307	41274
ath-miR159b-3p	51628	50239	15411	50307	41274
cas-miR159b-3p	51628	50239	15411	50307	41274
cas-miR159c-3p	51628	50239	15411	50307	41274
lus-miR159c	51628	50239	15411	50307	41274
aca-miR-21-5p	481	200	352	368	215
age-miR-21	481	200	352	368	215
cfa-miR-21	481	200	352	368	215
cgr-miR-21-5p	481	200	352	368	215
cja-miR-21	481	200	352	368	215
cli-miR-21-5p	481	200	352	368	215
cpi-miR-21-5p	481	200	352	368	215
eca-miR-21	481	200	352	368	215
gga-miR-21-5p	481	200	352	368	215
ggo-miR-21	481	200	352	368	215
hsa-miR-21-5p	481	200	352	368	215
mdo-miR-21-5p	481	200	352	368	215
mml-miR-21-5p	481	200	352	368	215
mmu-miR-21a-5p	481	200	352	368	215
mne-miR-21	481	200	352	368	215
oan-miR-21-5p	481	200	352	368	215
oha-miR-21-5p	481	200	352	368	215
pal-miR-21-5p	481	200	352	368	215
ppa-miR-21	481	200	352	368	215
ppy-miR-21	481	200	352	368	215
ptr-miR-21	481	200	352	368	215

rno-miR-21-5p	481	200	352	368	215
ssc-miR-21-5p	481	200	352	368	215
tch-miR-21-5p	481	200	352	368	215
tgu-miR-21-5p	481	200	352	368	215
age-miR-16	415	332	171	423	173
cfa-miR-16	415	332	171	423	173
cgr-miR-16-5p	415	332	171	423	173
cja-miR-16	415	332	171	423	173
cpi-miR-16a-5p	415	332	171	423	173
dma-miR-16	415	332	171	423	173
eca-miR-16	415	332	171	423	173
ggo-miR-16	415	332	171	423	173
hsa-miR-16-5p	415	332	171	423	173
lla-miR-16	415	332	171	423	173
mdo-miR-16-5p	415	332	171	423	173
mml-miR-16-5p	415	332	171	423	173
mmu-miR-16-5p	415	332	171	423	173
mne-miR-16	415	332	171	423	173
mze-miR-16a	415	332	171	423	173
nle-miR-16	415	332	171	423	173
oan-miR-16a-5p	415	332	171	423	173
oga-miR-16	415	332	171	423	173
oni-miR-16a	415	332	171	423	173
pal-miR-16-5p	415	332	171	423	173
pha-miR-16	415	332	171	423	173
ppa-miR-16	415	332	171	423	173
ptr-miR-16	415	332	171	423	173
rno-miR-16-5p	415	332	171	423	173
sbo-miR-16	415	332	171	423	173
sla-miR-16	415	332	171	423	173
ssa-miR-16c-5p	415	332	171	423	173
ssc-miR-16	415	332	171	423	173
gma-miR482c-3p	115	195	343	188	202
aof-miR171a	18981	26336	17317	24117	23314
aqc-miR171a	18981	26336	17317	24117	23314
aqc-miR171b	18981	26336	17317	24117	23314
aqc-miR171d	18981	26336	17317	24117	23314
ata-miR171b-3p	18981	26336	17317	24117	23314
ata-miR171d-3p	18981	26336	17317	24117	23314
bdi-miR171b	18981	26336	17317	24117	23314
bdi-miR171c-3p	18981	26336	17317	24117	23314
bdi-miR171d-3p	18981	26336	17317	24117	23314
bdi-miR171e	18981	26336	17317	24117	23314

cme-miR171c	18981	26336	17317	24117	23314
cme-miR171f	18981	26336	17317	24117	23314
cpa-miR171a	18981	26336	17317	24117	23314
cpa-miR171b	18981	26336	17317	24117	23314
cpa-miR171c	18981	26336	17317	24117	23314
cpa-miR171d	18981	26336	17317	24117	23314
crt-miR171	18981	26336	17317	24117	23314
csi-miR171c-3p	18981	26336	17317	24117	23314
csi-miR171d-3p	18981	26336	17317	24117	23314
csi-miR171f-3p	18981	26336	17317	24117	23314
csi-miR171h-3p	18981	26336	17317	24117	23314
csi-miR171i-3p	18981	26336	17317	24117	23314
far-miR171	18981	26336	17317	24117	23314
fve-miR171a	18981	26336	17317	24117	23314
fve-miR171c-3p	18981	26336	17317	24117	23314
fve-miR171d	18981	26336	17317	24117	23314
fve-miR171e	18981	26336	17317	24117	23314
fve-miR171g	18981	26336	17317	24117	23314
gma-miR171e	18981	26336	17317	24117	23314
gma-miR171f	18981	26336	17317	24117	23314
gma-miR171g	18981	26336	17317	24117	23314
gma-miR171j-3p	18981	26336	17317	24117	23314
gma-miR171u	18981	26336	17317	24117	23314
hpa-miR171a	18981	26336	17317	24117	23314
htu-miR171b	18981	26336	17317	24117	23314
htu-miR171c	18981	26336	17317	24117	23314
hvu-miR171-3p	18981	26336	17317	24117	23314
lja-miR171a	18981	26336	17317	24117	23314
lus-miR171b	18981	26336	17317	24117	23314
lus-miR171c	18981	26336	17317	24117	23314
lus-miR171e	18981	26336	17317	24117	23314
mdm-miR171g	18981	26336	17317	24117	23314
mdm-miR171h	18981	26336	17317	24117	23314
mes-miR171g	18981	26336	17317	24117	23314
mes-miR171h	18981	26336	17317	24117	23314
mes-miR171i	18981	26336	17317	24117	23314
mes-miR171j	18981	26336	17317	24117	23314
mes-miR171k	18981	26336	17317	24117	23314
mtr-miR171d	18981	26336	17317	24117	23314
nta-miR171c	18981	26336	17317	24117	23314
osa-miR171b	18981	26336	17317	24117	23314
osa-miR171c-3p	18981	26336	17317	24117	23314
osa-miR171d-3p	18981	26336	17317	24117	23314

osa-miR171e-3p	18981	26336	17317	24117	23314
osa-miR171f-3p	18981	26336	17317	24117	23314
pde-miR171	18981	26336	17317	24117	23314
ppe-miR171a	18981	26336	17317	24117	23314
ppe-miR171c	18981	26336	17317	24117	23314
ppe-miR171f	18981	26336	17317	24117	23314
ppe-miR171g	18981	26336	17317	24117	23314
ptc-miR171e	18981	26336	17317	24117	23314
ptc-miR171f	18981	26336	17317	24117	23314
ptc-miR171g-3p	18981	26336	17317	24117	23314
ptc-miR171h-3p	18981	26336	17317	24117	23314
ptc-miR171i	18981	26336	17317	24117	23314
rco-miR171c	18981	26336	17317	24117	23314
rco-miR171d	18981	26336	17317	24117	23314
rco-miR171e	18981	26336	17317	24117	23314
rco-miR171f	18981	26336	17317	24117	23314
sbi-miR171a	18981	26336	17317	24117	23314
sbi-miR171b	18981	26336	17317	24117	23314
sbi-miR171d	18981	26336	17317	24117	23314
sbi-miR171i	18981	26336	17317	24117	23314
sbi-miR171k	18981	26336	17317	24117	23314
sly-miR171a	18981	26336	17317	24117	23314
stu-miR171a-3p	18981	26336	17317	24117	23314
stu-miR171e	18981	26336	17317	24117	23314
tae-miR171a	18981	26336	17317	24117	23314
tcc-miR171d	18981	26336	17317	24117	23314
tcc-miR171e	18981	26336	17317	24117	23314
tcc-miR171f	18981	26336	17317	24117	23314
tcc-miR171g	18981	26336	17317	24117	23314
tcc-miR171h	18981	26336	17317	24117	23314
vvi-miR171a	18981	26336	17317	24117	23314
vvi-miR171c	18981	26336	17317	24117	23314
vvi-miR171d	18981	26336	17317	24117	23314
vvi-miR171i	18981	26336	17317	24117	23314
vvi-miR171j	18981	26336	17317	24117	23314
zma-miR171d-3p	18981	26336	17317	24117	23314
zma-miR171e-3p	18981	26336	17317	24117	23314
zma-miR171i-3p	18981	26336	17317	24117	23314
zma-miR171j-3p	18981	26336	17317	24117	23314
aly-miR159c-3p	143	159	52	148	104
ath-miR159c	143	159	52	148	104
cas-miR159a	143	159	52	148	104
zma-miR169a-3p	3225	6734	3860	4745	5231

zma-miR169b-3p	3225	6734	3860	4745	5231
gma-miR482a-3p	6550	10477	13426	7472	7453
vun-miR482	6550	10477	13426	7472	7453
atr-miR171b	355	690	319	428	500
gma-miR171c-3p	355	690	319	428	500
gma-miR171o-3p	355	690	319	428	500
gma-miR171q	355	690	319	428	500
mdm-miR171m	355	690	319	428	500
mdm-miR171n	355	690	319	428	500
zma-miR171f-3p	355	690	319	428	500
aca-miR-191-5p	477	428	181	576	207
bta-miR-191	477	428	181	576	207
cgr-miR-191-5p	477	428	181	576	207
cja-miR-191	477	428	181	576	207
cpo-miR-191-5p	477	428	181	576	207
dma-miR-191	477	428	181	576	207
dno-miR-191-5p	477	428	181	576	207
eca-miR-191a	477	428	181	576	207
gga-miR-191-5p	477	428	181	576	207
hsa-miR-191-5p	477	428	181	576	207
mml-miR-191-5p	477	428	181	576	207
mmr-miR-191	477	428	181	576	207
mmu-miR-191-5p	477	428	181	576	207
nle-miR-191	477	428	181	576	207
ocu-miR-191-5p	477	428	181	576	207
oga-miR-191	477	428	181	576	207
oha-miR-191-5p	477	428	181	576	207
pbv-miR-191-5p	477	428	181	576	207
pha-miR-191	477	428	181	576	207
ppa-miR-191	477	428	181	576	207
ppy-miR-191	477	428	181	576	207
ptr-miR-191	477	428	181	576	207
rno-miR-191a-5p	477	428	181	576	207
sbo-miR-191	477	428	181	576	207
ssc-miR-191	477	428	181	576	207
gma-miR171o-5p	84	80	19	34	90
cfa-miR-29a	75	30	84	70	34
cja-miR-29a	75	30	84	70	34
cpo-miR-29a-3p	75	30	84	70	34
dma-miR-29a	75	30	84	70	34
dno-miR-29a-3p	75	30	84	70	34
eca-miR-29a	75	30	84	70	34
hsa-miR-29a-3p	75	30	84	70	34

mmr-miR-29a	75	30	84	70	34
mmu-miR-29a-3p	75	30	84	70	34
nle-miR-29a	75	30	84	70	34
ocu-miR-29a-3p	75	30	84	70	34
oga-miR-29a	75	30	84	70	34
pal-miR-29a-3p	75	30	84	70	34
pha-miR-29a	75	30	84	70	34
rno-miR-29a-3p	75	30	84	70	34
csi-miR393b-5p	724	322	100	306	461
gma-miR393h	724	322	100	306	461
gma-miR393i	724	322	100	306	461
gma-miR393j	724	322	100	306	461
gma-miR393k	724	322	100	306	461
ami-miR-191-5p	194	181	119	234	96
cfa-miR-191	194	181	119	234	96
chi-miR-191-5p	194	181	119	234	96
cpi-miR-191-5p	194	181	119	234	96
mdo-miR-191-5p	194	181	119	234	96
oan-miR-191-5p	194	181	119	234	96
oar-miR-191	194	181	119	234	96
pal-miR-191-5p	194	181	119	234	96
tch-miR-191-5p	194	181	119	234	96
xla-miR-191-5p	194	181	119	234	96
xtr-miR-191	194	181	119	234	96
aly-miR169b-5p	146961	237557	30977	164185	155727
aly-miR169c-5p	146961	237557	30977	164185	155727
aqc-miR169c	146961	237557	30977	164185	155727
ata-miR169d-5p	146961	237557	30977	164185	155727
ath-miR169b-5p	146961	237557	30977	164185	155727
ath-miR169c	146961	237557	30977	164185	155727
bdi-miR169c-5p	146961	237557	30977	164185	155727
bdi-miR169f	146961	237557	30977	164185	155727
bna-miR169n	146961	237557	30977	164185	155727
cas-miR169b	146961	237557	30977	164185	155727
cme-miR169f	146961	237557	30977	164185	155727
cme-miR169h	146961	237557	30977	164185	155727
csi-miR169g-5p	146961	237557	30977	164185	155727
csi-miR169k-5p	146961	237557	30977	164185	155727
csi-miR169m-5p	146961	237557	30977	164185	155727
csi-miR169n-5p	146961	237557	30977	164185	155727
csi-miR169o-5p	146961	237557	30977	164185	155727
csi-miR169r-5p	146961	237557	30977	164185	155727
gma-miR169a	146961	237557	30977	164185	155727

gma-miR169f	146961	237557	30977	164185	155727
gma-miR169g	146961	237557	30977	164185	155727
gma-miR169m	146961	237557	30977	164185	155727
lus-miR169f	146961	237557	30977	164185	155727
lus-miR169h	146961	237557	30977	164185	155727
lus-miR169j	146961	237557	30977	164185	155727
mdm-miR169a	146961	237557	30977	164185	155727
mdm-miR169g	146961	237557	30977	164185	155727
mdm-miR169h	146961	237557	30977	164185	155727
mdm-miR169i	146961	237557	30977	164185	155727
mdm-miR169j	146961	237557	30977	164185	155727
mes-miR169a	146961	237557	30977	164185	155727
mes-miR169b	146961	237557	30977	164185	155727
mes-miR169c	146961	237557	30977	164185	155727
mes-miR169d	146961	237557	30977	164185	155727
mes-miR169e	146961	237557	30977	164185	155727
mtr-miR169b	146961	237557	30977	164185	155727
mtr-miR169g	146961	237557	30977	164185	155727
mtr-miR169l-5p	146961	237557	30977	164185	155727
nta-miR169q	146961	237557	30977	164185	155727
nta-miR169r	146961	237557	30977	164185	155727
nta-miR169s	146961	237557	30977	164185	155727
osa-miR169b	146961	237557	30977	164185	155727
osa-miR169c	146961	237557	30977	164185	155727
ppe-miR169a	146961	237557	30977	164185	155727
ppe-miR169b	146961	237557	30977	164185	155727
ppe-miR169c	146961	237557	30977	164185	155727
ptc-miR169d	146961	237557	30977	164185	155727
ptc-miR169e	146961	237557	30977	164185	155727
ptc-miR169f	146961	237557	30977	164185	155727
ptc-miR169g	146961	237557	30977	164185	155727
ptc-miR169h	146961	237557	30977	164185	155727
ptc-miR169p	146961	237557	30977	164185	155727
rco-miR169a	146961	237557	30977	164185	155727
rco-miR169b	146961	237557	30977	164185	155727
sbi-miR169b	146961	237557	30977	164185	155727
sbi-miR169k	146961	237557	30977	164185	155727
sly-miR169a	146961	237557	30977	164185	155727
tcc-miR169b	146961	237557	30977	164185	155727
tcc-miR169k	146961	237557	30977	164185	155727
tcc-miR169l	146961	237557	30977	164185	155727
vun-miR169	146961	237557	30977	164185	155727
vvi-miR169a	146961	237557	30977	164185	155727

vvi-miR169c	146961	237557	30977	164185	155727
vvi-miR169j	146961	237557	30977	164185	155727
vvi-miR169k	146961	237557	30977	164185	155727
vvi-miR169s	146961	237557	30977	164185	155727
vvi-miR169w	146961	237557	30977	164185	155727
zma-miR169c-5p	146961	237557	30977	164185	155727
zma-miR169r-5p	146961	237557	30977	164185	155727
aly-miR170-3p	15308	25886	3466	19075	16163
ath-miR170-3p	15308	25886	3466	19075	16163
stu-miR171c-3p	15308	25886	3466	19075	16163
cli-miR-146a-5p	343	393	170	459	165
cpo-miR-146a-5p	343	393	170	459	165
ocu-miR-146a-5p	343	393	170	459	165
dno-miR-146a-5p	390	443	190	506	189
gma-miR319d	4472	2104	493	3426	1420
gma-miR319o	4472	2104	493	3426	1420
gma-miR319i	4536	2115	515	3463	1429
cfa-miR-146a	341	392	170	457	164
cgr-miR-146a	341	392	170	457	164
cja-miR-146a	341	392	170	457	164
eca-miR-146a	341	392	170	457	164
gga-miR-146a-5p	341	392	170	457	164
hsa-miR-146a-5p	341	392	170	457	164
mdo-miR-146a-5p	341	392	170	457	164
mml-miR-146a-5p	341	392	170	457	164
mmr-miR-146a	341	392	170	457	164
mmu-miR-146a-5p	341	392	170	457	164
nle-miR-146a	341	392	170	457	164
pal-miR-146a-5p	341	392	170	457	164
pha-miR-146a	341	392	170	457	164
ppy-miR-146a	341	392	170	457	164
ptr-miR-146a	341	392	170	457	164
rno-miR-146a-5p	341	392	170	457	164
ssc-miR-146a-5p	341	392	170	457	164
tch-miR-146a-5p	341	392	170	457	164
tgu-miR-146c	341	392	170	457	164
efu-miR-22	731	372	963	618	328
xla-miR-22-3p	731	372	963	618	328
aly-miR171b-3p	424	544	1350	408	747
aly-miR171c-3p	424	544	1350	408	747
ata-miR171c-3p	424	544	1350	408	747
ath-miR171b-3p	424	544	1350	408	747
ath-miR171c-3p	424	544	1350	408	747

bna-miR171a	424	544	1350	408	747
bna-miR171b	424	544	1350	408	747
bna-miR171c	424	544	1350	408	747
bna-miR171d	424	544	1350	408	747
bna-miR171e	424	544	1350	408	747
bol-miR171a	424	544	1350	408	747
bra-miR171a	424	544	1350	408	747
bra-miR171b	424	544	1350	408	747
bra-miR171c	424	544	1350	408	747
bra-miR171d	424	544	1350	408	747
cas-miR171b	424	544	1350	408	747
cas-miR171c-3p	424	544	1350	408	747
cme-miR171b	424	544	1350	408	747
cme-miR171d	424	544	1350	408	747
gma-miR171i-3p	424	544	1350	408	747
lus-miR171i	424	544	1350	408	747
mdm-miR171f-3p	424	544	1350	408	747
mes-miR171b	424	544	1350	408	747
mes-miR171c	424	544	1350	408	747
mtr-miR171f	424	544	1350	408	747
ptc-miR171a-3p	424	544	1350	408	747
ptc-miR171b	424	544	1350	408	747
rco-miR171a	424	544	1350	408	747
rco-miR171b	424	544	1350	408	747
sly-miR171b-3p	424	544	1350	408	747
ssl-miR171a	424	544	1350	408	747
stu-miR171d-3p	424	544	1350	408	747
tae-miR171b	424	544	1350	408	747
age-miR-22	709	369	937	608	319
aja-miR-22	709	369	937	608	319
cfa-miR-22	709	369	937	608	319
cgr-miR-22-3p	709	369	937	608	319
cja-miR-22	709	369	937	608	319
cli-miR-22-3p	709	369	937	608	319
cpi-miR-22-3p	709	369	937	608	319
cpo-miR-22-3p	709	369	937	608	319
dma-miR-22	709	369	937	608	319
dno-miR-22-3p	709	369	937	608	319
eca-miR-22	709	369	937	608	319
gga-miR-22-3p	709	369	937	608	319
hsa-miR-22-3p	709	369	937	608	319
lca-miR-22	709	369	937	608	319
lla-miR-22	709	369	937	608	319

mml-miR-22	709	369	937	608	319
mmr-miR-22	709	369	937	608	319
mmu-miR-22-3p	709	369	937	608	319
mne-miR-22	709	369	937	608	319
nle-miR-22	709	369	937	608	319
oan-miR-22-3p	709	369	937	608	319
ocu-miR-22-3p	709	369	937	608	319
oga-miR-22	709	369	937	608	319
oha-miR-22a	709	369	937	608	319
pal-miR-22-3p	709	369	937	608	319
pbv-miR-22-3p	709	369	937	608	319
pha-miR-22	709	369	937	608	319
ppa-miR-22	709	369	937	608	319
ppy-miR-22	709	369	937	608	319
ptr-miR-22	709	369	937	608	319
rno-miR-22-3p	709	369	937	608	319
sbo-miR-22	709	369	937	608	319
sla-miR-22	709	369	937	608	319
ssc-miR-22-3p	709	369	937	608	319
tch-miR-22-3p	709	369	937	608	319
xtr-miR-22-3p	709	369	937	608	319
gma-miR319g	72394	42723	7142	58789	26709
gma-miR319l	72394	42723	7142	58789	26709
gma-miR319q	71606	42408	6869	58263	26449
aly-miR393a-5p	306	138	44	193	134
aly-miR393b-5p	306	138	44	193	134
ath-miR393a-5p	306	138	44	193	134
ath-miR393b-5p	306	138	44	193	134
atr-miR393	306	138	44	193	134
cas-miR393-5p	306	138	44	193	134
cpa-miR393	306	138	44	193	134
gma-miR393c-5p	306	138	44	193	134
gma-miR393d	306	138	44	193	134
gma-miR393e	306	138	44	193	134
gma-miR393f	306	138	44	193	134
gma-miR393g	306	138	44	193	134
htu-miR393a	306	138	44	193	134
htu-miR393b	306	138	44	193	134
htu-miR393c	306	138	44	193	134
mes-miR393b	306	138	44	193	134
stu-miR393-5p	306	138	44	193	134
tcc-miR393a	306	138	44	193	134
zma-miR393b-5p	306	138	44	193	134

aof-miR393b	174	86	26	102	86
fve-miR393b	174	86	26	102	86
ghr-miR393	174	86	26	102	86
mdm-miR393a	174	86	26	102	86
mdm-miR393b	174	86	26	102	86
mdm-miR393c	174	86	26	102	86
mes-miR393c	174	86	26	102	86
mes-miR393d	174	86	26	102	86
osa-miR393b-5p	174	86	26	102	86
zma-miR393a-5p	174	86	26	102	86
zma-miR393c-5p	174	86	26	102	86
smo-miR171a	54	99	106	64	80
atr-miR319a	10552	5675	5926	6787	3696
atr-miR319c	10552	5675	5926	6787	3696
cme-miR319a	10552	5675	5926	6787	3696
cme-miR319b	10552	5675	5926	6787	3696
ctr-miR319	10552	5675	5926	6787	3696
gma-miR319a	10552	5675	5926	6787	3696
gma-miR319b	10552	5675	5926	6787	3696
gma-miR319e	10552	5675	5926	6787	3696
lus-miR319b	10552	5675	5926	6787	3696
mtr-miR319a-3p	10552	5675	5926	6787	3696
mtr-miR319b-3p	10552	5675	5926	6787	3696
pab-miR319a	10552	5675	5926	6787	3696
pab-miR319b	10552	5675	5926	6787	3696
pab-miR319c	10552	5675	5926	6787	3696
pab-miR319f	10552	5675	5926	6787	3696
pab-miR319g	10552	5675	5926	6787	3696
pab-miR319i	10552	5675	5926	6787	3696
pab-miR319k	10552	5675	5926	6787	3696
pab-miR319l	10552	5675	5926	6787	3696
pab-miR319m	10552	5675	5926	6787	3696
pab-miR319n	10552	5675	5926	6787	3696
ppe-miR319a	10552	5675	5926	6787	3696
ptc-miR319a	10552	5675	5926	6787	3696
ptc-miR319b	10552	5675	5926	6787	3696
ptc-miR319c	10552	5675	5926	6787	3696
ptc-miR319d	10552	5675	5926	6787	3696
mtr-miR319c-3p	10669	5711	5950	6835	3724
vvi-miR319g	10669	5711	5950	6835	3724
csi-miR159c-3p	10896	5940	5944	7003	3829
ppt-miR319c	10896	5940	5944	7003	3829
ppt-miR319d-3p	10896	5940	5944	7003	3829

ppt-miR319e	10896	5940	5944	7003	3829
ath-miR8175	15	20	96	15	27
abu-miR-200a	0	2	202	0	0
bta-miR-200a	0	2	202	0	0
cgr-miR-200a	0	2	202	0	0
cli-miR-200a-3p	0	2	202	0	0
cpi-miR-200a-3p	0	2	202	0	0
cpo-miR-200a-3p	0	2	202	0	0
efu-miR-200a	0	2	202	0	0
mze-miR-200a	0	2	202	0	0
nbr-miR-200a	0	2	202	0	0
oan-miR-200a-3p	0	2	202	0	0
oha-miR-200a	0	2	202	0	0
oni-miR-200a	0	2	202	0	0
pal-miR-200a-3p	0	2	202	0	0
pbv-miR-200a-3p	0	2	202	0	0
pny-miR-200a	0	2	202	0	0
ssa-miR-200b-3p	0	2	202	0	0
tch-miR-200a-3p	0	2	202	0	0
tgu-miR-200a-3p	0	2	202	0	0
xla-miR-200a-3p	0	2	202	0	0
aau-miR162	2516	1966	8709	2401	1344
aly-miR162a-3p	2516	1966	8709	2401	1344
aly-miR162b-3p	2516	1966	8709	2401	1344
ath-miR162a-3p	2516	1966	8709	2401	1344
ath-miR162b-3p	2516	1966	8709	2401	1344
bra-miR162-3p	2516	1966	8709	2401	1344
cme-miR162	2516	1966	8709	2401	1344
cpa-miR162a	2516	1966	8709	2401	1344
csi-miR162-3p	2516	1966	8709	2401	1344
eun-miR162-3p	2516	1966	8709	2401	1344
fve-miR162-3p	2516	1966	8709	2401	1344
ghr-miR162a	2516	1966	8709	2401	1344
gma-miR162b	2516	1966	8709	2401	1344
gma-miR162c	2516	1966	8709	2401	1344
hpe-miR162a	2516	1966	8709	2401	1344
htu-miR162a	2516	1966	8709	2401	1344
lus-miR162a	2516	1966	8709	2401	1344
lus-miR162b	2516	1966	8709	2401	1344
mdm-miR162a	2516	1966	8709	2401	1344
mdm-miR162b	2516	1966	8709	2401	1344
mes-miR162	2516	1966	8709	2401	1344
mtr-miR162	2516	1966	8709	2401	1344

nta-miR162a	2516	1966	8709	2401	1344
nta-miR162b	2516	1966	8709	2401	1344
osa-miR162a	2516	1966	8709	2401	1344
pde-miR162	2516	1966	8709	2401	1344
ppe-miR162	2516	1966	8709	2401	1344
ptc-miR162a	2516	1966	8709	2401	1344
ptc-miR162b	2516	1966	8709	2401	1344
rco-miR162	2516	1966	8709	2401	1344
sbi-miR162	2516	1966	8709	2401	1344
sly-miR162	2516	1966	8709	2401	1344
stu-miR162a-3p	2516	1966	8709	2401	1344
stu-miR162b-3p	2516	1966	8709	2401	1344
tcc-miR162	2516	1966	8709	2401	1344
vun-miR162	2516	1966	8709	2401	1344
vvi-miR162	2516	1966	8709	2401	1344
gma-miR169s-5p	3996	5895	1244	4675	3356
mtr-miR169d-5p	3996	5895	1244	4675	3356
gma-miR169d	3762	5773	1252	4542	3103
aau-miR319	15967	7907	7713	9478	4930
aly-miR319a-3p	15967	7907	7713	9478	4930
aly-miR319b-3p	15967	7907	7713	9478	4930
amg-miR319	15967	7907	7713	9478	4930
aof-miR319a	15967	7907	7713	9478	4930
aqc-miR319	15967	7907	7713	9478	4930
ath-miR319a	15967	7907	7713	9478	4930
ath-miR319b	15967	7907	7713	9478	4930
bra-miR319-3p	15967	7907	7713	9478	4930
cca-miR319	15967	7907	7713	9478	4930
gma-miR319h	15967	7907	7713	9478	4930
gma-miR319j	15967	7907	7713	9478	4930
gma-miR319k	15967	7907	7713	9478	4930
gma-miR319m	15967	7907	7713	9478	4930
hbr-miR319	15967	7907	7713	9478	4930
lus-miR319a	15967	7907	7713	9478	4930
mdm-miR319a	15967	7907	7713	9478	4930
mdm-miR319b-3p	15967	7907	7713	9478	4930
mes-miR319a	15967	7907	7713	9478	4930
mes-miR319b	15967	7907	7713	9478	4930
mes-miR319c	15967	7907	7713	9478	4930
mes-miR319d	15967	7907	7713	9478	4930
mes-miR319e	15967	7907	7713	9478	4930
mtr-miR319d-3p	15967	7907	7713	9478	4930
nta-miR319a	15967	7907	7713	9478	4930

nta-miR319b	15967	7907	7713	9478	4930
rco-miR319a	15967	7907	7713	9478	4930
rco-miR319b	15967	7907	7713	9478	4930
rco-miR319c	15967	7907	7713	9478	4930
sly-miR319b	15967	7907	7713	9478	4930
stu-miR319a-3p	15967	7907	7713	9478	4930
tae-miR319	15967	7907	7713	9478	4930
vun-miR319a	15967	7907	7713	9478	4930
vvi-miR319b	15967	7907	7713	9478	4930
vvi-miR319c	15967	7907	7713	9478	4930
vvi-miR319f	15967	7907	7713	9478	4930
mtr-miR169e-5p	3708	5721	1198	4514	3024
vvi-miR169m	3708	5721	1198	4514	3024
vvi-miR169n	3708	5721	1198	4514	3024
vvi-miR169p	3708	5721	1198	4514	3024
vvi-miR169q	3708	5721	1198	4514	3024
csi-miR171a	52	95	103	56	74
zma-miR171b-3p	52	95	103	56	74
gma-miR166u	1208	580	1158	920	659
ami-miR-27b-3p	74	16	91	56	31
dma-miR-27b	74	16	91	56	31
gmo-miR-27b-3p	74	16	91	56	31
nle-miR-27b	74	16	91	56	31
oga-miR-27b	74	16	91	56	31
pha-miR-27b	74	16	91	56	31
cme-miR156j	21180	34742	3642	21446	16004
fve-miR156a	21179	34742	3642	21446	16004
fve-miR156b	21179	34742	3642	21446	16004
fve-miR156c	21179	34742	3642	21446	16004
fve-miR156e	21179	34742	3642	21446	16004
gma-miR156k	21179	34742	3642	21446	16004
gma-miR156n	21179	34742	3642	21446	16004
gma-miR156o	21179	34742	3642	21446	16004
aly-miR156a-5p	20768	34227	3548	21110	15698
aly-miR156b-5p	20768	34227	3548	21110	15698
aly-miR156c-5p	20768	34227	3548	21110	15698
aly-miR156d-5p	20768	34227	3548	21110	15698
aly-miR156e-5p	20768	34227	3548	21110	15698
aly-miR156f-5p	20768	34227	3548	21110	15698
aof-miR156a	20768	34227	3548	21110	15698
ata-miR156a-5p	20768	34227	3548	21110	15698
ata-miR156b-5p	20768	34227	3548	21110	15698
ata-miR156c-5p	20768	34227	3548	21110	15698

ata-miR156d-5p	20768	34227	3548	21110	15698
ata-miR156e-5p	20768	34227	3548	21110	15698
ath-miR156a-5p	20768	34227	3548	21110	15698
ath-miR156b-5p	20768	34227	3548	21110	15698
ath-miR156c-5p	20768	34227	3548	21110	15698
ath-miR156d-5p	20768	34227	3548	21110	15698
ath-miR156e	20768	34227	3548	21110	15698
ath-miR156f-5p	20768	34227	3548	21110	15698
atr-miR156b	20768	34227	3548	21110	15698
atr-miR156d	20768	34227	3548	21110	15698
bdi-miR156b-5p	20768	34227	3548	21110	15698
bdi-miR156c	20768	34227	3548	21110	15698
bdi-miR156d-5p	20768	34227	3548	21110	15698
bdi-miR156e-5p	20768	34227	3548	21110	15698
bdi-miR156f-5p	20768	34227	3548	21110	15698
bdi-miR156g-5p	20768	34227	3548	21110	15698
bdi-miR156h-5p	20768	34227	3548	21110	15698
bdi-miR156i-5p	20768	34227	3548	21110	15698
bna-miR156d	20768	34227	3548	21110	15698
bna-miR156e	20768	34227	3548	21110	15698
bna-miR156f	20768	34227	3548	21110	15698
bra-miR156a-5p	20768	34227	3548	21110	15698
bra-miR156b-5p	20768	34227	3548	21110	15698
bra-miR156c-5p	20768	34227	3548	21110	15698
bra-miR156d-5p	20768	34227	3548	21110	15698
bra-miR156e-5p	20768	34227	3548	21110	15698
bra-miR156f-5p	20768	34227	3548	21110	15698
bra-miR156g-5p	20768	34227	3548	21110	15698
cas-miR156a	20768	34227	3548	21110	15698
cas-miR156b-5p	20768	34227	3548	21110	15698
cas-miR156c-5p	20768	34227	3548	21110	15698
cas-miR156d-5p	20768	34227	3548	21110	15698
cas-miR156e-5p	20768	34227	3548	21110	15698
cas-miR156f-5p	20768	34227	3548	21110	15698
cas-miR156k-5p	20768	34227	3548	21110	15698
cca-miR156a	20768	34227	3548	21110	15698
cme-miR156a	20768	34227	3548	21110	15698
cme-miR156c	20768	34227	3548	21110	15698
cme-miR156d	20768	34227	3548	21110	15698
cme-miR156i	20768	34227	3548	21110	15698
cpa-miR156a	20768	34227	3548	21110	15698
cpa-miR156b	20768	34227	3548	21110	15698
cpa-miR156c	20768	34227	3548	21110	15698

cpa-miR156d	20768	34227	3548	21110	15698
csi-miR156a-5p	20768	34227	3548	21110	15698
csi-miR156b-5p	20768	34227	3548	21110	15698
csi-miR156c-5p	20768	34227	3548	21110	15698
ctr-miR156	20768	34227	3548	21110	15698
dpr-miR156b	20768	34227	3548	21110	15698
fve-miR156d	20768	34227	3548	21110	15698
ghr-miR156a	20768	34227	3548	21110	15698
ghr-miR156b	20768	34227	3548	21110	15698
ghr-miR156d	20768	34227	3548	21110	15698
gma-miR156a	20768	34227	3548	21110	15698
gma-miR156h	20768	34227	3548	21110	15698
gma-miR156u	20768	34227	3548	21110	15698
gma-miR156v	20768	34227	3548	21110	15698
gma-miR156w	20768	34227	3548	21110	15698
gma-miR156x	20768	34227	3548	21110	15698
gma-miR156y	20768	34227	3548	21110	15698
han-miR156a	20768	34227	3548	21110	15698
han-miR156b	20768	34227	3548	21110	15698
har-miR156a	20768	34227	3548	21110	15698
htu-miR156a	20768	34227	3548	21110	15698
lus-miR156a	20768	34227	3548	21110	15698
lus-miR156g	20768	34227	3548	21110	15698
mdm-miR156a	20768	34227	3548	21110	15698
mdm-miR156b	20768	34227	3548	21110	15698
mdm-miR156c	20768	34227	3548	21110	15698
mdm-miR156d	20768	34227	3548	21110	15698
mdm-miR156e	20768	34227	3548	21110	15698
mdm-miR156f	20768	34227	3548	21110	15698
mdm-miR156g	20768	34227	3548	21110	15698
mdm-miR156h	20768	34227	3548	21110	15698
mdm-miR156i	20768	34227	3548	21110	15698
mdm-miR156j	20768	34227	3548	21110	15698
mdm-miR156k	20768	34227	3548	21110	15698
mdm-miR156l	20768	34227	3548	21110	15698
mdm-miR156m	20768	34227	3548	21110	15698
mdm-miR156n	20768	34227	3548	21110	15698
mdm-miR156o	20768	34227	3548	21110	15698
mes-miR156a	20768	34227	3548	21110	15698
mes-miR156b	20768	34227	3548	21110	15698
mes-miR156c	20768	34227	3548	21110	15698
mes-miR156d	20768	34227	3548	21110	15698
mes-miR156e	20768	34227	3548	21110	15698

mes-miR156f	20768	34227	3548	21110	15698
mes-miR156g	20768	34227	3548	21110	15698
mtr-miR156b-5p	20768	34227	3548	21110	15698
mtr-miR156c-5p	20768	34227	3548	21110	15698
mtr-miR156d-5p	20768	34227	3548	21110	15698
mtr-miR156i-5p	20768	34227	3548	21110	15698
nta-miR156a	20768	34227	3548	21110	15698
nta-miR156b	20768	34227	3548	21110	15698
nta-miR156c	20768	34227	3548	21110	15698
nta-miR156d	20768	34227	3548	21110	15698
nta-miR156e	20768	34227	3548	21110	15698
osa-miR156a	20768	34227	3548	21110	15698
osa-miR156b-5p	20768	34227	3548	21110	15698
osa-miR156c-5p	20768	34227	3548	21110	15698
osa-miR156d	20768	34227	3548	21110	15698
osa-miR156e	20768	34227	3548	21110	15698
osa-miR156f-5p	20768	34227	3548	21110	15698
osa-miR156g-5p	20768	34227	3548	21110	15698
osa-miR156h-5p	20768	34227	3548	21110	15698
osa-miR156i	20768	34227	3548	21110	15698
osa-miR156j-5p	20768	34227	3548	21110	15698
pab-miR156a	20768	34227	3548	21110	15698
pab-miR156l	20768	34227	3548	21110	15698
ppe-miR156c	20768	34227	3548	21110	15698
ppe-miR156d	20768	34227	3548	21110	15698
ppe-miR156e	20768	34227	3548	21110	15698
ppt-miR156a	20768	34227	3548	21110	15698
ppt-miR156b	20768	34227	3548	21110	15698
ppt-miR156c	20768	34227	3548	21110	15698
ptc-miR156a	20768	34227	3548	21110	15698
ptc-miR156b	20768	34227	3548	21110	15698
ptc-miR156c	20768	34227	3548	21110	15698
ptc-miR156d	20768	34227	3548	21110	15698
ptc-miR156e	20768	34227	3548	21110	15698
ptc-miR156f	20768	34227	3548	21110	15698
sbi-miR156a	20768	34227	3548	21110	15698
sbi-miR156b	20768	34227	3548	21110	15698
sbi-miR156c	20768	34227	3548	21110	15698
sbi-miR156f	20768	34227	3548	21110	15698
sbi-miR156g	20768	34227	3548	21110	15698
sbi-miR156h	20768	34227	3548	21110	15698
sbi-miR156i	20768	34227	3548	21110	15698
sly-miR156d-5p	20768	34227	3548	21110	15698

sof-miR156	20768	34227	3548	21110	15698
stu-miR156e	20768	34227	3548	21110	15698
stu-miR156g-5p	20768	34227	3548	21110	15698
stu-miR156h-5p	20768	34227	3548	21110	15698
stu-miR156i-5p	20768	34227	3548	21110	15698
stu-miR156j-5p	20768	34227	3548	21110	15698
stu-miR156k-5p	20768	34227	3548	21110	15698
tcc-miR156b	20768	34227	3548	21110	15698
tcc-miR156c	20768	34227	3548	21110	15698
tcc-miR156d	20768	34227	3548	21110	15698
tcc-miR156g	20768	34227	3548	21110	15698
vca-miR156a-5p	20768	34227	3548	21110	15698
vun-miR156a	20768	34227	3548	21110	15698
vvi-miR156b	20768	34227	3548	21110	15698
vvi-miR156c	20768	34227	3548	21110	15698
vvi-miR156d	20768	34227	3548	21110	15698
zma-miR156a-5p	20768	34227	3548	21110	15698
zma-miR156b-5p	20768	34227	3548	21110	15698
zma-miR156c	20768	34227	3548	21110	15698
zma-miR156d-5p	20768	34227	3548	21110	15698
zma-miR156e-5p	20768	34227	3548	21110	15698
zma-miR156f-5p	20768	34227	3548	21110	15698
zma-miR156g-5p	20768	34227	3548	21110	15698
zma-miR156h-5p	20768	34227	3548	21110	15698
zma-miR156i-5p	20768	34227	3548	21110	15698
zma-miR156l-5p	20768	34227	3548	21110	15698
ama-miR156	20779	34249	3551	21127	15700
gma-miR169e	3672	5706	1196	4464	2983
gma-miR156q	20887	34400	3565	21195	15776
gma-miR156s	20887	34400	3565	21195	15776
ata-miR169h-5p	3720	5831	1223	4517	3047
bdi-miR169b	3720	5831	1223	4517	3047
mes-miR169f	3720	5831	1223	4517	3047
osa-miR169e	3720	5831	1223	4517	3047
sbi-miR169e	3720	5831	1223	4517	3047
sbi-miR169j	3720	5831	1223	4517	3047
ssp-miR169	3720	5831	1223	4517	3047
zma-miR169p-5p	3720	5831	1223	4517	3047
bna-miR156a	20891	34481	3564	21215	15781
hvu-miR156a	20891	34481	3564	21215	15781
hvu-miR156b	20891	34481	3564	21215	15781
rco-miR156a	20891	34481	3564	21215	15781
rco-miR156b	20891	34481	3564	21215	15781

rco-miR156c	20891	34481	3564	21215	15781
rco-miR156d	20891	34481	3564	21215	15781
ssl-miR156	20891	34481	3564	21215	15781
ssp-miR156	20891	34481	3564	21215	15781
tae-miR156	20891	34481	3564	21215	15781
gso-miR2218	212283	470943	271083	300516	243499
pvu-miR2118	212283	470943	271083	300516	243499
vun-miR2118	212283	470943	271083	300516	243499
aof-miR166b	1357	657	1354	1043	722
ahy-miR156a	187	211	101	167	113
aof-miR156c	187	211	101	167	113
ath-miR156j	187	211	101	167	113
bdi-miR156j	187	211	101	167	113
cas-miR156j	187	211	101	167	113
hpa-miR156a	187	211	101	167	113
ahy-miR167-3p	4463	5492	1307	2236	4610
ptc-miR167f-3p	4463	5492	1307	2236	4610
ptc-miR167g-3p	4463	5492	1307	2236	4610
ptc-miR167h-3p	4463	5492	1307	2236	4610
bdi-miR156a	193	211	103	169	114
far-miR156a	193	211	103	169	114
gma-miR156b	193	211	103	169	114
mtr-miR156a	193	211	103	169	114
osa-miR156k	193	211	103	169	114
rco-miR156e	193	211	103	169	114
sbi-miR156d	193	211	103	169	114
tcc-miR156a	193	211	103	169	114
zma-miR156j-5p	193	211	103	169	114
gma-miR2118a-3p	2919	4326	7841	4325	3577
gma-miR2118b-3p	2919	4326	7841	4325	3577
aqc-miR159	110	106	100	90	52
mtr-miR2118	77	252	70	111	89
gma-miR1515a	6869	8641	20282	4539	11745
gma-miR1515b	6869	8641	20282	4539	11745
aof-miR166a	15790	7474	18107	11179	9533
atr-miR166b	15790	7474	18107	11179	9533
bdi-miR166f	15790	7474	18107	11179	9533
csi-miR166b-3p	15790	7474	18107	11179	9533
csi-miR166d-3p	15790	7474	18107	11179	9533
csi-miR166g-3p	15790	7474	18107	11179	9533
gma-miR166h-3p	15790	7474	18107	11179	9533
gma-miR166k	15790	7474	18107	11179	9533
pab-miR166e	15790	7474	18107	11179	9533

sly-miR156e-3p	9056	10012	17656	9528	9902
stu-miR156g-3p	9056	10012	17656	9528	9902
cas-miR156k-3p	9076	10019	17678	9536	9910
mtr-miR156c-3p	9076	10019	17678	9536	9910
pvu-miR1514a	13941	9159	16954	12770	7637
aly-miR397a-5p	13	14	140	50	28
aly-miR397b-5p	13	14	140	50	28
ath-miR397a	13	14	140	50	28
bdi-miR397a	13	14	140	50	28
bna-miR397a	13	14	140	50	28
bna-miR397b	13	14	140	50	28
cas-miR397	13	14	140	50	28
cme-miR397	13	14	140	50	28
csi-miR397-5p	13	14	140	50	28
fve-miR397	13	14	140	50	28
gma-miR397a	13	14	140	50	28
gma-miR397b-5p	13	14	140	50	28
lus-miR397b	13	14	140	50	28
mes-miR397b	13	14	140	50	28
mtr-miR397-5p	13	14	140	50	28
osa-miR397a	13	14	140	50	28
ppe-miR397	13	14	140	50	28
ptc-miR397a	13	14	140	50	28
rco-miR397	13	14	140	50	28
sbi-miR397-5p	13	14	140	50	28
ssl-miR397	13	14	140	50	28
tcc-miR397	13	14	140	50	28
vca-miR397-5p	13	14	140	50	28
vvi-miR397a	13	14	140	50	28
pvu-miR482-3p	53	84	281	74	63
bdi-miR393a	133	78	12	81	58
bdi-miR393b-5p	133	78	12	81	58
bna-miR393	133	78	12	81	58
cme-miR393a	133	78	12	81	58
cme-miR393b	133	78	12	81	58
cme-miR393c	133	78	12	81	58
csi-miR393c-5p	133	78	12	81	58
fve-miR393a	133	78	12	81	58
gma-miR393a	133	78	12	81	58
lus-miR393a	133	78	12	81	58
lus-miR393b	133	78	12	81	58
lus-miR393c	133	78	12	81	58
lus-miR393d	133	78	12	81	58

mes-miR393a	133	78	12	81	58
mtr-miR393a	133	78	12	81	58
mtr-miR393b-5p	133	78	12	81	58
osa-miR393a	133	78	12	81	58
ppe-miR393b	133	78	12	81	58
ptc-miR393a-5p	133	78	12	81	58
ptc-miR393b-5p	133	78	12	81	58
ptc-miR393c	133	78	12	81	58
rco-miR393	133	78	12	81	58
sbi-miR393a	133	78	12	81	58
sbi-miR393b	133	78	12	81	58
tcc-miR393b	133	78	12	81	58
vca-miR393-5p	133	78	12	81	58
vvi-miR393a	133	78	12	81	58
vvi-miR393b	133	78	12	81	58
sly-miR171e	218	358	269	153	276
stu-miR171b-3p	218	358	269	153	276
aof-miR171c	212	347	248	146	267
csi-miR171e-3p	212	347	248	146	267
csi-miR171g-3p	212	347	248	146	267
ctr-miR171	212	347	248	146	267
fve-miR171h	212	347	248	146	267
mdm-miR171a	212	347	248	146	267
mdm-miR171b	212	347	248	146	267
mdm-miR171p	212	347	248	146	267
mes-miR171a	212	347	248	146	267
ppe-miR171h	212	347	248	146	267
efu-miR-126	173	35	497	123	79
bdi-miR160f	269	267	351	221	234
cas-miR160a	269	267	351	221	234
cas-miR160b-5p	269	267	351	221	234
gma-miR160b	269	267	351	221	234
gma-miR160c	269	267	351	221	234
gma-miR160d	269	267	351	221	234
gma-miR160e	269	267	351	221	234
htu-miR160a	269	267	351	221	234
pab-miR160c	269	267	351	221	234
pab-miR160e	269	267	351	221	234
pab-miR160f	269	267	351	221	234
gma-miR159e-5p	1346	1115	1126	751	1072
aca-miR-126-3p	165	35	490	120	78
ami-miR-126-3p	165	35	490	120	78
cgr-miR-126a	165	35	490	120	78

cja-miR-126	165	35	490	120	78
cli-miR-126-3p	165	35	490	120	78
cpi-miR-126-3p	165	35	490	120	78
cpo-miR-126-3p	165	35	490	120	78
dno-miR-126-3p	165	35	490	120	78
eca-miR-126-3p	165	35	490	120	78
gga-miR-126-3p	165	35	490	120	78
hsa-miR-126-3p	165	35	490	120	78
mdo-miR-126-3p	165	35	490	120	78
mml-miR-126	165	35	490	120	78
mmu-miR-126a-3p	165	35	490	120	78
oan-miR-126-3p	165	35	490	120	78
pbv-miR-126-3p	165	35	490	120	78
ppy-miR-126	165	35	490	120	78
ptr-miR-126	165	35	490	120	78
rno-miR-126a-3p	165	35	490	120	78
ssc-miR-126-3p	165	35	490	120	78
tgu-miR-126-3p	165	35	490	120	78
cme-miR168	1102	1956	779	1355	812
bra-miR168b-5p	1151	2054	812	1449	839
bra-miR168c-5p	1151	2054	812	1449	839
nta-miR168a	1151	2054	812	1449	839
nta-miR168b	1151	2054	812	1449	839
nta-miR168c	1151	2054	812	1449	839
sly-miR168a-5p	1151	2054	812	1449	839
sly-miR168b-5p	1151	2054	812	1449	839
csi-miR160b-5p	270	268	359	222	234
mes-miR160c	270	268	359	222	234
osa-miR160e-5p	270	268	359	222	234
zma-miR160f-5p	270	268	359	222	234
aly-miR167d-5p	52986	43732	40946	44083	24763
ath-miR167d	52986	43732	40946	44083	24763
cca-miR167	52986	43732	40946	44083	24763
eun-miR167b-5p	52986	43732	40946	44083	24763
nta-miR167a	52986	43732	40946	44083	24763
nta-miR167b	52986	43732	40946	44083	24763
nta-miR167c	52986	43732	40946	44083	24763
pab-miR167b	52986	43732	40946	44083	24763
rco-miR167c	52986	43732	40946	44083	24763
csi-miR393a	135	83	12	81	58
ghr-miR169b	72	100	50	52	73
aly-miR170-5p	6950	14810	10511	9105	8883
aly-miR171a-5p	6950	14810	10511	9105	8883

ath-miR170-5p	6950	14810	10511	9105	8883
ath-miR171a-5p	6950	14810	10511	9105	8883
cas-miR170	6950	14810	10511	9105	8883
cas-miR171a-5p	6950	14810	10511	9105	8883
csi-miR171f-5p	6950	14810	10511	9105	8883
gma-miR171j-5p	6950	14810	10511	9105	8883
sly-miR171f	6950	14810	10511	9105	8883
stu-miR171a-5p	6950	14810	10511	9105	8883
stu-miR171c-5p	6950	14810	10511	9105	8883
gma-miR482b-3p	2853	6453	1543	3760	1637
gma-miR482d-3p	2853	6453	1543	3760	1637
gma-miR159a-5p	1844	1295	2005	1030	1335
ptc-miR396e-3p	432	620	184	245	397
gma-miR319f	103	34	139	68	43
age-miR-19b	57	49	84	90	22
bta-miR-19b	57	49	84	90	22
cgr-miR-19b-3p	57	49	84	90	22
chi-miR-19b-3p	57	49	84	90	22
cja-miR-19b	57	49	84	90	22
cli-miR-19b-3p	57	49	84	90	22
cpo-miR-19b-3p	57	49	84	90	22
dno-miR-19b-3p	57	49	84	90	22
dre-miR-19b-3p	57	49	84	90	22
eca-miR-19b	57	49	84	90	22
fru-miR-19b	57	49	84	90	22
gga-miR-19b-3p	57	49	84	90	22
ggo-miR-19b	57	49	84	90	22
gmo-miR-19b-3p	57	49	84	90	22
hsa-miR-19b-3p	57	49	84	90	22
lca-miR-19b	57	49	84	90	22
lla-miR-19b	57	49	84	90	22
mdo-miR-19b-3p	57	49	84	90	22
mml-miR-19b	57	49	84	90	22
mmu-miR-19b-3p	57	49	84	90	22
mne-miR-19b	57	49	84	90	22
oan-miR-19b-3p	57	49	84	90	22
oar-miR-19b	57	49	84	90	22
ocu-miR-19b-3p	57	49	84	90	22
oha-miR-19b-3p	57	49	84	90	22
pal-miR-19-3p	57	49	84	90	22
pma-miR-19b-3p	57	49	84	90	22
ppa-miR-19b	57	49	84	90	22
ppy-miR-19b	57	49	84	90	22

ptr-miR-19b	57	49	84	90	22
rno-miR-19b-3p	57	49	84	90	22
sha-miR-19b	57	49	84	90	22
sla-miR-19b	57	49	84	90	22
ssc-miR-19b	57	49	84	90	22
tch-miR-19b-3p	57	49	84	90	22
tgu-miR-19b-3p	57	49	84	90	22
tni-miR-19b	57	49	84	90	22
xla-miR-19b	57	49	84	90	22
xtr-miR-19b	57	49	84	90	22
efu-miR-378	200	224	143	216	102
ggo-miR-378a	199	224	143	216	102
bta-miR-378	195	224	143	215	102
cfa-miR-378	195	224	143	215	102
cgr-miR-378-3p	195	224	143	215	102
chi-miR-378-3p	195	224	143	215	102
cja-miR-378	195	224	143	215	102
cpo-miR-378-3p	195	224	143	215	102
dno-miR-378-3p	195	224	143	215	102
hsa-miR-378a-3p	195	224	143	215	102
nle-miR-378a	195	224	143	215	102
ocu-miR-378-3p	195	224	143	215	102
oga-miR-378	195	224	143	215	102
pal-miR-378-3p	195	224	143	215	102
pha-miR-378	195	224	143	215	102
ppa-miR-378a	195	224	143	215	102
ssc-miR-378	195	224	143	215	102
tch-miR-378a-3p	195	224	143	215	102
efu-miR-19	58	50	84	91	22
xla-miR-19b-3p	58	50	84	91	22
gma-miR156f	12431	14883	2848	9875	6181
ahy-miR156c	12339	14785	2836	9790	6132
far-miR156b	12339	14785	2836	9790	6132
mdm-miR156t	12339	14785	2836	9790	6132
mdm-miR156u	12339	14785	2836	9790	6132
mdm-miR156v	12339	14785	2836	9790	6132
mdm-miR156w	12339	14785	2836	9790	6132
mes-miR156k	12339	14785	2836	9790	6132
gma-miR390b-5p	304	338	292	199	164
gma-miR390d	304	338	292	199	164
nta-miR390a	304	338	292	199	164
sly-miR390a-5p	304	338	292	199	164
stu-miR390-5p	304	338	292	199	164

csi-miR396f-3p	468	659	204	252	413
gma-miR396b-3p	468	659	204	252	413
gma-miR396k-3p	468	659	204	252	413
mtr-miR396a-3p	468	659	204	252	413
ahy-miR160-5p	95	80	217	96	42
aof-miR160a	95	80	217	96	42
bdi-miR160e-5p	95	80	217	96	42
cme-miR160d	95	80	217	96	42
cpa-miR160d	95	80	217	96	42
mes-miR160e	95	80	217	96	42
mes-miR160f	95	80	217	96	42
mtr-miR160c	95	80	217	96	42
osa-miR160f-5p	95	80	217	96	42
ptc-miR160e-5p	95	80	217	96	42
ptc-miR160f	95	80	217	96	42
rco-miR160c	95	80	217	96	42
sbi-miR160f	95	80	217	96	42
tcc-miR160a	95	80	217	96	42
vca-miR160-5p	95	80	217	96	42
vvi-miR160a	95	80	217	96	42
vvi-miR160b	95	80	217	96	42
lja-miR166-3p	41108	35806	93852	26586	32868
aly-miR166a-3p	39290	34477	91739	25385	31490
aly-miR166b-3p	39290	34477	91739	25385	31490
aly-miR166c-3p	39290	34477	91739	25385	31490
aly-miR166d-3p	39290	34477	91739	25385	31490
aly-miR166e-3p	39290	34477	91739	25385	31490
aly-miR166f-3p	39290	34477	91739	25385	31490
aly-miR166g-3p	39290	34477	91739	25385	31490
aly-miR166h-3p	39290	34477	91739	25385	31490
aof-miR166d	39290	34477	91739	25385	31490
aqc-miR166b	39290	34477	91739	25385	31490
aqc-miR166e	39290	34477	91739	25385	31490
ata-miR166a-3p	39290	34477	91739	25385	31490
ata-miR166b-3p	39290	34477	91739	25385	31490
ata-miR166d-3p	39290	34477	91739	25385	31490
ata-miR166e-3p	39290	34477	91739	25385	31490
ath-miR166a-3p	39290	34477	91739	25385	31490
ath-miR166b-3p	39290	34477	91739	25385	31490
ath-miR166c	39290	34477	91739	25385	31490
ath-miR166d	39290	34477	91739	25385	31490
ath-miR166e-3p	39290	34477	91739	25385	31490
ath-miR166f	39290	34477	91739	25385	31490

ath-miR166g	39290	34477	91739	25385	31490
atr-miR166a	39290	34477	91739	25385	31490
atr-miR166c	39290	34477	91739	25385	31490
atr-miR166d	39290	34477	91739	25385	31490
bdi-miR166a-3p	39290	34477	91739	25385	31490
bdi-miR166b-3p	39290	34477	91739	25385	31490
bdi-miR166c-3p	39290	34477	91739	25385	31490
bdi-miR166d-3p	39290	34477	91739	25385	31490
bdi-miR166i-3p	39290	34477	91739	25385	31490
bna-miR166a	39290	34477	91739	25385	31490
bna-miR166b	39290	34477	91739	25385	31490
bna-miR166c	39290	34477	91739	25385	31490
bna-miR166d	39290	34477	91739	25385	31490
bna-miR166e	39290	34477	91739	25385	31490
cme-miR166a	39290	34477	91739	25385	31490
cme-miR166b	39290	34477	91739	25385	31490
cme-miR166c	39290	34477	91739	25385	31490
cme-miR166d	39290	34477	91739	25385	31490
cme-miR166f	39290	34477	91739	25385	31490
cme-miR166h	39290	34477	91739	25385	31490
cpa-miR166a	39290	34477	91739	25385	31490
cpa-miR166b	39290	34477	91739	25385	31490
cpa-miR166c	39290	34477	91739	25385	31490
csi-miR166e-3p	39290	34477	91739	25385	31490
dpr-miR166b	39290	34477	91739	25385	31490
eun-miR166-3p	39290	34477	91739	25385	31490
fve-miR166a	39290	34477	91739	25385	31490
fve-miR166b	39290	34477	91739	25385	31490
fve-miR166c	39290	34477	91739	25385	31490
fve-miR166d-3p	39290	34477	91739	25385	31490
fve-miR166e	39290	34477	91739	25385	31490
fve-miR166f	39290	34477	91739	25385	31490
ghr-miR166b	39290	34477	91739	25385	31490
gma-miR166a-3p	39290	34477	91739	25385	31490
gma-miR166b	39290	34477	91739	25385	31490
gma-miR166c-3p	39290	34477	91739	25385	31490
gma-miR166d	39290	34477	91739	25385	31490
gma-miR166e	39290	34477	91739	25385	31490
gma-miR166f	39290	34477	91739	25385	31490
gma-miR166g	39290	34477	91739	25385	31490
gma-miR166i-3p	39290	34477	91739	25385	31490
gma-miR166n	39290	34477	91739	25385	31490
gma-miR166o	39290	34477	91739	25385	31490

hpa-miR166a	39290	34477	91739	25385	31490
hpe-miR166a	39290	34477	91739	25385	31490
hvu-miR166a	39290	34477	91739	25385	31490
hvu-miR166b	39290	34477	91739	25385	31490
hvu-miR166c	39290	34477	91739	25385	31490
lus-miR166a	39290	34477	91739	25385	31490
lus-miR166c	39290	34477	91739	25385	31490
lus-miR166d	39290	34477	91739	25385	31490
lus-miR166g	39290	34477	91739	25385	31490
lus-miR166h	39290	34477	91739	25385	31490
lus-miR166j	39290	34477	91739	25385	31490
mdm-miR166a	39290	34477	91739	25385	31490
mdm-miR166b	39290	34477	91739	25385	31490
mdm-miR166c	39290	34477	91739	25385	31490
mdm-miR166d	39290	34477	91739	25385	31490
mdm-miR166e	39290	34477	91739	25385	31490
mdm-miR166f	39290	34477	91739	25385	31490
mdm-miR166g	39290	34477	91739	25385	31490
mdm-miR166h	39290	34477	91739	25385	31490
mdm-miR166i	39290	34477	91739	25385	31490
mdm-miR166j	39290	34477	91739	25385	31490
mes-miR166a	39290	34477	91739	25385	31490
mes-miR166b	39290	34477	91739	25385	31490
mes-miR166c	39290	34477	91739	25385	31490
mes-miR166d	39290	34477	91739	25385	31490
mes-miR166e	39290	34477	91739	25385	31490
mes-miR166f	39290	34477	91739	25385	31490
mes-miR166g	39290	34477	91739	25385	31490
mtr-miR166a	39290	34477	91739	25385	31490
mtr-miR166e-3p	39290	34477	91739	25385	31490
mtr-miR166g-3p	39290	34477	91739	25385	31490
nta-miR166a	39290	34477	91739	25385	31490
nta-miR166b	39290	34477	91739	25385	31490
nta-miR166c	39290	34477	91739	25385	31490
nta-miR166d	39290	34477	91739	25385	31490
nta-miR166e	39290	34477	91739	25385	31490
nta-miR166f	39290	34477	91739	25385	31490
nta-miR166g	39290	34477	91739	25385	31490
nta-miR166h	39290	34477	91739	25385	31490
osa-miR166a-3p	39290	34477	91739	25385	31490
osa-miR166b-3p	39290	34477	91739	25385	31490
osa-miR166c-3p	39290	34477	91739	25385	31490
osa-miR166d-3p	39290	34477	91739	25385	31490

osa-miR166f	39290	34477	91739	25385	31490
osa-miR166j-3p	39290	34477	91739	25385	31490
pab-miR166f	39290	34477	91739	25385	31490
pab-miR166g	39290	34477	91739	25385	31490
pab-miR166h	39290	34477	91739	25385	31490
pab-miR166i	39290	34477	91739	25385	31490
ppe-miR166a	39290	34477	91739	25385	31490
ppe-miR166b	39290	34477	91739	25385	31490
ppe-miR166c	39290	34477	91739	25385	31490
ppe-miR166d	39290	34477	91739	25385	31490
ppe-miR166e	39290	34477	91739	25385	31490
ppt-miR166a	39290	34477	91739	25385	31490
ppt-miR166b	39290	34477	91739	25385	31490
ppt-miR166c	39290	34477	91739	25385	31490
ppt-miR166d	39290	34477	91739	25385	31490
ppt-miR166e	39290	34477	91739	25385	31490
ppt-miR166f	39290	34477	91739	25385	31490
ppt-miR166g	39290	34477	91739	25385	31490
ppt-miR166h	39290	34477	91739	25385	31490
ppt-miR166i	39290	34477	91739	25385	31490
pta-miR166a	39290	34477	91739	25385	31490
pta-miR166b	39290	34477	91739	25385	31490
ptc-miR166a	39290	34477	91739	25385	31490
ptc-miR166b	39290	34477	91739	25385	31490
ptc-miR166c	39290	34477	91739	25385	31490
ptc-miR166d	39290	34477	91739	25385	31490
ptc-miR166e	39290	34477	91739	25385	31490
ptc-miR166f	39290	34477	91739	25385	31490
ptc-miR166g	39290	34477	91739	25385	31490
ptc-miR166h	39290	34477	91739	25385	31490
ptc-miR166i	39290	34477	91739	25385	31490
ptc-miR166j	39290	34477	91739	25385	31490
ptc-miR166k	39290	34477	91739	25385	31490
ptc-miR166l	39290	34477	91739	25385	31490
ptc-miR166m	39290	34477	91739	25385	31490
pvu-miR166a	39290	34477	91739	25385	31490
rco-miR166a	39290	34477	91739	25385	31490
rco-miR166b	39290	34477	91739	25385	31490
rco-miR166c	39290	34477	91739	25385	31490
rco-miR166d	39290	34477	91739	25385	31490
rco-miR166e	39290	34477	91739	25385	31490
sly-miR166a	39290	34477	91739	25385	31490
sly-miR166b	39290	34477	91739	25385	31490

smo-miR166a	39290	34477	91739	25385	31490
smo-miR166b	39290	34477	91739	25385	31490
smo-miR166c	39290	34477	91739	25385	31490
ssl-miR166b	39290	34477	91739	25385	31490
ssp-miR166	39290	34477	91739	25385	31490
stu-miR166a-3p	39290	34477	91739	25385	31490
stu-miR166c-3p	39290	34477	91739	25385	31490
stu-miR166d-3p	39290	34477	91739	25385	31490
tcc-miR166a	39290	34477	91739	25385	31490
tcc-miR166d	39290	34477	91739	25385	31490
vca-miR166a-3p	39290	34477	91739	25385	31490
vca-miR166b-3p	39290	34477	91739	25385	31490
vca-miR166c-3p	39290	34477	91739	25385	31490
vvi-miR166c	39290	34477	91739	25385	31490
vvi-miR166d	39290	34477	91739	25385	31490
vvi-miR166e	39290	34477	91739	25385	31490
vvi-miR166f	39290	34477	91739	25385	31490
vvi-miR166g	39290	34477	91739	25385	31490
vvi-miR166h	39290	34477	91739	25385	31490
zma-miR166a-3p	39290	34477	91739	25385	31490
csi-miR166a-3p	39295	34481	91787	25387	31492
ctr-miR166	39295	34481	91787	25387	31492
hbr-miR166b	39295	34481	91787	25387	31492
lus-miR166i	39295	34481	91787	25387	31492
lus-miR166k	39295	34481	91787	25387	31492
cas-miR166c-3p	39375	34575	92370	25450	31533
cas-miR166d	39375	34575	92370	25450	31533
cas-miR166f-3p	39375	34575	92370	25450	31533
lja-miR168-5p	64684	135916	28128	81069	38549
aly-miR168a-5p	64535	135686	28082	80905	38434
aly-miR168b-5p	64535	135686	28082	80905	38434
aof-miR168a	64535	135686	28082	80905	38434
ath-miR168a-5p	64535	135686	28082	80905	38434
ath-miR168b-5p	64535	135686	28082	80905	38434
atr-miR168	64535	135686	28082	80905	38434
bna-miR168a	64535	135686	28082	80905	38434
bra-miR168a-5p	64535	135686	28082	80905	38434
cca-miR168a	64535	135686	28082	80905	38434
ccl-miR168	64535	135686	28082	80905	38434
crt-miR168	64535	135686	28082	80905	38434
csi-miR168-5p	64535	135686	28082	80905	38434
fve-miR168-5p	64535	135686	28082	80905	38434
gma-miR168a	64535	135686	28082	80905	38434

lus-miR168a	64535	135686	28082	80905	38434
lus-miR168b	64535	135686	28082	80905	38434
mdm-miR168a	64535	135686	28082	80905	38434
mdm-miR168b	64535	135686	28082	80905	38434
mes-miR168a	64535	135686	28082	80905	38434
mtr-miR168b	64535	135686	28082	80905	38434
mtr-miR168c-5p	64535	135686	28082	80905	38434
nta-miR168d	64535	135686	28082	80905	38434
nta-miR168e	64535	135686	28082	80905	38434
pab-miR168a	64535	135686	28082	80905	38434
ppe-miR168	64535	135686	28082	80905	38434
ptc-miR168a-5p	64535	135686	28082	80905	38434
ptc-miR168b-5p	64535	135686	28082	80905	38434
rco-miR168	64535	135686	28082	80905	38434
tcc-miR168	64535	135686	28082	80905	38434
vca-miR168a-5p	64535	135686	28082	80905	38434
vca-miR168b-5p	64535	135686	28082	80905	38434
vun-miR168	64535	135686	28082	80905	38434
vvi-miR168	64535	135686	28082	80905	38434
ahy-miR167-5p	32592	40851	39761	19815	28085
cme-miR167c	32592	40851	39761	19815	28085
cpa-miR167c	32592	40851	39761	19815	28085
csi-miR167b-5p	32592	40851	39761	19815	28085
gma-miR167e	32592	40851	39761	19815	28085
gma-miR167f	32592	40851	39761	19815	28085
lus-miR167b	32592	40851	39761	19815	28085
mes-miR167g	32592	40851	39761	19815	28085
mes-miR167h	32592	40851	39761	19815	28085
ptc-miR167f-5p	32592	40851	39761	19815	28085
ptc-miR167g-5p	32592	40851	39761	19815	28085
tcc-miR167c	32592	40851	39761	19815	28085
gma-miR403a	5565	3750	30300	4887	2458
gma-miR403b	5565	3750	30300	4887	2458
aly-miR396b-5p	1143	1233	2696	688	841
ama-miR396-5p	1143	1233	2696	688	841
aqc-miR396b	1143	1233	2696	688	841
ata-miR396c-5p	1143	1233	2696	688	841
ath-miR396b-5p	1143	1233	2696	688	841
atr-miR396b	1143	1233	2696	688	841
atr-miR396c	1143	1233	2696	688	841
atr-miR396e	1143	1233	2696	688	841
bcy-miR396b	1143	1233	2696	688	841
bdi-miR396e-5p	1143	1233	2696	688	841

bgy-miR396b	1143	1233	2696	688	841
bna-miR396a	1143	1233	2696	688	841
bra-miR396-5p	1143	1233	2696	688	841
cas-miR396b	1143	1233	2696	688	841
cca-miR396a-5p	1143	1233	2696	688	841
ccl-miR396	1143	1233	2696	688	841
cme-miR396a	1143	1233	2696	688	841
cme-miR396c	1143	1233	2696	688	841
cme-miR396d	1143	1233	2696	688	841
csi-miR396f-5p	1143	1233	2696	688	841
fve-miR396b-5p	1143	1233	2696	688	841
gma-miR396b-5p	1143	1233	2696	688	841
gma-miR396c	1143	1233	2696	688	841
gma-miR396k-5p	1143	1233	2696	688	841
lus-miR396b	1143	1233	2696	688	841
lus-miR396e	1143	1233	2696	688	841
mdm-miR396c	1143	1233	2696	688	841
mdm-miR396d	1143	1233	2696	688	841
mdm-miR396e	1143	1233	2696	688	841
mes-miR396c	1143	1233	2696	688	841
mes-miR396d	1143	1233	2696	688	841
mes-miR396e	1143	1233	2696	688	841
mes-miR396f	1143	1233	2696	688	841
mtr-miR396a-5p	1143	1233	2696	688	841
nta-miR396b	1143	1233	2696	688	841
nta-miR396c	1143	1233	2696	688	841
osa-miR396c-5p	1143	1233	2696	688	841
pab-miR396g	1143	1233	2696	688	841
pab-miR396h	1143	1233	2696	688	841
ppe-miR396b	1143	1233	2696	688	841
pta-miR396	1143	1233	2696	688	841
ptc-miR396c	1143	1233	2696	688	841
ptc-miR396d	1143	1233	2696	688	841
ptc-miR396e-5p	1143	1233	2696	688	841
rco-miR396	1143	1233	2696	688	841
sbi-miR396c	1143	1233	2696	688	841
sly-miR396b	1143	1233	2696	688	841
stu-miR396-5p	1143	1233	2696	688	841
tcc-miR396c	1143	1233	2696	688	841
tcc-miR396e	1143	1233	2696	688	841
zma-miR396e-5p	1143	1233	2696	688	841
zma-miR396f-5p	1143	1233	2696	688	841
gma-miR1511	1103	618	4493	521	1150

gma-miR5374-5p	554	502	295	428	210
mtr-miR171c	28	60	103	47	25
aly-miR166a-5p	15363	15709	1648	5141	10013
aly-miR166c-5p	15363	15709	1648	5141	10013
aly-miR166d-5p	15363	15709	1648	5141	10013
bdi-miR166e-5p	15363	15709	1648	5141	10013
cas-miR166a	15363	15709	1648	5141	10013
csi-miR166a-5p	15363	15709	1648	5141	10013
csi-miR166e-5p	15363	15709	1648	5141	10013
eun-miR166-5p	15363	15709	1648	5141	10013
gma-miR166a-5p	15363	15709	1648	5141	10013
gma-miR166c-5p	15363	15709	1648	5141	10013
gma-miR166l	15363	15709	1648	5141	10013
mtr-miR166g-5p	15363	15709	1648	5141	10013
osa-miR166d-5p	15363	15709	1648	5141	10013
stu-miR166a-5p	15363	15709	1648	5141	10013
vca-miR166b-5p	15363	15709	1648	5141	10013
zma-miR166c-5p	15363	15709	1648	5141	10013
gma-miR391-5p	85	61	167	59	39
gma-miR171m	9514	18038	18276	8015	9536
gma-miR171t	9514	18038	18276	8015	9536
aly-miR169a-5p	491	981	621	460	423
ata-miR169e-5p	491	981	621	460	423
ata-miR169f-5p	491	981	621	460	423
ata-miR169g-5p	491	981	621	460	423
ath-miR169a-5p	491	981	621	460	423
bdi-miR169a-5p	491	981	621	460	423
bna-miR169a	491	981	621	460	423
bna-miR169b	491	981	621	460	423
cas-miR169a	491	981	621	460	423
gma-miR169b	491	981	621	460	423
lus-miR169g	491	981	621	460	423
lus-miR169l	491	981	621	460	423
mes-miR169g	491	981	621	460	423
mtr-miR169a	491	981	621	460	423
nta-miR169a	491	981	621	460	423
nta-miR169b	491	981	621	460	423
nta-miR169c	491	981	621	460	423
nta-miR169d	491	981	621	460	423
nta-miR169e	491	981	621	460	423
nta-miR169f	491	981	621	460	423
nta-miR169g	491	981	621	460	423
nta-miR169h	491	981	621	460	423

nta-miR169i	491	981	621	460	423
nta-miR169j	491	981	621	460	423
nta-miR169k	491	981	621	460	423
nta-miR169l	491	981	621	460	423
nta-miR169m	491	981	621	460	423
nta-miR169o	491	981	621	460	423
nta-miR169p	491	981	621	460	423
osa-miR169a	491	981	621	460	423
ptc-miR169a	491	981	621	460	423
ptc-miR169b-5p	491	981	621	460	423
ptc-miR169c	491	981	621	460	423
sbi-miR169a	491	981	621	460	423
sly-miR169c	491	981	621	460	423
tcc-miR169a	491	981	621	460	423
tcc-miR169c	491	981	621	460	423
tcc-miR169e	491	981	621	460	423
vvi-miR169f	491	981	621	460	423
vvi-miR169g	491	981	621	460	423
zma-miR169a-5p	491	981	621	460	423
zma-miR169b-5p	491	981	621	460	423
gma-miR169u	487	966	649	440	429
mdm-miR167h	68755	87811	93911	40687	54233
mdm-miR167i	68755	87811	93911	40687	54233
mdm-miR167j	68755	87811	93911	40687	54233
ppe-miR167d	68755	87811	93911	40687	54233
ppe-miR398b	60	51	339	61	58
bna-miR167a	5635	8853	15331	4957	5190
bna-miR167b	5635	8853	15331	4957	5190
aly-miR167a-5p	5632	8844	15323	4951	5186
aly-miR167b-5p	5632	8844	15323	4951	5186
aof-miR167a	5632	8844	15323	4951	5186
ata-miR167a-5p	5632	8844	15323	4951	5186
ata-miR167c-5p	5632	8844	15323	4951	5186
ata-miR167e-5p	5632	8844	15323	4951	5186
ath-miR167a-5p	5632	8844	15323	4951	5186
ath-miR167b	5632	8844	15323	4951	5186
bdi-miR167a	5632	8844	15323	4951	5186
bdi-miR167b	5632	8844	15323	4951	5186
bdi-miR167f	5632	8844	15323	4951	5186
bna-miR167c	5632	8844	15323	4951	5186
bra-miR167a	5632	8844	15323	4951	5186
bra-miR167b	5632	8844	15323	4951	5186
bra-miR167c	5632	8844	15323	4951	5186

bra-miR167d	5632	8844	15323	4951	5186
cme-miR167a	5632	8844	15323	4951	5186
cme-miR167b	5632	8844	15323	4951	5186
cpa-miR167a	5632	8844	15323	4951	5186
cpa-miR167b	5632	8844	15323	4951	5186
csi-miR167d-5p	5632	8844	15323	4951	5186
csi-miR167e-5p	5632	8844	15323	4951	5186
dpr-miR167a	5632	8844	15323	4951	5186
dpr-miR167b	5632	8844	15323	4951	5186
ghr-miR167a	5632	8844	15323	4951	5186
ghr-miR167b	5632	8844	15323	4951	5186
gma-miR167a	5632	8844	15323	4951	5186
gma-miR167b	5632	8844	15323	4951	5186
gma-miR167d	5632	8844	15323	4951	5186
lus-miR167c	5632	8844	15323	4951	5186
lus-miR167d	5632	8844	15323	4951	5186
lus-miR167e	5632	8844	15323	4951	5186
lus-miR167h	5632	8844	15323	4951	5186
mdm-miR167b	5632	8844	15323	4951	5186
mdm-miR167c	5632	8844	15323	4951	5186
mdm-miR167d	5632	8844	15323	4951	5186
mdm-miR167e	5632	8844	15323	4951	5186
mdm-miR167f	5632	8844	15323	4951	5186
mdm-miR167g	5632	8844	15323	4951	5186
mes-miR167c	5632	8844	15323	4951	5186
mtr-miR167a	5632	8844	15323	4951	5186
nta-miR167d	5632	8844	15323	4951	5186
nta-miR167e	5632	8844	15323	4951	5186
osa-miR167a-5p	5632	8844	15323	4951	5186
osa-miR167b	5632	8844	15323	4951	5186
osa-miR167c-5p	5632	8844	15323	4951	5186
ppe-miR167a	5632	8844	15323	4951	5186
ppe-miR167b	5632	8844	15323	4951	5186
ptc-miR167a	5632	8844	15323	4951	5186
ptc-miR167b	5632	8844	15323	4951	5186
ptc-miR167c	5632	8844	15323	4951	5186
ptc-miR167d	5632	8844	15323	4951	5186
rco-miR167a	5632	8844	15323	4951	5186
rco-miR167b	5632	8844	15323	4951	5186
sbi-miR167a	5632	8844	15323	4951	5186
sbi-miR167b	5632	8844	15323	4951	5186
sbi-miR167i	5632	8844	15323	4951	5186
sly-miR167a	5632	8844	15323	4951	5186

stu-miR167a-5p	5632	8844	15323	4951	5186
stu-miR167b-5p	5632	8844	15323	4951	5186
stu-miR167c-5p	5632	8844	15323	4951	5186
stu-miR167d-5p	5632	8844	15323	4951	5186
tae-miR167a	5632	8844	15323	4951	5186
tcc-miR167a	5632	8844	15323	4951	5186
tcc-miR167b	5632	8844	15323	4951	5186
vvi-miR167b	5632	8844	15323	4951	5186
vvi-miR167d	5632	8844	15323	4951	5186
vvi-miR167e	5632	8844	15323	4951	5186
zma-miR167a-5p	5632	8844	15323	4951	5186
zma-miR167b-5p	5632	8844	15323	4951	5186
zma-miR167c-5p	5632	8844	15323	4951	5186
zma-miR167d-5p	5632	8844	15323	4951	5186
ppt-miR160b	33	24	341	30	17
ppt-miR160i	33	24	341	30	17
lus-miR398f	59	52	334	59	55
gma-miR159d	3954	2175	751	1985	1102
aof-miR398	6176	8152	22550	5826	6562
aqc-miR398b	6176	8152	22550	5826	6562
bdi-miR398a	6176	8152	22550	5826	6562
cca-miR398	6176	8152	22550	5826	6562
cme-miR398a	6176	8152	22550	5826	6562
csi-miR398b-3p	6176	8152	22550	5826	6562
gma-miR398c	6176	8152	22550	5826	6562
gma-miR398d	6176	8152	22550	5826	6562
lus-miR398a	6176	8152	22550	5826	6562
mdm-miR398b	6176	8152	22550	5826	6562
mdm-miR398c	6176	8152	22550	5826	6562
mes-miR398	6176	8152	22550	5826	6562
mtr-miR398b	6176	8152	22550	5826	6562
mtr-miR398c	6176	8152	22550	5826	6562
nta-miR398	6176	8152	22550	5826	6562
osa-miR398b	6176	8152	22550	5826	6562
ppe-miR398a-3p	6176	8152	22550	5826	6562
ptc-miR398b	6176	8152	22550	5826	6562
ptc-miR398c-3p	6176	8152	22550	5826	6562
rco-miR398b	6176	8152	22550	5826	6562
tcc-miR398a	6176	8152	22550	5826	6562
vvi-miR398b	6176	8152	22550	5826	6562
vvi-miR398c	6176	8152	22550	5826	6562
bdi-miR166e-3p	380	323	1408	247	290
ptc-miR169s	400	865	603	371	338

aof-miR171b	202	402	561	162	158
fve-miR171f-3p	202	402	561	162	158
gma-miR171k-3p	202	402	561	162	158
lja-miR171d-5p	202	402	561	162	158
mdm-miR171j	202	402	561	162	158
mdm-miR171k	202	402	561	162	158
mdm-miR171l	202	402	561	162	158
mes-miR171e	202	402	561	162	158
nta-miR171b	202	402	561	162	158
pab-miR171b	202	402	561	162	158
pab-miR171c	202	402	561	162	158
ppe-miR171b	202	402	561	162	158
ssl-miR171b	202	402	561	162	158
vvi-miR171f	202	402	561	162	158
lja-miR1511-3p	12708	10343	28977	6523	8375
htu-miR171a	21	50	99	36	17
fve-miR167d	1734	2867	4223	1487	1553
lus-miR167a	1609	2734	4204	1417	1469
vvi-miR167c	1609	2734	4204	1417	1469
bna-miR167d	1547	2691	4152	1384	1420
fve-miR167a	1547	2691	4152	1384	1420
fve-miR167b	1547	2691	4152	1384	1420
fve-miR167c	1547	2691	4152	1384	1420
gma-miR167l	1547	2691	4152	1384	1420
lja-miR167a	1547	2691	4152	1384	1420
lja-miR167b	1547	2691	4152	1384	1420
lja-miR167c	1547	2691	4152	1384	1420
mes-miR167b	1547	2691	4152	1384	1420
ptc-miR390d-3p	69	72	127	26	49
sly-miR390a-3p	69	72	127	26	49
cme-miR166g	322	277	935	199	221
csi-miR166c-3p	322	277	935	199	221
gma-miR166p	322	277	935	199	221
gma-miR166q	322	277	935	199	221
gma-miR166r	322	277	935	199	221
gma-miR166s	322	277	935	199	221
gma-miR166t	322	277	935	199	221
sbi-miR166a	322	277	935	199	221
sbi-miR166b	322	277	935	199	221
sbi-miR166c	322	277	935	199	221
sbi-miR166d	322	277	935	199	221
sbi-miR166h	322	277	935	199	221
sbi-miR166i	322	277	935	199	221

sbi-miR166j	322	277	935	199	221
tcc-miR166b	322	277	935	199	221
zma-miR166b-3p	322	277	935	199	221
zma-miR166c-3p	322	277	935	199	221
zma-miR166d-3p	322	277	935	199	221
zma-miR166e	322	277	935	199	221
zma-miR166f	322	277	935	199	221
zma-miR166g-3p	322	277	935	199	221
zma-miR166h-3p	322	277	935	199	221
zma-miR166i-3p	322	277	935	199	221
eun-miR167b-3p	464	825	474	344	315
csi-miR167c-3p	2180	2342	4079	1257	1598
ppt-miR390c-5p	244	380	768	230	183
csi-miR390b-5p	244	380	767	230	183
gma-miR390e	244	380	767	230	183
eca-miR-378	53	77	105	70	35
mml-miR-378a	53	77	105	70	35
mmu-miR-378a-3p	53	77	105	70	35
ptr-miR-378a	53	77	105	70	35
rno-miR-378a-3p	53	77	105	70	35
aof-miR167b	4141	6388	13239	3318	3696
ata-miR167b-5p	4141	6388	13239	3318	3696
ata-miR167d-5p	4141	6388	13239	3318	3696
bdi-miR167c-5p	4141	6388	13239	3318	3696
bdi-miR167d-5p	4141	6388	13239	3318	3696
bdi-miR167e-5p	4141	6388	13239	3318	3696
bdi-miR167g	4141	6388	13239	3318	3696
ccl-miR167a	4141	6388	13239	3318	3696
ccl-miR167b	4141	6388	13239	3318	3696
cpa-miR167d	4141	6388	13239	3318	3696
ctr-miR167	4141	6388	13239	3318	3696
eun-miR167a-5p	4141	6388	13239	3318	3696
gma-miR167g	4141	6388	13239	3318	3696
mes-miR167d	4141	6388	13239	3318	3696
mes-miR167e	4141	6388	13239	3318	3696
mes-miR167f	4141	6388	13239	3318	3696
ppe-miR167c	4141	6388	13239	3318	3696
vca-miR167a-5p	4141	6388	13239	3318	3696
vca-miR167b-5p	4141	6388	13239	3318	3696
cpa-miR166d	2329	1741	8028	1495	1533
gma-miR166j-3p	2329	1741	8028	1495	1533
mes-miR160h	8719	7677	23410	5160	4684
crt-miR166a	2333	1741	8038	1495	1535

mes-miR166h	2333	1741	8038	1495	1535
gma-miR390a-3p	3229	3523	12001	2369	3052
gma-miR390c	3229	3523	12001	2369	3052
mes-miR390	3229	3523	12001	2369	3052
aly-miR390a-3p	3489	3760	12662	2457	3259
ath-miR390a-3p	3489	3760	12662	2457	3259
cas-miR390a-3p	3489	3760	12662	2457	3259
csi-miR390a-3p	3489	3760	12662	2457	3259
lja-miR390a-3p	3489	3760	12662	2457	3259
lja-miR390b-3p	3489	3760	12662	2457	3259
sly-miR390b-3p	3489	3760	12662	2457	3259
aly-miR160a-5p	8586	7490	23233	5057	4547
aly-miR160b-5p	8586	7490	23233	5057	4547
aly-miR160c-5p	8586	7490	23233	5057	4547
aof-miR160c	8586	7490	23233	5057	4547
aqc-miR160b	8586	7490	23233	5057	4547
ata-miR160a-5p	8586	7490	23233	5057	4547
ata-miR160b-5p	8586	7490	23233	5057	4547
ata-miR160c-5p	8586	7490	23233	5057	4547
ath-miR160a-5p	8586	7490	23233	5057	4547
ath-miR160b	8586	7490	23233	5057	4547
ath-miR160c-5p	8586	7490	23233	5057	4547
atr-miR160	8586	7490	23233	5057	4547
bdi-miR160a-5p	8586	7490	23233	5057	4547
bdi-miR160b-5p	8586	7490	23233	5057	4547
bdi-miR160c-5p	8586	7490	23233	5057	4547
bdi-miR160d-5p	8586	7490	23233	5057	4547
bna-miR160a	8586	7490	23233	5057	4547
bna-miR160b	8586	7490	23233	5057	4547
bna-miR160c	8586	7490	23233	5057	4547
bna-miR160d	8586	7490	23233	5057	4547
bra-miR160a-5p	8586	7490	23233	5057	4547
cca-miR160b	8586	7490	23233	5057	4547
cme-miR160a	8586	7490	23233	5057	4547
cme-miR160b	8586	7490	23233	5057	4547
cme-miR160c	8586	7490	23233	5057	4547
cpa-miR160a	8586	7490	23233	5057	4547
cpa-miR160b	8586	7490	23233	5057	4547
cpa-miR160c-5p	8586	7490	23233	5057	4547
cpa-miR160e	8586	7490	23233	5057	4547
cpa-miR160f-5p	8586	7490	23233	5057	4547
eun-miR160-5p	8586	7490	23233	5057	4547
far-miR160	8586	7490	23233	5057	4547

fve-miR160a	8586	7490	23233	5057	4547
fve-miR160b	8586	7490	23233	5057	4547
gma-miR160a-5p	8586	7490	23233	5057	4547
gma-miR160f	8586	7490	23233	5057	4547
lus-miR160a	8586	7490	23233	5057	4547
lus-miR160b	8586	7490	23233	5057	4547
lus-miR160d	8586	7490	23233	5057	4547
lus-miR160e	8586	7490	23233	5057	4547
lus-miR160f	8586	7490	23233	5057	4547
lus-miR160h	8586	7490	23233	5057	4547
lus-miR160i	8586	7490	23233	5057	4547
lus-miR160j	8586	7490	23233	5057	4547
mdm-miR160a	8586	7490	23233	5057	4547
mdm-miR160b	8586	7490	23233	5057	4547
mdm-miR160c	8586	7490	23233	5057	4547
mdm-miR160d	8586	7490	23233	5057	4547
mdm-miR160e	8586	7490	23233	5057	4547
mes-miR160a	8586	7490	23233	5057	4547
mes-miR160b	8586	7490	23233	5057	4547
mes-miR160d	8586	7490	23233	5057	4547
mtr-miR160a	8586	7490	23233	5057	4547
mtr-miR160b	8586	7490	23233	5057	4547
mtr-miR160d	8586	7490	23233	5057	4547
mtr-miR160e	8586	7490	23233	5057	4547
nta-miR160a	8586	7490	23233	5057	4547
nta-miR160b	8586	7490	23233	5057	4547
nta-miR160c	8586	7490	23233	5057	4547
osa-miR160a-5p	8586	7490	23233	5057	4547
osa-miR160b-5p	8586	7490	23233	5057	4547
osa-miR160c-5p	8586	7490	23233	5057	4547
osa-miR160d-5p	8586	7490	23233	5057	4547
pab-miR160a	8586	7490	23233	5057	4547
pab-miR160b	8586	7490	23233	5057	4547
pab-miR160d	8586	7490	23233	5057	4547
ppe-miR160a	8586	7490	23233	5057	4547
ppe-miR160b	8586	7490	23233	5057	4547
ppt-miR160a	8586	7490	23233	5057	4547
ppt-miR160e	8586	7490	23233	5057	4547
ppt-miR160f	8586	7490	23233	5057	4547
ptc-miR160a	8586	7490	23233	5057	4547
ptc-miR160b-5p	8586	7490	23233	5057	4547
ptc-miR160c-5p	8586	7490	23233	5057	4547
ptc-miR160d	8586	7490	23233	5057	4547

rco-miR160a	8586	7490	23233	5057	4547
rco-miR160b	8586	7490	23233	5057	4547
sbi-miR160a	8586	7490	23233	5057	4547
sbi-miR160b	8586	7490	23233	5057	4547
sbi-miR160c	8586	7490	23233	5057	4547
sbi-miR160d	8586	7490	23233	5057	4547
sbi-miR160e	8586	7490	23233	5057	4547
sly-miR160a	8586	7490	23233	5057	4547
smo-miR160a	8586	7490	23233	5057	4547
smo-miR160b	8586	7490	23233	5057	4547
stu-miR160a-5p	8586	7490	23233	5057	4547
stu-miR160b	8586	7490	23233	5057	4547
tae-miR160	8586	7490	23233	5057	4547
tcc-miR160b	8586	7490	23233	5057	4547
ttu-miR160	8586	7490	23233	5057	4547
vun-miR160	8586	7490	23233	5057	4547
vvi-miR160c	8586	7490	23233	5057	4547
vvi-miR160d	8586	7490	23233	5057	4547
vvi-miR160e	8586	7490	23233	5057	4547
zma-miR160a-5p	8586	7490	23233	5057	4547
zma-miR160b-5p	8586	7490	23233	5057	4547
zma-miR160c-5p	8586	7490	23233	5057	4547
zma-miR160d-5p	8586	7490	23233	5057	4547
zma-miR160e	8586	7490	23233	5057	4547
zma-miR160g-5p	8586	7490	23233	5057	4547
mes-miR160g	8613	7512	23314	5065	4566
cas-miR166e	450	435	1699	337	287
csi-miR166f-3p	450	435	1699	337	287
osa-miR166m	450	435	1699	337	287
crt-miR166b	450	439	1702	337	288
ata-miR167f-5p	3638	5641	12623	2961	3288
tae-miR167c-5p	3638	5641	12623	2961	3288
aof-miR167c	3574	5613	12595	2914	3256
atr-miR167	3574	5613	12595	2914	3256
cme-miR167d	3574	5613	12595	2914	3256
cme-miR167f	3574	5613	12595	2914	3256
csi-miR167a-5p	3574	5613	12595	2914	3256
csi-miR167c-5p	3574	5613	12595	2914	3256
dpr-miR167c	3574	5613	12595	2914	3256
gma-miR167c	3574	5613	12595	2914	3256
gma-miR167j	3574	5613	12595	2914	3256
gso-miR167a	3574	5613	12595	2914	3256
lja-miR167	3574	5613	12595	2914	3256

lus-miR167f	3574	5613	12595	2914	3256
lus-miR167g	3574	5613	12595	2914	3256
lus-miR167i	3574	5613	12595	2914	3256
mes-miR167a	3574	5613	12595	2914	3256
mtr-miR167b-5p	3574	5613	12595	2914	3256
osa-miR167d-5p	3574	5613	12595	2914	3256
osa-miR167e-5p	3574	5613	12595	2914	3256
osa-miR167f	3574	5613	12595	2914	3256
osa-miR167g	3574	5613	12595	2914	3256
osa-miR167h-5p	3574	5613	12595	2914	3256
osa-miR167i-5p	3574	5613	12595	2914	3256
osa-miR167j	3574	5613	12595	2914	3256
ptc-miR167e	3574	5613	12595	2914	3256
sbi-miR167c	3574	5613	12595	2914	3256
sbi-miR167d	3574	5613	12595	2914	3256
sbi-miR167e	3574	5613	12595	2914	3256
sbi-miR167f	3574	5613	12595	2914	3256
sbi-miR167g	3574	5613	12595	2914	3256
sbi-miR167h	3574	5613	12595	2914	3256
sof-miR167a	3574	5613	12595	2914	3256
sof-miR167b	3574	5613	12595	2914	3256
ssp-miR167b	3574	5613	12595	2914	3256
vvi-miR167a	3574	5613	12595	2914	3256
zma-miR167e-5p	3574	5613	12595	2914	3256
zma-miR167f-5p	3574	5613	12595	2914	3256
zma-miR167g-5p	3574	5613	12595	2914	3256
zma-miR167h-5p	3574	5613	12595	2914	3256
zma-miR167i-5p	3574	5613	12595	2914	3256
zma-miR167j-5p	3574	5613	12595	2914	3256
aly-miR166g-5p	700	800	69	148	435
cas-miR166f-5p	700	800	69	148	435
csi-miR166b-5p	700	800	69	148	435
gma-miR166h-5p	700	800	69	148	435
gma-miR166j-5p	700	800	69	148	435
stu-miR166c-5p	700	800	69	148	435
aly-miR390a-5p	1490	1960	3675	965	866
aly-miR390b-5p	1490	1960	3675	965	866
aof-miR390	1490	1960	3675	965	866
ata-miR390-5p	1490	1960	3675	965	866
ath-miR390a-5p	1490	1960	3675	965	866
ath-miR390b-5p	1490	1960	3675	965	866
atr-miR390.2	1490	1960	3675	965	866
bdi-miR390a-5p	1490	1960	3675	965	866

bna-miR390a	1490	1960	3675	965	866
bna-miR390b	1490	1960	3675	965	866
bna-miR390c	1490	1960	3675	965	866
bra-miR390-5p	1490	1960	3675	965	866
cas-miR390a-5p	1490	1960	3675	965	866
cas-miR390b	1490	1960	3675	965	866
cme-miR390a	1490	1960	3675	965	866
cme-miR390b	1490	1960	3675	965	866
cme-miR390c	1490	1960	3675	965	866
cme-miR390d	1490	1960	3675	965	866
cpa-miR390a	1490	1960	3675	965	866
cpa-miR390b	1490	1960	3675	965	866
csi-miR390a-5p	1490	1960	3675	965	866
fve-miR390a	1490	1960	3675	965	866
fve-miR390b	1490	1960	3675	965	866
ghr-miR390a	1490	1960	3675	965	866
ghr-miR390b	1490	1960	3675	965	866
ghr-miR390c	1490	1960	3675	965	866
gma-miR390a-5p	1490	1960	3675	965	866
gma-miR390f	1490	1960	3675	965	866
gma-miR390g	1490	1960	3675	965	866
hex-miR390a	1490	1960	3675	965	866
hex-miR390b	1490	1960	3675	965	866
lja-miR390a-5p	1490	1960	3675	965	866
lja-miR390b-5p	1490	1960	3675	965	866
lus-miR390a	1490	1960	3675	965	866
lus-miR390b	1490	1960	3675	965	866
lus-miR390c	1490	1960	3675	965	866
lus-miR390d	1490	1960	3675	965	866
mdm-miR390a	1490	1960	3675	965	866
mdm-miR390b	1490	1960	3675	965	866
mdm-miR390c	1490	1960	3675	965	866
mdm-miR390d	1490	1960	3675	965	866
mdm-miR390e	1490	1960	3675	965	866
mdm-miR390f	1490	1960	3675	965	866
mes-miR390b	1490	1960	3675	965	866
mtr-miR390	1490	1960	3675	965	866
nta-miR390b	1490	1960	3675	965	866
nta-miR390c	1490	1960	3675	965	866
osa-miR390-5p	1490	1960	3675	965	866
pab-miR390a	1490	1960	3675	965	866
pab-miR390b	1490	1960	3675	965	866
ppe-miR390	1490	1960	3675	965	866

ppt-miR390a	1490	1960	3675	965	866
ppt-miR390b	1490	1960	3675	965	866
ptc-miR390a	1490	1960	3675	965	866
ptc-miR390b	1490	1960	3675	965	866
ptc-miR390c	1490	1960	3675	965	866
ptc-miR390d-5p	1490	1960	3675	965	866
rco-miR390a	1490	1960	3675	965	866
rco-miR390b	1490	1960	3675	965	866
sbi-miR390	1490	1960	3675	965	866
sly-miR390b-5p	1490	1960	3675	965	866
tcc-miR390a	1490	1960	3675	965	866
tcc-miR390b	1490	1960	3675	965	866
vvi-miR390	1490	1960	3675	965	866
zma-miR390a-5p	1490	1960	3675	965	866
zma-miR390b-5p	1490	1960	3675	965	866
csi-miR160a-5p	35	24	336	24	15
pab-miR166j	76	50	1329	38	57
mes-miR166i	15	10	174	5	15
gma-miR166m	69	36	1299	29	44
mtr-miR166e-5p	206	672	52	93	201
osa-miR166h-5p	206	672	52	93	201
zma-miR166m-5p	206	672	52	93	201
aly-miR168a-3p	434	484	5046	334	647
ath-miR168a-3p	434	484	5046	334	647
bra-miR168b-3p	434	484	5046	334	647
bra-miR168c-3p	434	484	5046	334	647
cas-miR168	434	484	5046	334	647
csi-miR168-3p	434	484	5046	334	647
fve-miR168-3p	434	484	5046	334	647
mtr-miR168c-3p	434	484	5046	334	647
ptc-miR168a-3p	434	484	5046	334	647
ptc-miR168b-3p	434	484	5046	334	647
sly-miR168b-3p	434	484	5046	334	647
lja-miR168-3p	436	488	5067	335	648
aof-miR166c	5	6	1623	3	11
ath-miR165a-3p	5	6	1623	3	11
ath-miR165b	5	6	1623	3	11
bna-miR166f	5	6	1623	3	11
cas-miR165a	5	6	1623	3	11
lus-miR166b	5	6	1623	3	11
gmo-miR-451-5p	12	192	761	11	7
cfa-miR-375	0	0	477	0	0
cpo-miR-375-3p	0	0	477	0	0

dno-miR-375-3p	0	0	477	0	0
ggo-miR-375	0	0	477	0	0
hsa-miR-375-3p	0	0	477	0	0
mml-miR-375	0	0	477	0	0
mmu-miR-375-3p	0	0	477	0	0
ocu-miR-375-3p	0	0	477	0	0
pal-miR-375-3p	0	0	477	0	0
ppy-miR-375	0	0	477	0	0
ptr-miR-375	0	0	477	0	0
rno-miR-375-3p	0	0	477	0	0
ssc-miR-375	0	0	477	0	0
bta-miR-375	0	0	486	0	0
efu-miR-375	0	0	486	0	0
mdo-miR-375	0	0	486	0	0
aae-miR-184	1	352	0	0	1
abu-miR-184a	1	352	0	0	1
ame-miR-184-3p	1	352	0	0	1
api-miR-184a	1	352	0	0	1
bbe-miR-184-3p	1	352	0	0	1
bdo-miR-184	1	352	0	0	1
bmo-miR-184-3p	1	352	0	0	1
ccr-miR-184	1	352	0	0	1
cin-miR-184	1	352	0	0	1
cqu-miR-184	1	352	0	0	1
cte-miR-184a	1	352	0	0	1
dan-miR-184-3p	1	352	0	0	1
der-miR-184-3p	1	352	0	0	1
dgr-miR-184-3p	1	352	0	0	1
dme-miR-184-3p	1	352	0	0	1
dmo-miR-184-3p	1	352	0	0	1
dpe-miR-184-3p	1	352	0	0	1
dps-miR-184	1	352	0	0	1
dre-miR-184	1	352	0	0	1
dse-miR-184-3p	1	352	0	0	1
dsi-miR-184-3p	1	352	0	0	1
dvi-miR-184-3p	1	352	0	0	1
dwi-miR-184-3p	1	352	0	0	1
dya-miR-184-3p	1	352	0	0	1
hme-miR-184	1	352	0	0	1
ipu-miR-184	1	352	0	0	1
isc-miR-184	1	352	0	0	1
lgi-miR-184	1	352	0	0	1
lva-miR-184-3p	1	352	0	0	1

mle-miR-184-3p	1	352	0	0	1
mse-miR-184	1	352	0	0	1
mze-miR-184a	1	352	0	0	1
nbr-miR-184a	1	352	0	0	1
ngi-miR-184	1	352	0	0	1
nlo-miR-184	1	352	0	0	1
nvi-miR-184	1	352	0	0	1
oni-miR-184a	1	352	0	0	1
pca-miR-184-3p	1	352	0	0	1
pmi-miR-184-3p	1	352	0	0	1
pny-miR-184a	1	352	0	0	1
pte-miR-184-3p	1	352	0	0	1
sko-miR-184-3p	1	352	0	0	1
spu-miR-184	1	352	0	0	1
tca-miR-184-3p	1	352	0	0	1
tcf-miR-184-3p	1	352	0	0	1
tur-miR-184-3p	1	352	0	0	1
aae-miR-2940-3p	0	673	2	0	0

X42_3	norm.H42_1	norm.H42_2	norm.H42_3	norm.X42_1	norm.X42_2	norm.X42_3
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1333	68	66	1485	40	93	629
139	14	13	194	5	24	66
1135	62	48	1451	31	72	535
80	186	891	58	98	327	38
80	186	891	58	98	327	38
80	186	891	58	98	327	38
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2726	391	642	5637	354	1052	1286
2737	393	647	5661	355	1054	1291
1235	5	8	1813	3	18	583
1235	5	8	1813	3	18	583
1235	5	8	1813	3	18	583
1235	5	8	1813	3	18	583
1235	5	8	1813	3	18	583
1235	5	8	1813	3	18	583
330	11	255	850	12	11	156
146	0	0	533	0	0	69
146	0	0	533	0	0	69

146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
146	0	0	533	0	0	69
147	0	0	543	0	0	69
147	0	0	543	0	0	69
147	0	0	543	0	0	69
14	1	467	0	0	2	7
14	1	467	0	0	2	7
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14	1	467	0	0	2	7
14	1	467	0	0	2	7

14	1	467	0	0	2	7
14	1	467	0	0	2	7
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14	1	467	0	0	2	7
14	1	467	0	0	2	7
14	1	467	0	0	2	7
14	1	467	0	0	2	7
14	1	467	0	0	2	7
14	1	467	0	0	2	7
14	1	467	0	0	2	7
7	0	893	2	0	0	3

baseMean	H2O	Xcf	FoldChange	log2FoldChan	stat	pvalue
31.3	5	58	1.023	3.5360529	2.311	0.02084639
31.3	5	58	1.023	3.5360529	2.311	0.02084639
31.3	5	58	1.023	3.5360529	2.311	0.02084639
31.3	5	58	1.023	3.5360529	2.311	0.02084639
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937

298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
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298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
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298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
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298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
298.79	474	124	0.99	-1.9345469	-2.058	0.03956937
300.18	476	124	0.99	-1.9406215	-2.069	0.03858368
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
747.37	1314	181	0.985	-2.8599037	-2.221	0.02635303
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
456.22	804	109	0.988	-2.8828674	-2.082	0.03737477
437.94	0	876	1.567	#DIV/0!	2.867	NA
403.97	0	808	1.51	#DIV/0!	2.837	NA
171.65	0	343	1.186	#DIV/0!	2.521	NA
141.75	0	283	3691349.76	#DIV/0!	5.902	NA
125.71	0	251	4829582.72	#DIV/0!	6.007	NA
125.08	0	250	4228034	#DIV/0!	5.955	NA
101.92	0	203	1.108	#DIV/0!	2.328	NA
86.64	0	173	3621108.59	#DIV/0!	5.894	NA
31.13	0	62	1416934	#DIV/0!	5.529	NA
30.9	0	62	1402888.26	#DIV/0!	5.525	NA
26.6	0	53	1.276	#DIV/0!	2.901	NA
24.4	0	48	1.229	#DIV/0!	2.845	NA
768.48	1	1536	1.526	10.5849625	2.851	NA
1282.5	2	2563	1.369	10.3236178	2.758	NA
2117.84	4	4232	1.273	10.0471239	2.67	NA
506.52	1	1012	1.311	9.98299357	2.696	NA

364.3	1	728	1.213	9.50779464	2.572	NA
274.52	1	548	1.156	9.09803208	2.467	NA
103.39	1	206	1.043	7.68650053	1.971	NA
146.88	7	287	1.685	5.357552	3.378	NA
34.8	2	68	1.121	5.08746284	2.828	NA
34.8	2	68	1.121	5.08746284	2.828	NA
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34.8	2	68	1.121	5.08746284	2.828	NA
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34.8	2	68	1.121	5.08746284	2.828	NA
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34.8	2	68	1.121	5.08746284	2.828	NA
34.8	2	68	1.121	5.08746284	2.828	NA
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52.09	5	99	1.085	4.30742853	2.804	NA
40.97	4	78	1.08	4.28540222	2.774	NA
137.78	17	259	1.032	3.92934545	2.42	NA
137.7	17	258	1.032	3.92376441	2.42	NA
137.7	17	258	1.032	3.92376441	2.42	NA
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137.7	17	258	1.032	3.92376441	2.42	NA
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137.7	17	258	1.032	3.92376441	2.42	NA
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137.7	17	258	1.032	3.92376441	2.42	NA
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137.7	17	258	1.032	3.92376441	2.42	NA

137.7	17	258	1.032	3.92376441	2.42	NA
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137.7	17	258	1.032	3.92376441	2.42	NA
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138.36	18	259	1.031	3.84688329	2.4	NA
152.59	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
152.51	22	283	1.033	3.68522662	2.488	NA
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42.45	14	70	1.007	2.32192809	1.802	0.07154974
185.39	62	309	1.008	2.31726672	1.839	0.06584198
184.76	62	308	1.008	2.31259023	1.836	0.0663934
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80.35	30	131	1.008	2.12653241	1.838	NA
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80.35	30	131	1.008	2.12653241	1.838	NA
62.97	24	102	1.004	2.08746284	1.309	0.1906123
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62.97	24	102	1.004	2.08746284	1.309	0.1906123
62.97	24	102	1.004	2.08746284	1.309	0.1906123
62.97	24	102	1.004	2.08746284	1.309	0.1906123
62.97	24	102	1.004	2.08746284	1.309	0.1906123
62.97	24	102	1.004	2.08746284	1.309	0.1906123
62.97	24	102	1.004	2.08746284	1.309	0.1906123
174.65	72	277	1.007	1.94381716	1.749	NA
174.65	72	277	1.007	1.94381716	1.749	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
173.75	72	275	1.007	1.93336281	1.738	NA
332.52	153	512	1.006	1.74261216	1.558	0.11912555

332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
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332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
332.52	153	512	1.006	1.74261216	1.558	0.11912555
324.22	153	496	1.007	1.69680847	1.736	0.08257385
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435

322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
322.17	152	492	1.007	1.69458699	1.734	0.08297435
268.79	130	408	1.003	1.65005753	1.052	NA
268.79	130	408	1.003	1.65005753	1.052	NA
268.79	130	408	1.003	1.65005753	1.052	NA
268.79	130	408	1.003	1.65005753	1.052	NA
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677

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427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
427.67	209	647	1.006	1.63026277	1.665	0.09598677
429.78	210	649	1.006	1.62782915	1.66	0.0969
271.66	134	409	1.003	1.60986784	1.04	NA
271.66	134	409	1.003	1.60986784	1.04	NA
239.51	122	357	1.003	1.54904293	0.982	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
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239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
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239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA

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239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
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239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.1	122	356	1.003	1.54499609	0.979	NA
239.78	123	357	1.003	1.53726576	0.975	NA
71.94	38	106	1.005	1.47999294	1.516	0.12940383

71.94	38	106	1.005	1.47999294	1.516	0.12940383
71.94	38	106	1.005	1.47999294	1.516	0.12940383
327.38	184	470	1.004	1.35295499	1.251	0.21108201
327.38	184	470	1.004	1.35295499	1.251	0.21108201
311.89	176	448	1.004	1.3479233	1.249	0.21180156
311.89	176	448	1.004	1.3479233	1.249	0.21180156
311.89	176	448	1.004	1.3479233	1.249	0.21180156
311.89	176	448	1.004	1.3479233	1.249	0.21180156
275.68	158	393	1.004	1.31460475	1.205	0.22830595
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
275.6	158	393	1.004	1.31460475	1.204	0.22849876
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097

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260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
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260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
260.91	151	371	1.004	1.29687064	1.192	0.23328097
81.33	48	115	1.003	1.26052755	1.05	0.29377339
81.33	48	115	1.003	1.26052755	1.05	0.29377339
81.33	48	115	1.003	1.26052755	1.05	0.29377339
81.33	48	115	1.003	1.26052755	1.05	0.29377339
81.33	48	115	1.003	1.26052755	1.05	0.29377339
81.33	48	115	1.003	1.26052755	1.05	0.29377339
81.33	48	115	1.003	1.26052755	1.05	0.29377339
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64.64	41	88	1.002	1.10187961	0.788	0.43061147
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3625.83	2373	4878	1.004	1.03957766	1.109	0.26755602
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3596.89	2357	4837	1.004	1.03716078	1.106	0.26866729
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374.21	246	503	1.003	1.03190008	0.99	0.32194986
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5686.85	3748	7625	1.003	1.02461638	0.895	0.37066403
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606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578

606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
606.25	426	786	1.004	0.88367588	1.032	0.30225578
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
50.96	36	65	1.003	0.85244281	0.919	0.35816764
259.42	187	332	1.002	0.82814497	0.76	0.4471115
91.75	67	117	1.003	0.80427553	0.816	0.41436939
90.75	67	114	1.002	0.76680082	0.779	0.4360549
90.75	67	114	1.002	0.76680082	0.779	0.4360549
90.75	67	114	1.002	0.76680082	0.779	0.4360549
48.29	36	61	1.001	0.76081234	0.561	NA
48.29	36	61	1.001	0.76081234	0.561	NA
52.03	39	66	1.002	0.7589919	0.759	0.44794427
52.03	39	66	1.002	0.7589919	0.759	0.44794427
52.03	39	66	1.002	0.7589919	0.759	0.44794427
52.03	39	66	1.002	0.7589919	0.759	0.44794427
52.03	39	66	1.002	0.7589919	0.759	0.44794427
91.19	68	115	1.002	0.75802721	0.78	0.43556478
91.35	68	115	1.002	0.75802721	0.772	0.43997876
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806

163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
163.67	122	205	1.002	0.74874276	0.766	0.44342806
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
89.27	67	112	1.002	0.74126573	0.763	0.44559638
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358

288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
288.94	218	360	1.003	0.72366877	0.867	0.38601358
52.48	40	65	1.002	0.70043972	0.566	NA
52.19	40	64	1.002	0.67807191	0.738	0.46037501
52.19	40	64	1.002	0.67807191	0.738	0.46037501
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989

76.76	59	94	1.003	0.6719458	0.778	0.43664989
76.76	59	94	1.003	0.6719458	0.778	0.43664989
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
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43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
43.71	34	53	1.002	0.64045761	0.617	0.53710245
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146

54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
54.95	43	67	1.002	0.63982444	0.58	0.56203146
493.51	387	600	1.003	0.63262893	0.768	0.44251288
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
69.58	55	84	1.002	0.61095771	0.64	0.52222472
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759

72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.4	57	87	1.002	0.61005348	0.691	0.48947759
72.06	57	87	1.002	0.61005348	0.562	0.5739466
72.06	57	87	1.002	0.61005348	0.562	0.5739466
72.06	57	87	1.002	0.61005348	0.562	0.5739466
72.06	57	87	1.002	0.61005348	0.562	0.5739466
72.06	57	87	1.002	0.61005348	0.562	0.5739466
72.06	57	87	1.002	0.61005348	0.562	0.5739466
72.06	57	87	1.002	0.61005348	0.562	0.5739466
468.33	371	566	1.003	0.60938287	0.733	0.46350316
468.33	371	566	1.003	0.60938287	0.733	0.46350316
134.08	106	161	1.002	0.60299642	0.64	0.52193757
134.08	106	161	1.002	0.60299642	0.64	0.52193757
72.9	58	88	1.002	0.60145062	0.696	0.48653258
1028.87	819	1239	1.002	0.59724083	0.578	0.56345612
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484

1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
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1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
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1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
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1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
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1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
1028.35	819	1238	1.002	0.59607596	0.577	0.56398484
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450.43	359	542	1.003	0.59430901	0.714	0.4749424
450.43	359	542	1.003	0.59430901	0.714	0.4749424
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450.43	359	542	1.003	0.59430901	0.714	0.4749424
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450.43	359	542	1.003	0.59430901	0.714	0.4749424

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450.43	359	542	1.003	0.59430901	0.714	0.4749424
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450.43	359	542	1.003	0.59430901	0.714	0.4749424
450.43	359	542	1.003	0.59430901	0.714	0.4749424
450.43	359	542	1.003	0.59430901	0.714	0.4749424
450.43	359	542	1.003	0.59430901	0.714	0.4749424
548.46	438	659	1.003	0.5893476	0.72	0.47152304
548.28	438	659	1.003	0.5893476	0.721	0.47064478
548.28	438	659	1.003	0.5893476	0.721	0.47064478
548.28	438	659	1.003	0.5893476	0.721	0.47064478
548.28	438	659	1.003	0.5893476	0.721	0.47064478
548.28	438	659	1.003	0.5893476	0.721	0.47064478
548.28	438	659	1.003	0.5893476	0.721	0.47064478
548.28	438	659	1.003	0.5893476	0.721	0.47064478
548.28	438	659	1.003	0.5893476	0.721	0.47064478
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548.28	438	659	1.003	0.5893476	0.721	0.47064478
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548.28	438	659	1.003	0.5893476	0.721	0.47064478
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548.28	438	659	1.003	0.5893476	0.721	0.47064478

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548.28	438	659	1.003	0.5893476	0.721	0.47064478
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67.72	54	81	1.001	0.5849625	0.437	0.66180834
67.72	54	81	1.001	0.5849625	0.437	0.66180834
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67.72	54	81	1.001	0.5849625	0.437	0.66180834
67.72	54	81	1.001	0.5849625	0.437	0.66180834
67.72	54	81	1.001	0.5849625	0.437	0.66180834
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67.72	54	81	1.001	0.5849625	0.437	0.66180834
67.72	54	81	1.001	0.5849625	0.437	0.66180834

67.72	54	81	1.001	0.5849625	0.437	0.66180834
67.72	54	81	1.001	0.5849625	0.437	0.66180834
68.75	55	82	1.001	0.57619229	0.433	0.6649149
125.01	101	149	1.002	0.56095704	0.61	0.5419706
125.01	101	149	1.002	0.56095704	0.61	0.5419706
125.01	101	149	1.002	0.56095704	0.61	0.5419706
125.01	101	149	1.002	0.56095704	0.61	0.5419706
125.01	101	149	1.002	0.56095704	0.61	0.5419706
125.01	101	149	1.002	0.56095704	0.61	0.5419706
125.01	101	149	1.002	0.56095704	0.61	0.5419706
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125.01	101	149	1.002	0.56095704	0.61	0.5419706
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125.01	101	149	1.002	0.56095704	0.61	0.5419706
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
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54.47	45	64	1.002	0.5081469	0.545	0.58546446
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54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
54.47	45	64	1.002	0.5081469	0.545	0.58546446
506.22	424	588	1.002	0.47175189	0.61	0.54159641
506.22	424	588	1.002	0.47175189	0.61	0.54159641
506.22	424	588	1.002	0.47175189	0.61	0.54159641

138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
138.11	117	160	1.001	0.45156338	0.46	0.64521595
465.43	394	537	1.002	0.44672646	0.573	0.56640241
465.43	394	537	1.002	0.44672646	0.573	0.56640241
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465.43	394	537	1.002	0.44672646	0.573	0.56640241
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465.9	395	537	1.002	0.44306943	0.573	0.56661469
465.9	395	537	1.002	0.44306943	0.573	0.56661469
465.9	395	537	1.002	0.44306943	0.573	0.56661469
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465.9	395	537	1.002	0.44306943	0.573	0.56661469
244.38	211	278	1.001	0.39784188	0.44	0.65978995

244.38	211	278	1.001	0.39784188	0.44	0.65978995
99.49	86	113	1.001	0.39391421	0.436	0.66254595
91.19	79	103	1.001	0.38271978	0.401	0.68863385
91.19	79	103	1.001	0.38271978	0.401	0.68863385
91.19	79	103	1.001	0.38271978	0.401	0.68863385
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91.19	79	103	1.001	0.38271978	0.401	0.68863385
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91.19	79	103	1.001	0.38271978	0.401	0.68863385
5884.56	5123	6647	1.001	0.37571446	0.363	0.71665988
4385.39	3827	4944	1.001	0.36946484	0.331	0.74060492
148.91	132	166	1.001	0.33064531	0.378	0.70579331
148.91	132	166	1.001	0.33064531	0.378	0.70579331
148.91	132	166	1.001	0.33064531	0.378	0.70579331
148.91	132	166	1.001	0.33064531	0.378	0.70579331
148.91	132	166	1.001	0.33064531	0.378	0.70579331
148.91	132	166	1.001	0.33064531	0.378	0.70579331
128.74	115	143	1.001	0.31438129	0.356	0.72163001
128.74	115	143	1.001	0.31438129	0.356	0.72163001
128.74	115	143	1.001	0.31438129	0.356	0.72163001
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128.74	115	143	1.001	0.31438129	0.356	0.72163001
128.74	115	143	1.001	0.31438129	0.356	0.72163001
128.74	115	143	1.001	0.31438129	0.356	0.72163001
150.56	135	166	1.001	0.29822383	0.349	0.727184
59.5	53	65	1.001	0.29444736	0.267	0.78983058
59.5	53	65	1.001	0.29444736	0.267	0.78983058
202.49	182	223	1.001	0.29310526	0.371	0.7103846
202.49	182	223	1.001	0.29310526	0.371	0.7103846
380.36	343	417	1.001	0.28183881	0.343	0.73148779
380.36	343	417	1.001	0.28183881	0.343	0.73148779
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380.01	343	417	1.001	0.28183881	0.343	0.73122458
145.09	131	159	1.001	0.27945995	0.206	0.83686919
148.47	135	161	1	0.25410128	0.19	0.84922835
3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
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3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
3509.51	3226	3793	1.001	0.23359293	0.306	0.75951581
279.49	257	302	1.001	0.23278019	0.25	0.80277995
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291.05	268	314	1.001	0.22853156	0.246	0.80573394
171.6	158	185	1	0.22760071	0.164	0.86972278
171.6	158	185	1	0.22760071	0.164	0.86972278
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171.6	158	185	1	0.22760071	0.164	0.86972278
172.25	159	186	1	0.22627586	0.167	0.86753177
197.57	183	212	1.001	0.21222062	0.264	0.7918615
197.57	183	212	1.001	0.21222062	0.264	0.7918615
186.85	173	200	1.001	0.20922796	0.26	0.79454113
186.85	173	200	1.001	0.20922796	0.26	0.79454113
186.85	173	200	1.001	0.20922796	0.26	0.79454113
186.85	173	200	1.001	0.20922796	0.26	0.79454113
186.85	173	200	1.001	0.20922796	0.26	0.79454113
186.85	173	200	1.001	0.20922796	0.26	0.79454113
186.85	173	200	1.001	0.20922796	0.26	0.79454113
186.85	173	200	1.001	0.20922796	0.26	0.79454113
327.25	304	350	1	0.2032836	0.163	0.87045425
318.09	296	340	1	0.19993757	0.164	0.86992485
533.46	497	570	1.001	0.19771607	0.223	0.82382762
533.46	497	570	1.001	0.19771607	0.223	0.82382762
305.55	285	326	1	0.19391005	0.153	0.8785945
305.55	285	326	1	0.19391005	0.153	0.8785945
305.55	285	326	1	0.19391005	0.153	0.8785945
305.1	285	325	1	0.1894778	0.15	0.8811123
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115.29	108	122	1.001	0.17584984	0.168	0.86626012
115.29	108	122	1.001	0.17584984	0.168	0.86626012
207.54	196	219	1.001	0.16007722	0.2	0.84177747
207.54	196	219	1.001	0.16007722	0.2	0.84177747
207.54	196	219	1.001	0.16007722	0.2	0.84177747
207.54	196	219	1.001	0.16007722	0.2	0.84177747
207.54	196	219	1.001	0.16007722	0.2	0.84177747
207.54	196	219	1.001	0.16007722	0.2	0.84177747
207.54	196	219	1.001	0.16007722	0.2	0.84177747
183.24	174	193	1	0.14951354	0.115	0.90880066
183.24	174	193	1	0.14951354	0.115	0.90880066
183.24	174	193	1	0.14951354	0.115	0.90880066
183.24	174	193	1	0.14951354	0.115	0.90880066
183.24	174	193	1	0.14951354	0.115	0.90880066
183.24	174	193	1	0.14951354	0.115	0.90880066
183.24	174	193	1	0.14951354	0.115	0.90880066

183.24	174	193	1	0.14951354	0.115	0.90880066
178.82	170	188	1.001	0.14519792	0.155	0.87666722
178.82	170	188	1.001	0.14519792	0.155	0.87666722
178.82	170	188	1.001	0.14519792	0.155	0.87666722
178.82	170	188	1.001	0.14519792	0.155	0.87666722
178.82	170	188	1.001	0.14519792	0.155	0.87666722
178.82	170	188	1.001	0.14519792	0.155	0.87666722
178.82	170	188	1.001	0.14519792	0.155	0.87666722
178.82	170	188	1.001	0.14519792	0.155	0.87666722
95.41	91	100	1	0.13606155	0.123	0.9020904
95.41	91	100	1	0.13606155	0.123	0.9020904
95.41	91	100	1	0.13606155	0.123	0.9020904
95.41	91	100	1	0.13606155	0.123	0.9020904
95.41	91	100	1	0.13606155	0.123	0.9020904
97.48	93	102	1.001	0.13326653	0.153	0.87801743
97.48	93	102	1.001	0.13326653	0.153	0.87801743
100.35	96	105	1	0.12928302	0.139	0.88976693
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
68.66	66	72	1	0.12553088	0.149	0.88183704
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
187.03	179	195	1	0.12351454	0.09	0.92816155
90.86	88	94	1	0.09515723	0.079	0.93668218
106.51	103	110	1	0.09485919	0.097	0.92234618
106.51	103	110	1	0.09485919	0.097	0.92234618

119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
119.17	116	123	1	0.08453351	0.101	0.91988506
121.76	118	125	1	0.08314124	0.103	0.91798369
110.33	107	113	1	0.07871198	0.095	0.92413182
110.33	107	113	1	0.07871198	0.095	0.92413182
256.62	250	264	1	0.07860983	0.082	0.93443419
291.88	285	299	1	0.06918357	0.092	0.92658997
56.08	55	57	1	0.0515303	0.046	0.96318627
461.71	454	470	1	0.04996846	0.062	0.95081656
461.71	454	470	1	0.04996846	0.062	0.95081656
461.71	454	470	1	0.04996846	0.062	0.95081656
461.71	454	470	1	0.04996846	0.062	0.95081656
63.99	63	65	1	0.04508789	0.025	0.97972935
63.99	63	65	1	0.04508789	0.025	0.97972935
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362

1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
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1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
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1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
1123962.24	1108777	1139147	1	0.03898469	0.037	0.97055362
19474.19	19244	19705	1	0.03415304	0.038	0.96979777
55.75	55	56	1	0.02599521	0.045	0.96400203
55.75	55	56	1	0.02599521	0.045	0.96400203
55.75	55	56	1	0.02599521	0.045	0.96400203
55.75	55	56	1	0.02599521	0.045	0.96400203
55.75	55	56	1	0.02599521	0.045	0.96400203
55.75	55	56	1	0.02599521	0.045	0.96400203
55.75	55	56	1	0.02599521	0.045	0.96400203
55.75	55	56	1	0.02599521	0.045	0.96400203
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645

37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
37566.59	37315	37818	1	0.01931738	0.02	0.98421645
6460.62	6419	6502	1	0.018535	0.021	0.98285815
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
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6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
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6433.82	6394	6473	1	0.01771576	0.021	0.98357156
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6433.82	6394	6473	1	0.01771576	0.021	0.98357156
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6433.82	6394	6473	1	0.01771576	0.021	0.98357156

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6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
6433.82	6394	6473	1	0.01771576	0.021	0.98357156
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6442.49	6403	6482	1	0.01769101	0.021	0.98339667
6442.49	6403	6482	1	0.01769101	0.021	0.98339667
6442.49	6403	6482	1	0.01769101	0.021	0.98339667
37699.49	37477	37922	1	0.01702958	0.017	0.98611562
43484.42	43461	43508	1	0.00155933	0.002	0.99873247
43484.42	43461	43508	1	0.00155933	0.002	0.99873247
43484.42	43461	43508	1	0.00155933	0.002	0.99873247
43484.42	43461	43508	1	0.00155933	0.002	0.99873247
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363.7	364	364	1	0	-0.003	0.9972818
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335.09	335	335	1	0	0	0.9996958
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335.09	335	335	1	0	0	0.9996958
335.09	335	335	1	0	0	0.9996958
247.64	249	247	1	-0.0116347	-0.012	0.99038722
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
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23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019

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23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
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23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
23635.07	23795	23475	1	-0.0195333	-0.021	0.98299019
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5299.88	5384	5216	1	-0.0457345	-0.05	0.96011256

5299.88	5384	5216	1	-0.0457345	-0.05	0.96011256
11348.02	11600	11096	1	-0.0640851	-0.079	0.93736682
11348.02	11600	11096	1	-0.0640851	-0.079	0.93736682
516.35	530	502	1	-0.078305	-0.088	0.93002306
516.35	530	502	1	-0.078305	-0.088	0.93002306
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388.68	400	378	1	-0.0816138	-0.094	0.92502052
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388.68	400	378	1	-0.0816138	-0.094	0.92502052
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388.68	400	378	1	-0.0816138	-0.094	0.92502052
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388.68	400	378	1	-0.0816138	-0.094	0.92502052
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388.68	400	378	1	-0.0816138	-0.094	0.92502052
388.68	400	378	1	-0.0816138	-0.094	0.92502052
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66.12	68	64	1	-0.0874628	-0.066	0.94756194
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65.25	67	63	1	-0.0888093	-0.094	0.92513432
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65.25	67	63	1	-0.0888093	-0.094	0.92513432
65.25	67	63	1	-0.0888093	-0.094	0.92513432
65.25	67	63	1	-0.0888093	-0.094	0.92513432
385.05	397	373	1	-0.0899634	-0.081	0.935329
385.05	397	373	1	-0.0899634	-0.081	0.935329
385.05	397	373	1	-0.0899634	-0.081	0.935329
385.05	397	373	1	-0.0899634	-0.081	0.935329
385.05	397	373	1	-0.0899634	-0.081	0.935329
176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
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176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
176.23	183	170	1	-0.1063089	-0.126	0.89950882
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325.4	340	311	0.999	-0.1286202	-0.149	0.88130482
325.4	340	311	0.999	-0.1286202	-0.149	0.88130482
325.4	340	311	0.999	-0.1286202	-0.149	0.88130482
367.54	384	351	0.999	-0.1296353	-0.147	0.88282692
2350.02	2457	2243	1	-0.1314682	-0.13	0.89684263
2350.02	2457	2243	1	-0.1314682	-0.13	0.89684263
2379.37	2489	2269	1	-0.1335096	-0.132	0.89478386
322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
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322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
322.21	339	306	0.999	-0.1477536	-0.172	0.86369006
705.37	743	668	0.999	-0.1535141	-0.192	0.84795306
705.37	743	668	0.999	-0.1535141	-0.192	0.84795306
826.88	871	783	0.999	-0.1536604	-0.168	0.86627939
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826.88	871	783	0.999	-0.1536604	-0.168	0.86627939
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687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
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687.88	725	651	0.999	-0.1553235	-0.196	0.84428396
40876.58	43295	38458	1	-0.1709167	-0.16	0.87261571
40876.58	43295	38458	1	-0.1709167	-0.16	0.87261571
40423.86	42817	38031	1	-0.1710078	-0.16	0.87313129
159.75	169	150	1	-0.1720607	-0.164	0.86979297
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92.94	99	86	0.999	-0.2030919	-0.23	0.81805809
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7356.39	7885	6827	0.999	-0.207859	-0.281	0.77896211
7406.14	7945	6867	0.999	-0.2103673	-0.284	0.7763552
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7548.95	8113	6985	0.999	-0.2159754	-0.291	0.77092824
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70.76	76	65	1	-0.2255597	-0.058	NA
70.76	76	65	1	-0.2255597	-0.058	NA
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3947.77	4270	3625	0.999	-0.2362551	-0.216	0.82914349
3947.77	4270	3625	0.999	-0.2362551	-0.216	0.82914349
3816	4149	3483	0.999	-0.2524332	-0.238	0.81214347
10245.5	11164	9327	0.999	-0.259369	-0.345	0.73025313
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3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
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3751.73	4090	3414	0.999	-0.2606378	-0.243	0.80805202
88	96	80	0.999	-0.2630344	-0.296	0.76754171
88	96	80	0.999	-0.2630344	-0.296	0.76754171
959.94	1050	869	0.999	-0.2729612	-0.348	0.72787069
57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
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57.82	63	52	0.999	-0.2768402	-0.285	0.77580654
20998.43	23080	18916	0.999	-0.2870362	-0.276	0.78260435
20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
20998.28	23080	18916	0.999	-0.2870362	-0.276	0.78261844
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3701.86	4072	3332	0.999	-0.2893492	-0.263	0.79265493
20737.94	22813	18663	0.999	-0.2896753	-0.278	0.78100729
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3772.21	4151	3393	0.999	-0.2908975	-0.266	0.79056893
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20761.15	22849	18673	0.999	-0.2911773	-0.279	0.77993646
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338667.77	372959	304377	0.999	-0.2931577	-0.343	0.73122556
338667.77	372959	304377	0.999	-0.2931577	-0.343	0.73122556
338667.77	372959	304377	0.999	-0.2931577	-0.343	0.73122556
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3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
3856.89	4256	3458	0.999	-0.2995603	-0.271	0.78650537
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
171.89	190	154	0.999	-0.3030691	-0.355	0.72240338
5152.37	5710	4595	0.999	-0.3134259	-0.373	0.70920272
5152.37	5710	4595	0.999	-0.3134259	-0.373	0.70920272
105.37	117	94	0.998	-0.3157759	-0.406	0.6848422
144.39	160	128	0.999	-0.3219281	-0.34	0.73378703
12048.53	13437	10660	0.999	-0.3340036	-0.357	0.72120175
12048.53	13437	10660	0.999	-0.3340036	-0.357	0.72120175
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434
13227.51	14790	11665	0.998	-0.3424357	-0.429	0.66819434

12257.71	13722	10793	0.999	-0.3463948	-0.413	0.67983967
12257.71	13722	10793	0.999	-0.3463948	-0.413	0.67983967
12271.67	13740	10804	0.999	-0.3468165	-0.413	0.67943045
12271.67	13740	10804	0.999	-0.3468165	-0.413	0.67943045
12988.06	14551	11425	0.998	-0.3489241	-0.456	0.64857196
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
55.15	62	48	0.999	-0.3692338	-0.321	0.74800089
140.2	158	122	0.999	-0.3730434	-0.362	0.71728644
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977

70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
70.17	79	61	0.999	-0.3730434	-0.293	0.76937977
286.36	324	249	0.999	-0.3798481	-0.424	0.67151471
286.36	324	249	0.999	-0.3798481	-0.424	0.67151471
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
273.16	309	237	0.999	-0.3827198	-0.425	0.6706357
222.36	252	192	0.999	-0.3923174	-0.367	0.71389273
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
289.54	329	250	0.998	-0.3961595	-0.483	0.62931211
1157.14	1317	998	0.998	-0.4001436	-0.469	0.63925448
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793

216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
216.86	247	186	0.999	-0.4092084	-0.383	0.70181793
1301.41	1486	1117	0.998	-0.4118049	-0.468	0.63987864
1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
1362.69	1556	1169	0.998	-0.4125671	-0.467	0.64070153
291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
291.81	333	250	0.998	-0.4135941	-0.497	0.61944521
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
44193.5	50500	37887	0.998	-0.4145805	-0.548	0.58337314
71.58	82	61	0.999	-0.4268147	-0.333	0.73912638
73.48	85	63	0.999	-0.432111	-0.424	0.67140481
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799

10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
10911.11	12551	9272	0.998	-0.4368498	-0.482	0.63009799
3700.6	4285	3116	0.998	-0.4596	-0.502	0.61583562
3700.6	4285	3116	0.998	-0.4596	-0.502	0.61583562
1617.32	1873	1362	0.998	-0.4596242	-0.567	0.57042232
405.15	472	338	0.998	-0.4817636	-0.486	0.62687205
83.92	98	70	0.998	-0.4854268	-0.542	0.58771849
59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
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59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
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59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
59.94	70	50	0.998	-0.4854268	-0.502	0.61600239
181.54	212	151	0.998	-0.4895157	-0.553	0.57998893
181.31	212	151	0.998	-0.4895157	-0.552	0.58089997
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
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180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
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180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
180.53	211	150	0.998	-0.4922805	-0.547	0.58469687
60.49	71	50	0.998	-0.5058909	-0.507	0.61247395
60.49	71	50	0.998	-0.5058909	-0.507	0.61247395
9637.02	11376	7899	0.998	-0.5262514	-0.541	0.58840402
9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
9567.8	11300	7836	0.998	-0.5281335	-0.543	0.58683539
295.68	349	242	0.997	-0.52822	-0.69	0.49031927
295.68	349	242	0.997	-0.52822	-0.69	0.49031927
295.68	349	242	0.997	-0.52822	-0.69	0.49031927
295.68	349	242	0.997	-0.52822	-0.69	0.49031927
295.68	349	242	0.997	-0.52822	-0.69	0.49031927

429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
429.97	508	352	0.998	-0.5292531	-0.536	0.5918884
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
121.28	145	98	0.998	-0.5651992	-0.639	0.52275261
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73901.6	89841	57963	0.998	-0.6322417	-0.649	0.51644109
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
34996.84	42660	27334	0.997	-0.6421874	-0.763	0.44520616
11945.94	14613	9279	0.998	-0.6552111	-0.598	0.55017117
11945.94	14613	9279	0.998	-0.6552111	-0.598	0.55017117
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083

1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1535.81	1893	1179	0.997	-0.6831107	-0.808	0.41892083
1843.9	2278	1410	0.998	-0.6920726	-0.675	0.49991687

402.47	498	307	0.997	-0.6979071	-0.802	0.42252068
59.11	73	45	0.998	-0.6979715	-0.744	0.45708247
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
9837.47	12174	7501	0.998	-0.6986484	-0.58	0.56200568
92.56	115	70	0.997	-0.716207	-0.808	0.41890161
14160.18	17640	10681	0.997	-0.7238038	-0.863	0.38813449
14160.18	17640	10681	0.997	-0.7238038	-0.863	0.38813449
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
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650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
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650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
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650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
650.99	812	489	0.997	-0.7316453	-0.851	0.3945691
651.18	815	487	0.997	-0.7428783	-0.867	0.38611964
75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
75236.85	94452	56022	0.997	-0.7535879	-0.918	0.35871936
131.91	167	97	0.998	-0.7837915	-0.753	0.45150374
8917.48	11316	6518	0.997	-0.7958628	-0.948	0.34324251
8917.48	11316	6518	0.997	-0.7958628	-0.948	0.34324251
8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
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8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
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8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
8910.85	11309	6513	0.997	-0.7960772	-0.948	0.34313428
116.13	148	85	0.998	-0.8000624	-0.622	NA
116.13	148	85	0.998	-0.8000624	-0.622	NA
129.88	165	94	0.998	-0.8117334	-0.772	0.43997844
1905.75	2429	1383	0.998	-0.8125613	-0.787	0.43113665
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
10865.99	13857	7875	0.997	-0.8152631	-0.916	0.35956605
610.96	781	441	0.997	-0.8245439	-0.878	0.38004258
567.3	727	408	0.996	-0.8333862	-0.981	0.32673794

348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
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348.86	447	250	0.997	-0.8383467	-0.962	0.33603045
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14920.99	19181	10661	0.996	-0.8473352	-1.001	0.31680124
50.52	65	36	0.997	-0.8524428	-0.867	0.38608549
2607.45	3361	1854	0.996	-0.8582493	-1.026	0.30488752
2518.33	3258	1779	0.996	-0.8729201	-1.037	0.2999259
2518.33	3258	1779	0.996	-0.8729201	-1.037	0.2999259
2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
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2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
2467.82	3201	1735	0.996	-0.883587	-1.047	0.2952488
76.6	100	54	0.997	-0.8889687	-1.001	0.31673814
76.6	100	54	0.997	-0.8889687	-1.001	0.31673814
436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
436.58	567	306	0.996	-0.8898171	-1.007	0.31406573
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523.23	681	366	0.996	-0.8958111	-1.051	0.29343267
2465.19	3209	1721	0.996	-0.8988767	-1.088	0.27662661
404.24	527	281	0.996	-0.9072328	-1.055	0.29121466
403.74	527	280	0.996	-0.9123761	-1.058	0.28988532
403.74	527	280	0.996	-0.9123761	-1.058	0.28988532
68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
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68.18	89	47	0.997	-0.9211446	-0.9	0.36830718
6857.55	8998	4716	0.996	-0.9320406	-1.081	0.27968845
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3396.98	4459	2335	0.997	-0.9332976	-1.014	0.31065541
3396.98	4459	2335	0.997	-0.9332976	-1.014	0.31065541
11221.4	14731	7712	0.996	-0.9336784	-1.083	0.27870223
3400.45	4464	2337	0.997	-0.9336793	-1.014	0.31054327

3400.45	4464	2337	0.997	-0.9336793	-1.014	0.31054327
5327.5	6997	3658	0.996	-0.9356814	-1.03	0.30308961
5327.5	6997	3658	0.996	-0.9356814	-1.03	0.30308961
5327.5	6997	3658	0.996	-0.9356814	-1.03	0.30308961
5649.44	7426	3873	0.996	-0.9391338	-1.035	0.30044327
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729.95	960	500	0.997	-0.9411063	-1.021	0.30744734
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396.88	540	254	0.998	-1.0881309	-0.783	NA
52.74	74	32	0.998	-1.2094534	-0.898	0.3693508
366.47	520	213	0.998	-1.2876582	-0.905	NA
266.39	378	154	0.997	-1.2954559	-1.081	0.27972876
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1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
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1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
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1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
1560.39	2223	897	0.997	-1.3093281	-1.141	0.25404287
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79.35	156	3	0.873	-5.7004397	-2.812	NA
79.35	156	3	0.873	-5.7004397	-2.812	NA
149.72	298	1	0.945	-8.2191685	-2.105	NA

padj	dispGeneEst	dispFit	dispMAP	dispersion	betaConv	maxCooks
0.99848065	2.1762	1.2612	1.6404	1.6404	TRUE	2.8769
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0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389

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0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
0.99848065	0.3739	0.9256	0.6296	0.6296	TRUE	0.1389
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0.99848065	0.3698	0.9254	0.6273	0.6273	TRUE	0.135
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NA	10	0.9691	3.9333	10	TRUE	38.054
NA	10	0.9796	3.908	10	TRUE	37.8974
NA	10	0.9801	3.907	10	TRUE	37.889
NA	10	1.0014	3.4243	10	TRUE	37.6283
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NA	10	1.266	3.8576	10	TRUE	34.3033
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NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
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NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
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NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
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NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
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NA	1.0098	0.9011	0.9533	0.9533	TRUE	24.9272
NA	1.0067	0.9009	0.951	0.951	TRUE	24.865
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
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0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
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0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
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0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
0.99848065	1.0335	1.1627	1.0966	1.0966	TRUE	1.0169
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0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
0.99848065	1.2889	0.9498	1.1313	1.1313	TRUE	7.2958
0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
0.99848065	0.9874	1.1188	1.0516	1.0516	TRUE	1.6529
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NA	0.9482	0.9047	0.912	0.912	TRUE	23.4869

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0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
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0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
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0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
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0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
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0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628
0.99848065	1.2644	0.9673	1.1198	1.1198	TRUE	6.3628

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NA	0.9152	1.0323	0.969	0.969	TRUE	21.098
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0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
0.99848065	2.7906	1.0726	1.7796	1.7796	TRUE	8.7809
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0.99848065	0.8814	0.9216	0.9019	0.9019	TRUE	9.129
0.99848065	0.8814	0.9216	0.9019	0.9019	TRUE	9.129
0.99848065	0.8814	0.9216	0.9019	0.9019	TRUE	9.129
0.99848065	0.8814	0.9216	0.9019	0.9019	TRUE	9.129
0.99848065	0.8814	0.9216	0.9019	0.9019	TRUE	9.129
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0.99848065	0.8814	0.9216	0.9019	0.9019	TRUE	9.129
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NA	2.6272	0.93	1.7627	1.7627	TRUE	19.4662
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NA	2.6272	0.93	1.7627	1.7627	TRUE	19.4662
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0.99848065	0.4932	0.9136	0.6894	0.6894	TRUE	11.9383
NA	2.5286	0.9295	1.7188	1.7188	TRUE	21.0823
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NA	2.6557	0.9353	1.7794	1.7794	TRUE	23.6516
NA	2.6627	0.9354	1.7832	1.7832	TRUE	23.6343
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NA	2.6668	0.9352	1.7851	1.7851	TRUE	23.7809
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0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
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0.99848065	1.0325	1.0306	1.0317	1.0317	TRUE	14.9934
0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
0.99848065	0.6597	0.9976	0.8185	0.8185	TRUE	16.2617
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	0.7804	1.1955	0.9855	0.9855	TRUE	1.4791
0.99848065	1.6677	1.0678	1.363	1.363	TRUE	1.2491
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444

0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	1.6666	1.068	1.3625	1.3625	TRUE	1.2444
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796

0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5793	0.9088	0.7349	0.7349	TRUE	1.1796
0.99848065	0.5787	0.9087	0.7345	0.7345	TRUE	1.2044
0.99848065	0.5787	0.9087	0.7345	0.7345	TRUE	1.2044
0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
0.99848065	0.4117	0.8895	0.6332	0.6332	TRUE	11.6504
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.4124	0.8896	0.6336	0.6336	TRUE	11.6664
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942

0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.652	0.9177	0.7786	0.7786	TRUE	0.5942
0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
0.99848065	0.9952	0.8884	0.9436	0.9436	TRUE	0.5118
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.639	0.9153	0.7704	0.7704	TRUE	0.4762
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597
0.99848065	0.2791	1.0998	0.6545	0.6545	TRUE	1.9597

0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4581	1.0873	0.7502	0.7502	TRUE	2.2587
0.99848065	0.4614	1.0822	0.7498	0.7498	TRUE	2.1389
0.99848065	0.2185	0.9056	0.5292	0.5292	TRUE	1.28
0.99848065	0.2185	0.9056	0.5292	0.5292	TRUE	1.28
0.99848065	0.2185	0.9056	0.5292	0.5292	TRUE	1.28
0.99848065	0.2185	0.9056	0.5292	0.5292	TRUE	1.28
0.99848065	0.2185	0.9056	0.5292	0.5292	TRUE	1.28
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392

0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
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0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
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0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.2172	0.9057	0.5285	0.5285	TRUE	1.2392
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.1506	1.1166	0.5953	0.5953	TRUE	1.22
0.99848065	0.7787	0.9315	0.8514	0.8514	TRUE	0.4832
0.99848065	0.3817	1.0142	0.6778	0.6778	TRUE	5.3986
0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
0.99848065	0.3922	1.0156	0.6842	0.6842	TRUE	6.2365
NA	1.6013	1.1293	1.3727	1.3727	TRUE	22.8793
NA	1.6013	1.1293	1.3727	1.3727	TRUE	22.8793
0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
0.99848065	0.4492	1.1118	0.7557	0.7557	TRUE	8.3175
0.99848065	0.3783	1.015	0.6759	0.6759	TRUE	7.2141
0.99848065	0.3895	1.0147	0.6823	0.6823	TRUE	5.4956
0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
0.99848065	0.4784	0.958	0.7017	0.7017	TRUE	11.7551
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0.99848065	0.3862	1.0177	0.6818	0.6818	TRUE	5.9548
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0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483

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0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
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0.99848065	0.1459	0.9269	0.4931	0.4931	TRUE	3.7483
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NA	1.2555	1.1099	1.1857	1.1857	TRUE	20.02
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0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663
0.99848065	0.1057	1.0392	0.5276	0.5276	TRUE	0.4663

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0.99848065	0.4974	1.1548	0.8022	0.8022	TRUE	11.1961
0.99848065	0.4974	1.1548	0.8022	0.8022	TRUE	11.1961
0.99848065	0.4974	1.1548	0.8022	0.8022	TRUE	11.1961
0.99848065	0.4974	1.1548	0.8022	0.8022	TRUE	11.1961
0.99848065	0.4974	1.1548	0.8022	0.8022	TRUE	11.1961
0.99848065	0.4974	1.1548	0.8022	0.8022	TRUE	11.1961
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0.99848065	0.5752	1.0998	0.8265	0.8265	TRUE	2.5804
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0.99848065	0.5752	1.0998	0.8265	0.8265	TRUE	2.5804
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0.99848065	0.3373	0.9738	0.6332	0.6332	TRUE	0.5599
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0.99848065	0.6522	0.8977	0.7685	0.7685	TRUE	0.3985
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0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
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0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
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0.99848065	0.6555	0.8977	0.7703	0.7703	TRUE	0.3993
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
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0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
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0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965

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0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1495	0.9123	0.4911	0.4911	TRUE	1.965
0.99848065	0.1365	0.9077	0.4803	0.4803	TRUE	0.9055
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
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0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
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0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
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0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
0.99848065	0.1366	0.9077	0.4804	0.4804	TRUE	0.9049
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0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
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0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
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0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
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0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
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0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218

0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4605	1.0596	1.265	1.265	TRUE	5.7218
0.99848065	1.4311	1.057	1.2486	1.2486	TRUE	5.0296
0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
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0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
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0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
0.99848065	0.3328	0.9802	0.6336	0.6336	TRUE	0.564
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
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0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
0.99848065	0.1487	1.1017	0.5747	0.5747	TRUE	2.184
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0.99848065	0.057	0.9095	0.4289	0.4289	TRUE	0.3274
0.99848065	0.057	0.9095	0.4289	0.4289	TRUE	0.3274
0.99848065	0.057	0.9095	0.4289	0.4289	TRUE	0.3274

0.99848065	0.4043	0.9713	0.666	0.666	TRUE	1.6884
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0.99848065	0.4043	0.9713	0.666	0.666	TRUE	1.6884
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0.99848065	0.0567	0.9115	0.4313	0.4313	TRUE	0.2611
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0.99848065	0.0567	0.9115	0.4313	0.4313	TRUE	0.2611
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0.99848065	0.0567	0.9115	0.4313	0.4313	TRUE	0.2572
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0.99848065	0.2934	0.9343	0.5826	0.5826	TRUE	3.5417

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0.99848065	0.3142	1.0042	0.6308	0.6308	TRUE	4.182
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.3598	1.015	0.6622	0.6622	TRUE	3.0186
0.99848065	0.6941	0.8883	0.7717	0.7717	TRUE	1.0172
0.99848065	0.9043	0.889	0.8974	0.8974	TRUE	0.5704
0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
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0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
0.99848065	0.186	0.9651	0.5415	0.5415	TRUE	0.8406
0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
0.99848065	0.1941	0.9774	0.553	0.553	TRUE	2.7677
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0.99848065	0.5592	1.0835	0.8027	0.8027	TRUE	5.2847
0.99848065	0.5592	1.0835	0.8027	0.8027	TRUE	5.2847
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0.99848065	0.0755	0.9442	0.4607	0.4607	TRUE	0.299
0.99848065	0.1305	0.9171	0.4815	0.4815	TRUE	1.1233
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0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353

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0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
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0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
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0.99848065	0.1315	0.9172	0.4822	0.4822	TRUE	1.1353
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0.99848065	1.6087	0.9672	1.2919	1.2919	TRUE	3.7481
0.99848065	1.5678	0.9653	1.2711	1.2711	TRUE	5.9406
0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
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0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
0.99848065	0.0552	0.8896	0.4186	0.4186	TRUE	0.8472
0.99848065	0.3303	0.9283	0.6052	0.6052	TRUE	0.3087
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0.99848065	0.3159	0.9266	0.5961	0.5961	TRUE	0.3301
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0.99848065	0.0633	0.9457	0.4545	0.4545	TRUE	1.2571
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0.99848065	0.2652	0.9083	0.5569	0.5569	TRUE	1.9845
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0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	1.2591	0.9248	1.0953	1.0953	TRUE	0.3559
0.99848065	0.5081	0.9881	0.7317	0.7317	TRUE	3.3237
0.99848065	0.5081	0.9881	0.7317	0.7317	TRUE	3.3237
0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
0.99848065	0.0803	0.9428	0.464	0.464	TRUE	1.2933
0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491

0.99848065	1.5661	0.9503	1.2624	1.2624	TRUE	1.1491
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.3017	0.9519	0.5997	0.5997	TRUE	2.6316
0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
0.99848065	0.7832	1.0093	0.8927	0.8927	TRUE	1.5532
0.99848065	0.1091	1.0067	0.5141	0.5141	TRUE	0.23
0.99848065	0.1091	1.0067	0.5141	0.5141	TRUE	0.23
0.99848065	0.1036	1.0032	0.5088	0.5088	TRUE	0.237
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	0.2465	1.0572	0.6187	0.6187	TRUE	0.4444
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	1.7755	0.949	1.3488	1.3488	TRUE	0.409
0.99848065	0.792	1.0154	0.8978	0.8978	TRUE	0.3103
0.99848065	0.1605	0.9965	0.5385	0.5385	TRUE	0.2503
0.99848065	0.1605	0.9965	0.5385	0.5385	TRUE	0.2503

0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1586	0.9848	0.5324	0.5324	TRUE	0.4223
0.99848065	0.1459	0.9827	0.5237	0.5237	TRUE	0.4203
0.99848065	0.1594	0.9926	0.536	0.536	TRUE	0.2103
0.99848065	0.1594	0.9926	0.536	0.536	TRUE	0.2103
0.99848065	0.3389	0.932	0.6116	0.6116	TRUE	0.3884
0.99848065	0.0147	0.9265	0.41	0.41	TRUE	0.2902
0.99848065	0.3436	1.0955	0.6931	0.6931	TRUE	0.8144
0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
0.99848065	0.1347	0.9117	0.4814	0.4814	TRUE	1.5426
0.99848065	0.8108	1.0697	0.9368	0.9368	TRUE	1.3683
0.99848065	0.8108	1.0697	0.9368	0.9368	TRUE	1.3683
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651

0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3769	0.8863	0.8042	0.8042	TRUE	0.6651
0.99848065	0.3276	0.8869	0.5846	0.5846	TRUE	0.6523
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.3398	1.0967	0.6917	0.6917	TRUE	0.8016
0.99848065	0.5143	0.8866	0.6886	0.6886	TRUE	0.4812
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0.99848065	0.5143	0.8866	0.6886	0.6886	TRUE	0.4812
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0.99848065	0.5143	0.8866	0.6886	0.6886	TRUE	0.4812

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0.99848065	0.5143	0.8866	0.6886	0.6886	TRUE	0.4812
0.99848065	0.5143	0.8866	0.6886	0.6886	TRUE	0.4812
0.99848065	0.5143	0.8866	0.6886	0.6886	TRUE	0.4812
0.99848065	0.208	0.8881	0.5227	0.5227	TRUE	5.7055
0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
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0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
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0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
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0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
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0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
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0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
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0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
0.99848065	0.2084	0.8881	0.5231	0.5231	TRUE	5.7214
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0.99848065	0.2086	0.8881	0.5232	0.5232	TRUE	5.7287
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0.99848065	0.5149	0.8866	0.6889	0.6889	TRUE	0.4773
0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
0.9996958	0.5517	0.8866	0.7089	0.7089	TRUE	0.5047
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303

0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.0299	0.9186	0.4168	0.4168	TRUE	0.6303
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.9996958	0.1213	0.9213	0.4778	0.4778	TRUE	0.8586
0.99848065	0.2221	0.9337	0.5449	0.5449	TRUE	0.2481
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303

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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
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0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3683	0.8868	0.6076	0.6076	TRUE	0.3303
0.99848065	0.3053	0.976	0.6128	0.6128	TRUE	0.2175
0.99848065	0.3053	0.976	0.6128	0.6128	TRUE	0.2175
0.99848065	0.3053	0.976	0.6128	0.6128	TRUE	0.2175
0.99848065	0.3593	0.8885	0.6035	0.6035	TRUE	0.2656

0.99848065	0.3593	0.8885	0.6035	0.6035	TRUE	0.2656
0.99848065	0.1494	0.8873	0.4786	0.4786	TRUE	2.258
0.99848065	0.1494	0.8873	0.4786	0.4786	TRUE	2.258
0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
0.99848065	0.3297	0.909	0.5959	0.5959	TRUE	0.5677
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.2796	0.9165	0.5702	0.5702	TRUE	0.4627
0.99848065	0.8624	1.0637	0.9577	0.9577	TRUE	1.3669
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
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0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833

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0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.076	1.0661	0.5231	0.5231	TRUE	0.1833
0.99848065	0.9235	0.9168	0.9198	0.9198	TRUE	0.358
0.99848065	0.9235	0.9168	0.9198	0.9198	TRUE	0.358
0.99848065	0.9235	0.9168	0.9198	0.9198	TRUE	0.358
0.99848065	0.9235	0.9168	0.9198	0.9198	TRUE	0.358
0.99848065	0.9235	0.9168	0.9198	0.9198	TRUE	0.358
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.1262	0.9529	0.4948	0.4948	TRUE	0.4709
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
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0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
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0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243
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0.99848065	0.5792	0.8864	0.9414	0.9414	TRUE	0.4243

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0.99848065	1.0949	0.887	0.9941	0.9941	TRUE	0.4982
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0.99848065	0.5965	0.8912	0.7353	0.7353	TRUE	0.342
0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
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0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
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0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
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0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
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0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
0.99848065	0.2507	0.9227	0.5561	0.5561	TRUE	0.4734
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0.99848065	0.3342	0.9005	0.5947	0.5947	TRUE	0.5843
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0.99848065	0.772	0.8866	0.8266	0.8266	TRUE	0.5818
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0.99848065	0.197	1.0126	0.567	0.567	TRUE	2.0055
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0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
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0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
0.99848065	0.0227	0.8879	0.3951	0.3951	TRUE	0.3956
0.99848065	0.0232	0.8879	0.3955	0.3955	TRUE	0.4118
0.99848065	0.0232	0.8879	0.3955	0.3955	TRUE	0.4118
0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012

0.99848065	0.0241	0.8879	0.396	0.396	TRUE	0.3012
0.99848065	0.6705	1.1445	0.8923	0.8923	TRUE	1.1361
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0.99848065	0.8402	0.8893	0.8636	0.8636	TRUE	0.4448
0.99848065	0.8402	0.8893	0.8636	0.8636	TRUE	0.4448
0.99848065	0.7437	0.8894	0.813	0.813	TRUE	0.4832
0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
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0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
0.99848065	0.042	0.8874	0.4079	0.4079	TRUE	0.4585
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0.99848065	0.7749	0.8894	0.8294	0.8294	TRUE	0.4725
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0.99848065	0.1947	1.0196	0.5692	0.5692	TRUE	2.0003
0.99848065	0.1947	1.0196	0.5692	0.5692	TRUE	2.0003
0.99848065	0.0874	0.8985	0.4443	0.4443	TRUE	0.5052
0.99848065	0.2408	1.0892	0.6336	0.6336	TRUE	0.2183
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0.99848065	0.6833	0.8869	0.7798	0.7798	TRUE	0.3573
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0.99848065	0.853	0.8895	0.8715	0.8715	TRUE	0.4951
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0.99848065	0.6876	0.8869	0.7821	0.7821	TRUE	0.3595
0.99848065	0.8421	0.8894	0.8647	0.8647	TRUE	0.5022
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0.99848065	0.8421	0.8894	0.8647	0.8647	TRUE	0.5022
0.99848065	0.8421	0.8894	0.8647	0.8647	TRUE	0.5022
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0.99848065	0.8421	0.8894	0.8647	0.8647	TRUE	0.5022
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0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
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0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611

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0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
0.99848065	0.6887	0.8869	0.7827	0.7827	TRUE	0.3611
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0.99848065	0.2234	0.8863	0.5249	0.5249	TRUE	0.7719
0.99848065	0.2234	0.8863	0.5249	0.5249	TRUE	0.7719
0.99848065	0.2234	0.8863	0.5249	0.5249	TRUE	0.7719
0.99848065	0.0828	0.8971	0.4406	0.4406	TRUE	0.283
0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
0.99848065	0.1528	0.9555	0.5129	0.5129	TRUE	0.4177
0.99848065	0.8752	0.8893	0.8814	0.8814	TRUE	0.5692
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0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1463	0.9546	0.5085	0.5085	TRUE	0.3534
0.99848065	0.1776	0.8886	0.5085	0.5085	TRUE	0.1556
0.99848065	0.1776	0.8886	0.5085	0.5085	TRUE	0.1556
0.99848065	0.0109	0.9976	0.4432	0.4432	TRUE	0.2926
0.99848065	0.3774	0.9676	0.6502	0.6502	TRUE	9.0847
0.99848065	0.3655	0.8873	0.6313	0.6313	TRUE	0.6019
0.99848065	0.3655	0.8873	0.6313	0.6313	TRUE	0.6019
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339
0.99848065	0.1133	0.8872	0.4602	0.4602	TRUE	0.2339

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0.99848065	0.1728	0.8873	0.5075	0.5075	TRUE	0.2563
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0.99848065	0.0627	0.8872	0.4222	0.4222	TRUE	0.8517
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
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0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
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0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.8088	1.099	0.9466	0.9466	TRUE	14.8254
0.99848065	0.4707	0.97	0.7029	0.7029	TRUE	0.8753
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
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0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657

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0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
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0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	1.1702	1.0535	1.1139	1.1139	TRUE	3.1657
0.99848065	0.2943	0.9273	0.5838	0.5838	TRUE	0.8903
0.99848065	0.2943	0.9273	0.5838	0.5838	TRUE	0.8903
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
0.99848065	0.3127	0.9293	0.5955	0.5955	TRUE	1.2671
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0.99848065	0.6933	0.9391	0.8195	0.8195	TRUE	1.0902
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.1532	0.9268	0.4997	0.4997	TRUE	0.4204
0.99848065	0.2203	0.8964	0.5261	0.5261	TRUE	1.181
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214

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0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
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0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
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0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
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0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.7046	0.9404	0.8173	0.8173	TRUE	1.214
0.99848065	0.2909	0.8953	0.5586	0.5586	TRUE	5.1055
0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
0.99848065	0.2972	0.8949	0.5636	0.5636	TRUE	5.1739
0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
0.99848065	0.1526	0.9265	0.4991	0.4991	TRUE	0.4218
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	0.0446	0.8866	0.4118	0.4118	TRUE	0.7664
0.99848065	1.1796	1.0502	1.1171	1.1171	TRUE	6.9224
0.99848065	0.5311	1.046	0.771	0.771	TRUE	0.4632
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606

0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.276	0.8874	0.593	0.593	TRUE	0.2606
0.99848065	0.4067	0.8895	0.6039	0.6039	TRUE	3.4941
0.99848065	0.4067	0.8895	0.6039	0.6039	TRUE	3.4941
0.99848065	0.1377	0.8936	0.4743	0.4743	TRUE	2.3521
0.99848065	0.5386	0.9153	0.7151	0.7151	TRUE	0.7391
0.99848065	0.1594	1.0261	0.5525	0.5525	TRUE	0.1968
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848

0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.3443	1.082	0.6828	0.6828	TRUE	1.7848
0.99848065	0.2604	0.9509	0.5746	0.5746	TRUE	0.6009
0.99848065	0.263	0.951	0.5761	0.5761	TRUE	0.6047
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.2634	0.9513	0.5765	0.5765	TRUE	0.6187
0.99848065	0.346	1.0803	0.683	0.683	TRUE	1.847
0.99848065	0.346	1.0803	0.683	0.683	TRUE	1.847
0.99848065	0.5005	0.8875	0.6815	0.6815	TRUE	0.1437
0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
0.99848065	0.4993	0.8875	0.6808	0.6808	TRUE	0.1442
0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668
0.99848065	0.0346	0.926	0.4234	0.4234	TRUE	0.4668

0.99848065	0.5184	0.9136	0.7033	0.7033	TRUE	0.7433
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0.99848065	0.5184	0.9136	0.7033	0.7033	TRUE	0.7433
0.99848065	0.5184	0.9136	0.7033	0.7033	TRUE	0.7433
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
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0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.1881	0.983	0.5474	0.5474	TRUE	2.5751
0.99848065	0.2138	0.8865	0.5076	0.5076	TRUE	2.0271
0.99848065	0.2212	0.8865	0.5119	0.5119	TRUE	2.0247
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0.99848065	1.0239	0.8873	0.8665	0.8665	TRUE	16.2164
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0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
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0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462

0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2265	0.9043	0.5307	0.5307	TRUE	0.4462
0.99848065	0.2206	0.9043	0.5279	0.5279	TRUE	0.3113
0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
0.99848065	0.1717	0.8865	0.4858	0.4858	TRUE	2.5645
0.99848065	0.5817	0.9753	0.766	0.766	TRUE	5.8724
0.99848065	0.1759	0.8876	0.508	0.508	TRUE	0.1534
0.99848065	0.1759	0.8876	0.508	0.508	TRUE	0.1534
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0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
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0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
0.99848065	0.176	0.8876	0.508	0.508	TRUE	0.1529
NA	1.3338	0.9873	1.1659	1.1659	TRUE	19.7433
NA	1.3338	0.9873	1.1659	1.1659	TRUE	19.7433
0.99848065	0.5797	0.9766	0.7656	0.7656	TRUE	6.8216
0.99848065	0.6576	0.8925	0.7687	0.7687	TRUE	0.9719
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.3169	0.8874	0.5707	0.5707	TRUE	0.527
0.99848065	0.4035	0.9055	0.6362	0.6362	TRUE	5.1643
0.99848065	0.201	0.907	0.5221	0.5221	TRUE	0.2014

0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2276	0.9199	0.5414	0.5414	TRUE	0.908
0.99848065	0.2307	0.8871	0.5163	0.5163	TRUE	3.7539
0.99848065	0.3279	1.1185	0.6909	0.6909	TRUE	0.1222
0.99848065	0.1886	0.8908	0.5043	0.5043	TRUE	0.4283
0.99848065	0.199	0.891	0.5107	0.5107	TRUE	0.314
0.99848065	0.199	0.891	0.5107	0.5107	TRUE	0.314
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.2032	0.8911	0.5132	0.5132	TRUE	0.3126
0.99848065	0.187	1.0395	0.5773	0.5773	TRUE	0.2223
0.99848065	0.187	1.0395	0.5773	0.5773	TRUE	0.2223
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642

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0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2699	0.9132	0.5629	0.5629	TRUE	4.1642
0.99848065	0.2055	0.9087	0.523	0.523	TRUE	0.9043
0.99848065	0.1794	0.8911	0.4919	0.4919	TRUE	0.2225
0.99848065	0.2111	0.9153	0.5293	0.5293	TRUE	0.1463
0.99848065	0.2105	0.9154	0.5289	0.5289	TRUE	0.1455
0.99848065	0.2105	0.9154	0.5289	0.5289	TRUE	0.1455
0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
0.99848065	0.4572	1.0584	0.7364	0.7364	TRUE	1.84
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
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0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.2251	0.888	0.5355	0.5355	TRUE	0.1592
0.99848065	0.3703	0.8898	0.6103	0.6103	TRUE	9.5306
0.99848065	0.3703	0.8898	0.6103	0.6103	TRUE	9.5306
0.99848065	0.2728	0.8873	0.5354	0.5354	TRUE	2.5672
0.99848065	0.3706	0.8898	0.6104	0.6104	TRUE	9.536

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0.99848065	0.3795	0.8885	0.5946	0.5946	TRUE	1.4073
0.99848065	0.3795	0.8885	0.5946	0.5946	TRUE	1.4073
0.99848065	0.3795	0.8885	0.5946	0.5946	TRUE	1.4073
0.99848065	0.3759	0.8884	0.5926	0.5926	TRUE	1.4126
0.99848065	0.3759	0.8884	0.5926	0.5926	TRUE	1.4126
0.99848065	0.3759	0.8884	0.5926	0.5926	TRUE	1.4126
0.99848065	0.3759	0.8884	0.5926	0.5926	TRUE	1.4126
0.99848065	0.3759	0.8884	0.5926	0.5926	TRUE	1.4126
0.99848065	0.3759	0.8884	0.5926	0.5926	TRUE	1.4126
0.99848065	0.3759	0.8884	0.5926	0.5926	TRUE	1.4126
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
0.99848065	0.2806	0.8874	0.5389	0.5389	TRUE	2.8617
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0.99848065	0.3633	0.9024	0.6122	0.6122	TRUE	3.1789
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0.99848065	0.3633	0.9024	0.6122	0.6122	TRUE	3.1789
0.99848065	0.3628	0.9023	0.6119	0.6119	TRUE	2.9924
0.99848065	0.25	0.8882	0.5496	0.5496	TRUE	0.2022
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0.99848065	1.2476	0.9126	1.0847	1.0847	TRUE	0.3571
0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
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0.99848065	0.1596	0.8921	0.494	0.494	TRUE	0.1337
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NA	1.3182	0.9938	1.1611	1.1611	TRUE	19.3212
NA	1.8446	0.9159	1.3852	1.3852	TRUE	27.308
0.99848065	1.4413	1.1088	1.2777	1.2777	TRUE	3.8058
NA	1.9927	0.9183	1.4593	1.4593	TRUE	28.4691
0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
0.99848065	1.1259	0.9303	1.0314	1.0314	TRUE	1.4759
0.99848065	1.0306	0.8938	0.9485	0.9485	TRUE	16.7866
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0.99848065	1.0296	0.8938	0.9479	0.9479	TRUE	16.4382
NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
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NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
NA	4.2054	0.9153	2.49	2.49	TRUE	35.125
0.99848065	1.9474	0.9407	1.4455	1.4455	TRUE	0.3724
NA	10	1.0033	4.5623	10	TRUE	32.3951
NA	10	1.0033	4.5623	10	TRUE	32.3951

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aggcaagaugcuggcauagcugu	Phvul.009G006000.3	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.2	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G198200.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.3	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.2	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G006000.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G198200.1	2.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G214600.7	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G150800.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G261000.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G214600.7	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G150800.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G261000.1	3	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G022900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G128900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.4	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.3	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.2	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G174100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G040500.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G018100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G290000.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G040800.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.3	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.2	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G022900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G128900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.4	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.3	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G219900.2	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G174100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G040500.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G018100.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G290000.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G040800.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.3	3.5	-1	1

aggcaagaugcuggcauagcugu	Phvul.010G000700.1	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G000700.2	3.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G032100.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G243500.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G061200.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G061900.3	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G061900.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G061900.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G226500.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G226500.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.3	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.4	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G133900.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G106900.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G036300.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G192300.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G112400.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G032100.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G243500.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G061200.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G061900.3	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G061900.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G061900.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G226500.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G226500.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.3	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.4	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G242900.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G133900.2	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G106900.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G036300.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G192300.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G112400.1	4	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G151200.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G104300.2	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G104300.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G033500.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G038200.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G022400.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.L001644.1	4.5	-1	1

aggcaagaugcuggcauagcugu	Phvul.001G264132.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G019100.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G073900.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G159700.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G151200.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G104300.2	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G104300.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G033500.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.008G038200.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G022400.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.L001644.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G264132.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G019100.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G073900.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.003G159700.1	4.5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G214600.7	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G228600.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G035800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G134100.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G134000.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G130800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G081100.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G133300.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.007G247800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G172000.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G031700.2	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G031700.3	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G105800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G021200.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G226800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G162000.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G038300.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.007G188300.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G084688.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.L001859.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G027900.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G180700.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G153700.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.001G214600.7	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G228600.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G035800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G134100.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G134000.1	5	-1	1

aggcaagaugcuggcauagcugu	Phvul.011G130800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G081100.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.011G133300.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.007G247800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G172000.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G031700.2	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.010G031700.3	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G105800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G021200.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.009G226800.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.006G162000.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G038300.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.007G188300.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G084688.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.L001859.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.002G027900.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.005G180700.1	5	-1	1
aggcaagaugcuggcauagcugu	Phvul.004G153700.1	5	-1	1

miRNA_end	Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition
23	1845	1867	AGGCAAGAU	.::::::::::::.::::..	UGGAUUAUG	Cleavage
23	1845	1867	AGGCAAGAU	.::::::::::::.::::..	UGGAUUAUG	Cleavage
23	1031	1053	AGGCAAGAU	::::::::::.: ::::.:	CAAGCUAUG	Cleavage
23	1656	1678	AGGCAAGAU	::::::::::.: ::::.:	CAAGCUAUG	Cleavage
23	1656	1678	AGGCAAGAU	::::::::::.: ::::.:	CAAGCUAUG	Cleavage
23	775	797	AGGCAAGAU	: : .::::::::.:::::::.	AAACUUAUG	Cleavage
23	1031	1053	AGGCAAGAU	::::::::::.: ::::.:	CAAGCUAUG	Cleavage
23	1656	1678	AGGCAAGAU	::::::::::.: ::::.:	CAAGCUAUG	Cleavage
23	1656	1678	AGGCAAGAU	::::::::::.: ::::.:	CAAGCUAUG	Cleavage
23	775	797	AGGCAAGAU	: : .::::::::.:::::::.	AAACUUAUG	Cleavage
23	1055	1077	AGGCAAGAU	:: :::::...:::::::: :	UCAUCUAUG	Cleavage
23	1403	1425	AGGCAAGAU	: : :: :::.:::::.:::..	AGAACUCUG	Cleavage
23	1694	1716	AGGCAAGAU	:: ::.::::::.:::::	UCUCCUUUG	Cleavage
23	1055	1077	AGGCAAGAU	:: :::::...:::::::: :	UCAUCUAUG	Cleavage
23	1403	1425	AGGCAAGAU	: : :: :::.:::::.:::..	AGAACUCUG	Cleavage
23	1694	1716	AGGCAAGAU	:: ::.::::::.:::::	UCUCCUUUG	Cleavage
23	94	116	AGGCAAGAU	::: ::.:: ::::::.::::.	ACAACUGUG	Cleavage
23	798	820	AGGCAAGAU	:: ::.::::::.:: :::::	CCAACUGUG	Cleavage
23	573	595	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	573	595	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	1468	1490	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	1468	1490	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	2981	3002	AGGCAAGAU	.:: :::: ::::::::::::.	GCACCUAU-C	Cleavage
23	1638	1660	AGGCAAGAU	: :::::..::.: :::::.	GAAACUAUG	Cleavage
23	1884	1906	AGGCAAGAU	.::::::.:::: .::::.	AGCAUUAUG	Cleavage
23	1140	1162	AGGCAAGAU	:: : .::: ::::::::::.	ACUUCAGUG	Cleavage
23	1074	1096	AGGCAAGAU	: :: :::..::::.::::..	UAACCUCUG	Cleavage
23	1003	1025	AGGCAAGAU	::::: : ::::::::::	CAUUCUAUG	Cleavage
23	1003	1025	AGGCAAGAU	::::: : ::::::::::	CAUUCUAUG	Cleavage
23	1003	1025	AGGCAAGAU	::::: : ::::::::::	CAUUCUAUG	Cleavage
23	94	116	AGGCAAGAU	::: ::.:: ::::::.::::.	ACAACUGUG	Cleavage
23	798	820	AGGCAAGAU	:: ::.::::::.:: :::::	CCAACUGUG	Cleavage
23	573	595	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	573	595	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	1468	1490	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	1468	1490	AGGCAAGAU	.: : ::: .:::.::::::.:	GCUGAUAUA	Cleavage
23	2981	3002	AGGCAAGAU	.:: :::: ::::::::::::.	GCACCUAU-C	Cleavage
23	1638	1660	AGGCAAGAU	: :::::..::.: :::::.	GAAACUAUG	Cleavage
23	1884	1906	AGGCAAGAU	.::::::.:::: .::::.	AGCAUUAUG	Cleavage
23	1140	1162	AGGCAAGAU	:: : .::: ::::::::::.	ACUUCAGUG	Cleavage
23	1074	1096	AGGCAAGAU	: :: :::..::::.::::..	UAACCUCUG	Cleavage
23	1003	1025	AGGCAAGAU	::::: : ::::::::::	CAUUCUAUG	Cleavage

23	1003	1025	AGGCAAGAU	:::: : :::::::::	CAUUCUAUG	Cleavage
23	1003	1025	AGGCAAGAU	:::: : :::::::::	CAUUCUAUG	Cleavage
23	1342	1364	AGGCAAGAU	..::::::::.: : :::::.	CUGGCUAUG	Translation
23	1154	1176	AGGCAAGAU	: :::::: :..::::::: .:	AAAGCUAUA	Cleavage
23	624	646	AGGCAAGAU	..::: :::: ::::: ::	CUGGCUCUG	Translation
23	1814	1836	AGGCAAGAU	: :::::::..:..: ::::.	CCCGCUAUGC	Cleavage
23	1817	1839	AGGCAAGAU	: :::::::..:..: ::::.	CCCGCUAUGC	Cleavage
23	1743	1765	AGGCAAGAU	: :::::::..:..: ::::.	CCCGCUAUGC	Cleavage
23	1851	1873	AGGCAAGAU	...: :: :.:::::::: ::	GUGGAUACG	Cleavage
23	1852	1874	AGGCAAGAU	...: :: :.:::::::: ::	GUGGAUACG	Cleavage
23	664	687	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	617	640	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	654	677	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	664	687	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	467	489	AGGCAAGAU	: .:.::..::.::.::::	UGACUUGUG	Cleavage
23	1109	1131	AGGCAAGAU	::: :::..::: .::::	UAUGCUUUG	Cleavage
23	400	422	AGGCAAGAU	:::.:: :.::::.: :::	AAUGCUGUG	Cleavage
23	1207	1229	AGGCAAGAU	.: :. :: :..::::.::::	GCUGUAAUU	Cleavage
23	1672	1694	AGGCAAGAU	.:.::: ::::::::::.:	GAGGUUAUA	Cleavage
23	1342	1364	AGGCAAGAU	..::::::::.: : :::::.	CUGGCUAUG	Translation
23	1154	1176	AGGCAAGAU	: :::::: :..::::::: .:	AAAGCUAUA	Cleavage
23	624	646	AGGCAAGAU	..::: :::: ::::: ::	CUGGCUCUG	Translation
23	1814	1836	AGGCAAGAU	: :::::::..:..: ::::.	CCCGCUAUGC	Cleavage
23	1817	1839	AGGCAAGAU	: :::::::..:..: ::::.	CCCGCUAUGC	Cleavage
23	1743	1765	AGGCAAGAU	: :::::::..:..: ::::.	CCCGCUAUGC	Cleavage
23	1851	1873	AGGCAAGAU	...: :: :.:::::::: ::	GUGGAUACG	Cleavage
23	1852	1874	AGGCAAGAU	...: :: :.:::::::: ::	GUGGAUACG	Cleavage
23	664	687	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	617	640	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	654	677	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	664	687	AGGCAAGAU	:::: ::..:.::.:::	GGUGCUAUU	Cleavage
23	467	489	AGGCAAGAU	: .:.::..::.::.::::	UGACUUGUG	Cleavage
23	1109	1131	AGGCAAGAU	::: :::..::: .::::	UAUGCUUUG	Cleavage
23	400	422	AGGCAAGAU	:::.:: :.::::.: :::	AAUGCUGUG	Cleavage
23	1207	1229	AGGCAAGAU	.: :. :: :..::::.::::	GCUGUAAUU	Cleavage
23	1672	1694	AGGCAAGAU	.:.::: ::::::::::.:	GAGGUUAUA	Cleavage
23	1590	1612	AGGCAAGAU	:.::.::::.. :::::::::	AUAGUUAUG	Translation
23	1336	1358	AGGCAAGAU	:. ::::::. .:.::.::::	AUUGCUAUG	Cleavage
23	1352	1374	AGGCAAGAU	:. ::::::. .:.::.::::	AUUGCUAUG	Cleavage
23	839	861	AGGCAAGAU	.::.: ::::::..:::: .	UUAGUUUUG	Cleavage
23	56	78	AGGCAAGAU	:: : :.::: :::: :::::	ACUGGUGUG	Cleavage
23	1146	1168	AGGCAAGAU	:.: ::::::.:::::. : .:	AUACCUAUG	Cleavage
23	1123	1145	AGGCAAGAU	.:::: :: ::::::.:::..	GCAGCCAUCA	Cleavage

23	912	934	AGGCAAGAU	::::: ::::.::::::::	UCAGCUUAC	Cleavage
23	26	48	AGGCAAGAU	:: ::.:::: :.: ::::.	CCAACUGUG	Translation
23	168	191	AGGCAAGAU	: :::::.::: .::::::.	UAAACUAUG	Translation
23	1464	1486	AGGCAAGAU	::: : ::::.::: ::::.:	ACAUGUCUG	Cleavage
23	1590	1612	AGGCAAGAU	:.::.::::.. :::::::::	AUAGUUAUG	Translation
23	1336	1358	AGGCAAGAU	:. ::::::. .:.::.::::	AUUGCUAUG	Cleavage
23	1352	1374	AGGCAAGAU	:. ::::::. .:.::.::::	AUUGCUAUG	Cleavage
23	839	861	AGGCAAGAU	.::.: ::::::..:::: .	UUAGUUUUG	Cleavage
23	56	78	AGGCAAGAU	:: : :.::: :::: :::::	ACUGGUGUG	Cleavage
23	1146	1168	AGGCAAGAU	:.: ::::::.:::::. : .:	AUACCUAUG	Cleavage
23	1123	1145	AGGCAAGAU	.:::: :: ::::::.:::..	GCAGCCAUC	Cleavage
23	912	934	AGGCAAGAU	::::: ::::.::::::::	UCAGCUUAC	Cleavage
23	26	48	AGGCAAGAU	:: ::.:::: :.: ::::.	CCAACUGUG	Translation
23	168	191	AGGCAAGAU	: :::::.::: .::::::.	UAAACUAUG	Translation
23	1464	1486	AGGCAAGAU	::: : ::::.::: ::::.:	ACAUGUCUG	Cleavage
23	1004	1026	AGGCAAGAU	: :::::::..:::::::::	AAAGCUAUG	Cleavage
23	366	388	AGGCAAGAU	:..::::::::::.: ::::.	AUGGCUAUG	Cleavage
23	859	881	AGGCAAGAU	.::::::::::..: : ::::..	GCAGCUAUG	Translation
23	895	917	AGGCAAGAU	:.::::::: ..::::::: .:	AUAGCUAUG	Cleavage
23	1000	1022	AGGCAAGAU	:.::: :::: :::::::: ::	AUAGCCAUG	Cleavage
23	1000	1022	AGGCAAGAU	:.::::::: ..::::::: .:	AUAGCUAUG	Cleavage
23	1064	1086	AGGCAAGAU	:.::: :::...:::::: ::	AUAGCAAUG	Cleavage
23	1000	1022	AGGCAAGAU	:.::::::: ..::::::: .:	AUAGCUAUG	Cleavage
23	1232	1255	AGGCAAGAU	:::::::...: :::::::	CAAGCUAUG	Translation
23	1770	1792	AGGCAAGAU	:::.: ::.::::::. ::..	UCAGUUUUG	Cleavage
23	2276	2298	AGGCAAGAU	.::::.: ::.::..:.::::.	GCAGUUUCG	Cleavage
23	2353	2375	AGGCAAGAU	.:::.: ::.::..:.::::.	GCAGUUUCG	Cleavage
23	1513	1535	AGGCAAGAU	:.::: :::::::..: :..	AUAGCACUG	Cleavage
23	733	755	AGGCAAGAU	.::. ::::.:: ::::::.:	UUAGUAAUG	Translation
23	809	831	AGGCAAGAU	:: :::: :.: ::::.::::.	ACUGCUAAG	Cleavage
23	1197	1220	AGGCA-AGAU	:::::::.::.::.: :::	GGUGCUAUG	Cleavage
23	1385	1407	AGGCAAGAU	:. ::::::. .:..:.::::	AUUGCUAUG	Cleavage
23	277	299	AGGCAAGAU	::: : .::::::. ::::::.	ACACCCGUG	Cleavage
23	2137	2159	AGGCAAGAU	..:.:.::.::::.:: :::	UUGGUUGUG	Cleavage
23	693	716	AGGCAAGAU	.: ::.::::: ::::::::	UUAUCUGUG	Translation
23	34	56	AGGCAAGAU	: :::: :::: .::::: .	AAAGCUUUG	Translation
23	1702	1724	AGGCAAGAU	:..: : ::::.:..:::: ::	AUGGAUUUG	Cleavage
23	606	628	AGGCAAGAU	::: :::::::: : ::..	UGAGCAAUG	Cleavage
23	1004	1026	AGGCAAGAU	: :::::::..:::::::::	AAAGCUAUG	Cleavage
23	366	388	AGGCAAGAU	:..::::::::::.: ::::.	AUGGCUAUG	Cleavage
23	859	881	AGGCAAGAU	.::::::::::..: : ::::..	GCAGCUAUG	Translation
23	895	917	AGGCAAGAU	:.::::::: ..::::::: .:	AUAGCUAUG	Cleavage
23	1000	1022	AGGCAAGAU	:.::: :::: :::::::: ::	AUAGCCAUG	Cleavage

23	1000	1022	AGGCAAGAU	:.::::::: ..::::::: .:	AUAGCUAUG	Cleavage
23	1064	1086	AGGCAAGAU	:.::: :::...::::::: ::	AUAGCAAUG	Cleavage
23	1000	1022	AGGCAAGAU	:.::::::: ..::::::: .:	AUAGCUAUG	Cleavage
23	1232	1255	AGGCAAGAU	::::::::...: ::::::::	CAAGCUAUG	Translation
23	1770	1792	AGGCAAGAU	:::.: ::.:::::. ::..	UCAGUUUUG	Cleavage
23	2276	2298	AGGCAAGAU	.:::.: ::.::..:.::::.	GCAGUUUCG	Cleavage
23	2353	2375	AGGCAAGAU	.:::.: ::.::..:.::::.	GCAGUUUCG	Cleavage
23	1513	1535	AGGCAAGAU	:.::: ::::::::.: :..	AUAGCACUG	Cleavage
23	733	755	AGGCAAGAU	.::. ::::.:: ::::::.:	UUAGUAAUG	Translation
23	809	831	AGGCAAGAU	:: :::: :.: ::::.::::.	ACUGCUAAG	Cleavage
23	1197	1220	AGGCA-AGAU	:::::::.::.::.: :::	GGUGCUAUG	Cleavage
23	1385	1407	AGGCAAGAU	:. ::::::. .:..:.::::	AUUGCUAUG	Cleavage
23	277	299	AGGCAAGAU	::: : .::::::. ::::::.	ACACCCGUGC	Cleavage
23	2137	2159	AGGCAAGAU	..:.:.::.::::.:: :::	UUGGUUGUG	Cleavage
23	693	716	AGGCAAGAU	.: ::.:::::: ::::::::	UUAUCUGUG	Translation
23	34	56	AGGCAAGAU	: :::: ::::: .:::::: .	AAAGCUUUG	Translation
23	1702	1724	AGGCAAGAU	:...: : ::::.:..:::: ::	AUGGAUUUG	Cleavage
23	606	628	AGGCAAGAU	::: ::::::::: : ::..	UGAGCAAUG	Cleavage

Target_Desc.	Multiplicity	Target_Acc.	locusName	Pfam
pacid=371666	1	Phvul.007G103100	Phvul.007G103100	PF02127
pacid=371666	1	Phvul.007G103100	Phvul.007G103100	PF02127
pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650
pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650
pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650
pacid=371750	1	Phvul.002G198200	Phvul.002G198200	PF12847
pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650
pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650
pacid=371508	1	Phvul.009G006000	Phvul.009G006000	PF00650
pacid=371750	1	Phvul.002G198200	Phvul.002G198200	PF12847
pacid=371692	2	Phvul.001G214600	Phvul.001G214600	0
pacid=371516	1	Phvul.009G150800	Phvul.009G150800	PF03151
pacid=371743	1	Phvul.002G261000	Phvul.002G261000	PF12070
pacid=371692	2	Phvul.001G214600	Phvul.001G214600	0
pacid=371516	1	Phvul.009G150800	Phvul.009G150800	PF03151
pacid=371743	1	Phvul.002G261000	Phvul.002G261000	PF12070
pacid=371685	1	Phvul.001G022900	Phvul.001G022900	PF00447
pacid=371580	1	Phvul.008G128900	Phvul.008G128900	PF00097
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371478	1	Phvul.003G174100	Phvul.003G174100	PF03144,PF0
pacid=371593	1	Phvul.008G040500	Phvul.008G040500	PF00854
pacid=371633	1	Phvul.004G018100	Phvul.004G018100	PF02705
pacid=371602	1	Phvul.008G290000	Phvul.008G290000	PF00627,PF0
pacid=371525	1	Phvul.005G040800	Phvul.005G040800	PF04652
pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11
pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11
pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11
pacid=371685	1	Phvul.001G022900	Phvul.001G022900	PF00447
pacid=371580	1	Phvul.008G128900	Phvul.008G128900	PF00097
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371709	1	Phvul.001G219900	Phvul.001G219900	PF00483
pacid=371478	1	Phvul.003G174100	Phvul.003G174100	PF03144,PF0
pacid=371593	1	Phvul.008G040500	Phvul.008G040500	PF00854
pacid=371633	1	Phvul.004G018100	Phvul.004G018100	PF02705
pacid=371602	1	Phvul.008G290000	Phvul.008G290000	PF00627,PF0
pacid=371525	1	Phvul.005G040800	Phvul.005G040800	PF04652
pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11

pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11
pacid=371440	1	Phvul.010G000700	Phvul.010G000700	PF12295,PF11
pacid=371489	1	Phvul.009G032100	Phvul.009G032100	PF04674
pacid=371515	1	Phvul.009G243500	Phvul.009G243500	PF00856
pacid=371751	1	Phvul.002G061200	Phvul.002G061200	PF08244,PF11
pacid=371613	1	Phvul.008G061900	Phvul.008G061900	PF07690
pacid=371613	1	Phvul.008G061900	Phvul.008G061900	PF07690
pacid=371613	1	Phvul.008G061900	Phvul.008G061900	PF07690
pacid=371514	1	Phvul.009G226500	Phvul.009G226500	PF16124,PF00
pacid=371514	1	Phvul.009G226500	Phvul.009G226500	PF16124,PF00
pacid=371506	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371506	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371506	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371505	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371774	1	Phvul.002G133900	Phvul.002G133900	0
pacid=371497	1	Phvul.009G106900	Phvul.009G106900	PF10255
pacid=371504	1	Phvul.009G036300	Phvul.009G036300	PF00249
pacid=371489	1	Phvul.009G192300	Phvul.009G192300	PF13414
pacid=371446	1	Phvul.003G112400	Phvul.003G112400	PF04802
pacid=371489	1	Phvul.009G032100	Phvul.009G032100	PF04674
pacid=371515	1	Phvul.009G243500	Phvul.009G243500	PF00856
pacid=371751	1	Phvul.002G061200	Phvul.002G061200	PF08244,PF11
pacid=371613	1	Phvul.008G061900	Phvul.008G061900	PF07690
pacid=371613	1	Phvul.008G061900	Phvul.008G061900	PF07690
pacid=371613	1	Phvul.008G061900	Phvul.008G061900	PF07690
pacid=371514	1	Phvul.009G226500	Phvul.009G226500	PF16124,PF00
pacid=371514	1	Phvul.009G226500	Phvul.009G226500	PF16124,PF00
pacid=371506	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371506	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371506	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371505	1	Phvul.009G242900	Phvul.009G242900	PF07687,PF01
pacid=371774	1	Phvul.002G133900	Phvul.002G133900	0
pacid=371497	1	Phvul.009G106900	Phvul.009G106900	PF10255
pacid=371504	1	Phvul.009G036300	Phvul.009G036300	PF00249
pacid=371489	1	Phvul.009G192300	Phvul.009G192300	PF13414
pacid=371446	1	Phvul.003G112400	Phvul.003G112400	PF04802
pacid=371734	1	Phvul.006G151200	Phvul.006G151200	PF00849
pacid=371721	1	Phvul.006G104300	Phvul.006G104300	PF06101
pacid=371721	1	Phvul.006G104300	Phvul.006G104300	PF06101
pacid=371563	1	Phvul.011G033500	Phvul.011G033500	PF01535,PF13
pacid=371588	1	Phvul.008G038200	Phvul.008G038200	PF00249
pacid=371787	1	Phvul.002G022400	Phvul.002G022400	PF01535,PF13
pacid=371742	1	Phvul.L001644	Phvul.L001644	PF14432,PF01

pacid=371686	1	Phvul.001G264132	Phvul.001G264132	PF00270
pacid=371502	1	Phvul.009G019100	Phvul.009G019100	PF01399,PF08
pacid=371514	1	Phvul.009G073900	Phvul.009G073900	0
pacid=371469	1	Phvul.003G159700	Phvul.003G159700	PF08263,PF13
pacid=371734	1	Phvul.006G151200	Phvul.006G151200	PF00849
pacid=371721	1	Phvul.006G104300	Phvul.006G104300	PF06101
pacid=371721	1	Phvul.006G104300	Phvul.006G104300	PF06101
pacid=371563	1	Phvul.011G033500	Phvul.011G033500	PF01535,PF13
pacid=371588	1	Phvul.008G038200	Phvul.008G038200	PF00249
pacid=371787	1	Phvul.002G022400	Phvul.002G022400	PF01535,PF13
pacid=371742	1	Phvul.L001644	Phvul.L001644	PF14432,PF01
pacid=371686	1	Phvul.001G264132	Phvul.001G264132	PF00270
pacid=371502	1	Phvul.009G019100	Phvul.009G019100	PF01399,PF08
pacid=371514	1	Phvul.009G073900	Phvul.009G073900	0
pacid=371469	1	Phvul.003G159700	Phvul.003G159700	PF08263,PF13
pacid=371692	2	Phvul.001G214600	Phvul.001G214600	0
pacid=371486	1	Phvul.009G228600	Phvul.009G228600	PF06596
pacid=371491	1	Phvul.009G035800	Phvul.009G035800	PF07714,PF14
pacid=371564	1	Phvul.011G134100	Phvul.011G134100	PF08246,PF00
pacid=371557	1	Phvul.011G134000	Phvul.011G134000	PF08246,PF00
pacid=371547	1	Phvul.011G130800	Phvul.011G130800	PF08246,PF00
pacid=371568	1	Phvul.011G081100	Phvul.011G081100	PF08246,PF00
pacid=371571	1	Phvul.011G133300	Phvul.011G133300	PF08246,PF00
pacid=371674	1	Phvul.007G247800	Phvul.007G247800	PF12922,PF12
pacid=371622	1	Phvul.004G172000	Phvul.004G172000	0
pacid=371435	1	Phvul.010G031700	Phvul.010G031700	PF04130
pacid=371435	1	Phvul.010G031700	Phvul.010G031700	PF04130
pacid=371533	1	Phvul.005G105800	Phvul.005G105800	PF05623
pacid=371519	1	Phvul.009G021200	Phvul.009G021200	0
pacid=371493	1	Phvul.009G226800	Phvul.009G226800	PF04525
pacid=371719	1	Phvul.006G162000	Phvul.006G162000	PF00097,PF05
pacid=371757	1	Phvul.002G038300	Phvul.002G038300	PF06101
pacid=371658	1	Phvul.007G188300	Phvul.007G188300	PF11721,PF07
pacid=371636	1	Phvul.004G084688	Phvul.004G084688	PF08263,PF00
pacid=371521	1	Phvul.L001859	Phvul.L001859	0
pacid=371753	1	Phvul.002G027900	Phvul.002G027900	PF00190
pacid=371530	1	Phvul.005G180700	Phvul.005G180700	PF00690,PF00
pacid=371631	1	Phvul.004G153700	Phvul.004G153700	PF13041,PF01
pacid=371692	2	Phvul.001G214600	Phvul.001G214600	0
pacid=371486	1	Phvul.009G228600	Phvul.009G228600	PF06596
pacid=371491	1	Phvul.009G035800	Phvul.009G035800	PF07714,PF14
pacid=371564	1	Phvul.011G134100	Phvul.011G134100	PF08246,PF00
pacid=371557	1	Phvul.011G134000	Phvul.011G134000	PF08246,PF00

pacid=371547	1	Phvul.011G130800	Phvul.011G130800	PF08246,PF00
pacid=371568	1	Phvul.011G081100	Phvul.011G081100	PF08246,PF00
pacid=371571	1	Phvul.011G133300	Phvul.011G133300	PF08246,PF00
pacid=371674	1	Phvul.007G247800	Phvul.007G247800	PF12922,PF12
pacid=371622	1	Phvul.004G172000	Phvul.004G172000	0
pacid=371435	1	Phvul.010G031700	Phvul.010G031700	PF04130
pacid=371435	1	Phvul.010G031700	Phvul.010G031700	PF04130
pacid=371533	1	Phvul.005G105800	Phvul.005G105800	PF05623
pacid=371519	1	Phvul.009G021200	Phvul.009G021200	0
pacid=371493	1	Phvul.009G226800	Phvul.009G226800	PF04525
pacid=371719	1	Phvul.006G162000	Phvul.006G162000	PF00097,PF05
pacid=371757	1	Phvul.002G038300	Phvul.002G038300	PF06101
pacid=371658	1	Phvul.007G188300	Phvul.007G188300	PF11721,PF07
pacid=371636	1	Phvul.004G084688	Phvul.004G084688	PF08263,PF00
pacid=371521	1	Phvul.L001859	Phvul.L001859	0
pacid=371753	1	Phvul.002G027900	Phvul.002G027900	PF00190
pacid=371530	1	Phvul.005G180700	Phvul.005G180700	PF00690,PF00
pacid=371631	1	Phvul.004G153700	Phvul.004G153700	PF13041,PF01

Panther	KOG	KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
PTHR28570,P	0	3.4.11.21	K01267	GO:0008270,(	AT5G04710.1	0
PTHR28570,P	0	3.4.11.21	K01267	GO:0008270,(	AT5G04710.1	0
PTHR23324,P	0	0	0	0	AT4G39170.1	0
PTHR23324,P	0	0	0	0	AT4G39170.1	0
PTHR23324,P	0	0	0	0	AT4G39170.1	0
PTHR21404	KOG1045	0	0	GO:0008173,(	AT4G20910.1	CRM2,HEN1
PTHR23324,P	0	0	0	0	AT4G39170.1	0
PTHR23324,P	0	0	0	0	AT4G39170.1	0
PTHR23324,P	0	0	0	0	AT4G39170.1	0
PTHR21404	KOG1045	0	0	GO:0008173,(	AT4G20910.1	CRM2,HEN1
PTHR34210,P	0	0	0	0	AT3G62330.1	0
PTHR11132,P	KOG1444	0	K15356	0	AT2G13650.1	GONST1
PTHR21243,P	0	0	0	GO:0006351,(	AT4G40050.1	0
PTHR34210,P	0	0	0	0	AT3G62330.1	0
PTHR11132,P	KOG1444	0	K15356	0	AT2G13650.1	GONST1
PTHR21243,P	0	0	0	GO:0006351,(	AT4G40050.1	0
PTHR10015,P	0	0	K09419	GO:0043565,(	AT1G46264.1	AT-HSFB4,HSF
PTHR10825,P	0	6.3.2.19	K10695	GO:0046872	AT5G44280.1	ATRING1A,RIN
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR23115,P	0	3.6.5.3	K12852	GO:0005525	AT1G06220.1	CLO,GFA1,ME
PTHR11654,P	0	0	0	GO:0016020,(	AT1G32450.1	NRT1.5
PTHR30540,P	0	0	K03549	GO:0071805,(	AT5G14880.1	0
PTHR13779,P	0	3.6.1.3	K07478	GO:0005524	AT1G24290.1	0
PTHR12741,P	0	2.4.1.34	K11000	GO:0003843	AT2G31960.2	ATGSL03,ATG
PTHR15245,P	KOG1895	0	0	0	AT5G01400.1	ESP4
PTHR15245,P	KOG1895	0	0	0	AT5G01400.1	ESP4
PTHR15245,P	KOG1895	0	0	0	AT5G01400.1	ESP4
PTHR10015,P	0	0	K09419	GO:0043565,(	AT1G46264.1	AT-HSFB4,HSF
PTHR10825,P	0	6.3.2.19	K10695	GO:0046872	AT5G44280.1	ATRING1A,RIN
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR22572,P	KOG1322	2.7.7.27	0	GO:0016779,(	AT1G27680.1	APL2
PTHR23115,P	0	3.6.5.3	K12852	GO:0005525	AT1G06220.1	CLO,GFA1,ME
PTHR11654,P	0	0	0	GO:0016020,(	AT1G32450.1	NRT1.5
PTHR30540,P	0	0	K03549	GO:0071805,(	AT5G14880.1	0
PTHR13779,P	0	3.6.1.3	K07478	GO:0005524	AT1G24290.1	0
PTHR12741,P	0	2.4.1.34	K11000	GO:0003843	AT2G31960.2	ATGSL03,ATG
PTHR15245,P	KOG1895	0	0	0	AT5G01400.1	ESP4

PTHR15245,P	KOG1895		0	0	0	AT5G01400.1 ESP4
PTHR15245,P	KOG1895		0	0	0	AT5G01400.1 ESP4
PTHR31279,P	0	0	0	0	AT4G08950.1	EXO
PTHR13271,P	0	2.1.1.127	0	GO:0005515	AT4G20130.1	PTAC14
PTHR31953,P	0	3.2.1.26	K01193	GO:0004575,	AT1G12240.1	ATBETAFRUCT
PTHR11662,P	KOG2532	0	0	GO:0055085,	AT4G00370.1	ANTR2,PHT4;
PTHR11662,P	KOG2532	0	0	GO:0055085,	AT4G00370.1	ANTR2,PHT4;
PTHR11662,P	KOG2532	0	0	GO:0055085,	AT4G00370.1	ANTR2,PHT4;
PTHR13710,P	KOG0352	3.6.4.12	K10901	GO:0005524,	AT4G35740.1	ATRECQ3,Rec
PTHR13710,P	KOG0352	3.6.4.12	K10901	GO:0005524,	AT4G35740.1	ATRECQ3,Rec
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
0	0	0	0	0	0	0
PTHR13242	KOG3677	0	K15029	GO:0005852,	AT5G25754.1	0
PTHR21717,P	0	0	0	0	AT1G09710.2	0
PTHR16193	KOG1128	0	0	0	AT5G17270.1	0
PTHR23318,P	KOG2175	0	K17491	0	AT3G06670.1	0
PTHR31279,P	0	0	0	0	AT4G08950.1	EXO
PTHR13271,P	0	2.1.1.127	0	GO:0005515	AT4G20130.1	PTAC14
PTHR31953,P	0	3.2.1.26	K01193	GO:0004575,	AT1G12240.1	ATBETAFRUCT
PTHR11662,P	KOG2532	0	0	GO:0055085,	AT4G00370.1	ANTR2,PHT4;
PTHR11662,P	KOG2532	0	0	GO:0055085,	AT4G00370.1	ANTR2,PHT4;
PTHR11662,P	KOG2532	0	0	GO:0055085,	AT4G00370.1	ANTR2,PHT4;
PTHR13710,P	KOG0352	3.6.4.12	K10901	GO:0005524,	AT4G35740.1	ATRECQ3,Rec
PTHR13710,P	KOG0352	3.6.4.12	K10901	GO:0005524,	AT4G35740.1	ATRECQ3,Rec
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
PTHR32494,P	0	3.5.3.9	0	GO:0016787,	AT4G20070.1	AAH,ATAAH
0	0	0	0	0	0	0
PTHR13242	KOG3677	0	K15029	GO:0005852,	AT5G25754.1	0
PTHR21717,P	0	0	0	0	AT1G09710.2	0
PTHR16193	KOG1128	0	0	0	AT5G17270.1	0
PTHR23318,P	KOG2175	0	K17491	0	AT3G06670.1	0
PTHR11079,P	KOG1919	5.4.99.24	0	GO:0009982,	AT4G21770.1	0
PTHR17204,P	0	0	0	0	AT3G04350.1	0
PTHR17204,P	0	0	0	0	AT3G04350.1	0
PTHR24015,P	0	0	0	0	AT2G21090.1	0
PTHR10641,P	0	0	0	0	AT1G66370.1	AtMYB113,MY
PTHR24015,P	0	0	0	0	AT3G50420.1	0
PTHR24015,P	0	0	0	0	AT1G25360.1	0

PTHR18934,P	0	3.6.4.13	0	GO:0005524,(	AT3G26560.1	0
PTHR10758,P	0	0	K03033	GO:0005515,(	AT1G20200.1	EMB2719,HAI
PTHR37613	0	0	0	0	0	0
PTHR27008,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT2G26730.1	0
PTHR11079,P	KOG1919	5.4.99.24	0	GO:0009982,(	AT4G21770.1	0
PTHR17204,P	0	0	0	0	AT3G04350.1	0
PTHR17204,P	0	0	0	0	AT3G04350.1	0
PTHR24015,P	0	0	0	0	AT2G21090.1	0
PTHR10641,P	0	0	0	0	AT1G66370.1	AtMYB113,MY
PTHR24015,P	0	0	0	0	AT3G50420.1	0
PTHR24015,P	0	0	0	0	AT1G25360.1	0
PTHR18934,P	0	3.6.4.13	0	GO:0005524,(	AT3G26560.1	0
PTHR10758,P	0	0	K03033	GO:0005515,(	AT1G20200.1	EMB2719,HAI
PTHR37613	0	0	0	0	0	0
PTHR27008,P	KOG1187	2.7.11.1	0	GO:0005515,(	AT2G26730.1	0
PTHR34210,P	0	0	0	0	AT3G62330.1	0
PTHR34455,P	0	0	0	GO:0016020,(	AT2G06520.1	PSBX
PTHR23257,P	KOG0192	2.7.11.1	0	GO:0006468,(	AT4G24480.1	0
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR14222,P	0	0	K06677	GO:0007076	AT3G57060.2	0
PTHR35505,P	0	0	0	0	AT5G11780.1	0
PTHR19302,P	0	0	K16569	GO:0005815,(	AT5G17410.2	0
PTHR19302,P	0	0	K16569	GO:0005815,(	AT5G17410.2	0
PTHR31343,P	0	0	0	0	AT4G03420.1	0
PTHR34936,P	0	0	0	0	AT1G20460.1	0
PTHR31087,P	0	0	0	0	AT2G05910.1	0
PTHR21319,P	KOG1940	6.3.2.19	K10144	GO:0046872,(	AT5G18650.1	0
PTHR17204,P	0	0	0	0	AT5G43950.1	0
PTHR27003,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G28680.1	ANX2
PTHR27000,P	KOG1187	2.7.10.1	0	GO:0005515,(	AT1G34420.1	0
0	0	0	0	0	0	0
PTHR31189,P	0	0	0	GO:0045735	AT2G18540.1	0
PTHR24093,P	0	3.6.3.6	K01535	GO:0046872,(	AT1G80660.1	AHA9,HA9
PTHR24015,P	0	0	0	0	AT5G66520.1	0
PTHR34210,P	0	0	0	0	AT3G62330.1	0
PTHR34455,P	0	0	0	GO:0016020,(	AT2G06520.1	PSBX
PTHR23257,P	KOG0192	2.7.11.1	0	GO:0006468,(	AT4G24480.1	0
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12

PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR12411,P	KOG1543	3.4.22.33	0	GO:0008234,(	AT5G45890.1	SAG12
PTHR14222,P	0	0	K06677	GO:0007076	AT3G57060.2	0
PTHR35505,P	0	0	0	0	AT5G11780.1	0
PTHR19302,P	0	0	K16569	GO:0005815,(	AT5G17410.2	0
PTHR19302,P	0	0	K16569	GO:0005815,(	AT5G17410.2	0
PTHR31343,P	0	0	0	0	AT4G03420.1	0
PTHR34936,P	0	0	0	0	AT1G20460.1	0
PTHR31087,P	0	0	0	0	AT2G05910.1	0
PTHR21319,P	KOG1940	6.3.2.19	K10144	GO:0046872,(	AT5G18650.1	0
PTHR17204,P	0	0	0	0	AT5G43950.1	0
PTHR27003,P	KOG1187	2.7.11.1	0	GO:0006468,(	AT5G28680.1	ANX2
PTHR27000,P	KOG1187	2.7.10.1	0	GO:0005515,(	AT1G34420.1	0
0	0	0	0	0	0	0
PTHR31189,P	0	0	0	GO:0045735	AT2G18540.1	0
PTHR24093,P	0	3.6.3.6	K01535	GO:0046872,(	AT1G80660.1	AHA9,HA9
PTHR24015,P	0	0	0	0	AT5G66520.1	0

arabi-defline	ID	Annot_defline	IDENTIFIER
Zn-dependent exopeptidases superfamily prot	Phvul.007G10	PTHR28570:S	Phvul.007G10
Zn-dependent exopeptidases superfamily prot	Phvul.007G10	PTHR28570:S	Phvul.007G10
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00	PTHR23324:S	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00	PTHR23324:S	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00	PTHR23324:S	Phvul.009G00
double-stranded RNA binding protein-related	Phvul.002G19	PTHR21404 -	Phvul.002G19
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00	PTHR23324:S	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00	PTHR23324:S	Phvul.009G00
Sec14p-like phosphatidylinositol transfer famil	Phvul.009G00	PTHR23324:S	Phvul.009G00
double-stranded RNA binding protein-related	Phvul.002G19	PTHR21404 -	Phvul.002G19
Zinc knuckle (CCHC-type) family protein	0	0	Phvul.001G21
golgi nucleotide sugar transporter 1	Phvul.009G15	K15356 - GDP	Phvul.009G15
Protein of unknown function (DUF3550/UPF0	Phvul.002G26	PF12070 - Pro	Phvul.002G26
Zinc knuckle (CCHC-type) family protein	0	0	Phvul.001G21
golgi nucleotide sugar transporter 1	Phvul.009G15	K15356 - GDP	Phvul.009G15
Protein of unknown function (DUF3550/UPF0	Phvul.002G26	PF12070 - Pro	Phvul.002G26
heat shock transcription factor B4	Phvul.001G02	PTHR10015:S	Phvul.001G02
RING 1A	Phvul.008G12	PTHR10825:S	Phvul.008G12
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
Ribosomal protein S5/Elongation factor G/III/V	Phvul.003G17	K12852 - 116	Phvul.003G17
nitrate transporter 1.5	Phvul.008G04	PTHR11654:S	Phvul.008G04
Potassium transporter family protein	Phvul.004G01	PTHR30540:S	Phvul.004G01
AAA-type ATPase family protein	Phvul.008G29	K07478 - puta	Phvul.008G29
glucan synthase-like 3	Phvul.005G04	PTHR12741:S	Phvul.005G04
HEAT repeat-containing protein	Phvul.010G00	PTHR15245//	Phvul.010G00
HEAT repeat-containing protein	Phvul.010G00	PTHR15245//	Phvul.010G00
HEAT repeat-containing protein	Phvul.010G00	PTHR15245//	Phvul.010G00
heat shock transcription factor B4	Phvul.001G02	PTHR10015:S	Phvul.001G02
RING 1A	Phvul.008G12	PTHR10825:S	Phvul.008G12
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
ADPGLC-PPase large subunit	Phvul.001G21	PTHR22572//	Phvul.001G21
Ribosomal protein S5/Elongation factor G/III/V	Phvul.003G17	K12852 - 116	Phvul.003G17
nitrate transporter 1.5	Phvul.008G04	PTHR11654:S	Phvul.008G04
Potassium transporter family protein	Phvul.004G01	PTHR30540:S	Phvul.004G01
AAA-type ATPase family protein	Phvul.008G29	K07478 - puta	Phvul.008G29
glucan synthase-like 3	Phvul.005G04	PTHR12741:S	Phvul.005G04
HEAT repeat-containing protein	Phvul.010G00	PTHR15245//	Phvul.010G00

HEAT repeat-containing protein	Phvul.010G00	PTHR15245//	Phvul.010G00
HEAT repeat-containing protein	Phvul.010G00	PTHR15245//	Phvul.010G00
Phosphate-responsive 1 family protein	Phvul.009G03	PTHR31279:S	Phvul.009G03
plastid transcriptionally active 14	Phvul.009G24	PTHR13271:S	Phvul.009G24
Glycosyl hydrolases family 32 protein	Phvul.002G06	PTHR31953:S	Phvul.002G06
Major facilitator superfamily protein	Phvul.008G06	PTHR11662:S	Phvul.008G06
Major facilitator superfamily protein	Phvul.008G06	PTHR11662:S	Phvul.008G06
Major facilitator superfamily protein	Phvul.008G06	PTHR11662:S	Phvul.008G06
DEAD/DEAH box RNA helicase family protein	Phvul.009G22	PTHR13710:S	Phvul.009G22
DEAD/DEAH box RNA helicase family protein	Phvul.009G22	PTHR13710:S	Phvul.009G22
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
0	0	0	Phvul.002G13
RNA polymerase I-associated factor PAF67	Phvul.009G10	K15029 - tran	Phvul.009G10
Homeodomain-like superfamily protein	Phvul.009G03	PTHR21717:S	Phvul.009G03
Protein prenylyltransferase superfamily protei	Phvul.009G19	KOG1128 - Un	Phvul.009G19
binding	Phvul.003G11	K17491 - prot	Phvul.003G11
Phosphate-responsive 1 family protein	Phvul.009G03	PTHR31279:S	Phvul.009G03
plastid transcriptionally active 14	Phvul.009G24	PTHR13271:S	Phvul.009G24
Glycosyl hydrolases family 32 protein	Phvul.002G06	PTHR31953:S	Phvul.002G06
Major facilitator superfamily protein	Phvul.008G06	PTHR11662:S	Phvul.008G06
Major facilitator superfamily protein	Phvul.008G06	PTHR11662:S	Phvul.008G06
Major facilitator superfamily protein	Phvul.008G06	PTHR11662:S	Phvul.008G06
DEAD/DEAH box RNA helicase family protein	Phvul.009G22	PTHR13710:S	Phvul.009G22
DEAD/DEAH box RNA helicase family protein	Phvul.009G22	PTHR13710:S	Phvul.009G22
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
allantoate amidohydrolase	Phvul.009G24	K02083 - allan	Phvul.009G24
0	0	0	Phvul.002G13
RNA polymerase I-associated factor PAF67	Phvul.009G10	K15029 - tran	Phvul.009G10
Homeodomain-like superfamily protein	Phvul.009G03	PTHR21717:S	Phvul.009G03
Protein prenylyltransferase superfamily protei	Phvul.009G19	KOG1128 - Un	Phvul.009G19
binding	Phvul.003G11	K17491 - prot	Phvul.003G11
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S	Phvul.006G15
Plant protein of unknown function (DUF946)	Phvul.006G10	PTHR17204//	Phvul.006G10
Plant protein of unknown function (DUF946)	Phvul.006G10	PTHR17204//	Phvul.006G10
Pentatricopeptide repeat (PPR-like) superfamil	Phvul.011G03	PF01535//PF1	Phvul.011G03
myb domain protein 113	Phvul.008G03	PTHR10641:S	Phvul.008G03
Pentatricopeptide repeat (PPR) superfamily pr	Phvul.002G02	PF01535//PF1	Phvul.002G02
Pentatricopeptide repeat (PPR) superfamily pr	Phvul.L00164	PF01535//PF1	Phvul.L00164

ATP-dependent RNA helicase, putative	Phvul.001G26	PTHR18934//	Phvul.001G26
PAM domain (PCI/PINT associated module) pr	Phvul.009G01	K03033 - 26S	Phvul.009G01
0	0	0	Phvul.009G07
Leucine-rich repeat protein kinase family prot	Phvul.003G15	PF00069//PF	Phvul.003G15
Pseudouridine synthase family protein	Phvul.006G15	PTHR11079:S	Phvul.006G15
Plant protein of unknown function (DUF946)	Phvul.006G10	PTHR17204//	Phvul.006G10
Plant protein of unknown function (DUF946)	Phvul.006G10	PTHR17204//	Phvul.006G10
Pentatricopeptide repeat (PPR-like) superfami	Phvul.011G03	PF01535//PF1	Phvul.011G03
myb domain protein 113	Phvul.008G03	PTHR10641:S	Phvul.008G03
Pentatricopeptide repeat (PPR) superfamily pr	Phvul.002G02	PF01535//PF1	Phvul.002G02
Pentatricopeptide repeat (PPR) superfamily pr	Phvul.L00164	PF01535//PF1	Phvul.L00164
ATP-dependent RNA helicase, putative	Phvul.001G26	PTHR18934//	Phvul.001G26
PAM domain (PCI/PINT associated module) pr	Phvul.009G01	K03033 - 26S	Phvul.009G01
0	0	0	Phvul.009G07
Leucine-rich repeat protein kinase family prot	Phvul.003G15	PF00069//PF	Phvul.003G15
Zinc knuckle (CCHC-type) family protein	0	0	Phvul.001G21
photosystem II subunit X	Phvul.009G22	PTHR34455:S	Phvul.009G22
Protein kinase superfamily protein	Phvul.009G03	PTHR23257:S	Phvul.009G03
senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13
senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13
senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13
senescence-associated gene 12	Phvul.011G08	PTHR12411//	Phvul.011G08
senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13
binding	Phvul.007G24	K06677 - conc	Phvul.007G24
0	0	0	Phvul.004G17
Spc97 / Spc98 family of spindle pole body (SBP	Phvul.010G03	K16569 - gam	Phvul.010G03
Spc97 / Spc98 family of spindle pole body (SBP	Phvul.010G03	K16569 - gam	Phvul.010G03
Protein of unknown function (DUF789)	Phvul.005G10	PTHR31343:S	Phvul.005G10
0	0	0	Phvul.009G02
Protein of unknown function (DUF567)	Phvul.009G22	PTHR31087:S	Phvul.009G22
CHY-type/CTCHY-type/RING-type Zinc finger p	Phvul.006G16	PTHR21319//	Phvul.006G16
Plant protein of unknown function (DUF946)	Phvul.002G03	PTHR17204//	Phvul.002G03
Malectin/receptor-like protein kinase family p	Phvul.007G18	PTHR27003:S	Phvul.007G18
leucine-rich repeat transmembrane protein ki	Phvul.004G08	PTHR27000:S	Phvul.004G08
0	0	0	Phvul.L00185
RmlC-like cupins superfamily protein	Phvul.002G02	PTHR31189:S	Phvul.002G02
H(+)-ATPase 9	Phvul.005G18	PTHR24093:S	Phvul.005G18
Tetratricopeptide repeat (TPR)-like superfami	Phvul.004G15	PF01535//PF1	Phvul.004G15
Zinc knuckle (CCHC-type) family protein	0	0	Phvul.001G21
photosystem II subunit X	Phvul.009G22	PTHR34455:S	Phvul.009G22
Protein kinase superfamily protein	Phvul.009G03	PTHR23257:S	Phvul.009G03
senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13
senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13

senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13
senescence-associated gene 12	Phvul.011G08	PTHR12411//	Phvul.011G08
senescence-associated gene 12	Phvul.011G13	PTHR12411:S	Phvul.011G13
binding	Phvul.007G24	K06677 - conc	Phvul.007G24
0	0	0	Phvul.004G17
Spc97 / Spc98 family of spindle pole body (SBP	Phvul.010G03	K16569 - gam	Phvul.010G03
Spc97 / Spc98 family of spindle pole body (SBP	Phvul.010G03	K16569 - gam	Phvul.010G03
Protein of unknown function (DUF789)	Phvul.005G10	PTHR31343:S	Phvul.005G10
0	0	0	Phvul.009G02
Protein of unknown function (DUF567)	Phvul.009G22	PTHR31087:S	Phvul.009G22
CHY-type/CTCHY-type/RING-type Zinc finger p	Phvul.006G16	PTHR21319//	Phvul.006G16
Plant protein of unknown function (DUF946)	Phvul.002G03	PTHR17204//	Phvul.002G03
Malectin/receptor-like protein kinase family p	Phvul.007G18	PTHR27003:S	Phvul.007G18
leucine-rich repeat transmembrane protein ki	Phvul.004G08	PTHR27000:S	Phvul.004G08
0	0	0	Phvul.L00185
RmlC-like cupins superfamily protein	Phvul.002G02	PTHR31189:S	Phvul.002G02
H(+)-ATPase 9	Phvul.005G18	PTHR24093:S	Phvul.005G18
Tetratricopeptide repeat (TPR)-like superfamil	Phvul.004G15	PF01535//PF1	Phvul.004G15

NAME	DESCRIPTION
Protein home	M18-class aspartyl aminopeptidase (DAP) (original description: pacid=37166631 tran
Protein home	M18-class aspartyl aminopeptidase (DAP) (original description: pacid=37166631 tran
not assigned.	(original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.
not assigned.	(original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.
not assigned.	(original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.
RNA processi	miRNA/siRNA methyltransferase (HEN1) (original description: pacid=37175057 trans
not assigned.	(original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.
not assigned.	(original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.
not assigned.	(original description: pacid=37150821 transcript=Phvul.009G006000.3 locus=Phvul.
RNA processi	miRNA/siRNA methyltransferase (HEN1) (original description: pacid=37175057 trans
not assigned.	no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu
Solute transp	nucleotide sugar transporter (GONST1|2|3|4) (original description: pacid=37151677
not assigned.	no hits & (original description: pacid=37174363 transcript=Phvul.002G261000.1 locu
not assigned.	no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu
Solute transp	nucleotide sugar transporter (GONST1|2|3|4) (original description: pacid=37151677
not assigned.	no hits & (original description: pacid=37174363 transcript=Phvul.002G261000.1 locu
RNA biosynth	transcription factor (HSF) (original description: pacid=37168548 transcript=Phvul.001
Chromatin or	modification writer component RING1 of modification writer protein components (o
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
RNA processi	protein factor SNU114/U5-116kDa of U5 small nuclear ribonucleoprotein particle (sn
Solute transp	anion transporter (NRT1/PTR) (original description: pacid=37159373 transcript=Phvu
Solute transp	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37163324 tr
not assigned.	no hits & (original description: pacid=37160223 transcript=Phvul.008G290000.1 locu
not assigned.	(original description: pacid=37152506 transcript=Phvul.005G040800.1 locus=Phvul.
RNA processi	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
RNA processi	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
RNA processi	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
RNA biosynth	transcription factor (HSF) (original description: pacid=37168548 transcript=Phvul.001
Chromatin or	modification writer component RING1 of modification writer protein components (o
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
Carbohydrate	ADP-glucose pyrophosphorylase (original description: pacid=37170950 transcript=Ph
RNA processi	protein factor SNU114/U5-116kDa of U5 small nuclear ribonucleoprotein particle (sn
Solute transp	anion transporter (NRT1/PTR) (original description: pacid=37159373 transcript=Phvu
Solute transp	potassium cation transporter (HAK/KUP/KT) (original description: pacid=37163324 tr
not assigned.	no hits & (original description: pacid=37160223 transcript=Phvul.008G290000.1 locu
not assigned.	(original description: pacid=37152506 transcript=Phvul.005G040800.1 locus=Phvul.
RNA processi	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF

RNA processir	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
RNA processir	component Symplekin/Pta1 of Cleavage and Polyadenylation Specificity Factor (CPSF
not assigned.a	(original description: pacid=37148991 transcript=Phvul.009G032100.1 locus=Phvul.0
RNA biosynth	PAP7/TAC14 cofactor of plastid-encoded RNA polymerase (original description: pacic
Carbohydrate	acid beta-fructofuranosidase (VIN) (original description: pacid=37175113 transcript=
Solute transpo	phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
Solute transpo	phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
Solute transpo	phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
not assigned.a	(original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.0
not assigned.a	(original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.0
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
not assigned.r	no hits & (original description: pacid=37177485 transcript=Phvul.002G133900.2 locu
Protein biosyr	component eIF3l of eIF3 mRNA-to-PIC binding complex (original description: pacid=3
RNA biosynth	transcription factor (MYB-related) (original description: pacid=37150497 transcript=F
not assigned.r	no hits & (original description: pacid=37148905 transcript=Phvul.009G192300.1 locu
Protein modif	regulatory component PP4R3 of PP4 phosphatase complex (original description: paci
not assigned.a	(original description: pacid=37148991 transcript=Phvul.009G032100.1 locus=Phvul.0
RNA biosynth	PAP7/TAC14 cofactor of plastid-encoded RNA polymerase (original description: pacic
Carbohydrate	acid beta-fructofuranosidase (VIN) (original description: pacid=37175113 transcript=
Solute transpo	phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
Solute transpo	phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
Solute transpo	phosphate transporter (PHT4) (original description: pacid=37161312 transcript=Phvu
not assigned.a	(original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.0
not assigned.a	(original description: pacid=37151468 transcript=Phvul.009G226500.2 locus=Phvul.0
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
Nucleotide me	allantoate amidohydrolase (original description: pacid=37150600 transcript=Phvul.00
not assigned.r	no hits & (original description: pacid=37177485 transcript=Phvul.002G133900.2 locu
Protein biosyr	component eIF3l of eIF3 mRNA-to-PIC binding complex (original description: pacid=3
RNA biosynth	transcription factor (MYB-related) (original description: pacid=37150497 transcript=F
not assigned.r	no hits & (original description: pacid=37148905 transcript=Phvul.009G192300.1 locu
Protein modif	regulatory component PP4R3 of PP4 phosphatase complex (original description: paci
not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1 locus=Phvul.0
not assigned.r	no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
not assigned.r	no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
not assigned.a	(original description: pacid=37156354 transcript=Phvul.011G033500.1 locus=Phvul.0
RNA biosynth	transcription factor (MYB) (original description: pacid=37158898 transcript=Phvul.00
not assigned.a	(original description: pacid=37178778 transcript=Phvul.002G022400.1 locus=Phvul.0
not assigned.a	(original description: pacid=37174264 transcript=Phvul.L001644.1 locus=Phvul.L001

not assigned.a	(original description: pacid=37168645 transcript=Phvul.001G264132.1 locus=Phvul.0
Protein home	regulatory component RPN3 of 26S proteasome (original description: pacid=371502
not assigned.n	no hits & (original description: pacid=37151497 transcript=Phvul.009G073900.1 locu
Protein modif	protein kinase (LRR-III) (original description: pacid=37146991 transcript=Phvul.003G1
not assigned.a	(original description: pacid=37173420 transcript=Phvul.006G151200.1 locus=Phvul.0
not assigned.n	no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
not assigned.n	no hits & (original description: pacid=37172154 transcript=Phvul.006G104300.2 locu
not assigned.a	(original description: pacid=37156354 transcript=Phvul.011G033500.1 locus=Phvul.0
RNA biosynth	transcription factor (MYB) (original description: pacid=37158898 transcript=Phvul.00
not assigned.a	(original description: pacid=37178778 transcript=Phvul.002G022400.1 locus=Phvul.0
not assigned.a	(original description: pacid=37174264 transcript=Phvul.L001644.1 locus=Phvul.L001
not assigned.a	(original description: pacid=37168645 transcript=Phvul.001G264132.1 locus=Phvul.0
Protein home	regulatory component RPN3 of 26S proteasome (original description: pacid=371502
not assigned.n	no hits & (original description: pacid=37151497 transcript=Phvul.009G073900.1 locu
Protein modif	protein kinase (LRR-III) (original description: pacid=37146991 transcript=Phvul.003G1
not assigned.n	no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu
Photosynthesi	component PsbX of PS-II complex (original description: pacid=37148668 transcript=P
Protein modif	protein kinase (MAP3K-RAF) (original description: pacid=37149156 transcript=Phvul.
Protein home	protease (Papain) (original description: pacid=37156473 transcript=Phvul.011G1341
Protein home	protease (Papain) (original description: pacid=37155727 transcript=Phvul.011G1340
Protein home	protease (Papain) (original description: pacid=37154718 transcript=Phvul.011G1308
Protein home	protease (Papain) (original description: pacid=37156814 transcript=Phvul.011G0811
Protein home	protease (Papain) (original description: pacid=37157156 transcript=Phvul.011G1333
Cell cycle orga	component CAP-D2A of condensin I complex (original description: pacid=37167459 t
not assigned.n	no hits & (original description: pacid=37162297 transcript=Phvul.004G172000.1 locu
Cytoskeleton	component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
Cytoskeleton	component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
not assigned.n	no hits & (original description: pacid=37153352 transcript=Phvul.005G105800.1 locu
not assigned.n	no hits & (original description: pacid=37151943 transcript=Phvul.009G021200.1 locu
not assigned.a	(original description: pacid=37149394 transcript=Phvul.009G226800.1 locus=Phvul.0
not assigned.a	(original description: pacid=37171980 transcript=Phvul.006G162000.1 locus=Phvul.0
not assigned.n	no hits & (original description: pacid=37175715 transcript=Phvul.002G038300.1 locu
Protein modif	protein kinase (CrlRLK1) (original description: pacid=37165831 transcript=Phvul.007
Protein modif	protein kinase (LRR-Xc) (original description: pacid=37163699 transcript=Phvul.004G
not assigned.n	no hits & (original description: pacid=37152177 transcript=Phvul.L001859.1 locus=P
not assigned.a	(original description: pacid=37175319 transcript=Phvul.002G027900.2 locus=Phvul.0
Solute transp	P3A-type proton-translocating ATPase (AHA) (original description: pacid=37153023 t
not assigned.a	(original description: pacid=37163120 transcript=Phvul.004G153700.1 locus=Phvul.0
not assigned.n	no hits & (original description: pacid=37169210 transcript=Phvul.001G214600.7 locu
Photosynthesi	component PsbX of PS-II complex (original description: pacid=37148668 transcript=P
Protein modif	protein kinase (MAP3K-RAF) (original description: pacid=37149156 transcript=Phvul.
Protein home	protease (Papain) (original description: pacid=37156473 transcript=Phvul.011G1341
Protein home	protease (Papain) (original description: pacid=37155727 transcript=Phvul.011G1340

Protein home	protease (Papain) (original description: pacid=37154718 transcript=Phvul.011G1308
Protein home	protease (Papain) (original description: pacid=37156814 transcript=Phvul.011G0811
Protein home	protease (Papain) (original description: pacid=37157156 transcript=Phvul.011G1333
Cell cycle orga	component CAP-D2A of condensin I complex (original description: pacid=37167459 t
not assigned.r	no hits & (original description: pacid=37162297 transcript=Phvul.004G172000.1 locu
Cytoskeleton	component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
Cytoskeleton	component GCP2 of gamma-Tubulin ring complex (gamma-TuRC) (original descriptio
not assigned.r	no hits & (original description: pacid=37153352 transcript=Phvul.005G105800.1 locu
not assigned.r	no hits & (original description: pacid=37151943 transcript=Phvul.009G021200.1 locu
not assigned.a	(original description: pacid=37149394 transcript=Phvul.009G226800.1 locus=Phvul.
not assigned.a	(original description: pacid=37171980 transcript=Phvul.006G162000.1 locus=Phvul.
not assigned.r	no hits & (original description: pacid=37175715 transcript=Phvul.002G038300.1 locu
Protein modif	protein kinase (CrlRLK1) (original description: pacid=37165831 transcript=Phvul.007
Protein modif	protein kinase (LRR-Xc) (original description: pacid=37163699 transcript=Phvul.004G
not assigned.r	no hits & (original description: pacid=37152177 transcript=Phvul.L001859.1 locus=P
not assigned.a	(original description: pacid=37175319 transcript=Phvul.002G027900.2 locus=Phvul.
Solute transp	P3A-type proton-translocating ATPase (AHA) (original description: pacid=37153023 t
not assigned.a	(original description: pacid=37163120 transcript=Phvul.004G153700.1 locus=Phvul.

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09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
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09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
09G006000 ID=Phvul.009G006000.3.v2.1 annot-version=v2.1) & Phosphatidylinositol/phosphatidy
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s=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)
transcript=Phvul.009G150800.1 locus=Phvul.009G150800 ID=Phvul.009G150800.1.v2.1 annot-vers
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s=Phvul.001G214600 ID=Phvul.001G214600.7.v2.1 annot-version=v2.1)
transcript=Phvul.009G150800.1 locus=Phvul.009G150800 ID=Phvul.009G150800.1.v2.1 annot-vers
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vul.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
vul.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
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s=Phvul.008G290000 ID=Phvul.008G290000.1.v2.1 annot-version=v2.1)
05G040800 ID=Phvul.005G040800.1.v2.1 annot-version=v2.1) & Callose synthase 2 OS=Arabidopsi
) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
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riginal description: pacid=37158087 transcript=Phvul.008G128900.1 locus=Phvul.008G128900 ID=P
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vul.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
vul.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
vul.001G219900.4 locus=Phvul.001G219900 ID=Phvul.001G219900.4.v2.1 annot-version=v2.1) &
RNP) (original description: pacid=37147800 transcript=Phvul.003G174100.1 locus=Phvul.003G1741
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ranscript=Phvul.004G018100.1 locus=Phvul.004G018100 ID=Phvul.004G018100.1.v2.1 annot-versio
s=Phvul.008G290000 ID=Phvul.008G290000.1.v2.1 annot-version=v2.1)
05G040800 ID=Phvul.005G040800.1.v2.1 annot-version=v2.1) & Callose synthase 2 OS=Arabidopsi
) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G

F) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
F) complex (original description: pacid=37144029 transcript=Phvul.010G000700.3 locus=Phvul.010G
009G032100 ID=Phvul.009G032100.1.v2.1 annot-version=v2.1) & Protein EXORDIUM OS=Arabidops
d=37151543 transcript=Phvul.009G243500.2 locus=Phvul.009G243500 ID=Phvul.009G243500.2.v2.
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ul.008G061900.3 locus=Phvul.008G061900 ID=Phvul.008G061900.3.v2.1 annot-version=v2.1) &
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009G226500 ID=Phvul.009G226500.2.v2.1 annot-version=v2.1) & ATP-dependent DNA helicase Q-li
009G226500 ID=Phvul.009G226500.2.v2.1 annot-version=v2.1) & ATP-dependent DNA helicase Q-li
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
us=Phvul.002G133900 ID=Phvul.002G133900.2.v2.1 annot-version=v2.1)
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009G032100 ID=Phvul.009G032100.1.v2.1 annot-version=v2.1) & Protein EXORDIUM OS=Arabidops
d=37151543 transcript=Phvul.009G243500.2 locus=Phvul.009G243500 ID=Phvul.009G243500.2.v2.
Phvul.002G061200.1 locus=Phvul.002G061200 ID=Phvul.002G061200.1.v2.1 annot-version=v2.1) &
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ul.008G061900.3 locus=Phvul.008G061900 ID=Phvul.008G061900.3.v2.1 annot-version=v2.1) &
009G226500 ID=Phvul.009G226500.2.v2.1 annot-version=v2.1) & ATP-dependent DNA helicase Q-li
009G226500 ID=Phvul.009G226500.2.v2.1 annot-version=v2.1) & ATP-dependent DNA helicase Q-li
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
09G242900.4 locus=Phvul.009G242900 ID=Phvul.009G242900.4.v2.1 annot-version=v2.1) &
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Phvul.009G036300.1 locus=Phvul.009G036300 ID=Phvul.009G036300.1.v2.1 annot-version=v2.1) &
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006G151200 ID=Phvul.006G151200.1.v2.1 annot-version=v2.1) & RNA pseudouridine synthase 6, c
us=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)
us=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)
011G033500 ID=Phvul.011G033500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
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002G022400 ID=Phvul.002G022400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
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us=Phvul.009G073900 ID=Phvul.009G073900.1.v2.1 annot-version=v2.1)
159700.1 locus=Phvul.003G159700 ID=Phvul.003G159700.1.v2.1 annot-version=v2.1) &
006G151200 ID=Phvul.006G151200.1.v2.1 annot-version=v2.1) & RNA pseudouridine synthase 6, ch
us=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)
us=Phvul.006G104300 ID=Phvul.006G104300.2.v2.1 annot-version=v2.1)
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08G038200.1 locus=Phvul.008G038200 ID=Phvul.008G038200.1.v2.1 annot-version=v2.1) &
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02 transcript=Phvul.009G019100.1 locus=Phvul.009G019100 ID=Phvul.009G019100.1.v2.1 annot-ve
us=Phvul.009G073900 ID=Phvul.009G073900.1.v2.1 annot-version=v2.1)
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us=Phvul.004G172000 ID=Phvul.004G172000.1.v2.1 annot-version=v2.1)
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on: pacid=37143582 transcript=Phvul.010G031700.5 locus=Phvul.010G031700 ID=Phvul.010G03170
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006G162000 ID=Phvul.006G162000.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase MIEL1
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:v2.1) &
:v2.1) &
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'lcholine transfer protein SFH8 OS=Arabidopsis thaliana (sp|f4ihj0|sfh8_arath : 681.0)
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sion=v2.1) &

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ke 3 OS=Arabidopsis thaliana (sp|q9ft72|rql3_arath : 811.0)
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loroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)

ing protein At2g21090 OS=Arabidopsis thaliana (sp|q9skq4|pp167_arath : 607.0)

ing protein At3g50420 OS=Arabidopsis thaliana (sp|q9sct2|pp277_arath : 413.0)
t1g25360 OS=Arabidopsis thaliana (sp|q9fri5|ppr57_arath : 1008.0)

ɔr ATP-dependent RNA helicase DEAH5 OS=Arabidopsis thaliana (sp|q38953|deah5_arath : 438.0)
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hloroplastic OS=Arabidopsis thaliana (sp|q9svs0|pus6_arath : 622.0)

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ing protein At3g50420 OS=Arabidopsis thaliana (sp|q9sct2|pp277_arath : 413.0)
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on=v2.1) &

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aaaccguuacca	Phvul.009G196100.1	3.5	-1	1	22
aaaccguuacca	Phvul.008G199900.1	3.5	-1	1	22
aaaccguuacca	Phvul.007G157000.1	3.5	-1	1	22
aaaccguuacca	Phvul.009G104850.1	3.5	-1	1	22
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aaaccguuacca	Phvul.L001604.3	3.5	-1	1	22
aaaccguuacca	Phvul.L001604.2	3.5	-1	1	22
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Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
119	140	AAACCGUUAC	::. :: :::::::.:::::	GCCUUUGUC	Cleavage	pacid=371619
646	667	AAACCGUUAC	:.: ::::::::: ::::	AUAUUAAUA	Cleavage	pacid=371509
1051	1072	AAACCGUUAC	: : :::::::.:.:::::	UCGUGAAUA	Cleavage	pacid=371614
118	140	AAACCGUUAC	::. :: :::::::.::::	GGCCUUUGU	Cleavage	pacid=371619
645	667	AAACCGUUAC	:.: ::::::::: :::	UAUAUUAAU	Cleavage	pacid=371509
118	140	AAACCGUUAC	::. :: :::::::.::::	GGCCUUUGU	Cleavage	pacid=371619
645	667	AAACCGUUAC	:.: ::::::::: :::	UAUAUUAAU	Cleavage	pacid=371509
138	159	AAACCGUUAC	::.::::::.:: :::.::::	AAUUCAGUA	Translation	pacid=371489
645	666	AAACCGUUAC	..::::::::: ::: .::::	GGCUCAGUA	Translation	pacid=371593
1217	1238	AAACCGUUAC	: : ::::::::::.:.:: ::	ACCACAGUAA	Cleavage	pacid=371664
193	214	AAACCGUUAC	.:..::..::::...::::	GUUUUGGUG	Cleavage	pacid=371513
1819	1840	AAACCGUUAC	::::: :::: :.:.::::	UUCUCAGAA	Translation	pacid=371635
2711	2732	AAACCGUUAC	..::.:::::.:.:::::	AUAAUGGUG	Cleavage	pacid=371550
2714	2735	AAACCGUUAC	..::.:::::.:.:::::	AUAAUGGUG	Cleavage	pacid=371550
321	342	AAACCGUUAC	.:::: :.::::::. ::::	GUUUCAGAA	Cleavage	pacid=371574
298	319	AAACCGUUAC	.:::: :.::::::. ::::	GUUUCAGAA	Cleavage	pacid=371574
316	337	AAACCGUUAC	.:::: :.::::::. ::::	GUUUCAGAA	Cleavage	pacid=371574
28	49	AAACCGUUAC	::: ::::: ::::::::	GAGACAGCA	Cleavage	pacid=371620
1182	1203	AAACCGUUAC	:::: .::::::..::::	AUAUCAGAG	Cleavage	pacid=371556
1264	1285	AAACCGUUAC	:::: .::::::..::::	AUAUCAGAG	Cleavage	pacid=371556
1264	1285	AAACCGUUAC	:::: .::::::..::::	AUAUCAGAG	Cleavage	pacid=371556
43	64	AAACCGUUAC	:.. :.:::::::..::::	GUAUUGAUG	Cleavage	pacid=371470
43	64	AAACCGUUAC	:.. :.:::::::..::::	GUAUUGAUG	Cleavage	pacid=371470
121	142	AAACCGUUAC	:::: ::::::.: ::::	CCAUCAGCAA	Cleavage	pacid=371453
137	159	AAACCGUUAC	::.::::::.:: :::.::::	CAAUUCAGU	Translation	pacid=371489
644	666	AAACCGUUAC	...:::::::: ::: .::::	GGGCUCAGU	Translation	pacid=371593
1216	1238	AAACCGUUAC	:: : ::::::::::.:.:: :	AACCACAGUA	Cleavage	pacid=371664
27	49	AAACCGUUAC	:.: ::: ::::: ::::::	AGAGACAGC	Cleavage	pacid=371620
192	214	AAACCGUUAC	.:..::..::::...::::	GGUUUUGGU	Cleavage	pacid=371513
320	342	AAACCGUUAC	:. .:::: :.::::::. :::	AGUUUCAGA	Cleavage	pacid=371574
297	319	AAACCGUUAC	:. .:::: :.::::::. :::	AGUUUCAGA	Cleavage	pacid=371574
315	337	AAACCGUUAC	:. .:::: :.::::::. :::	AGUUUCAGA	Cleavage	pacid=371574
1818	1840	AAACCGUUAC	::::: :::: :.:.::::	GUUCUCAGA	Translation	pacid=371635
2710	2732	AAACCGUUAC	..::.:::::.:.::::	AAUAAUGGU	Cleavage	pacid=371550
2713	2735	AAACCGUUAC	..::.:::::.:.::::	AAUAAUGGU	Cleavage	pacid=371550
137	159	AAACCGUUAC	::.::::::.:: :::.::::	CAAUUCAGU	Translation	pacid=371489
644	666	AAACCGUUAC	...:::::::: ::: .::::	GGGCUCAGU	Translation	pacid=371593
1216	1238	AAACCGUUAC	:: : ::::::::::.:.:: :	AACCACAGUA	Cleavage	pacid=371664
27	49	AAACCGUUAC	:.: ::: ::::: ::::::	AGAGACAGC	Cleavage	pacid=371620
192	214	AAACCGUUAC	.:..::..::::...::::	GGUUUUGGU	Cleavage	pacid=371513
320	342	AAACCGUUAC	:. .:::: :.::::::. :::	AGUUUCAGA	Cleavage	pacid=371574
297	319	AAACCGUUAC	:. .:::: :.::::::. :::	AGUUUCAGA	Cleavage	pacid=371574
315	337	AAACCGUUAC	:. .:::: :.::::::. :::	AGUUUCAGA	Cleavage	pacid=371574
1818	1840	AAACCGUUAC	::::: :::: :.:.::::	GUUCUCAGA	Translation	pacid=371635
2710	2732	AAACCGUUAC	..::.:::::.:.::::	AAUAAUGGU	Cleavage	pacid=371550

2713	2735	AAACCGUUA	..::.:::::.:.::::	AAUAAUGGU	Cleavage	pacid=371550
1940	1961	AAACCGUUA	:: :.:::: :::.: ::::	AAAUUAGUA	Cleavage	pacid=371781
1944	1965	AAACCGUUA	:: :.:::: :::.: ::::	AAAUUAGUA	Cleavage	pacid=371781
1972	1993	AAACCGUUA	:: :.:::: :::.: ::::	AAAUUAGUA	Cleavage	pacid=371781
156	177	AAACCGUUA	.: :::::::::.:::	GUUUGAGUA	Cleavage	pacid=371748
1163	1184	AAACCGUUA	: :::.:: :::: ..::::	AUCUCGGUC	Cleavage	pacid=371440
1130	1151	AAACCGUUA	.:: .:: :::::::.::::	GACAAGGUC	Cleavage	pacid=371723
968	989	AAACCGUUA	: : .:::.::: :::.::::	AUCAUAGUG	Translation	pacid=371726
968	989	AAACCGUUA	: : .:::.::: :::.::::	AUCAUAGUG	Translation	pacid=371726
968	989	AAACCGUUA	: : .:::.::: :::.::::	AUCAUAGUG	Translation	pacid=371726
968	989	AAACCGUUA	: : .:::.::: :::.::::	AUCAUAGUG	Translation	pacid=371726
711	732	AAACCGUUA	:::::::: :.::::	AUGCAAGUA	Cleavage	pacid=371777
2616	2637	AAACCGUUA	::::::::::.::: ::	GUGGCAGUA	Cleavage	pacid=371537
2616	2637	AAACCGUUA	::::::::::.::: ::	GUGGCAGUA	Cleavage	pacid=371537
2616	2637	AAACCGUUA	::::::::::.::: ::	GUGGCAGUA	Cleavage	pacid=371537
2616	2637	AAACCGUUA	::::::::::.::: ::	GUGGCAGUA	Cleavage	pacid=371537
3174	3195	AAACCGUUA	.:..:::: :::: ::::::	UCUUUGGUA	Cleavage	pacid=371783
2616	2637	AAACCGUUA	::::::::::.::: ::	GUGGCAGUA	Cleavage	pacid=371537
2616	2637	AAACCGUUA	::::::::::.::: ::	GUGGCAGUA	Cleavage	pacid=371537
724	745	AAACCGUUA	..::..::::..::::::	CAGGUGGUG	Cleavage	pacid=371648
702	723	AAACCGUUA	:::::.: :::..::::	CCGUCAGUG	Cleavage	pacid=371659
1489	1510	AAACCGUUA	:..: : :::::::.:: ::	CAUUAACUA	Cleavage	pacid=371463
1252	1273	AAACCGUUA	::::.::: ::..::::	UUAACAGUG	Translation	pacid=371746
503	524	AAACCGUUA	.::::.:: :::.:::::	GUAGUAGUA	Translation	pacid=371631
240	261	AAACCGUUA	.:: :..::::.::::::	GUUUCCCUG	Cleavage	pacid=371598
342	363	AAACCGUUA	.:: :..::::..:::::	GUUUCCCUG	Cleavage	pacid=371598
990	1011	AAACCGUUA	.: :.:: ::::::.. :::::	GAAUUAGCA	Cleavage	pacid=371773
1310	1331	AAACCGUUA	...::: ::::: ::.::::::	GGUUCAACA	Cleavage	pacid=371619
381	402	AAACCGUUA	.: :::: :::: ::::::::	GAAUCAGAA	Translation	pacid=371707
1572	1593	AAACCGUUA	.: :::::::::.: ::::	CUUUGAGUA	Cleavage	pacid=371530
1575	1596	AAACCGUUA	.: :::::::::.: ::::	CUUUGAGUA	Cleavage	pacid=371530
1939	1961	AAACCGUUA	::: :.:::: :::.: ::::	AAAAUUAGU	Cleavage	pacid=371781
1943	1965	AAACCGUUA	::: :.:::: :::.: ::::	AAAAUUAGU	Cleavage	pacid=371781
1971	1993	AAACCGUUA	::: :.:::: :::.: ::::	AAAAUUAGU	Cleavage	pacid=371781
155	177	AAACCGUUA	:. .: :::::::::::.:::	AGUUUGAGU	Cleavage	pacid=371748
1129	1151	AAACCGUUA	..:: .:: :::::::.::::	GGACAAGGU	Cleavage	pacid=371723
1162	1184	AAACCGUUA	: :::.:: ::::: ..::::	CAUCUCGGU	Cleavage	pacid=371440
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
239	261	AAACCGUUA	.:: :..::::..:::::	GGUUUCCCU	Cleavage	pacid=371598
341	363	AAACCGUUA	.:: :..::::..:::::	GGUUUCCCU	Cleavage	pacid=371598
380	402	AAACCGUUA	..: :::: :::: :::::::	GGAAUCAGA	Translation	pacid=371707
1939	1961	AAACCGUUA	::: :.:::: :::.: ::::	AAAAUUAGU	Cleavage	pacid=371781
1943	1965	AAACCGUUA	::: :.:::: :::.: ::::	AAAAUUAGU	Cleavage	pacid=371781

1971	1993	AAACCGUUA	::: :.:::: :::.: ::::	AAAAUUAGU	Cleavage	pacid=371781
155	177	AAACCGUUA	:. .: :::::::::::.:::	AGUUUGAGU	Cleavage	pacid=371748
1129	1151	AAACCGUUA	..:: .:: :::::::.::::	GGACAAGGU	Cleavage	pacid=371723
1162	1184	AAACCGUUA	: :::.:: :::: ..::::	CAUCUCGGU	Cleavage	pacid=371440
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
967	989	AAACCGUUA	: : .:::.::: :::.::::	CAUCAUAGU	Translation	pacid=371726
239	261	AAACCGUUA	.:: :..::::..:::::	GGUUUCCCU	Cleavage	pacid=371598
341	363	AAACCGUUA	.:: :..::::..:::::	GGUUUCCCU	Cleavage	pacid=371598
380	402	AAACCGUUA	..: :::: :::: :::::::	GGAAUCAGA	Translation	pacid=371707
520	541	AAACCGUUA	::: ::::..:::::: :::	AACACAGUG	Cleavage	pacid=371712
188	209	AAACCGUUA	::.:.:::.: ::::.::: ::	AAUUUAGUG	Cleavage	pacid=371425
550	571	AAACCGUUA	::.:.:::.: ::::.::: ::	AAUUUAGUG	Cleavage	pacid=371425
1347	1370	AAACCGUUA	.::: ::::::::: ::.:::	GACUGACAG	Cleavage	pacid=371501
1394	1417	AAACCGUUA	.::: ::::::::: ::.:::	GACUGACAG	Cleavage	pacid=371501
1475	1498	AAACCGUUA	.::: ::::::::: ::.:::	GACUGACAG	Cleavage	pacid=371501
1480	1503	AAACCGUUA	.::: ::::::::: ::.:::	GACUGACAG	Cleavage	pacid=371501
593	614	AAACCGUUA	::. ::::..:::::: :::	AAUACAGUG	Cleavage	pacid=371679
1109	1130	AAACCGUUA	::::. :..::::.:.::::	AACUUCAUG	Cleavage	pacid=371611
224	245	AAACCGUUA	.:.:::::.:::::.. :: :	GAUUCAGUA	Cleavage	pacid=371431
1397	1418	AAACCGUUA	:::::: ::::: : .:::::	UACUCAGCA	Cleavage	pacid=371726
676	697	AAACCGUUA	::::.:::::::.:::	AUGACAGUG	Cleavage	pacid=371501
789	810	AAACCGUUA	.:.::::.::::..::::	CUUUUAGUA	Cleavage	pacid=371645
820	841	AAACCGUUA	.:: .::::::::: :::	UUACUAGAG	Cleavage	pacid=371457
665	686	AAACCGUUA	..::..::::....:::::	GUGGUGGUG	Cleavage	pacid=371548
6	27	AAACCGUUA	::. . ::. :::::::::::::	AAUAUUGUG	Cleavage	pacid=371690
868	889	AAACCGUUA	.::::::::::::.:::	GUAGUAGUA	Cleavage	pacid=371654
868	889	AAACCGUUA	.::::::::::::.:::	GUAGUAGUA	Cleavage	pacid=371654
495	516	AAACCGUUA	: ::.::..::::.::::	CAAUCGGUG	Cleavage	pacid=371552
1238	1259	AAACCGUUA	.:: .:: ::::::..:::::	GACAAGGUC	Cleavage	pacid=371723
1031	1052	AAACCGUUA	..: .:: ::::::..:::::	GGCAAGGUC	Cleavage	pacid=371723
791	812	AAACCGUUA	:..::: ::: : :::.:::::	AGUUCAUUA	Translation	pacid=371763
988	1009	AAACCGUUA	.:: :: :..::::...:::::	GACACAUUG	Cleavage	pacid=371655
584	605	AAACCGUUA	..::::::::::::::	AUAAUGGUA	Cleavage	pacid=371741
1386	1407	AAACCGUUA	:::::.::::::: :::	CUAUCAGUG	Cleavage	pacid=371423
160	181	AAACCGUUA	::: ::::::::::: :::	CACUAUGUA	Cleavage	pacid=371773
448	469	AAACCGUUA	:::::.::::::::: :	AUGUCAGUG	Cleavage	pacid=371702
501	522	AAACCGUUA	:::::.::::::::: :	AUGUCAGUG	Cleavage	pacid=371702
517	538	AAACCGUUA	:::::.::::::::: :	AUGUCAGUG	Cleavage	pacid=371702
3048	3069	AAACCGUUA	..:::::.:: ::: :::::	UGUUCAGUG	Translation	pacid=371717
814	835	AAACCGUUA	..::.::.::: :.::: :::	UGUUCGGUG	Translation	pacid=371439
443	464	AAACCGUUA	.:::.:: .::::. .:::::	UGCUCGGUU	Cleavage	pacid=371670
1174	1195	AAACCGUUA	:..::..::::.:.::: :	GUGUUGGUG	Cleavage	pacid=371670
32	53	AAACCGUUA	:: ..::.:::::.:.::::	AAAAUGGUG	Cleavage	pacid=371540
37	58	AAACCGUUA	:: ..::.:::::.:.::::	AAAAUGGUG	Cleavage	pacid=371540

442	463	AAACCGUUA	.::::.:: .::::. .:::::	UGCUCGGUU	Cleavage	pacid=371668
1173	1194	AAACCGUUA	:..::..::::.:.::: :	GUGUUGGUG	Cleavage	pacid=371668
41	62	AAACCGUUA	:: ..::.:::::.:.::::	AAAAUGGUG	Cleavage	pacid=371540
113	134	AAACCGUUA	:: :.::: ::: :::.::::	AAAUUAGUU	Translation	pacid=371600
291	312	AAACCGUUA	.:.:. :..::::..:::::	GAUUUCCUG	Cleavage	pacid=371598
278	299	AAACCGUUA	.: :.::::: ::..: ::::	GAAUUAGUA	Translation	pacid=371432
278	299	AAACCGUUA	.: :.::::: ::..: ::::	GAAUUAGUA	Translation	pacid=371432
1831	1852	AAACCGUUA	:: :.: :.: ::::..:::::	AAGUUAAUG	Cleavage	pacid=371641
1059	1080	AAACCGUUA	:::::.:::::: : :::	ACAGCAGUA	Cleavage	pacid=371626
2504	2525	AAACCGUUA	:: :::: ::: : ::.::::	AAAUCAGAA	Translation	pacid=371527
187	209	AAACCGUUA	:::.:.:::.: ::::.::: :	AAAUUUAGU	Cleavage	pacid=371425
549	571	AAACCGUUA	:::.:.:::.: ::::.::: :	AAAUUUAGU	Cleavage	pacid=371425
519	541	AAACCGUUA	::: ::::..::::::: :::	UAACACAGU	Cleavage	pacid=371712
1108	1130	AAACCGUUA	.::::. :..::::.:.::::	GAACUUCAU	Cleavage	pacid=371611
1346	1370	AAACCGUUA	.::: ::::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
1393	1417	AAACCGUUA	.::: ::::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
1474	1498	AAACCGUUA	.::: ::::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
1479	1503	AAACCGUUA	.::: ::::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
592	614	AAACCGUUA	::. ::::..::::::: :::	CAAUACAGU	Cleavage	pacid=371679
223	245	AAACCGUUA	..:::::::.:::::.. ::	UGAUUCAGU	Cleavage	pacid=371431
664	686	AAACCGUUA	..::..::::...::::	GGUGGUGGU	Cleavage	pacid=371548
1237	1259	AAACCGUUA	..:: .:: ::::::..::::	GGACAAGGU	Cleavage	pacid=371723
1030	1052	AAACCGUUA	...: .:: ::::::..::::	GGGCAAGGU	Cleavage	pacid=371723
277	299	AAACCGUUA	:.: :.::::: ::..: :::	AGAAUUAGU	Translation	pacid=371432
277	299	AAACCGUUA	:.: :.::::: ::..: :::	AGAAUUAGU	Translation	pacid=371432
1058	1080	AAACCGUUA	:::::.:::::: : ::	AACAGCAGU	Cleavage	pacid=371626
790	812	AAACCGUUA	.:..::: ::: : :::.::::	GAGUUCAUU	Translation	pacid=371763
987	1009	AAACCGUUA	..:: :: :..::::...::::	GGACACAUU	Cleavage	pacid=371655
1396	1418	AAACCGUUA	:::::: ::::: : .::::	UUACUCAGC	Cleavage	pacid=371726
675	697	AAACCGUUA	::::.::::::::.:::	UAUGACAGU	Cleavage	pacid=371501
788	810	AAACCGUUA	.:.::::.::::..::::	ACUUUUAGU	Cleavage	pacid=371645
819	841	AAACCGUUA	.:: .::::::::: ::	UUUACUAGA	Cleavage	pacid=371457
31	53	AAACCGUUA	.:: ..::.:::::.:.::::	GAAAAUGGU	Cleavage	pacid=371540
36	58	AAACCGUUA	.:: ..::.:::::.:.::::	GAAAAUGGU	Cleavage	pacid=371540
5	27	AAACCGUUA	::. . ::. :::::::::::	CAAUAUUGU	Cleavage	pacid=371690
867	889	AAACCGUUA	.::::::::::::.:::	AGUAGUAGU	Cleavage	pacid=371654
867	889	AAACCGUUA	.::::::::::::.:::	AGUAGUAGU	Cleavage	pacid=371654
494	516	AAACCGUUA	: ::.::..::::.:::::	GCAAUCGGU	Cleavage	pacid=371552
40	62	AAACCGUUA	.:: ..::.:::::.:.::::	GAAAAUGGU	Cleavage	pacid=371540
112	134	AAACCGUUA	.:: :.::: ::: :::.::::	GAAAUUAGU	Translation	pacid=371600
343	365	AAACCGUUA	:: .::::: :::::.:: : :	AACUUCAGU	Cleavage	pacid=371523
583	605	AAACCGUUA	..:::::::::::::	UAUAAUGGU	Cleavage	pacid=371741
3047	3069	AAACCGUUA	: ..:::::.:: ::: :::::	AUGUUCAGU	Translation	pacid=371717
290	312	AAACCGUUA	..:.:. :..::::..:::::	GGAUUUCCU	Cleavage	pacid=371598
323	345	AAACCGUUA	::. ::::::::: .::: ::	AAGGACAGU	Cleavage	pacid=371570
1385	1407	AAACCGUUA	:::::.::::::: :::	ACUAUCAGU	Cleavage	pacid=371423

159	181	AAACCGUUAC	::: :::::::::: :::	GCACUAUGU	Cleavage	pacid=371773
1830	1852	AAACCGUUAC	.:: :.: :.: ::::..::::	GAAGUUAAU	Cleavage	pacid=371641
447	469	AAACCGUUAC	:::::.:::::::: :	GAUGUCAGU	Cleavage	pacid=371702
187	209	AAACCGUUAC	:::.:.:::.: ::::.::: :	AAAUUUAGU	Cleavage	pacid=371425
549	571	AAACCGUUAC	:::.:.:::.: ::::.::: :	AAAUUUAGU	Cleavage	pacid=371425
519	541	AAACCGUUAC	::: ::::..:::::: :::	UAACACAGU	Cleavage	pacid=371712
1108	1130	AAACCGUUAC	.::::. :..::::.:.::::	GAACUUCAU	Cleavage	pacid=371611
1346	1370	AAACCGUUAC	.::: :::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
1393	1417	AAACCGUUAC	.::: :::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
1474	1498	AAACCGUUAC	.::: :::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
1479	1503	AAACCGUUAC	.::: :::::::: ::.::	CGACUGACA	Cleavage	pacid=371501
592	614	AAACCGUUAC	::. ::::..:::::: :::	CAAUACAGU	Cleavage	pacid=371679
223	245	AAACCGUUAC	.:.:::::.:::::.. ::	UGAUUCAGU	Cleavage	pacid=371431
664	686	AAACCGUUAC	..::..::::...::::	GGUGGUGGU	Cleavage	pacid=371548
1237	1259	AAACCGUUAC	..:: .:: ::::::..::::	GGACAAGGU	Cleavage	pacid=371723
1030	1052	AAACCGUUAC	...: .:: ::::::..::::	GGGCAAGGU	Cleavage	pacid=371723
277	299	AAACCGUUAC	:.: :.::::: ::..: :::	AGAAUUAGU	Translation	pacid=371432
277	299	AAACCGUUAC	:.: :.::::: ::..: :::	AGAAUUAGU	Translation	pacid=371432
1058	1080	AAACCGUUAC	:::::.:::::: : ::	AACAGCAGU	Cleavage	pacid=371626
790	812	AAACCGUUAC	.:..::: ::: : :::.::::	GAGUUCAUU	Translation	pacid=371763
987	1009	AAACCGUUAC	..:: :: :..::::...::::	GGACACAUU	Cleavage	pacid=371655
1396	1418	AAACCGUUAC	:::::: :::: : .::::	UUACUCAGC	Cleavage	pacid=371726
675	697	AAACCGUUAC	::::.:::::::.:::	UAUGACAGU	Cleavage	pacid=371501
788	810	AAACCGUUAC	.:.:::::::::::.::::	ACUUUUAGU	Cleavage	pacid=371645
819	841	AAACCGUUAC	.:: .:::::::: ::	UUUACUAGA	Cleavage	pacid=371457
31	53	AAACCGUUAC	.:: ..::.:::::.:.::::	GAAAAUGGU	Cleavage	pacid=371540
36	58	AAACCGUUAC	.:: ..::.:::::.:.::::	GAAAAUGGU	Cleavage	pacid=371540
5	27	AAACCGUUAC	::. . ::. ::::::::::	CAAUAUUGU	Cleavage	pacid=371690
867	889	AAACCGUUAC	.:::::::::::.:::	AGUAGUAGU	Cleavage	pacid=371654
867	889	AAACCGUUAC	.:::::::::::.:::	AGUAGUAGU	Cleavage	pacid=371654
494	516	AAACCGUUAC	: ::.::..::::.:::::	GCAAUCGGU	Cleavage	pacid=371552
40	62	AAACCGUUAC	.:: ..::.:::::.:.::::	GAAAAUGGU	Cleavage	pacid=371540
112	134	AAACCGUUAC	.:: :.::: ::: :::.::::	GAAAUUAGU	Translation	pacid=371600
343	365	AAACCGUUAC	:: .::::: :::::.:: : :	AACUUCAGU	Cleavage	pacid=371523
583	605	AAACCGUUAC	..:::::::::::::	UAUAAUGGU	Cleavage	pacid=371741
3047	3069	AAACCGUUAC	: ..:::::.:: ::: :::::	AUGUUCAGU	Translation	pacid=371717
290	312	AAACCGUUAC	..:.:. :..::::..:::::	GGAUUUCCU	Cleavage	pacid=371598
323	345	AAACCGUUAC	::. ::::::::: .::: ::	AAGGACAGU	Cleavage	pacid=371570
1385	1407	AAACCGUUAC	:::::.:::::: :::	ACUAUCAGU	Cleavage	pacid=371423
159	181	AAACCGUUAC	::: :::::::::: :::	GCACUAUGU	Cleavage	pacid=371773
1830	1852	AAACCGUUAC	.:: :.: :.: ::::..::::	GAAGUUAAU	Cleavage	pacid=371641
447	469	AAACCGUUAC	:::::.:::::::: :	GAUGUCAGU	Cleavage	pacid=371702
500	522	AAACCGUUAC	:::::.:::::::: :	GAUGUCAGU	Cleavage	pacid=371702
1264	1285	AAACCGUUAC	.:.::.::..::::..::::	GAUUCGGUG	Cleavage	pacid=371548
514	535	AAACCGUUAC	.: :..: :: :::...:::::	GAAUUGGCA	Cleavage	pacid=371548
838	859	AAACCGUUAC	.: :..: :: :::...:::::	GAAUUGGCA	Cleavage	pacid=371548

904	925	AAACCGUUAC	.: :..: :: :::...:::::	GAAUUGGCA	Cleavage	pacid=371548
1102	1123	AAACCGUUAC	.: :..: :: :::...:::::	GAAUUGGCA	Cleavage	pacid=371548
1054	1075	AAACCGUUAC	.: .::..::::..::: ::	GUUUAGGUG	Cleavage	pacid=371548
1535	1556	AAACCGUUAC	::: ::::::::::.. :: :	AACACAGUAA	Cleavage	pacid=371621
1540	1561	AAACCGUUAC	::: ::::::::::.. :: :	AACACAGUAA	Cleavage	pacid=371621
625	646	AAACCGUUAC	.::..::::...:::::	GAGCAGGUG	Cleavage	pacid=371513
715	736	AAACCGUUAC	.::..::::...:::::	GAGCAGGUG	Cleavage	pacid=371513
859	880	AAACCGUUAC	.::..::::...:::::	GAGCAGGUG	Cleavage	pacid=371513
958	979	AAACCGUUAC	.:: :.:::: :::..:::::	GACCCGGUAA	Cleavage	pacid=371460
509	530	AAACCGUUAC	:.: ..::.:::::...::::	AGCGUGGUG	Cleavage	pacid=371718
522	543	AAACCGUUAC	:::::: ::::::::: :::	AACUCACAAA	Cleavage	pacid=371779
311	332	AAACCGUUAC	.:.:..::..::::...::: :	GAUUUGGUG	Cleavage	pacid=371548
328	349	AAACCGUUAC	::. ::::.: :::.: :::::	AAUGCAGUG	Cleavage	pacid=371642
132	153	AAACCGUUAC	::: ::: ::::::...:: ::	AACACAGCAA	Cleavage	pacid=371533
1460	1481	AAACCGUUAC	: ..:: :::::::..::::	GUCAUGGUU	Cleavage	pacid=371723
1020	1041	AAACCGUUAC	..::..::.::: : :.:::::	GGCUUGGUG	Translation	pacid=371550
608	629	AAACCGUUAC	..:: ::::::::.::: :	AUUAUGGUU	Cleavage	pacid=371741
3142	3163	AAACCGUUAC	:.:::: :.::::::..:::	UAUUCAGCA	Cleavage	pacid=371544
2698	2719	AAACCGUUAC	::.::: ::.::: ::.:: ::	AAUUCACUA	Cleavage	pacid=371680
1224	1245	AAACCGUUAC	:.:::::.:: ::.::: ::	UAUUCAGUG	Translation	pacid=371578
155	176	AAACCGUUAC	:...:: :::::::.:::	UUCUUGGUC	Cleavage	pacid=371617
210	231	AAACCGUUAC	.::::..::::....:::	GUUUCAGUG	Cleavage	pacid=371708
797	818	AAACCGUUAC	.:....:::: ::::::	GUUUUGGUA	Translation	pacid=371501
361	382	AAACCGUUAC	:.::::::::..::::	GUGGCGGUA	Cleavage	pacid=371573
788	809	AAACCGUUAC	..:::::::::....:::	GGAGUGGUA	Cleavage	pacid=371583
682	703	AAACCGUUAC	..:::::::::....:::	GGAGUGGUA	Cleavage	pacid=371731
350	371	AAACCGUUAC	.:::: :..::::::.:: ::	GACUCCCUG	Cleavage	pacid=371712
550	571	AAACCGUUAC	...:..::..::::...:: ::	GGUUUGGUG	Cleavage	pacid=371609
2	23	AAACCGUUAC	::: :: .::::::::: :::	AACACAUAGA	Cleavage	pacid=371609
1144	1165	AAACCGUUAC	: ::.:::.: :::.:.: :::	AUCUUAGUG	Cleavage	pacid=371512
2	23	AAACCGUUAC	::: :: .::::::::: :::	AACACAUAGA	Cleavage	pacid=371609
419	440	AAACCGUUAC	.:::: :..::::::.:: ::	GACUCCCUG	Cleavage	pacid=371741
712	733	AAACCGUUAC	: :.:::..::::.:.:::	CAAUUAGUG	Cleavage	pacid=371699
1245	1266	AAACCGUUAC	::.:::..::::. .::::	GUCUUAGUG	Cleavage	pacid=371562
265	286	AAACCGUUAC	:..:::: ::::: :..: :::	AGUUCAGAA	Cleavage	pacid=371626
445	466	AAACCGUUAC	:..: .::..::::.:. ::::	AGUUAGGUG	Cleavage	pacid=371737
1970	1991	AAACCGUUAC	..:.: :::::::..:::	UGUUUACUA	Cleavage	pacid=371509
1324	1345	AAACCGUUAC	..::::::::::.:::	GCUAUGGUA	Cleavage	pacid=371526
1263	1285	AAACCGUUAC	..:.::.::..::::..::::	GGAUUCGGU	Cleavage	pacid=371548
513	535	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGC	Cleavage	pacid=371548
837	859	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGC	Cleavage	pacid=371548
903	925	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGC	Cleavage	pacid=371548
1101	1123	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGC	Cleavage	pacid=371548
1053	1075	AAACCGUUAC	.: .::..::::..::: :	GGUUUAGGU	Cleavage	pacid=371548
508	530	AAACCGUUAC	::.: ..::.:::::...::::	AAGCGUGGU	Cleavage	pacid=371718
521	543	AAACCGUUAC	::::::: ::::::::: ::	AAACUCACAA	Cleavage	pacid=371779

131	153	AAACCGUUAC	:::: ::: :::::::...:: :	AAACACAGCA	Cleavage	pacid=371533
1534	1556	AAACCGUUAC	.::: :::::::::::.. ::	GAACACAGUA	Cleavage	pacid=371621
1539	1561	AAACCGUUAC	.::: :::::::::::.. ::	GAACACAGUA	Cleavage	pacid=371621
1019	1041	AAACCGUUAC	:..::..::.::: : :.:::	AGGCUUGGUC	Translation	pacid=371550
709	732	AAACCGUUAC	:::. :: ::::::: :.:::	AAAUGCAAGU	Cleavage	pacid=371777
349	371	AAACCGUUAC	:.:::: :..::::::.:: :	AGACUCCCUG	Cleavage	pacid=371712
310	332	AAACCGUUAC	..:.:..::..::::...:::	GGAUUUGGU	Cleavage	pacid=371548
418	440	AAACCGUUAC	:.:::: :..::::::.:: :	AGACUCCCUG	Cleavage	pacid=371741
714	736	AAACCGUUAC	.::..::::...::::	GGAGCAGGUC	Cleavage	pacid=371513
858	880	AAACCGUUAC	.::..::::...::::	GGAGCAGGUC	Cleavage	pacid=371513
624	646	AAACCGUUAC	.::..::::...::::	GGAGCAGGUC	Cleavage	pacid=371513
957	979	AAACCGUUAC	.:: :.:::: :::..:::::	UGACCCGGUA	Cleavage	pacid=371460
209	231	AAACCGUUAC	:. .:::::..::::...:::	AGUUUCAGUC	Cleavage	pacid=371708
2329	2350	AAACCGUUAC	:..:.::::: :::: :..::::	AGAUUCAGUC	Cleavage	pacid=371623
327	349	AAACCGUUAC	::. ::::.: :::.: ::::	CAAUGCAGUC	Cleavage	pacid=371642
818	840	AAACCGUUAC	:: :::: :.:::::..:: ::	AACCUCAUUG	Cleavage	pacid=371492
1223	1245	AAACCGUUAC	: :.:::::.:: ::.::: ::	AUAUUCAGUC	Translation	pacid=371578
736	758	AAACCGUUAC	:..:::: :::: .::::::	AGGCUCACCA	Cleavage	pacid=371570
331	353	AAACCGUUAC	:.: :::::.::::::. :: :	AGAAUCAGUC	Cleavage	pacid=371433
740	762	AAACCGUUAC	:: :::: :.:::::..:: ::	AACCUCAUUG	Cleavage	pacid=371492
607	629	AAACCGUUAC	.: . ..:: ::::::::.:::	GAUUAUGGU	Cleavage	pacid=371741
3141	3163	AAACCGUUAC	:.:::: :::::::..:::	GUAUUCAGCA	Cleavage	pacid=371544
2697	2719	AAACCGUUAC	::.::: ::.::: ::.:: :	UAAUUCACUA	Cleavage	pacid=371680
154	176	AAACCGUUAC	::. :.:::.::: :.:.: ::	AAGAUUAGUC	Translation	pacid=371718
295	317	AAACCGUUAC	: :: :: :::::::: :::	UCAGUCUGUC	Cleavage	pacid=371718
549	571	AAACCGUUAC	....:..::..::::...:: :	GGGUUUGGU	Cleavage	pacid=371609
1176	1198	AAACCGUUAC	::.. :: ::.::::.:.:: :	AAGUACACUA	Cleavage	pacid=371552
1	23	AAACCGUUAC	.::: :: .:::::::: ::	GAACACAUAG	Cleavage	pacid=371609
1	23	AAACCGUUAC	.::: :: .:::::::: ::	GAACACAUAG	Cleavage	pacid=371609
264	286	AAACCGUUAC	.:..:::: :::: :..: ::	GAGUUCAGAA	Cleavage	pacid=371626
444	466	AAACCGUUAC	.:..: .::..::::.:. :::	GAGUUAGGU	Cleavage	pacid=371737
1325	1347	AAACCGUUAC	:: : :::::::: .:.:: :	AACCACAGUA	Cleavage	pacid=371640
1263	1285	AAACCGUUAC	..:.::.::..::::..::::	GGAUUCGGUC	Cleavage	pacid=371548
513	535	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGCA	Cleavage	pacid=371548
837	859	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGCA	Cleavage	pacid=371548
903	925	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGCA	Cleavage	pacid=371548
1101	1123	AAACCGUUAC	..: :..: :: :::...::::	GGAAUUGGCA	Cleavage	pacid=371548
1053	1075	AAACCGUUAC	.: .::..::::..::: :	GGUUUAGGU	Cleavage	pacid=371548
508	530	AAACCGUUAC	::.: ..::.:::::...::::	AAGCGUGGUC	Cleavage	pacid=371718
521	543	AAACCGUUAC	:::::: :::::::: ::	AAACUCACAA	Cleavage	pacid=371779
131	153	AAACCGUUAC	:::: ::: :::::::...:: :	AAACACAGCA	Cleavage	pacid=371533
1534	1556	AAACCGUUAC	.::: :::::::::::.. ::	GAACACAGUA	Cleavage	pacid=371621
1539	1561	AAACCGUUAC	.::: :::::::::::.. ::	GAACACAGUA	Cleavage	pacid=371621
1019	1041	AAACCGUUAC	:..::..::.::: : :.:::	AGGCUUGGUC	Translation	pacid=371550
709	732	AAACCGUUAC	:::. :: ::::::: :.:::	AAAUGCAAGU	Cleavage	pacid=371777
349	371	AAACCGUUAC	:.:::: :..::::::.:: :	AGACUCCCUG	Cleavage	pacid=371712

310	332	AAACCGUUA	..:.:..::..::::...:::	GGAUUUGGU	Cleavage	pacid=371548
418	440	AAACCGUUA	:..:::: :..::::::.:: :	AGACUCCCU	Cleavage	pacid=371741
714	736	AAACCGUUA	.::..::::...::::	GGAGCAGGU	Cleavage	pacid=371513
858	880	AAACCGUUA	.::..::::...::::	GGAGCAGGU	Cleavage	pacid=371513
624	646	AAACCGUUA	.::..::::...::::	GGAGCAGGU	Cleavage	pacid=371513
957	979	AAACCGUUA	.:: :.:::: :::..:::::	UGACCCGGU	Cleavage	pacid=371460
209	231	AAACCGUUA	:. .:::::..::::...:::	AGUUUCAGU	Cleavage	pacid=371708
2329	2350	AAACCGUUA	:..:.::::: :::: :..::::	AGAUUCAGU	Cleavage	pacid=371623
327	349	AAACCGUUA	::. ::::.: :::.: ::::	CAAUGCAGU	Cleavage	pacid=371642
818	840	AAACCGUUA	:: :::: :.:::::..:: ::	AACCUCAUU	Cleavage	pacid=371492
1223	1245	AAACCGUUA	: :.:::::.:: ::.::: ::	AUAUUCAGU	Translation	pacid=371578
736	758	AAACCGUUA	:..:::: ::::: .::::::	AGGCUCACC	Cleavage	pacid=371570
331	353	AAACCGUUA	:..: :::::.::::::. :: :	AGAAUCAGU	Cleavage	pacid=371433
740	762	AAACCGUUA	:: :::: :.:::::..:: ::	AACCUCAUU	Cleavage	pacid=371492
607	629	AAACCGUUA	.: . ..:: :::::::.:::	GAUUAUGGU	Cleavage	pacid=371741
3141	3163	AAACCGUUA	:.:::: :.:::::..:::	GUAUUCAGC	Cleavage	pacid=371544
2697	2719	AAACCGUUA	::.::: ::.::: ::.:: :	UAAUUCACU	Cleavage	pacid=371680
154	176	AAACCGUUA	::. :.:::.::: :.:.: ::	AAGAUUAGU	Translation	pacid=371718
295	317	AAACCGUUA	: :: :: :::::.:: :::	UCAGUCUGU	Cleavage	pacid=371718
549	571	AAACCGUUA	....:..::..::::...:: :	GGGUUUGGU	Cleavage	pacid=371609
1176	1198	AAACCGUUA	::.. :: ::.::::.:.:: :	AAGUACACU	Cleavage	pacid=371552
1	23	AAACCGUUA	.::: :: .:::::::: ::	GAACACAUA	Cleavage	pacid=371609
1	23	AAACCGUUA	.::: :: .:::::::: ::	GAACACAUA	Cleavage	pacid=371609
264	286	AAACCGUUA	.:..:::: ::::: :..: ::	GAGUUCAGA	Cleavage	pacid=371626
444	466	AAACCGUUA	.:..: .::..:::::. :::	GAGUUAGGU	Cleavage	pacid=371737
1325	1347	AAACCGUUA	:: : ::::::::: .:.:: :	AACCACAGU	Cleavage	pacid=371640

Multiplicity	peptideName	locusName	Pfam	Panther	KOG
1	Phvul.004G064100	Phvul.004G064100	PF00445	PTHR11240,P	KOG1642
1	Phvul.009G096000	Phvul.009G096000	PF03330	PTHR22595,P	0
1	Phvul.008G049000	Phvul.008G049000	PF00793	PTHR21057,P	0
1	Phvul.004G064100	Phvul.004G064100	PF00445	PTHR11240,P	KOG1642
1	Phvul.009G096000	Phvul.009G096000	PF03330	PTHR22595,P	0
1	Phvul.004G064100	Phvul.004G064100	PF00445	PTHR11240,P	KOG1642
1	Phvul.009G096000	Phvul.009G096000	PF03330	PTHR22595,P	0
1	Phvul.009G196100	Phvul.009G196100	0	PTHR33494,P	0
1	Phvul.008G199900	Phvul.008G199900	PF05653	PTHR12570,P	KOG2922
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
1	Phvul.004G038100	Phvul.004G038100	PF10250	PTHR36050,P	0
1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02	PTHR31384,P	0
1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02	PTHR31384,P	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.004G160700	Phvul.004G160700	PF00293,PF15	PTHR13622,P	KOG4313
1	Phvul.011G152300	Phvul.011G152300	PF08276,PF0	PTHR27002,P	KOG1187
1	Phvul.011G152300	Phvul.011G152300	PF08276,PF0	PTHR27002,P	KOG1187
1	Phvul.011G152300	Phvul.011G152300	PF08276,PF0	PTHR27002,P	KOG1187
1	Phvul.003G229300	Phvul.003G229300	PF10260	PTHR13527,P	KOG3249
1	Phvul.003G229300	Phvul.003G229300	PF10260	PTHR13527,P	KOG3249
1	Phvul.003G178200	Phvul.003G178200	PF02153	PTHR11811,P	0
1	Phvul.009G196100	Phvul.009G196100	0	PTHR33494,P	0
1	Phvul.008G199900	Phvul.008G199900	PF05653	PTHR12570,P	KOG2922
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.004G160700	Phvul.004G160700	PF00293,PF15	PTHR13622,P	KOG4313
4	Phvul.009G104850	Phvul.009G104850	0	0	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.004G038100	Phvul.004G038100	PF10250	PTHR36050,P	0
1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02	PTHR31384,P	0
1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02	PTHR31384,P	0
1	Phvul.009G196100	Phvul.009G196100	0	PTHR33494,P	0
1	Phvul.008G199900	Phvul.008G199900	PF05653	PTHR12570,P	KOG2922
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.004G160700	Phvul.004G160700	PF00293,PF15	PTHR13622,P	KOG4313
4	Phvul.009G104850	Phvul.009G104850	0	0	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.L001604	Phvul.L001604	0	PTHR36390	0
1	Phvul.004G038100	Phvul.004G038100	PF10250	PTHR36050,P	0
1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02	PTHR31384,P	0

1	Phvul.011G073600	Phvul.011G073600	PF02309,PF02	PTHR31384,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G041900	Phvul.002G041900	0	PTHR35105,P	0
1	Phvul.010G108300	Phvul.010G108300	PF01176	PTHR21668,P	KOG3403
4	Phvul.006G148800	Phvul.006G148800	0	0	0
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.002G231800	Phvul.002G231800	PF00011	PTHR11527,P	KOG0710
1	Phvul.005G137000	Phvul.005G137000	PF02037,PF02	PTHR10782,P	KOG2169
1	Phvul.005G137000	Phvul.005G137000	PF02037,PF02	PTHR10782,P	KOG2169
1	Phvul.005G137000	Phvul.005G137000	PF02037,PF02	PTHR10782,P	KOG2169
1	Phvul.005G137000	Phvul.005G137000	PF02037,PF02	PTHR10782,P	KOG2169
1	Phvul.002G226900	Phvul.002G226900	PF03031,PF0	PTHR23081,P	KOG0323
1	Phvul.005G137000	Phvul.005G137000	PF02037,PF02	PTHR10782,P	KOG2169
1	Phvul.005G137000	Phvul.005G137000	PF02037,PF02	PTHR10782,P	KOG2169
1	Phvul.007G222000	Phvul.007G222000	0	0	0
1	Phvul.007G029200	Phvul.007G029200	PF07797	PTHR33130,P	0
1	Phvul.003G058400	Phvul.003G058400	PF14416,PF13	PTHR32285,P	0
1	Phvul.002G250000	Phvul.002G250000	PF02493,PF01	PTHR23086,P	0
1	Phvul.004G028100	Phvul.004G028100	PF00271,PF12	PTHR12131,P	0
3	Phvul.008G216700	Phvul.008G216700	0	0	0
3	Phvul.008G216700	Phvul.008G216700	0	0	0
1	Phvul.002G190100	Phvul.002G190100	PF00467,PF01	PTHR10497	KOG3418
1	Phvul.004G087000	Phvul.004G087000	PF07731,PF07	PTHR11709,P	KOG1263
1	Phvul.001G036500	Phvul.001G036500	0	PTHR10593,P	0
1	Phvul.005G102100	Phvul.005G102100	PF13639	PTHR22763,P	0
1	Phvul.005G102100	Phvul.005G102100	PF13639	PTHR22763,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G041900	Phvul.002G041900	0	PTHR35105,P	0
3	Phvul.006G148800	Phvul.006G148800	0	0	0
1	Phvul.010G108300	Phvul.010G108300	PF01176	PTHR21668,P	KOG3403
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
3	Phvul.008G216700	Phvul.008G216700	0	0	0
3	Phvul.008G216700	Phvul.008G216700	0	0	0
1	Phvul.001G036500	Phvul.001G036500	0	PTHR10593,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0

1	Phvul.002G289600	Phvul.002G289600	PF00153	PTHR24089,P	0
1	Phvul.002G041900	Phvul.002G041900	0	PTHR35105,P	0
3	Phvul.006G148800	Phvul.006G148800	0	0	0
1	Phvul.010G108300	Phvul.010G108300	PF01176	PTHR21668,P	KOG3403
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.006G214700	Phvul.006G214700	PF02493,PF01	PTHR23086,P	KOG0229
3	Phvul.008G216700	Phvul.008G216700	0	0	0
3	Phvul.008G216700	Phvul.008G216700	0	0	0
1	Phvul.001G036500	Phvul.001G036500	0	PTHR10593,P	0
1	Phvul.001G052300	Phvul.001G052300	0	PTHR35697,P	0
1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.001G073300	Phvul.001G073300	0	PTHR35697,P	0
1	Phvul.008G279750	Phvul.008G279750	PF03552	PTHR13301,P	0
1	Phvul.010G152600	Phvul.010G152600	PF11145	PTHR33389,P	0
1	Phvul.006G021500	Phvul.006G021500	PF14577,PF14	PTHR33232,P	0
1	Phvul.009G177300	Phvul.009G177300	PF00787,PF13	PTHR12326,P	0
1	Phvul.007G147400	Phvul.007G147400	PF00005,PF0C	PTHR24221,P	0
1	Phvul.003G178100	Phvul.003G178100	PF00226,PF01	PTHR24078,P	KOG0714
2	Phvul.011G102400	Phvul.011G102400	0	0	0
1	Phvul.001G106800	Phvul.001G106800	PF00249	PTHR10641,P	KOG0048
1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936
1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936
1	Phvul.011G187600	Phvul.011G187600	PF11605,PF04	PTHR13128,P	KOG2760
4	Phvul.006G148800	Phvul.006G148800	0	0	0
4	Phvul.006G148800	Phvul.006G148800	0	0	0
1	Phvul.002G044500	Phvul.002G044500	PF14432,PF13	PTHR24015,P	0
1	Phvul.007G113300	Phvul.007G113300	PF08031,PF01	PTHR32448,P	0
2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P	0
1	Phvul.010G144900	Phvul.010G144900	PF00349,PF03	PTHR19443,P	0
1	Phvul.002G083800	Phvul.002G083800	PF00249	PTHR10641,P	0
1	Phvul.001G067500	Phvul.001G067500	0	PTHR34194,P	0
1	Phvul.001G067500	Phvul.001G067500	0	PTHR34194,P	0
1	Phvul.001G067500	Phvul.001G067500	0	PTHR34194,P	0
1	Phvul.006G045600	Phvul.006G045600	PF00439	PTHR22881,P	0
1	Phvul.010G156000	Phvul.010G156000	PF04525	PTHR31087,P	0
2	Phvul.007G055500	Phvul.007G055500	PF07690	PTHR23500,P	KOG0254
2	Phvul.007G055500	Phvul.007G055500	PF07690	PTHR23500,P	KOG0254
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0

2	Phvul.007G055200	Phvul.007G055200	PF07690	PTHR23500,P	KOG0254
2	Phvul.007G055200	Phvul.007G055200	PF07690	PTHR23500,P	KOG0254
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.008G273100	Phvul.008G273100	PF00149	PTHR11668,P	0
3	Phvul.008G216700	Phvul.008G216700	0	0	0
1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338
1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338
1	Phvul.007G270500	Phvul.007G270500	PF00400,PF08	PTHR22840	0
1	Phvul.004G125900	Phvul.004G125900	PF00999	PTHR16254,P	KOG1650
1	Phvul.005G027200	Phvul.005G027200	PF00931	PTHR23155,P	KOG4658
1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
1	Phvul.001G052300	Phvul.001G052300	0	PTHR35697,P	0
1	Phvul.008G279750	Phvul.008G279750	PF03552	PTHR13301,P	0
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.001G073300	Phvul.001G073300	0	PTHR35697,P	0
1	Phvul.010G152600	Phvul.010G152600	PF11145	PTHR33389,P	0
2	Phvul.011G102400	Phvul.011G102400	0	0	0
3	Phvul.006G148800	Phvul.006G148800	0	0	0
3	Phvul.006G148800	Phvul.006G148800	0	0	0
1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338
1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338
1	Phvul.004G125900	Phvul.004G125900	PF00999	PTHR16254,P	KOG1650
1	Phvul.002G044500	Phvul.002G044500	PF14432,PF13	PTHR24015,P	0
1	Phvul.007G113300	Phvul.007G113300	PF08031,PF01	PTHR32448,P	0
1	Phvul.006G021500	Phvul.006G021500	PF14577,PF14	PTHR33232,P	0
1	Phvul.009G177300	Phvul.009G177300	PF00787,PF13	PTHR12326,P	0
1	Phvul.007G147400	Phvul.007G147400	PF00005,PF00	PTHR24221,P	0
1	Phvul.003G178100	Phvul.003G178100	PF00226,PF01	PTHR24078,P	KOG0714
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.001G106800	Phvul.001G106800	PF00249	PTHR10641,P	KOG0048
1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936
1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936
1	Phvul.011G187600	Phvul.011G187600	PF11605,PF04	PTHR13128,P	KOG2760
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.008G273100	Phvul.008G273100	PF00149	PTHR11668,P	0
1	Phvul.005G065300	Phvul.005G065300	PF11145	PTHR33389,P	0
2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P	0
1	Phvul.006G045600	Phvul.006G045600	PF00439	PTHR22881,P	0
3	Phvul.008G216700	Phvul.008G216700	0	0	0
1	Phvul.011G111800	Phvul.011G111800	0	0	0
1	Phvul.010G144900	Phvul.010G144900	PF00349,PF03	PTHR19443,P	0

1	Phvul.002G083800	Phvul.002G083800	PF00249	PTHR10641,P	0
1	Phvul.007G270500	Phvul.007G270500	PF00400,PF08	PTHR22840	0
1	Phvul.001G067500	Phvul.001G067500	0	PTHR34194,P	0
1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
1	Phvul.010G110700	Phvul.010G110700	PF08167	PTHR34105	0
1	Phvul.001G052300	Phvul.001G052300	0	PTHR35697,P	0
1	Phvul.008G279750	Phvul.008G279750	PF03552	PTHR13301,P	0
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.009G100000	Phvul.009G100000	PF00240,PF13	PTHR24006	KOG1863
1	Phvul.001G073300	Phvul.001G073300	0	PTHR35697,P	0
1	Phvul.010G152600	Phvul.010G152600	PF11145	PTHR33389,P	0
2	Phvul.011G102400	Phvul.011G102400	0	0	0
3	Phvul.006G148800	Phvul.006G148800	0	0	0
3	Phvul.006G148800	Phvul.006G148800	0	0	0
1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338
1	Phvul.010G121200	Phvul.010G121200	PF03372	PTHR12121,P	KOG2338
1	Phvul.004G125900	Phvul.004G125900	PF00999	PTHR16254,P	KOG1650
1	Phvul.002G044500	Phvul.002G044500	PF14432,PF13	PTHR24015,P	0
1	Phvul.007G113300	Phvul.007G113300	PF08031,PF01	PTHR32448,P	0
1	Phvul.006G021500	Phvul.006G021500	PF14577,PF14	PTHR33232,P	0
1	Phvul.009G177300	Phvul.009G177300	PF00787,PF13	PTHR12326,P	0
1	Phvul.007G147400	Phvul.007G147400	PF00005,PF0	PTHR24221,P	0
1	Phvul.003G178100	Phvul.003G178100	PF00226,PF01	PTHR24078,P	KOG0714
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.001G106800	Phvul.001G106800	PF00249	PTHR10641,P	KOG0048
1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936
1	Phvul.007G261100	Phvul.007G261100	PF08327,PF09	PTHR13009,P	KOG2936
1	Phvul.011G187600	Phvul.011G187600	PF11605,PF04	PTHR13128,P	KOG2760
1	Phvul.005G154600	Phvul.005G154600	PF04266	PTHR34204,P	0
1	Phvul.008G273100	Phvul.008G273100	PF00149	PTHR11668,P	0
1	Phvul.005G065300	Phvul.005G065300	PF11145	PTHR33389,P	0
2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P	0
1	Phvul.006G045600	Phvul.006G045600	PF00439	PTHR22881,P	0
3	Phvul.008G216700	Phvul.008G216700	0	0	0
1	Phvul.011G111800	Phvul.011G111800	0	0	0
1	Phvul.010G144900	Phvul.010G144900	PF00349,PF03	PTHR19443,P	0
1	Phvul.002G083800	Phvul.002G083800	PF00249	PTHR10641,P	0
1	Phvul.007G270500	Phvul.007G270500	PF00400,PF08	PTHR22840	0
1	Phvul.001G067500	Phvul.001G067500	0	PTHR34194,P	0
1	Phvul.001G067500	Phvul.001G067500	0	PTHR34194,P	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0

6	Phvul.011G133575	Phvul.011G133575	0	0	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0
1	Phvul.004G019300	Phvul.004G019300	PF14416,PF13	PTHR32285,P	0
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4	Phvul.009G104850	Phvul.009G104850	0	0	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
1	Phvul.003G158800	Phvul.003G158800	PF00704	PTHR11177,P	KOG2806
1	Phvul.006G173500	Phvul.006G173500	PF00847	PTHR31194,P	0
1	Phvul.002G183700	Phvul.002G183700	0	0	0
2	Phvul.011G102400	Phvul.011G102400	0	0	0
1	Phvul.007G027000	Phvul.007G027000	PF00847	PTHR31194,P	0
1	Phvul.005G043000	Phvul.005G043000	PF06101	PTHR17204,P	0
4	Phvul.006G148800	Phvul.006G148800	0	0	0
1	Phvul.011G069000	Phvul.011G069000	PF01535,PF13	PTHR24015,P	0
2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P	0
1	Phvul.005G054600	Phvul.005G054600	PF01926,PF11	PTHR23115,P	0
1	Phvul.001G024200	Phvul.001G024200	PF00225	PTHR24115,P	0
1	Phvul.008G060700	Phvul.008G060700	PF01554	PTHR11206,P	KOG1347
1	Phvul.004G147900	Phvul.004G147900	PF14531	PTHR24361,P	KOG0581
1	Phvul.001G057200	Phvul.001G057200	PF01269	PTHR10335	KOG1596
1	Phvul.009G046200	Phvul.009G046200	PF07145,PF14	PTHR24012	KOG0131
1	Phvul.011G133400	Phvul.011G133400	0	PTHR35420	0
1	Phvul.008G111100	Phvul.008G111100	PF13639	PTHR14155,P	0
1	Phvul.006G070000	Phvul.006G070000	PF13639	PTHR14155,P	KOG4172
1	Phvul.L001687	Phvul.L001687	PF02458	PTHR31642,P	0
1	Phvul.008G033500	Phvul.008G033500	PF00076	PTHR24012	0
1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P	0
1	Phvul.009G198900	Phvul.009G198900	PF05185	PTHR11006,P	KOG1499
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1	Phvul.006G037000	Phvul.006G037000	PF02458	PTHR31642,P	0
1	Phvul.001G205600	Phvul.001G205600	PF13414,PF11	PTHR17130,P	0
1	Phvul.011G159400	Phvul.011G159400	PF14259,PF0	PTHR24012,P	KOG4205
1	Phvul.004G061900	Phvul.004G061900	PF07690	PTHR23500,P	KOG0254
1	Phvul.006G048000	Phvul.006G048000	PF00026	PTHR13683,P	KOG1339
1	Phvul.009G007900	Phvul.009G007900	0	0	0
1	Phvul.005G067950	Phvul.005G067950	PF03634	PTHR31072,P	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0
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1	Phvul.006G173500	Phvul.006G173500	PF00847	PTHR31194,P	0
1	Phvul.002G183700	Phvul.002G183700	0	0	0

1	Phvul.005G043000	Phvul.005G043000	PF06101	PTHR17204,P	0
1	Phvul.004G019300	Phvul.004G019300	PF14416,PF13	PTHR32285,P	0
1	Phvul.004G019300	Phvul.004G019300	PF14416,PF13	PTHR32285,P	0
1	Phvul.011G069000	Phvul.011G069000	PF01535,PF13	PTHR24015,P	0
1	Phvul.002G231800	Phvul.002G231800	PF00011	PTHR11527,P	KOG0710
1	Phvul.L001687	Phvul.L001687	PF02458	PTHR31642,P	0
2	Phvul.011G102400	Phvul.011G102400	0	0	0
1	Phvul.006G037000	Phvul.006G037000	PF02458	PTHR31642,P	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
1	Phvul.003G158800	Phvul.003G158800	PF00704	PTHR11177,P	KOG2806
1	Phvul.001G057200	Phvul.001G057200	PF01269	PTHR10335	KOG1596
1	Phvul.004G057900	Phvul.004G057900	PF01535,PF13	PTHR24015,P	0
1	Phvul.007G027000	Phvul.007G027000	PF00847	PTHR31194,P	0
1	Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513
1	Phvul.008G060700	Phvul.008G060700	PF01554	PTHR11206,P	KOG1347
1	Phvul.011G110000	Phvul.011G110000	PF02984,PF0	PTHR10177,P	KOG0656
1	Phvul.010G003800	Phvul.010G003800	PF00854	PTHR11654,P	KOG1237
1	Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513
2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P	0
1	Phvul.005G054600	Phvul.005G054600	PF01926,PF11	PTHR23115,P	0
1	Phvul.001G024200	Phvul.001G024200	PF00225	PTHR24115,P	0
2	Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P	0
2	Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P	0
1	Phvul.008G033500	Phvul.008G033500	PF00076	PTHR24012	0
1	Phvul.011G028900	Phvul.011G028900	PF01966	PTHR33594,P	0
1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P	0
1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P	0
1	Phvul.004G061900	Phvul.004G061900	PF07690	PTHR23500,P	KOG0254
1	Phvul.006G048000	Phvul.006G048000	PF00026	PTHR13683,P	KOG1339
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
6	Phvul.011G133575	Phvul.011G133575	0	0	0
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6	Phvul.011G133575	Phvul.011G133575	0	0	0
1	Phvul.006G173500	Phvul.006G173500	PF00847	PTHR31194,P	0
1	Phvul.002G183700	Phvul.002G183700	0	0	0
1	Phvul.005G043000	Phvul.005G043000	PF06101	PTHR17204,P	0
1	Phvul.004G019300	Phvul.004G019300	PF14416,PF13	PTHR32285,P	0
1	Phvul.004G019300	Phvul.004G019300	PF14416,PF13	PTHR32285,P	0
1	Phvul.011G069000	Phvul.011G069000	PF01535,PF13	PTHR24015,P	0
1	Phvul.002G231800	Phvul.002G231800	PF00011	PTHR11527,P	KOG0710
1	Phvul.L001687	Phvul.L001687	PF02458	PTHR31642,P	0

2	Phvul.011G102400	Phvul.011G102400	0	0	0
1	Phvul.006G037000	Phvul.006G037000	PF02458	PTHR31642,P	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
4	Phvul.009G104850	Phvul.009G104850	0	0	0
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1	Phvul.003G158800	Phvul.003G158800	PF00704	PTHR11177,P	KOG2806
1	Phvul.001G057200	Phvul.001G057200	PF01269	PTHR10335	KOG1596
1	Phvul.004G057900	Phvul.004G057900	PF01535,PF13	PTHR24015,P	0
1	Phvul.007G027000	Phvul.007G027000	PF00847	PTHR31194,P	0
1	Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513
1	Phvul.008G060700	Phvul.008G060700	PF01554	PTHR11206,P	KOG1347
1	Phvul.011G110000	Phvul.011G110000	PF02984,PF0	PTHR10177,P	KOG0656
1	Phvul.010G003800	Phvul.010G003800	PF00854	PTHR11654,P	KOG1237
1	Phvul.009G063500	Phvul.009G063500	PF01734	PTHR32176	KOG0513
2	Phvul.006G206800	Phvul.006G206800	PF00806	PTHR12537,P	0
1	Phvul.005G054600	Phvul.005G054600	PF01926,PF11	PTHR23115,P	0
1	Phvul.001G024200	Phvul.001G024200	PF00225	PTHR24115,P	0
2	Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P	0
2	Phvul.006G098000	Phvul.006G098000	PF13302	PTHR13256,P	0
1	Phvul.008G033500	Phvul.008G033500	PF00076	PTHR24012	0
1	Phvul.011G028900	Phvul.011G028900	PF01966	PTHR33594,P	0
1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P	0
1	Phvul.008G036100	Phvul.008G036100	PF13445	PTHR13139,P	0
1	Phvul.004G061900	Phvul.004G061900	PF07690	PTHR23500,P	KOG0254
1	Phvul.006G048000	Phvul.006G048000	PF00026	PTHR13683,P	KOG1339
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0

KEGG	KOG	GO	Best-hit-arabi	arabi-symbol
3.1.27.1	K01166	GO:0033897,	AT1G14220.1	0
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2.5.1.55	K01627	GO:0009058,	AT1G79500.4	AtkdsA1
3.1.27.1	K01166	GO:0033897,	AT1G14220.1	0
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0	0	0	AT2G24100.1	0
0	0	GO:0016021,	AT1G34470.1	0
0	0	0	AT2G37570.1	SLT1
0	0	0	0	0
0	0	0	AT4G17430.1	0
0	0	GO:0006355,	AT5G60450.1	ARF4
0	0	GO:0006355,	AT5G60450.1	ARF4
0	0	0	AT5G07890.1	0
0	0	0	AT5G07890.1	0
0	0	0	AT5G07890.1	0
2.7.6.2	0	GO:0016787	AT5G19460.1	atnudt20,NU
2.7.11.1	0	GO:0048544,	AT4G27290.1	0
2.7.11.1	0	GO:0048544,	AT4G27290.1	0
2.7.11.1	0	GO:0048544,	AT4G27290.1	0
0	0	0	AT2G35360.1	0
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1.3.1.78	K15227	GO:0055114,	AT5G34930.1	0
0	0	0	AT2G24100.1	0
0	0	GO:0016021,	AT1G34470.1	0
0	0	0	AT2G37570.1	SLT1
2.7.6.2	0	GO:0016787	AT5G19460.1	atnudt20,NU
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0	0	0	AT5G07890.1	0
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0	0	0	AT5G07890.1	0
0	0	0	AT4G17430.1	0
0	0	GO:0006355,	AT5G60450.1	ARF4
0	0	GO:0006355,	AT5G60450.1	ARF4
0	0	0	AT2G24100.1	0
0	0	GO:0016021,	AT1G34470.1	0
0	0	0	AT2G37570.1	SLT1
2.7.6.2	0	GO:0016787	AT5G19460.1	atnudt20,NU
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	0		0	0	AT4G11440.1	0
	0		0	0	AT1G64980.1	0
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3.4.19.12	K11858	GO:0005515	AT3G49600.1	ATUBP26,SUP
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3.1.3.16	K15423	GO:0016787	AT5G55260.1	PPX-2,PPX2
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3.6.5.3	K02519	GO:0005525	AT1G17220.1	FUG1
3.6.4.4	K10395	GO:0008017,(	AT5G47820.1	FRA1
0	K03327	GO:0055085,(	AT4G00350.1	0
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3.6.4.13	K14563	GO:0008168,(	AT5G52470.1	ATFBR1,ATFIB
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0	K12741	GO:0003676	AT5G61030.1	GR-RBP3
2.7.11.1	0	0	AT3G29270.2	0
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3.6.5.3	K02519	GO:0005525	AT1G17220.1	FUG1
3.6.4.4	K10395	GO:0008017,(	AT5G47820.1	FRA1
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2.3.1.1	0	GO:0008080	AT3G22560.1	0
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0	K06950	0	AT1G17330.1	0
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3.6.5.3	K02519	GO:0005525	AT1G17220.1	FUG1
3.6.4.4	K10395	GO:0008017,(	AT5G47820.1	FRA1
2.3.1.1	0	GO:0008080	AT3G22560.1	0
2.3.1.1	0	GO:0008080	AT3G22560.1	0
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arabi-defline	ID	Annot_defline	IDENTIFIER
Ribonuclease T2 family protein	Phvul.004G06	PTHR11240:S	Phvul.004G06
plant natriuretic peptide A	Phvul.009G09	PTHR22595//I	Phvul.009G09
Aldolase-type TIM barrel family protein	Phvul.008G04	2.5.1.55 - 3-de	Phvul.008G04
Ribonuclease T2 family protein	Phvul.004G06	PTHR11240:S	Phvul.004G06
plant natriuretic peptide A	Phvul.009G09	PTHR22595//I	Phvul.009G09
Ribonuclease T2 family protein	Phvul.004G06	PTHR11240:S	Phvul.004G06
plant natriuretic peptide A	Phvul.009G09	PTHR22595//I	Phvul.009G09
0	0	0	Phvul.009G19
Protein of unknown function (DUF803)	Phvul.008G19	KOG2922 - Un	Phvul.008G19
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:S	Phvul.007G15
0	0	0	Phvul.009G10
O-fucosyltransferase family protein	Phvul.004G03	PF10250 - GD	Phvul.004G03
auxin response factor 4	Phvul.011G07	PTHR31384:S	Phvul.011G07
auxin response factor 4	Phvul.011G07	PTHR31384:S	Phvul.011G07
myosin heavy chain-related	0	0	Phvul.L00160
myosin heavy chain-related	0	0	Phvul.L00160
myosin heavy chain-related	0	0	Phvul.L00160
nudix hydrolase homolog 20	Phvul.004G16	2.7.6.2 - Thian	Phvul.004G16
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S	Phvul.011G15
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S	Phvul.011G15
S-locus lectin protein kinase family protein	Phvul.011G15	PTHR27002:S	Phvul.011G15
ubiquitin family protein	Phvul.003G22	PTHR13527:S	Phvul.003G22
ubiquitin family protein	Phvul.003G22	PTHR13527:S	Phvul.003G22
arogenate dehydrogenase	Phvul.003G17	1.3.1.78 - Aro	Phvul.003G17
0	0	0	Phvul.009G19
Protein of unknown function (DUF803)	Phvul.008G19	KOG2922 - Un	Phvul.008G19
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:S	Phvul.007G15
nudix hydrolase homolog 20	Phvul.004G16	2.7.6.2 - Thian	Phvul.004G16
0	0	0	Phvul.009G10
myosin heavy chain-related	0	0	Phvul.L00160
myosin heavy chain-related	0	0	Phvul.L00160
myosin heavy chain-related	0	0	Phvul.L00160
O-fucosyltransferase family protein	Phvul.004G03	PF10250 - GD	Phvul.004G03
auxin response factor 4	Phvul.011G07	PTHR31384:S	Phvul.011G07
auxin response factor 4	Phvul.011G07	PTHR31384:S	Phvul.011G07
0	0	0	Phvul.009G19
Protein of unknown function (DUF803)	Phvul.008G19	KOG2922 - Un	Phvul.008G19
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:S	Phvul.007G15
nudix hydrolase homolog 20	Phvul.004G16	2.7.6.2 - Thian	Phvul.004G16
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myosin heavy chain-related	0	0	Phvul.L00160
myosin heavy chain-related	0	0	Phvul.L00160
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O-fucosyltransferase family protein	Phvul.004G03	PF10250 - GD	Phvul.004G03
auxin response factor 4	Phvul.011G07	PTHR31384:S	Phvul.011G07

auxin response factor 4	Phvul.011G07	PTHR31384:SI	Phvul.011G07
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Nucleotide-diphospho-sugar transferases superf	0	0	Phvul.002G04
Nucleic acid-binding, OB-fold-like protein	Phvul.010G10	K03236 - tran:	Phvul.010G10
0	0	0	Phvul.006G14
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
HSP20-like chaperones superfamily protein	Phvul.002G23	PTHR11527:SI	Phvul.002G23
DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:SI	Phvul.005G13
DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:SI	Phvul.005G13
DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:SI	Phvul.005G13
DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:SI	Phvul.005G13
C-terminal domain phosphatase-like 1	Phvul.002G22	PTHR23081:SI	Phvul.002G22
DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:SI	Phvul.005G13
DNA-binding protein with MIZ/SP-RING zinc fing	Phvul.005G13	PTHR10782:SI	Phvul.005G13
0	0	0	Phvul.007G22
Protein of unknown function (DUF1639)	Phvul.007G02	PF07797 - Pro	Phvul.007G02
TRICHOME BIREFRINGENCE-LIKE 37	Phvul.003G05	PTHR32285:SI	Phvul.003G05
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.002G25	PTHR23086:SI	Phvul.002G25
ATP-dependent RNA helicase, mitochondrial, pu	Phvul.004G02	PTHR12131:SI	Phvul.004G02
0	0	0	Phvul.008G21
0	0	0	Phvul.008G21
Ribosomal L27e protein family	Phvul.002G19	K02901 - large	Phvul.002G19
Laccase/Diphenol oxidase family protein	Phvul.004G08	PTHR11709:SI	Phvul.004G08
indeterminate(ID)-domain 2	Phvul.001G03	PTHR10593:SI	Phvul.001G03
RING/U-box superfamily protein	Phvul.005G10	PTHR22763:SI	Phvul.005G10
RING/U-box superfamily protein	Phvul.005G10	PTHR22763:SI	Phvul.005G10
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Nucleotide-diphospho-sugar transferases superf	0	0	Phvul.002G04
0	0	0	Phvul.006G14
Nucleic acid-binding, OB-fold-like protein	Phvul.010G10	K03236 - tran:	Phvul.010G10
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
0	0	0	Phvul.008G21
0	0	0	Phvul.008G21
indeterminate(ID)-domain 2	Phvul.001G03	PTHR10593:SI	Phvul.001G03
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28

Mitochondrial substrate carrier family protein	Phvul.002G28	PTHR24089:SI	Phvul.002G28
Nucleotide-diphospho-sugar transferases superf	0	0	Phvul.002G04
0	0	0	Phvul.006G14
Nucleic acid-binding, OB-fold-like protein	Phvul.010G10	K03236 - tran:	Phvul.010G10
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
Phosphatidylinositol-4-phosphate 5-kinase famil	Phvul.006G21	PTHR23086:SI	Phvul.006G21
0	0	0	Phvul.008G21
0	0	0	Phvul.008G21
indeterminate(ID)-domain 2	Phvul.001G03	PTHR10593:SI	Phvul.001G03
tracheary element differentiation-related 7	0	0	Phvul.001G05
0	Phvul.010G11	PF08167 - rRN	Phvul.010G11
0	Phvul.010G11	PF08167 - rRN	Phvul.010G11
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
tracheary element differentiation-related 6	0	0	Phvul.001G07
cellulose synthase like E1	Phvul.008G27	PTHR13301//I	Phvul.008G27
Protein of unknown function (DUF2921)	Phvul.010G15	PF11145 - Pro	Phvul.010G15
0	Phvul.006G02	PF14577 - Sie	Phvul.006G02
Phox (PX) domain-containing protein	Phvul.009G17	PTHR12326 - I	Phvul.009G17
ATP binding cassette subfamily B1	Phvul.007G14	PTHR24221:SI	Phvul.007G14
DNAJ heat shock family protein	Phvul.003G17	PTHR24078:SI	Phvul.003G17
0	0	0	Phvul.011G10
myb domain protein 56	Phvul.001G10	PTHR10641:SI	Phvul.001G10
Aha1 domain-containing protein	Phvul.007G26	PTHR13009 - I	Phvul.007G26
Aha1 domain-containing protein	Phvul.007G26	PTHR13009 - I	Phvul.007G26
EAP30/Vps36 family protein	Phvul.011G18	K12190 - ESCF	Phvul.011G18
0	0	0	Phvul.006G14
0	0	0	Phvul.006G14
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.002G04	PF01535//PF1	Phvul.002G04
FAD-binding Berberine family protein	Phvul.007G11	PF01565//PFC	Phvul.007G11
pumilio 7	Phvul.006G20	PTHR12537:SI	Phvul.006G20
hexokinase 2	Phvul.010G14	PTHR19443//I	Phvul.010G14
myb domain protein 105	Phvul.002G08	PTHR10641:SI	Phvul.002G08
0	Phvul.001G06	PTHR34194:SI	Phvul.001G06
0	Phvul.001G06	PTHR34194:SI	Phvul.001G06
0	Phvul.001G06	PTHR34194:SI	Phvul.001G06
DNA-binding bromodomain-containing protein	Phvul.006G04	PTHR22881:SI	Phvul.006G04
Protein of unknown function (DUF567)	Phvul.010G15	PTHR31087:SI	Phvul.010G15
Major facilitator superfamily protein	Phvul.007G05	PTHR23500:SI	Phvul.007G05
Major facilitator superfamily protein	Phvul.007G05	PTHR23500:SI	Phvul.007G05
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:SI	Phvul.005G15
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:SI	Phvul.005G15

Major facilitator superfamily protein	Phvul.007G05	PTHR23500:S	Phvul.007G05
Major facilitator superfamily protein	Phvul.007G05	PTHR23500:S	Phvul.007G05
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:S	Phvul.005G15
protein phosphatase X 2	Phvul.008G27	K15423 - seri	Phvul.008G27
0	0	0	Phvul.008G21
Calcium-binding endonuclease/exonuclease/ph	Phvul.010G12	PTHR12121//	Phvul.010G12
Calcium-binding endonuclease/exonuclease/ph	Phvul.010G12	PTHR12121//	Phvul.010G12
MOS4-associated complex 3B	Phvul.007G27	K10599 - pre-	Phvul.007G27
K+ efflux antiporter 5	Phvul.004G12	PTHR16254:S	Phvul.004G12
NB-ARC domain-containing disease resistance p	Phvul.005G02	PTHR23155//	Phvul.005G02
0	Phvul.010G11	PF08167 - rR	Phvul.010G11
0	Phvul.010G11	PF08167 - rR	Phvul.010G11
tracheary element differentiation-related 7	0	0	Phvul.001G05
cellulose synthase like E1	Phvul.008G27	PTHR13301//	Phvul.008G27
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
tracheary element differentiation-related 6	0	0	Phvul.001G07
Protein of unknown function (DUF2921)	Phvul.010G15	PF11145 - Pro	Phvul.010G15
0	0	0	Phvul.011G10
0	0	0	Phvul.006G14
0	0	0	Phvul.006G14
Calcium-binding endonuclease/exonuclease/ph	Phvul.010G12	PTHR12121//	Phvul.010G12
Calcium-binding endonuclease/exonuclease/ph	Phvul.010G12	PTHR12121//	Phvul.010G12
K+ efflux antiporter 5	Phvul.004G12	PTHR16254:S	Phvul.004G12
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.002G04	PF01535//PF1	Phvul.002G04
FAD-binding Berberine family protein	Phvul.007G11	PF01565//PF	Phvul.007G11
0	Phvul.006G02	PF14577 - Sie	Phvul.006G02
Phox (PX) domain-containing protein	Phvul.009G17	PTHR12326 -	Phvul.009G17
ATP binding cassette subfamily B1	Phvul.007G14	PTHR24221:S	Phvul.007G14
DNAJ heat shock family protein	Phvul.003G17	PTHR24078:S	Phvul.003G17
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:S	Phvul.005G15
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:S	Phvul.005G15
myb domain protein 56	Phvul.001G10	PTHR10641:S	Phvul.001G10
Aha1 domain-containing protein	Phvul.007G26	PTHR13009 -	Phvul.007G26
Aha1 domain-containing protein	Phvul.007G26	PTHR13009 -	Phvul.007G26
EAP30/Vps36 family protein	Phvul.011G18	K12190 - ESC	Phvul.011G18
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:S	Phvul.005G15
protein phosphatase X 2	Phvul.008G27	K15423 - seri	Phvul.008G27
Protein of unknown function (DUF2921)	Phvul.005G06	PF11145 - Pro	Phvul.005G06
pumilio 7	Phvul.006G20	PTHR12537:S	Phvul.006G20
DNA-binding bromodomain-containing protein	Phvul.006G04	PTHR22881:S	Phvul.006G04
0	0	0	Phvul.008G21
embryo defective 1923	0	0	Phvul.011G11
hexokinase 2	Phvul.010G14	PTHR19443//	Phvul.010G14

myb domain protein 105	Phvul.002G08	PTHR10641:S	Phvul.002G08
MOS4-associated complex 3B	Phvul.007G27	K10599 - pre-	Phvul.007G27
0	Phvul.001G06	PTHR34194:S	Phvul.001G06
0	Phvul.010G11	PF08167 - rR	Phvul.010G11
0	Phvul.010G11	PF08167 - rR	Phvul.010G11
tracheary element differentiation-related 7	0	0	Phvul.001G05
cellulose synthase like E1	Phvul.008G27	PTHR13301//	Phvul.008G27
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
ubiquitin-specific protease 26	Phvul.009G10	K11858 - ubiq	Phvul.009G10
tracheary element differentiation-related 6	0	0	Phvul.001G07
Protein of unknown function (DUF2921)	Phvul.010G15	PF11145 - Pro	Phvul.010G15
0	0	0	Phvul.011G10
0	0	0	Phvul.006G14
0	0	0	Phvul.006G14
Calcium-binding endonuclease/exonuclease/ph	Phvul.010G12	PTHR12121//	Phvul.010G12
Calcium-binding endonuclease/exonuclease/ph	Phvul.010G12	PTHR12121//	Phvul.010G12
K+ efflux antiporter 5	Phvul.004G12	PTHR16254:S	Phvul.004G12
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.002G04	PF01535//PF1	Phvul.002G04
FAD-binding Berberine family protein	Phvul.007G11	PF01565//PF	Phvul.007G11
0	Phvul.006G02	PF14577 - Sie	Phvul.006G02
Phox (PX) domain-containing protein	Phvul.009G17	PTHR12326 -	Phvul.009G17
ATP binding cassette subfamily B1	Phvul.007G14	PTHR24221:S	Phvul.007G14
DNAJ heat shock family protein	Phvul.003G17	PTHR24078:S	Phvul.003G17
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:S	Phvul.005G15
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:S	Phvul.005G15
myb domain protein 56	Phvul.001G10	PTHR10641:S	Phvul.001G10
Aha1 domain-containing protein	Phvul.007G26	PTHR13009 -	Phvul.007G26
Aha1 domain-containing protein	Phvul.007G26	PTHR13009 -	Phvul.007G26
EAP30/Vps36 family protein	Phvul.011G18	K12190 - ESC	Phvul.011G18
RNA-binding ASCH domain protein	Phvul.005G15	PTHR34204:S	Phvul.005G15
protein phosphatase X 2	Phvul.008G27	K15423 - serir	Phvul.008G27
Protein of unknown function (DUF2921)	Phvul.005G06	PF11145 - Pro	Phvul.005G06
pumilio 7	Phvul.006G20	PTHR12537:S	Phvul.006G20
DNA-binding bromodomain-containing protein	Phvul.006G04	PTHR22881:S	Phvul.006G04
0	0	0	Phvul.008G21
embryo defective 1923	0	0	Phvul.011G11
hexokinase 2	Phvul.010G14	PTHR19443//	Phvul.010G14
myb domain protein 105	Phvul.002G08	PTHR10641:S	Phvul.002G08
MOS4-associated complex 3B	Phvul.007G27	K10599 - pre-	Phvul.007G27
0	Phvul.001G06	PTHR34194:S	Phvul.001G06
0	Phvul.001G06	PTHR34194:S	Phvul.001G06
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13

0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:S	Phvul.004G01
TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:S	Phvul.004G01
0	0	0	Phvul.009G10
0	0	0	Phvul.009G10
0	0	0	Phvul.009G10
Glycosyl hydrolase family protein with chitinase	Phvul.003G15	PTHR11177//	Phvul.003G15
related to AP2 11	Phvul.006G17	PTHR31194//	Phvul.006G17
0	0	0	Phvul.002G18
0	0	0	Phvul.011G10
Integrase-type DNA-binding superfamily protein	Phvul.007G02	PTHR31194//	Phvul.007G02
Plant protein of unknown function (DUF946)	Phvul.005G04	PTHR17204:S	Phvul.005G04
0	0	0	Phvul.006G14
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.011G06	PF01535//PF1	Phvul.011G06
pumilio 7	Phvul.006G20	PTHR12537:S	Phvul.006G20
Translation initiation factor 2, small GTP-binding	Phvul.005G05	PTHR23115:S	Phvul.005G05
P-loop containing nucleoside triphosphate hydr	Phvul.001G02	K10395 - kine	Phvul.001G02
MATE efflux family protein	Phvul.008G06	PTHR11206:S	Phvul.008G06
MAP kinase kinase 9	Phvul.004G14	PTHR24361:S	Phvul.004G14
fibrillarin 1	Phvul.001G05	K14563 - rRN	Phvul.001G05
CTC-interacting domain 12	Phvul.009G04	PF00076//PF	Phvul.009G04
0	0	0	Phvul.011G13
TOXICOS EN LEVADURA 2	Phvul.008G11	PTHR14155:S	Phvul.008G11
TOXICOS EN LEVADURA 63	Phvul.006G07	PTHR14155:S	Phvul.006G07
spermidine hydroxycinnamoyl transferase	Phvul.L00168	PTHR31642:S	Phvul.L00168
glycine-rich RNA-binding protein 3	Phvul.008G03	K12741 - hete	Phvul.008G03
RING/U-box superfamily protein	Phvul.008G03	PTHR13139 -	Phvul.008G03
protein arginine methyltransferase 10	Phvul.009G19	PTHR11006:S	Phvul.009G19
RING/U-box superfamily protein	Phvul.008G03	PTHR13139 -	Phvul.008G03
spermidine hydroxycinnamoyl transferase	Phvul.006G03	K13065 - shiki	Phvul.006G03
tetratricopeptide repeat (TPR)-containing protei	Phvul.001G20	PTHR17130:S	Phvul.001G20
RNA-binding (RRM/RBD/RNP motifs) family prot	Phvul.011G15	PTHR24012:S	Phvul.011G15
plastidic GLC translocator	Phvul.004G06	PTHR23500:S	Phvul.004G06
Eukaryotic aspartyl protease family protein	Phvul.006G04	PTHR13683:S	Phvul.006G04
0	0	0	Phvul.009G00
TCP family transcription factor 4	Phvul.005G06	PTHR31072:S	Phvul.005G06
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
related to AP2 11	Phvul.006G17	PTHR31194//	Phvul.006G17
0	0	0	Phvul.002G18

Plant protein of unknown function (DUF946)	Phvul.005G04	PTHR17204:S	Phvul.005G04
TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:S	Phvul.004G01
TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:S	Phvul.004G01
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.011G06	PF01535//PF1	Phvul.011G06
HSP20-like chaperones superfamily protein	Phvul.002G23	PTHR11527:S	Phvul.002G23
spermidine hydroxycinnamoyl transferase	Phvul.L00168	PTHR31642:S	Phvul.L00168
0	0	0	Phvul.011G10
spermidine hydroxycinnamoyl transferase	Phvul.006G03	K13065 - shiki	Phvul.006G03
0	0	0	Phvul.009G10
0	0	0	Phvul.009G10
0	0	0	Phvul.009G10
Glycosyl hydrolase family protein with chitinase	Phvul.003G15	PTHR11177//	Phvul.003G15
fibrillarin 1	Phvul.001G05	K14563 - rRN	Phvul.001G05
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.004G05	PF01535//PF1	Phvul.004G05
Integrase-type DNA-binding superfamily protein	Phvul.007G02	PTHR31194//	Phvul.007G02
phospholipase A 2A	Phvul.009G06	KOG0513 - Ca	Phvul.009G06
MATE efflux family protein	Phvul.008G06	PTHR11206:S	Phvul.008G06
Cyclin D6;1	Phvul.011G11	K18812 - cycli	Phvul.011G11
Major facilitator superfamily protein	Phvul.010G00	PTHR11654//	Phvul.010G00
phospholipase A 2A	Phvul.009G06	KOG0513 - Ca	Phvul.009G06
pumilio 7	Phvul.006G20	PTHR12537:S	Phvul.006G20
Translation initiation factor 2, small GTP-binding	Phvul.005G05	PTHR23115:S	Phvul.005G05
P-loop containing nucleoside triphosphate hydr	Phvul.001G02	K10395 - kine	Phvul.001G02
Acyl-CoA N-acyltransferases (NAT) superfamily	Phvul.006G09	PTHR13256:S	Phvul.006G09
Acyl-CoA N-acyltransferases (NAT) superfamily	Phvul.006G09	PTHR13256:S	Phvul.006G09
glycine-rich RNA-binding protein 3	Phvul.008G03	K12741 - hete	Phvul.008G03
Metal-dependent phosphohydrolase	Phvul.011G02	K06950 - unch	Phvul.011G02
RING/U-box superfamily protein	Phvul.008G03	PTHR13139 -	Phvul.008G03
RING/U-box superfamily protein	Phvul.008G03	PTHR13139 -	Phvul.008G03
plastidic GLC translocator	Phvul.004G06	PTHR23500:S	Phvul.004G06
Eukaryotic aspartyl protease family protein	Phvul.006G04	PTHR13683:S	Phvul.006G04
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:S	Phvul.007G15
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
0	0	0	Phvul.011G13
related to AP2 11	Phvul.006G17	PTHR31194//	Phvul.006G17
0	0	0	Phvul.002G18
Plant protein of unknown function (DUF946)	Phvul.005G04	PTHR17204:S	Phvul.005G04
TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:S	Phvul.004G01
TRICHOME BIREFRINGENCE-LIKE 22	Phvul.004G01	PTHR32285:S	Phvul.004G01
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.011G06	PF01535//PF1	Phvul.011G06
HSP20-like chaperones superfamily protein	Phvul.002G23	PTHR11527:S	Phvul.002G23
spermidine hydroxycinnamoyl transferase	Phvul.L00168	PTHR31642:S	Phvul.L00168

0	0	0	Phvul.011G10
spermidine hydroxycinnamoyl transferase	Phvul.006G03	K13065 - shiki	Phvul.006G03
0	0	0	Phvul.009G10
0	0	0	Phvul.009G10
0	0	0	Phvul.009G10
Glycosyl hydrolase family protein with chitinase	Phvul.003G15	PTHR11177//I	Phvul.003G15
fibrillarin 1	Phvul.001G05	K14563 - rRN/	Phvul.001G05
Pentatricopeptide repeat (PPR) superfamily prot	Phvul.004G05	PF01535//PF1	Phvul.004G05
Integrase-type DNA-binding superfamily protein	Phvul.007G02	PTHR31194//I	Phvul.007G02
phospholipase A 2A	Phvul.009G06	KOG0513 - Ca	Phvul.009G06
MATE efflux family protein	Phvul.008G06	PTHR11206:SI	Phvul.008G06
Cyclin D6;1	Phvul.011G11	K18812 - cycli	Phvul.011G11
Major facilitator superfamily protein	Phvul.010G00	PTHR11654//I	Phvul.010G00
phospholipase A 2A	Phvul.009G06	KOG0513 - Ca	Phvul.009G06
pumilio 7	Phvul.006G20	PTHR12537:SI	Phvul.006G20
Translation initiation factor 2, small GTP-binding	Phvul.005G05	PTHR23115:SI	Phvul.005G05
P-loop containing nucleoside triphosphate hydro	Phvul.001G02	K10395 - kine	Phvul.001G02
Acyl-CoA N-acyltransferases (NAT) superfamily p	Phvul.006G09	PTHR13256:SI	Phvul.006G09
Acyl-CoA N-acyltransferases (NAT) superfamily p	Phvul.006G09	PTHR13256:SI	Phvul.006G09
glycine-rich RNA-binding protein 3	Phvul.008G03	K12741 - hete	Phvul.008G03
Metal-dependent phosphohydrolase	Phvul.011G02	K06950 - uncl	Phvul.011G02
RING/U-box superfamily protein	Phvul.008G03	PTHR13139 - I	Phvul.008G03
RING/U-box superfamily protein	Phvul.008G03	PTHR13139 - I	Phvul.008G03
plastidic GLC translocator	Phvul.004G06	PTHR23500:SI	Phvul.004G06
Eukaryotic aspartyl protease family protein	Phvul.006G04	PTHR13683:SI	Phvul.006G04
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:SI	Phvul.007G15

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RNA biosynth	transcription factor (ARF) (original description: pacid=37155087 transcript=Phvul.011
Solute transp	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
Solute transp	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
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Protein biosyn	assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv
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Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
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Protein home	SUMO E3 ligase (SIZ1) (original description: pacid=37153775 transcript=Phvul.005G1
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Protein biosyn	component RPL27 of LSU proteome component (original description: pacid=3717730
Enzyme classi	Laccase-15 OS=Arabidopsis thaliana (sp|q84j37|lac15_arath : 554.0) & Enzyme class
RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript
not assigned.	(original description: pacid=37153077 transcript=Phvul.005G102100.2 locus=Phvul.0
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Solute transp	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
Solute transp	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
Solute transp	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
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Protein biosyn	assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
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not assigned.r	no hits & (original description: pacid=37159849 transcript=Phvul.008G216700.1 locu
RNA biosynth	C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript
Solute transp	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
Solute transp	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00

Solute transpo	solute transporter (MTCC) (original description: pacid=37178109 transcript=Phvul.00
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Protein biosyn	assembly factor (eIF1A) of eIF1 (original description: pacid=37144013 transcript=Phv
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37172
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RNA biosynthe	C2H2 zinc finger transcription factor (original description: pacid=37170711 transcript
Cell wall organ	TED-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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Protein homeo	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
Protein homeo	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
Protein homeo	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
Protein homeo	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
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Solute transpo	subfamily ABCB transporter (original description: pacid=37164519 transcript=Phvul.0
Protein homeo	co-chaperone (Hsp40) (original description: pacid=37145763 transcript=Phvul.003G1
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Solute transpo	monosaccharide transporter (STP) (original description: pacid=37167067 transcript=P
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Solute transp	monosaccharide transporter (STP) (original description: pacid=37166808 transcript=
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Protein modif	catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3
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not assigned.a	(original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.0
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Protein home	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
Protein home	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
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Solute transp	subfamily ABCB transporter (original description: pacid=37164519 transcript=Phvul.0
Protein home	co-chaperone (Hsp40) (original description: pacid=37145763 transcript=Phvul.003G1
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RNA biosynth	transcription factor (MYB) (original description: pacid=37169002 transcript=Phvul.00
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Vesicle traffic	component VPS36 of ESCRT-II complex (original description: pacid=37155231 transcr
not assigned.n	no hits & (original description: pacid=37154072 transcript=Phvul.005G154600.3 locu
Protein modif	catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3
not assigned.n	no hits & (original description: pacid=37152330 transcript=Phvul.005G065300.1 locu
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Carbohydrate	hexokinase (original description: pacid=37142381 transcript=Phvul.010G144900.1 lo

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RNA processir	component MAC3 of non-snRNP MOS4-associated complex (original description: pac
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Cell wall orgar	TED-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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Protein home	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
Protein home	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
Protein home	deubiquitinase (UBP26) (original description: pacid=37150180 transcript=Phvul.009G
Cell wall orgar	TED-type cellulose synthase CSC-interactive protein (original description: pacid=3716
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not assigned.r	no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
not assigned.r	no hits & (original description: pacid=37172393 transcript=Phvul.006G148800.1 locu
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not assigned.a	(original description: pacid=37143248 transcript=Phvul.010G121200.2 locus=Phvul.0
Solute transpo	proton:potassium cation antiporter (KEA) (original description: pacid=37162662 tran
not assigned.a	(original description: pacid=37176369 transcript=Phvul.002G044500.1 locus=Phvul.0
Enzyme classi	Enzyme classification.EC_1 oxidoreductases.EC_1.1 oxidoreductase acting on CH-OH
not assigned.a	(original description: pacid=37172660 transcript=Phvul.006G021500.1 locus=Phvul.0
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Solute transpo	subfamily ABCB transporter (original description: pacid=37164519 transcript=Phvul.0
Protein home	co-chaperone (Hsp40) (original description: pacid=37145763 transcript=Phvul.003G1
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RNA biosynth	transcription factor (MYB) (original description: pacid=37169002 transcript=Phvul.00
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Vesicle traffic	component VPS36 of ESCRT-II complex (original description: pacid=37155231 transcr
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Protein modif	catalytic component PP4c of PP4 phosphatase complex (original description: pacid=3
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Carbohydrate	hexokinase (original description: pacid=37142381 transcript=Phvul.010G144900.1 lo
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not assigned.a	(original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.0
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Enzyme classi	no description available(sp|a0a072ur65|cht5b_medtr : 395.0) & Enzyme classificatio
External stimu	transcription factor (ERN1) (original description: pacid=37171836 transcript=Phvul.00
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Cytoskeleton (	motor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001
Solute transpo	metabolite transporter (DTX) (original description: pacid=37157842 transcript=Phvul
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Enzyme classi	Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 24.7) (origina
RNA processin	RNA editing factor (ORRM) (original description: pacid=37160922 transcript=Phvul.00
Protein home	RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
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Photosynthesi	LPA1 protein involved in PS-II assembly (original description: pacid=37169924 transcr
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Solute transpo	hexose transporter (SGB/GlcT) (original description: pacid=37162603 transcript=Phvu
Protein home	pepsin-type protease (original description: pacid=37173754 transcript=Phvul.006G04
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RNA biosynthe	transcription factor (TCP) (original description: pacid=37152688 transcript=Phvul.005
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not assigned.r	no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
not assigned.r	no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
not assigned.r	no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
not assigned.r	no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
not assigned.r	no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
External stimu	transcription factor (ERN1) (original description: pacid=37171836 transcript=Phvul.00
not assigned.r	no hits & (original description: pacid=37177963 transcript=Phvul.002G183700.1 locu

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not assigned.a	(original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37162149 transcript=Phvul.004G019300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37155075 transcript=Phvul.011G069000.1 locus=Phvul.0
Protein home	class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t
Enzyme classi	Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 24.7) (origina
not assigned.r	no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
Enzyme classi	Spermidine hydroxycinnamoyl transferase OS=Arabidopsis thaliana (sp|o64470|sht_
not assigned.r	no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
not assigned.r	no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
not assigned.r	no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
Enzyme classi	no description available(sp|a0a072ur65|cht5b_medtr : 395.0) & Enzyme classificatic
Protein biosyr	methyltransferase component Nop1/fibrillarin of snoRNP rRNA methylation complex
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RNA biosynth	transcription factor (ERF) (original description: pacid=37164213 transcript=Phvul.007
Lipid metaboli	phospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.0
Solute transp	metabolite transporter (DTX) (original description: pacid=37157842 transcript=Phvul
Cell cycle orga	cyclin (CYCD) (original description: pacid=37157024 transcript=Phvul.011G110000.1 l
Solute transp	anion transporter (NRT1/PTR) (original description: pacid=37143370 transcript=Phvu
Lipid metaboli	phospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.0
not assigned.a	(original description: pacid=37174127 transcript=Phvul.006G206800.1 locus=Phvul.0
Protein biosyr	IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv
Cytoskeleton	motor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001
not assigned.r	no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
not assigned.r	no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
RNA processir	RNA editing factor (ORRM) (original description: pacid=37160922 transcript=Phvul.0
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Protein home	RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
Solute transp	hexose transporter (SGB/GlcT) (original description: pacid=37162603 transcript=Phvu
Protein home	pepsin-type protease (original description: pacid=37173754 transcript=Phvul.006G0
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not assigned.r	no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
not assigned.r	no hits & (original description: pacid=37154875 transcript=Phvul.011G133575.1 locu
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External stimu	transcription factor (ERN1) (original description: pacid=37171836 transcript=Phvul.0
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Protein home	class-C-I small heat-shock-responsive protein (original description: pacid=37177788 t
Enzyme classi	Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 24.7) (origina

not assigned.r	no hits & (original description: pacid=37154896 transcript=Phvul.011G102400.1 locu
Enzyme classi	Spermidine hydroxycinnamoyl transferase OS=Arabidopsis thaliana (sp|o64470|sht_
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not assigned.r	no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
not assigned.r	no hits & (original description: pacid=37151350 transcript=Phvul.009G104850.1 locu
Enzyme classi	no description available(sp|a0a072ur65|cht5b_medtr : 395.0) & Enzyme classificatic
Protein biosyr	methyltransferase component Nop1/fibrillarin of snoRNP rRNA methylation complex
not assigned.a	(original description: pacid=37162384 transcript=Phvul.004G057900.1 locus=Phvul.0
RNA biosynth	transcription factor (ERF) (original description: pacid=37164213 transcript=Phvul.007
Lipid metaboli	phospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(
Solute transpc	metabolite transporter (DTX) (original description: pacid=37157842 transcript=Phvul
Cell cycle orga	cyclin (CYCD) (original description: pacid=37157024 transcript=Phvul.011G110000.1 l
Solute transpc	anion transporter (NRT1/PTR) (original description: pacid=37143370 transcript=Phvu
Lipid metaboli	phospholipase A2 (pPLA2-II) (original description: pacid=37149281 transcript=Phvul.(
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Protein biosyr	IF-2 translation initiation factor (original description: pacid=37154471 transcript=Phv
Cytoskeleton	motor protein (Kinesin-4) (original description: pacid=37168025 transcript=Phvul.001
not assigned.r	no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
not assigned.r	no hits & (original description: pacid=37171812 transcript=Phvul.006G098000.1 locu
RNA processir	RNA editing factor (ORRM) (original description: pacid=37160922 transcript=Phvul.0(
not assigned.r	no hits & (original description: pacid=37155232 transcript=Phvul.011G028900.1 locu
Protein home	RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
Protein home	RING-HC-class E3 ligase (original description: pacid=37160948 transcript=Phvul.008G
Solute transpc	hexose transporter (SGB/GlcT) (original description: pacid=37162603 transcript=Phvu
Protein home	pepsin-type protease (original description: pacid=37173754 transcript=Phvul.006G0
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04G160700 ID=Phvul.004G160700.1.v2.1 annot-version=v2.1) & Nudix hydrolase 20, chloroplastic
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2300.3 locus=Phvul.011G152300 ID=Phvul.011G152300.3.v2.1 annot-version=v2.1) &
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1G073600.2 locus=Phvul.011G073600 ID=Phvul.011G073600.2.v2.1 annot-version=v2.1) &
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2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
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transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi
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37000.6 locus=Phvul.005G137000 ID=Phvul.005G137000.6.v2.1 annot-version=v2.1) &
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t=Phvul.001G036500.1 locus=Phvul.001G036500 ID=Phvul.001G036500.1.v2.1 annot-version=v2.1)
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2G289600.3 locus=Phvul.002G289600 ID=Phvul.002G289600.3.v2.1 annot-version=v2.1) &

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02G041900 ID=Phvul.002G041900.1.v2.1 annot-version=v2.1) & Protein CDI OS=Arabidopsis thalia
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2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
2657 transcript=Phvul.006G214700.4 locus=Phvul.006G214700 ID=Phvul.006G214700.4.v2.1 annot-
us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
t=Phvul.001G036500.1 locus=Phvul.001G036500 ID=Phvul.001G036500.1.v2.1 annot-version=v2.1)
71276 transcript=Phvul.001G052300.1 locus=Phvul.001G052300 ID=Phvul.001G052300.1.v2.1 anno
us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
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08G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein E6
us=Phvul.010G152600 ID=Phvul.010G152600.2.v2.1 annot-version=v2.1)
06G021500 ID=Phvul.006G021500.1.v2.1 annot-version=v2.1) & Protein SIEVE ELEMENT OCCLUSI
us=Phvul.009G177300 ID=Phvul.009G177300.1.v2.1 annot-version=v2.1)
07G147400.1 locus=Phvul.007G147400 ID=Phvul.007G147400.1.v2.1 annot-version=v2.1) &
78100.1 locus=Phvul.003G178100 ID=Phvul.003G178100.1.v2.1 annot-version=v2.1) &
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us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)
02G044500 ID=Phvul.002G044500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
group of donor(50.1.1 : 747.9) & Reticuline oxidase OS=Papaver somniferum (sp|p93479|reto_pa
06G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
cus=Phvul.010G144900 ID=Phvul.010G144900.1.v2.1 annot-version=v2.1) &
2G083800.1 locus=Phvul.002G083800 ID=Phvul.002G083800.1.v2.1 annot-version=v2.1) &
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10G156000 ID=Phvul.010G156000.1.v2.1 annot-version=v2.1) & Protein LURP-one-related 12 OS=
Phvul.007G055500.1 locus=Phvul.007G055500 ID=Phvul.007G055500.1.v2.1 annot-version=v2.1) &
Phvul.007G055500.1 locus=Phvul.007G055500 ID=Phvul.007G055500.1.v2.1 annot-version=v2.1) &
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us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)

Phvul.007G055200.1 locus=Phvul.007G055200 ID=Phvul.007G055200.1.v2.1 annot-version=v2.1) &
Phvul.007G055200.1 locus=Phvul.007G055200 ID=Phvul.007G055200.1.v2.1 annot-version=v2.1) &
us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
37160063 transcript=Phvul.008G273100.1 locus=Phvul.008G273100 ID=Phvul.008G273100.1.v2.1 ar
us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding
010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding
cid=37164150 transcript=Phvul.007G270500.1 locus=Phvul.007G270500 ID=Phvul.007G270500.1.v2
nscript=Phvul.004G125900.1 locus=Phvul.004G125900 ID=Phvul.004G125900.1.v2.1 annot-version=
005G027200 ID=Phvul.005G027200.1.v2.1 annot-version=v2.1) & Putative disease resistance protei
us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)
71276 transcript=Phvul.001G052300.1 locus=Phvul.001G052300 ID=Phvul.001G052300.1.v2.1 anno
008G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein E6
G100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
G100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
G100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &
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57914 transcript=Phvul.001G073300.1 locus=Phvul.001G073300 ID=Phvul.001G073300.1.v2.1 anno
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010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding
010G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding
nscript=Phvul.004G125900.1 locus=Phvul.004G125900 ID=Phvul.004G125900.1.v2.1 annot-version=
002G044500 ID=Phvul.002G044500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
group of donor(50.1.1 : 747.9) & Reticuline oxidase OS=Papaver somniferum (sp|p93479|reto_pap
006G021500 ID=Phvul.006G021500.1.v2.1 annot-version=v2.1) & Protein SIEVE ELEMENT OCCLUSIO
us=Phvul.009G177300 ID=Phvul.009G177300.1.v2.1 annot-version=v2.1)
007G147400.1 locus=Phvul.007G147400 ID=Phvul.007G147400.1.v2.1 annot-version=v2.1) &
178100.1 locus=Phvul.003G178100 ID=Phvul.003G178100.1.v2.1 annot-version=v2.1) &
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01G106800.2 locus=Phvul.001G106800 ID=Phvul.001G106800.2.v2.1 annot-version=v2.1) &
us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
us=Phvul.007G261100 ID=Phvul.007G261100.2.v2.1 annot-version=v2.1)
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us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)
37160063 transcript=Phvul.008G273100.1 locus=Phvul.008G273100 ID=Phvul.008G273100.1.v2.1 ar
us=Phvul.005G065300 ID=Phvul.005G065300.1.v2.1 annot-version=v2.1)
006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
us=Phvul.006G045600 ID=Phvul.006G045600.1.v2.1 annot-version=v2.1)
us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)
us=Phvul.011G111800 ID=Phvul.011G111800.1.v2.1 annot-version=v2.1)
cus=Phvul.010G144900 ID=Phvul.010G144900.1.v2.1 annot-version=v2.1) &

2G083800.1 locus=Phvul.002G083800 ID=Phvul.002G083800.1.v2.1 annot-version=v2.1) &

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us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)

us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)

us=Phvul.010G110700 ID=Phvul.010G110700.2.v2.1 annot-version=v2.1)

71276 transcript=Phvul.001G052300.1 locus=Phvul.001G052300 ID=Phvul.001G052300.1.v2.1 anno

08G279750 ID=Phvul.008G279750.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein E6

100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &

100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &

100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &

100000.5 locus=Phvul.009G100000 ID=Phvul.009G100000.5.v2.1 annot-version=v2.1) &

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us=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)

us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)

us=Phvul.006G148800 ID=Phvul.006G148800.1.v2.1 annot-version=v2.1)

10G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding

10G121200 ID=Phvul.010G121200.2.v2.1 annot-version=v2.1) & Uncharacterized calcium-binding

script=Phvul.004G125900.1 locus=Phvul.004G125900 ID=Phvul.004G125900.1.v2.1 annot-version=

02G044500 ID=Phvul.002G044500.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

group of donor(50.1.1 : 747.9) & Reticuline oxidase OS=Papaver somniferum (sp|p93479|reto_pap

06G021500 ID=Phvul.006G021500.1.v2.1 annot-version=v2.1) & Protein SIEVE ELEMENT OCCLUSI

us=Phvul.009G177300 ID=Phvul.009G177300.1.v2.1 annot-version=v2.1)

07G147400.1 locus=Phvul.007G147400 ID=Phvul.007G147400.1.v2.1 annot-version=v2.1) &

78100.1 locus=Phvul.003G178100 ID=Phvul.003G178100.1.v2.1 annot-version=v2.1) &

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us=Phvul.005G154600 ID=Phvul.005G154600.3.v2.1 annot-version=v2.1)

7160063 transcript=Phvul.008G273100.1 locus=Phvul.008G273100 ID=Phvul.008G273100.1.v2.1 a

us=Phvul.005G065300 ID=Phvul.005G065300.1.v2.1 annot-version=v2.1)

06G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor

us=Phvul.006G045600 ID=Phvul.006G045600.1.v2.1 annot-version=v2.1)

us=Phvul.008G216700 ID=Phvul.008G216700.1.v2.1 annot-version=v2.1)

us=Phvul.011G111800 ID=Phvul.011G111800.1.v2.1 annot-version=v2.1)

cus=Phvul.010G144900 ID=Phvul.010G144900.1.v2.1 annot-version=v2.1) &

2G083800.1 locus=Phvul.002G083800 ID=Phvul.002G083800.1.v2.1 annot-version=v2.1) &

id=37164150 transcript=Phvul.007G270500.1 locus=Phvul.007G270500 ID=Phvul.007G270500.1.v2

us=Phvul.001G067500 ID=Phvul.001G067500.3.v2.1 annot-version=v2.1)

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004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
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on.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr
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7G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &
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011G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
vul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &
1G024200.1 locus=Phvul.001G024200 ID=Phvul.001G024200.1.v2.1 annot-version=v2.1) &
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009G046200 ID=Phvul.009G046200.1.v2.1 annot-version=v2.1) & Polyadenylate-binding protein-int
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G111100.1 locus=Phvul.008G111100 ID=Phvul.008G111100.1.v2.1 annot-version=v2.1) &
G070000.2 locus=Phvul.006G070000 ID=Phvul.006G070000.2.v2.1 annot-version=v2.1) &
al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687
08G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &
G036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
009G198900 ID=Phvul.009G198900.1.v2.1 annot-version=v2.1) & Protein arginine N-methyltransfer
G036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
_arath : 311.0) & Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 22.0) (origi
ript=Phvul.001G205600.1 locus=Phvul.001G205600 ID=Phvul.001G205600.1.v2.1 annot-version=v2
011G159400 ID=Phvul.011G159400.1.v2.1 annot-version=v2.1) & UBP1-associated protein 2C OS=A
ul.004G061900.1 locus=Phvul.004G061900 ID=Phvul.004G061900.1.v2.1 annot-version=v2.1) &
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5G067950.1 locus=Phvul.005G067950 ID=Phvul.005G067950.1.v2.1 annot-version=v2.1) &
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004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
011G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi
al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687
us=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
_arath : 311.0) & Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 22.0) (origi
us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
on.EC_3 hydrolases.EC_3.2 glycosylase(50.3.2 : 132.1) (original description: pacid=37146097 transcr
x (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 ID
004G057900 ID=Phvul.004G057900.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
7G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &
009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
l.008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &
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009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
vul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &
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004G019300 ID=Phvul.004G019300.2.v2.1 annot-version=v2.1) & Protein ALTERED XYLOGLUCAN 4-
011G069000 ID=Phvul.011G069000.1.v2.1 annot-version=v2.1) & Putative pentatricopeptide repeat
transcript=Phvul.002G231800.1 locus=Phvul.002G231800 ID=Phvul.002G231800.1.v2.1 annot-versi
al description: pacid=37171282 transcript=Phvul.L001687.1 locus=Phvul.L001687 ID=Phvul.L001687

us=Phvul.011G102400 ID=Phvul.011G102400.1.v2.1 annot-version=v2.1)
_arath : 311.0) & Enzyme classification.EC_2 transferases.EC_2.3 acyltransferase(50.2.3 : 22.0) (origi
us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
us=Phvul.009G104850 ID=Phvul.009G104850.1.v2.1 annot-version=v2.1)
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x (original description: pacid=37170855 transcript=Phvul.001G057200.1 locus=Phvul.001G057200 ID
004G057900 ID=Phvul.004G057900.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
7G027000.1 locus=Phvul.007G027000 ID=Phvul.007G027000.1.v2.1 annot-version=v2.1) &
009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
l.008G060700.1 locus=Phvul.008G060700 ID=Phvul.008G060700.1.v2.1 annot-version=v2.1) &
locus=Phvul.011G110000 ID=Phvul.011G110000.1.v2.1 annot-version=v2.1) &
ul.010G003800.1 locus=Phvul.010G003800 ID=Phvul.010G003800.1.v2.1 annot-version=v2.1) &
009G063500.2 locus=Phvul.009G063500 ID=Phvul.009G063500.2.v2.1 annot-version=v2.1) &
006G206800 ID=Phvul.006G206800.1.v2.1 annot-version=v2.1) & Putative pumilio homolog 7, chlor
vul.005G054600.1 locus=Phvul.005G054600 ID=Phvul.005G054600.1.v2.1 annot-version=v2.1) &
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us=Phvul.006G098000 ID=Phvul.006G098000.1.v2.1 annot-version=v2.1)
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08G033500.1 locus=Phvul.008G033500 ID=Phvul.008G033500.1.v2.1 annot-version=v2.1) &
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G036100.2 locus=Phvul.008G036100 ID=Phvul.008G036100.2.v2.1 annot-version=v2.1) &
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us=Phvul.007G156900 ID=Phvul.007G156900.1.v2.1 annot-version=v2.1)

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aliana (sp|p42814|rns2_arath : 111.0)

aliana (sp|p42814|rns2_arath : 111.0)

NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3_arath : 384.0)

idopsis thaliana (sp|q1jpm5|oft30_arath : 545.0)

OS=Arabidopsis thaliana (sp|q8vxz0|nud20_arath : 429.0)

NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3_arath : 384.0)

OS=Arabidopsis thaliana (sp|q8vxz0|nud20_arath : 429.0)

idopsis thaliana (sp|q1jpm5|oft30_arath : 545.0)

NIPA3 OS=Arabidopsis thaliana (sp|q9lnk7|nipa3_arath : 384.0)

OS=Arabidopsis thaliana (sp|q8vxz0|nud20_arath : 429.0)

idopsis thaliana (sp|q1jpm5|oft30_arath : 545.0) ana (sp|q9xip8|cdi_arath : 441.0)

-version=v2.1) &
-version=v2.1) &
-version=v2.1) &
-version=v2.1) &
on=v2.1) &

ke 37 OS=Arabidopsis thaliana (sp|o22960|tbl37_arath : 515.0)
-version=v2.1) &
elicase DExH18, mitochondrial OS=Arabidopsis thaliana (sp|f4kfv7|suv3l_arath : 1000.0)

ersion=v2.1) &
donor(50.1.10 : 222.3) (original description: pacid=37161921 transcript=Phvul.004G087000.1 locus
&
23|fly1_arath : 853.0)
23|fly1_arath : 853.0)

ana (sp|q9xip8|cdi_arath : 441.0)

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

&

ına (sp|q9xip8|cdi_arath : 441.0)

-version=v2.1) &

-version=v2.1) &

-version=v2.1) &

-version=v2.1) &

&

ıt-version=v2.1) &

ıt-version=v2.1) &

ı OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)

ON B OS=Arabidopsis thaliana (sp|q9ss87|seob_arath : 193.0)

.1) &

ing protein At4g14820 OS=Arabidopsis thaliana (sp|o23337|pp311_arath : 842.0)

ɔso : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007

roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

Arabidopsis thaliana (sp|q9lvz8|lor12_arath : 212.0)

nnot-version=v2.1) &

protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)
protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)
2.1 annot-version=v2.1) &
v2.1) &
in RGA1 OS=Solanum bulbocastanum (sp|q7xa42|rga1_solbu : 363.0)

t-version=v2.1) &
OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)

t-version=v2.1) &

protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)
protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)
v2.1) &
ing protein At4g14820 OS=Arabidopsis thaliana (sp|o23337|pp311_arath : 842.0)
oso : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007
N B OS=Arabidopsis thaliana (sp|q9ss87|seob_arath : 193.0)

.1) &

nnot-version=v2.1) &

roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

2.1 annot-version=v2.1) &

t-version=v2.1) &
OS=Oryza sativa subsp. japonica (sp|q651x6|csle6_orysj : 667.0)

t-version=v2.1) &

protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)
protein At1g02270 OS=Arabidopsis thaliana (sp|o81916|yc22_arath : 560.0)
v2.1) &
ing protein At4g14820 OS=Arabidopsis thaliana (sp|o23337|pp311_arath : 842.0)
so : 452.0) (original description: pacid=37165503 transcript=Phvul.007G113300.1 locus=Phvul.007
N B OS=Arabidopsis thaliana (sp|q9ss87|seob_arath : 193.0)

.1) &

nnot-version=v2.1) &

roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

2.1 annot-version=v2.1) &

-like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)
-like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)

ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.

t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5_arath : 632.0)
roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &
teracting protein 12 OS=Arabidopsis thaliana (sp|q9s7n9|cid12_arath : 405.0)

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

rase PRMT10 OS=Arabidopsis thaliana (sp|q9mat5|anm10_arath : 573.0)

inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phv
2.1) &
Arabidopsis thaliana (sp|q9lka4|uba2c_arath : 315.0)

-like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)
-like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)
t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5_arath : 632.0)
on=v2.1) &
'.1.v2.1 annot-version=v2.1) &

inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phv

ipt=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.
)=Phvul.001G057200.1.v2.1 annot-version=v2.1) &
ing protein At1g79490, mitochondrial OS=Arabidopsis thaliana (sp|q9sak0|pp132_arath : 1241.0)

roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

-like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)
-like OS=Arabidopsis thaliana (sp|q9lrs2|tbl22_arath : 415.0)
t-containing protein At1g02420 OS=Arabidopsis thaliana (sp|q9fz19|ppr5_arath : 632.0)
on=v2.1) &
'.1.v2.1 annot-version=v2.1) &

inal description: pacid=37174189 transcript=Phvul.006G037000.1 locus=Phvul.006G037000 ID=Phv

ript=Phvul.003G158800.1 locus=Phvul.003G158800 ID=Phvul.003G158800.1.v2.1 annot-version=v2.
D=Phvul.001G057200.1.v2.1 annot-version=v2.1) &
ing protein At1g79490, mitochondrial OS=Arabidopsis thaliana (sp|q9sak0|pp132_arath : 1241.0)

roplastic OS=Arabidopsis thaliana (sp|q9c9r6|pum7_arath : 433.0)

=Phvul.004G087000 ID=Phvul.004G087000.1.v2.1 annot-version=v2.1) &

G113300 ID=Phvul.007G113300.1.v2.1 annot-version=v2.1) &

G113300 ID=Phvul.007G113300.1.v2.1 annot-version=v2.1) &

G113300 ID=Phvul.007G113300.1.v2.1 annot-version=v2.1) &

.1) &

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.1) &

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.1) &

miRNA_Acc.	Target_Acc.	Expectation	UPE$	miRNA_start	miRNA_end
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
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uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
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uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	21
uggagaagcagg	Phvul.009G186000.1	0.5	-1	1	21
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uggagaagcagg	Phvul.003G189000.1	0.5	-1	1	22
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uggagaagcagg	Phvul.005G055400.1	1	-1	1	21
uggagaagcagg	Phvul.005G074500.1	1	-1	1	21
uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
uggagaagcagg	Phvul.005G055400.1	1	-1	1	21
uggagaagcagg	Phvul.005G074500.1	1	-1	1	21
uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
uggagaagcagg	Phvul.005G055400.1	1	-1	1	21

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uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
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uggagaagcagg	Phvul.005G055400.1	1	-1	1	21
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uggagaagcagg	Phvul.005G055400.1	1	-1	1	21
uggagaagcagg	Phvul.005G074500.1	1	-1	1	21
uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
uggagaagcagg	Phvul.005G055400.1	1	-1	1	21
uggagaagcagg	Phvul.005G074500.1	1	-1	1	21
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uggagaagcagg	Phvul.011G160400.1	1	-1	1	21
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uggagaagcagg	Phvul.005G074500.1	1	-1	1	22
uggagaagcagg	Phvul.011G160400.1	1	-1	1	22
uggagaagcagg	Phvul.005G055400.1	1	-1	1	22
uggagaagcagg	Phvul.006G169300.1	2.5	-1	1	21

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uggagaagcagg	Phvul.011G065700.3	2.5	-1	1	21
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uggagaagcagg	Phvul.004G172600.1	2.5	-1	1	21
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uggagaagcagg	Phvul.004G172600.1	2.5	-1	1	21
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uggagaagcagg	Phvul.006G086200.1	3	-1	1	21
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uggagaagcagg	Phvul.010G089100.2	3	-1	1	21
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uggagaagcagg	Phvul.006G086200.1	3	-1	1	21
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uggagaagcagg	Phvul.008G147100.3	3	-1	1	21
uggagaagcagg	Phvul.006G086200.1	3	-1	1	21
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uggagaagcagg	Phvul.006G086200.1	3	-1	1	21
uggagaagcagg	Phvul.010G128500.1	3	-1	1	21
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uggagaagcagg	Phvul.008G147100.3	3	-1	1	21
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uggagaagcagg	Phvul.005G001200.1	3	-1	1	21
uggagaagcagg	Phvul.008G147100.2	3	-1	1	21
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uggagaagcagg	Phvul.008G147100.3	3	-1	1	21
uggagaagcagg	Phvul.006G086200.1	3	-1	1	21
uggagaagcagg	Phvul.010G128500.1	3	-1	1	21
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uggagaagcagg	Phvul.002G325300.2	3	-1	1	22
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uggagaagcagg	Phvul.007G083500.1	3.5	-1	1	21
uggagaagcagg	Phvul.007G083500.2	3.5	-1	1	21
uggagaagcagg	Phvul.011G079800.1	3.5	-1	1	21
uggagaagcagg	Phvul.008G077800.1	3.5	-1	1	21
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uggagaagcagg	Phvul.002G017700.2	4.5	-1	1	21
uggagaagcagg	Phvul.002G017700.1	4.5	-1	1	21
uggagaagcagg	Phvul.007G022500.3	4.5	-1	1	21
uggagaagcagg	Phvul.010G115000.1	4.5	-1	1	21

uggagaagcagg	Phvul.010G115000.2	4.5	-1	1	21
uggagaagcagg	Phvul.006G154900.1	4.5	-1	1	21
uggagaagcagg	Phvul.006G047000.1	4.5	-1	1	21
uggagaagcagg	Phvul.005G001000.1	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.1	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.2	4.5	-1	1	21
uggagaagcagg	Phvul.008G017200.1	4.5	-1	1	21
uggagaagcagg	Phvul.008G017200.2	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.3	4.5	-1	1	21
uggagaagcagg	Phvul.007G106300.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G034400.1	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.2	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.1	4.5	-1	1	21
uggagaagcagg	Phvul.008G070000.1	4.5	-1	1	21
uggagaagcagg	Phvul.010G156200.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G217000.1	4.5	-1	1	21
uggagaagcagg	Phvul.008G043500.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G079400.3	4.5	-1	1	21
uggagaagcagg	Phvul.001G193000.3	4.5	-1	1	21
uggagaagcagg	Phvul.001G193000.4	4.5	-1	1	21
uggagaagcagg	Phvul.003G154400.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G030200.1	4.5	-1	1	21
uggagaagcagg	Phvul.004G166100.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G160200.1	4.5	-1	1	21
uggagaagcagg	Phvul.002G119600.1	4.5	-1	1	21
uggagaagcagg	Phvul.002G150800.1	4.5	-1	1	21
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uggagaagcagg	Phvul.002G017700.2	4.5	-1	1	21
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uggagaagcagg	Phvul.009G034400.1	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.2	4.5	-1	1	21

uggagaagcagg	Phvul.L002444.1	4.5	-1	1	21
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uggagaagcagg	Phvul.010G115000.2	4.5	-1	1	21
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uggagaagcagg	Phvul.002G017700.2	4.5	-1	1	21
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uggagaagcagg	Phvul.010G115000.1	4.5	-1	1	21
uggagaagcagg	Phvul.010G115000.2	4.5	-1	1	21
uggagaagcagg	Phvul.006G154900.1	4.5	-1	1	21
uggagaagcagg	Phvul.006G047000.1	4.5	-1	1	21
uggagaagcagg	Phvul.005G001000.1	4.5	-1	1	21

uggagaagcagg	Phvul.003G056900.1	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.2	4.5	-1	1	21
uggagaagcagg	Phvul.008G017200.1	4.5	-1	1	21
uggagaagcagg	Phvul.008G017200.2	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.3	4.5	-1	1	21
uggagaagcagg	Phvul.007G106300.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G034400.1	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.2	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.1	4.5	-1	1	21
uggagaagcagg	Phvul.008G070000.1	4.5	-1	1	21
uggagaagcagg	Phvul.010G156200.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G217000.1	4.5	-1	1	21
uggagaagcagg	Phvul.008G043500.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G079400.3	4.5	-1	1	21
uggagaagcagg	Phvul.001G193000.3	4.5	-1	1	21
uggagaagcagg	Phvul.001G193000.4	4.5	-1	1	21
uggagaagcagg	Phvul.003G154400.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G030200.1	4.5	-1	1	21
uggagaagcagg	Phvul.004G166100.1	4.5	-1	1	21
uggagaagcagg	Phvul.009G160200.1	4.5	-1	1	21
uggagaagcagg	Phvul.002G119600.1	4.5	-1	1	21
uggagaagcagg	Phvul.002G150800.1	4.5	-1	1	21
uggagaagcagg	Phvul.002G271400.1	4.5	-1	1	21
uggagaagcagg	Phvul.011G166200.1	4.5	-1	1	21
uggagaagcagg	Phvul.001G110100.1	4.5	-1	1	21
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uggagaagcagg	Phvul.002G017700.2	4.5	-1	1	21
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uggagaagcagg	Phvul.007G022500.3	4.5	-1	1	21
uggagaagcagg	Phvul.010G115000.1	4.5	-1	1	21
uggagaagcagg	Phvul.010G115000.2	4.5	-1	1	21
uggagaagcagg	Phvul.006G154900.1	4.5	-1	1	21
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uggagaagcagg	Phvul.003G056900.1	4.5	-1	1	21
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uggagaagcagg	Phvul.003G056900.3	4.5	-1	1	21
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uggagaagcagg	Phvul.009G034400.1	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.2	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.1	4.5	-1	1	21
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uggagaagcagg	Phvul.010G156200.1	4.5	-1	1	21
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uggagaagcagg	Phvul.001G193000.3	4.5	-1	1	21
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uggagaagcagg	Phvul.004G166100.1	4.5	-1	1	21
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uggagaagcagg	Phvul.002G119600.1	4.5	-1	1	21
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uggagaagcagg	Phvul.002G017700.2	4.5	-1	1	21
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uggagaagcagg	Phvul.007G022500.3	4.5	-1	1	21
uggagaagcagg	Phvul.010G115000.1	4.5	-1	1	21
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uggagaagcagg	Phvul.006G154900.1	4.5	-1	1	21
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uggagaagcagg	Phvul.005G001000.1	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.1	4.5	-1	1	21
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uggagaagcagg	Phvul.009G034400.1	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.2	4.5	-1	1	21
uggagaagcagg	Phvul.L002444.1	4.5	-1	1	21
uggagaagcagg	Phvul.008G070000.1	4.5	-1	1	21
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uggagaagcagg	Phvul.001G193000.3	4.5	-1	1	21
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uggagaagcagg	Phvul.002G017700.2	4.5	-1	1	21
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uggagaagcagg	Phvul.006G154900.1	4.5	-1	1	21
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uggagaagcagg	Phvul.005G001000.1	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.1	4.5	-1	1	21
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uggagaagcagg	Phvul.002G017700.2	4.5	-1	1	21
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uggagaagcagg	Phvul.006G154900.1	4.5	-1	1	21
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uggagaagcagg	Phvul.003G056900.2	4.5	-1	1	21
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uggagaagcagg	Phvul.L002444.1	4.5	-1	1	21
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uggagaagcagg	Phvul.001G110100.1	4.5	-1	1	21
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uggagaagcagg	Phvul.010G115000.1	4.5	-1	1	21
uggagaagcagg	Phvul.010G115000.2	4.5	-1	1	21
uggagaagcagg	Phvul.006G154900.1	4.5	-1	1	21
uggagaagcagg	Phvul.006G047000.1	4.5	-1	1	21
uggagaagcagg	Phvul.005G001000.1	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.1	4.5	-1	1	21
uggagaagcagg	Phvul.003G056900.2	4.5	-1	1	21
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uggagaagcagg	Phvul.003G056900.3	4.5	-1	1	21
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uggagaagcagg	Phvul.L002444.2	4.5	-1	1	21
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uggagaagcagg	Phvul.008G070000.1	4.5	-1	1	21
uggagaagcagg	Phvul.010G156200.1	4.5	-1	1	22
uggagaagcagg	Phvul.009G160200.1	4.5	-1	1	22
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uggagaagcagg	Phvul.009G079400.3	4.5	-1	1	22
uggagaagcagg	Phvul.001G193000.3	4.5	-1	1	22
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uggagaagcagg	Phvul.009G167700.2	4.5	-1	1	22
uggagaagcagg	Phvul.003G154400.1	4.5	-1	1	22
uggagaagcagg	Phvul.L003746.2	4.5	-1	1	22
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uggagaagcagg	Phvul.009G030200.1	4.5	-1	1	22
uggagaagcagg	Phvul.004G166100.1	4.5	-1	1	22
uggagaagcagg	Phvul.002G119600.1	4.5	-1	1	22
uggagaagcagg	Phvul.002G150800.1	4.5	-1	1	22
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uggagaagcagg	Phvul.006G067900.1	4.5	-1	1	22
uggagaagcagg	Phvul.001G110100.1	4.5	-1	1	22
uggagaagcagg	Phvul.002G037500.1	4.5	-1	1	22
uggagaagcagg	Phvul.010G115000.1	4.5	-1	1	22
uggagaagcagg	Phvul.010G115000.2	4.5	-1	1	22
uggagaagcagg	Phvul.002G157000.1	4.5	-1	1	22
uggagaagcagg	Phvul.009G222600.1	5	-1	1	21
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uggagaagcagg	Phvul.005G059700.1	5	-1	1	21
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uggagaagcagg	Phvul.004G088300.1	5	-1	1	21
uggagaagcagg	Phvul.004G088300.3	5	-1	1	21
uggagaagcagg	Phvul.004G088300.2	5	-1	1	21
uggagaagcagg	Phvul.009G201600.1	5	-1	1	21
uggagaagcagg	Phvul.005G155100.1	5	-1	1	21
uggagaagcagg	Phvul.005G155100.3	5	-1	1	21
uggagaagcagg	Phvul.009G201600.2	5	-1	1	21
uggagaagcagg	Phvul.004G088300.4	5	-1	1	21
uggagaagcagg	Phvul.009G222600.1	5	-1	1	21
uggagaagcagg	Phvul.002G106900.1	5	-1	1	21
uggagaagcagg	Phvul.005G099500.1	5	-1	1	21
uggagaagcagg	Phvul.003G181900.1	5	-1	1	21
uggagaagcagg	Phvul.003G181900.2	5	-1	1	21
uggagaagcagg	Phvul.003G121200.1	5	-1	1	21
uggagaagcagg	Phvul.003G121200.2	5	-1	1	21
uggagaagcagg	Phvul.006G075600.1	5	-1	1	21
uggagaagcagg	Phvul.008G284900.1	5	-1	1	21
uggagaagcagg	Phvul.007G163400.1	5	-1	1	21
uggagaagcagg	Phvul.001G266600.1	5	-1	1	21
uggagaagcagg	Phvul.006G091100.2	5	-1	1	21
uggagaagcagg	Phvul.006G091100.1	5	-1	1	21
uggagaagcagg	Phvul.003G037500.1	5	-1	1	21
uggagaagcagg	Phvul.009G007300.1	5	-1	1	21
uggagaagcagg	Phvul.003G100200.1	5	-1	1	21
uggagaagcagg	Phvul.003G100200.2	5	-1	1	21
uggagaagcagg	Phvul.002G262600.1	5	-1	1	21
uggagaagcagg	Phvul.002G262600.2	5	-1	1	21
uggagaagcagg	Phvul.002G299004.1	5	-1	1	21
uggagaagcagg	Phvul.002G299004.3	5	-1	1	21
uggagaagcagg	Phvul.007G156200.1	5	-1	1	21
uggagaagcagg	Phvul.002G006400.1	5	-1	1	21
uggagaagcagg	Phvul.002G006400.3	5	-1	1	21
uggagaagcagg	Phvul.005G001000.1	5	-1	1	21
uggagaagcagg	Phvul.002G006400.2	5	-1	1	21
uggagaagcagg	Phvul.008G243700.1	5	-1	1	21
uggagaagcagg	Phvul.007G201400.1	5	-1	1	21

uggagaagcagg	Phvul.007G157500.2	5	-1	1	21
uggagaagcagg	Phvul.007G157500.2	5	-1	1	21
uggagaagcagg	Phvul.007G157500.1	5	-1	1	21
uggagaagcagg	Phvul.007G157500.1	5	-1	1	21
uggagaagcagg	Phvul.003G181600.1	5	-1	1	21
uggagaagcagg	Phvul.007G157500.5	5	-1	1	21
uggagaagcagg	Phvul.007G157500.5	5	-1	1	21
uggagaagcagg	Phvul.006G164800.1	5	-1	1	21
uggagaagcagg	Phvul.007G157500.3	5	-1	1	21
uggagaagcagg	Phvul.007G157500.3	5	-1	1	21
uggagaagcagg	Phvul.005G059700.1	5	-1	1	21
uggagaagcagg	Phvul.007G157500.4	5	-1	1	21
uggagaagcagg	Phvul.007G157500.4	5	-1	1	21
uggagaagcagg	Phvul.005G059500.1	5	-1	1	21
uggagaagcagg	Phvul.002G116800.1	5	-1	1	21
uggagaagcagg	Phvul.008G103100.1	5	-1	1	21
uggagaagcagg	Phvul.008G075300.1	5	-1	1	21
uggagaagcagg	Phvul.003G262800.1	5	-1	1	21
uggagaagcagg	Phvul.008G072300.1	5	-1	1	21
uggagaagcagg	Phvul.008G072300.2	5	-1	1	21
uggagaagcagg	Phvul.004G088300.1	5	-1	1	21
uggagaagcagg	Phvul.004G088300.3	5	-1	1	21
uggagaagcagg	Phvul.004G088300.2	5	-1	1	21
uggagaagcagg	Phvul.009G201600.1	5	-1	1	21
uggagaagcagg	Phvul.005G155100.1	5	-1	1	21
uggagaagcagg	Phvul.005G155100.3	5	-1	1	21
uggagaagcagg	Phvul.009G201600.2	5	-1	1	21
uggagaagcagg	Phvul.004G088300.4	5	-1	1	21
uggagaagcagg	Phvul.006G075600.1	5	-1	1	22
uggagaagcagg	Phvul.008G284900.1	5	-1	1	22
uggagaagcagg	Phvul.006G091100.2	5	-1	1	22
uggagaagcagg	Phvul.009G222600.1	5	-1	1	22
uggagaagcagg	Phvul.006G091100.1	5	-1	1	22
uggagaagcagg	Phvul.002G106900.1	5	-1	1	22
uggagaagcagg	Phvul.005G099500.1	5	-1	1	22
uggagaagcagg	Phvul.003G181900.1	5	-1	1	22
uggagaagcagg	Phvul.003G181900.2	5	-1	1	22
uggagaagcagg	Phvul.003G121200.1	5	-1	1	22
uggagaagcagg	Phvul.003G121200.2	5	-1	1	22
uggagaagcagg	Phvul.005G059700.1	5	-1	1	22
uggagaagcagg	Phvul.005G059500.1	5	-1	1	22
uggagaagcagg	Phvul.008G072300.1	5	-1	1	22
uggagaagcagg	Phvul.008G072300.2	5	-1	1	22
uggagaagcagg	Phvul.009G201600.1	5	-1	1	22
uggagaagcagg	Phvul.005G155100.1	5	-1	1	22
uggagaagcagg	Phvul.005G155100.3	5	-1	1	22

uggagaagcagg	Phvul.009G201600.2	5	-1	1	22
uggagaagcagg	Phvul.005G155100.2	5	-1	1	22
uggagaagcagg	Phvul.009G114400.1	5	-1	1	22
uggagaagcagg	Phvul.003G240100.1	5	-1	1	22
uggagaagcagg	Phvul.002G283000.3	5	-1	1	22
uggagaagcagg	Phvul.002G283000.1	5	-1	1	22
uggagaagcagg	Phvul.002G283000.2	5	-1	1	22
uggagaagcagg	Phvul.003G170100.1	5	-1	1	22
uggagaagcagg	Phvul.011G173600.1	5	-1	1	22
uggagaagcagg	Phvul.003G283500.1	5	-1	1	22
uggagaagcagg	Phvul.007G163400.1	5	-1	1	22
uggagaagcagg	Phvul.003G037500.1	5	-1	1	22
uggagaagcagg	Phvul.001G266600.1	5	-1	1	22
uggagaagcagg	Phvul.001G243500.2	5	-1	1	22
uggagaagcagg	Phvul.006G067900.1	5	-1	1	22
uggagaagcagg	Phvul.008G140600.1	5	-1	1	22

Target_start	Target_end	miRNA_aligne	alignment	Target_aligne	Inhibition	Target_Desc.
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
847	867	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371453
750	770	UGGAGAAGC	.::::::::::::::::::	CUUACGUGC	Cleavage	pacid=371489
846	867	UGGAGAAGC	.::::::::::::::::::	GCUUACGUG	Cleavage	pacid=371453
749	770	UGGAGAAGC	.::::::::::::::::::	CCUUACGUG	Cleavage	pacid=371489
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538

1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1273	1293	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371528
973	993	UGGAGAAGC	:::::::.::::.:::::::	AGCACGUGU	Cleavage	pacid=371560
727	747	UGGAGAAGC	::: ::::::::::::::::	AGCAAGUGC	Cleavage	pacid=371538
1272	1293	UGGAGAAGC	:::::::.::::.:::::::	GAGCACGUG	Cleavage	pacid=371528
972	993	UGGAGAAGC	:::::::.::::.:::::::	GAGCACGUG	Cleavage	pacid=371560
726	747	UGGAGAAGC	::: ::::::::::::::::	GAGCAAGUG	Cleavage	pacid=371538
191	211	UGGAGAAGC	::: :::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718

496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574

213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: ::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.::::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574

351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
191	211	UGGAGAAGC	::: :::::.:::::.:.::	AGCAAGUGC	Cleavage	pacid=371718
496	516	UGGAGAAGC	:.:::::::::::.:: :	CCCGCGUGCC	Cleavage	pacid=371641
876	896	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
351	371	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
349	369	UGGAGAAGC	..: ::.::::::::::::	CUUGCUUGU	Cleavage	pacid=371574
213	233	UGGAGAAGC	::: : ::.::::::::::	CACACUUCCC	Cleavage	pacid=371629
190	211	UGGAGAAGC	::: :::::.:::::.:.::	CAGCAAGUG	Cleavage	pacid=371718
495	516	UGGAGAAGC	:.:::::::::::.:: :	UCCCGCGUG	Cleavage	pacid=371641
875	896	UGGAGAAGC	..: ::.::::::::::::	UCUUGCUUG	Cleavage	pacid=371574
350	371	UGGAGAAGC	..: ::.::::::::::::	UCUUGCUUG	Cleavage	pacid=371574
348	369	UGGAGAAGC	..: ::.::::::::::::	UCUUGCUUG	Cleavage	pacid=371574
212	233	UGGAGAAGC	::: : ::.::::::::::	UCACACUUCC	Cleavage	pacid=371629
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: ::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.:::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: ::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.:::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: ::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.:::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: ::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542

182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.:::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.:::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.:::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.:::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.:::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.::::::: :::	GACACUUGC	Cleavage	pacid=371578

182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGCU	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	::::::::::: : ::::::	UGCACGUGCC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: :::: :::::::.::	AACAGGUGCC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGCU	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	::::::::::: : ::::::	UGCACGUGCC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: :::: :::::::.::	AACAGGUGCC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGCU	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	::::::::::: : ::::::	UGCACGUGCC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: :::: :::::::.::	AACAGGUGCC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGCU	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	::::::::::: : ::::::	UGCACGUGCC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: :::: :::::::.::	AACAGGUGCC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGCU	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.::::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	::::::::::: : ::::::	UGCACGUGCC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: :::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: :::: :::::::.::	AACAGGUGCC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGCU	Cleavage	pacid=371578

182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.:::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: ::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.:::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: ::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.:::::::.::	CACAC-UGCU	Cleavage	pacid=371439
180	200	UGGAGAAGC	:::::::::::: : ::::::	UGCACGUGC	Cleavage	pacid=371438
508	528	UGGAGAAGC	::: ::::::::::::	ACUCCGUCCC	Cleavage	pacid=371767
186	206	UGGAGAAGC	::::: ..:::.:::::.:	CUCACGUUU	Cleavage	pacid=371619
340	360	UGGAGAAGC	:: ::::: :::::::.::	AACAGGUGC	Translation	pacid=371542
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
182	202	UGGAGAAGC	::: :::.:::::: :::	GACACUUGC	Cleavage	pacid=371578
286	306	UGGAGAAGC	::. ::.::::::::::	ACCAUUGGC	Cleavage	pacid=371732
79	98	UGGAGAAGC	::: :::.:::::::.::	CACAC-UGCU	Cleavage	pacid=371439
179	200	UGGAGAAGC	:::::::::::: : ::::::	GUGCACGUG	Cleavage	pacid=371438
507	528	UGGAGAAGC	::: ::::::::::::	AACUCCGUCC	Cleavage	pacid=371767
185	206	UGGAGAAGC	::::: ..:::.:::::.:	UCUCACGUU	Cleavage	pacid=371619
339	360	UGGAGAAGC	:: ::::: :::::::.::	CAACAGGUG	Translation	pacid=371542
181	202	UGGAGAAGC	::: :::.:::::: :::	GGACACUUG	Cleavage	pacid=371578
181	202	UGGAGAAGC	::: :::.:::::: :::	GGACACUUG	Cleavage	pacid=371578
181	202	UGGAGAAGC	::: :::.:::::: :::	GGACACUUG	Cleavage	pacid=371578
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	:::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	:::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470

134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: :::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	:::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	:::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.::::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	::::.:.: ::::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	:::::...: ::::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: :::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	:::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	:::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.::::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	::::.:.: ::::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	:::::...: ::::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: :::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	:::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	:::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.::::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	::::.:.: ::::::::	CCAACGUGU	Cleavage	pacid=371597

349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	:::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:...: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	:::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:...: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	:::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:...: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552

3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: ::::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: ::::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.:::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: ::::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: ::::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.:::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: ::::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: ::::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.:::::::	UCAGCAUGU	Cleavage	pacid=371594

1550	1570	UGGAGAAGC/	::: :::::::.::.::.	CUCACUUGCC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC/	::: ::.:.::.:::::..	ACCACUUGUC	Cleavage	pacid=371488
609	629	UGGAGAAGC/	::::: .:: ::::.::::	GUCACGUUU(	Translation	pacid=371524
904	924	UGGAGAAGC/	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC/	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC/	: .:: : :::::::::::	UCUACAUUCC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC/	:::: :::.::::::.:::.	UGCAGCUGCU	Cleavage	pacid=371672
1459	1479	UGGAGAAGC/	:::: :::.::::::.:::.	UGCAGCUGCU	Cleavage	pacid=371672
3334	3354	UGGAGAAGC/	:.::::::::::::.:.:	UUAAUGUGC(	Cleavage	pacid=371569
395	415	UGGAGAAGC/	:::::.:.: ::::::::	CCAACGUGUC	Cleavage	pacid=371597
349	369	UGGAGAAGC/	:.::::::.:::::.:..	CUCGCGUGCC	Cleavage	pacid=371564
398	418	UGGAGAAGC/	::::::..: ::::::::	CCAACGUGCU	Cleavage	pacid=371609
2339	2359	UGGAGAAGC/	::::::::.::.::: .:.	AACACGUGCC	Cleavage	pacid=371543
512	532	UGGAGAAGC/	:::::: ::::::::. :	GCCACGUGCA	Cleavage	pacid=371586
749	769	UGGAGAAGC/	::.:::.:.:::::.:: :	CACAUGUGU(	Cleavage	pacid=371470
134	154	UGGAGAAGC/	:..: : ::::::::::.::	GGUGCAUUC(	Cleavage	pacid=371704
6862	6882	UGGAGAAGC/	.: ::.::::.::::::	UCAGCAUGU(	Cleavage	pacid=371594
1550	1570	UGGAGAAGC/	::: :::::::.::.::.	CUCACUUGCC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC/	::: ::.:.::.:::::..	ACCACUUGUC	Cleavage	pacid=371488
609	629	UGGAGAAGC/	::::: .:: ::::.::::	GUCACGUUU(	Translation	pacid=371524
904	924	UGGAGAAGC/	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC/	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC/	: .:: : :::::::::::	UCUACAUUCC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC/	:::: :::.::::::.:::.	UGCAGCUGCU	Cleavage	pacid=371672
1459	1479	UGGAGAAGC/	:::: :::.::::::.:::.	UGCAGCUGCU	Cleavage	pacid=371672
3334	3354	UGGAGAAGC/	:.::::::::::::.:.:	UUAAUGUGC(	Cleavage	pacid=371569
395	415	UGGAGAAGC/	:::::.:.: ::::::::	CCAACGUGUC	Cleavage	pacid=371597
349	369	UGGAGAAGC/	:.::::::.:::::.:..	CUCGCGUGCC	Cleavage	pacid=371564
398	418	UGGAGAAGC/	::::::..: ::::::::	CCAACGUGCU	Cleavage	pacid=371609
2339	2359	UGGAGAAGC/	::::::::.::.::: .:.	AACACGUGCC	Cleavage	pacid=371543
512	532	UGGAGAAGC/	:::::: ::::::::. :	GCCACGUGCA	Cleavage	pacid=371586
749	769	UGGAGAAGC/	::.:::.:.:::::.:: :	CACAUGUGU(	Cleavage	pacid=371470
134	154	UGGAGAAGC/	:..: : ::::::::::.::	GGUGCAUUC(	Cleavage	pacid=371704
6862	6882	UGGAGAAGC/	.: ::.::::.::::::	UCAGCAUGU(	Cleavage	pacid=371594
1550	1570	UGGAGAAGC/	::: :::::::.::.::.	CUCACUUGCC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC/	::: ::.:.::.:::::..	ACCACUUGUC	Cleavage	pacid=371488
609	629	UGGAGAAGC/	::::: .:: ::::.::::	GUCACGUUU(	Translation	pacid=371524
904	924	UGGAGAAGC/	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC/	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC/	: .:: : :::::::::::	UCUACAUUCC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC/	:::: :::.::::::.:::.	UGCAGCUGCU	Cleavage	pacid=371672
1459	1479	UGGAGAAGC/	:::: :::.::::::.:::.	UGCAGCUGCU	Cleavage	pacid=371672
3334	3354	UGGAGAAGC/	:.::::::::::::.:.:	UUAAUGUGC(	Cleavage	pacid=371569
395	415	UGGAGAAGC/	:::::.:.: ::::::::	CCAACGUGUC	Cleavage	pacid=371597
349	369	UGGAGAAGC/	:.::::::.:::::.:..	CUCGCGUGCC	Cleavage	pacid=371564
398	418	UGGAGAAGC/	::::::..: ::::::::	CCAACGUGCU	Cleavage	pacid=371609

2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGCC	Cleavage	pacid=371543
512	532	UGGAGAAGC	:::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	:::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	:::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : ::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGCC	Cleavage	pacid=371543
512	532	UGGAGAAGC	:::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	:::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	:::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : ::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	::::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGCC	Cleavage	pacid=371543
512	532	UGGAGAAGC	:::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	:::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	:::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : ::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672

1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	:::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.:::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	:::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.:::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488
609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..::::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1540	1560	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
1459	1479	UGGAGAAGC	:::: :::.::::::.:::.	UGCAGCUGC	Cleavage	pacid=371672
3334	3354	UGGAGAAGC	:.:::::::::::.:.:	UUAAUGUGC	Cleavage	pacid=371569
395	415	UGGAGAAGC	:::::.:.: :::::::	CCAACGUGU	Cleavage	pacid=371597
349	369	UGGAGAAGC	:.::::::.:::::.:..	CUCGCGUGC	Cleavage	pacid=371564
398	418	UGGAGAAGC	:::::..: :::::::	CCAACGUGC	Cleavage	pacid=371609
2339	2359	UGGAGAAGC	::::::::.::.::: .:.	AACACGUGC	Cleavage	pacid=371543
512	532	UGGAGAAGC	::::::: ::::::::. :	GCCACGUGC	Cleavage	pacid=371586
749	769	UGGAGAAGC	::.:::.:.:::::.:: :	CACAUGUGU	Cleavage	pacid=371470
134	154	UGGAGAAGC	:..: : ::::::::::.::	GGUGCAUUC	Cleavage	pacid=371704
6862	6882	UGGAGAAGC	.: ::.::::.:::::::	UCAGCAUGU	Cleavage	pacid=371594
1550	1570	UGGAGAAGC	::: ::::::::.::.::.	CUCACUUGC	Cleavage	pacid=371472
1368	1388	UGGAGAAGC	::: ::.:.::.:::::..	ACCACUUGU	Cleavage	pacid=371488

609	629	UGGAGAAGC	::::: .:: ::::.::::	GUCACGUUU	Translation	pacid=371524
904	924	UGGAGAAGC	.:.:: ..:::::::.::	ACUAUGUUU	Cleavage	pacid=371508
335	355	UGGAGAAGC	::::: :.:::: :::::.	CCCACGUCCU	Cleavage	pacid=371552
3330	3350	UGGAGAAGC	: .:: : :::::::::::	UCUACAUUC	Cleavage	pacid=371560
1539	1560	UGGAGAAGC	:::: :::.::::::.:::.	CUGCAGCUG	Cleavage	pacid=371672
1458	1479	UGGAGAAGC	:::: :::.::::::.:::.	CUGCAGCUG	Cleavage	pacid=371672
3333	3354	UGGAGAAGC	:.::::::::::.:.:	GUUAAUGUG	Cleavage	pacid=371569
3329	3350	UGGAGAAGC	:: .:: : :::::::::::	UUCUACAUU	Cleavage	pacid=371560
394	415	UGGAGAAGC	:::::.:.: ::::::::	UCCAACGUG	Cleavage	pacid=371597
348	369	UGGAGAAGC	:.::::::.:::::.:..	UCUCGCGUG	Cleavage	pacid=371564
397	418	UGGAGAAGC	::::::..: ::::::::	UCCAACGUG	Cleavage	pacid=371609
2338	2359	UGGAGAAGC	::::::::.::.::: .:.	GAACACGUG	Cleavage	pacid=371543
440	461	UGGAGAAGC	:: : . ::::.::.::::::::	UUCCCUAUG	Cleavage	pacid=371782
412	433	UGGAGAAGC	:: : . ::::.::.::::::::	UUCCCUUUG	Cleavage	pacid=371745
354	375	UGGAGAAGC	:: : . ::::.::.::::::::	UUCCCUUUG	Cleavage	pacid=371745
511	532	UGGAGAAGC	::::::: ::::::::. :	AGCCACGUG	Cleavage	pacid=371586
748	769	UGGAGAAGC	::.:::.:.:::::.:: :	CCACAUGUG	Cleavage	pacid=371470
133	154	UGGAGAAGC	:..: : ::::::::::.::	GGGUGCAUU	Cleavage	pacid=371704
6861	6882	UGGAGAAGC	.: ::.::::.:::::::	AUCAGCAUG	Cleavage	pacid=371594
1549	1570	UGGAGAAGC	::: :::::::.::.::.	ACUCACUUG	Cleavage	pacid=371472
1367	1388	UGGAGAAGC	::: ::.:.::.::::::..	UACCACUUG	Cleavage	pacid=371488
21	41	UGGAGAAGC	::::: : .::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .:::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. ::::::::.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :..: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::..: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.::::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.::::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.::::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: :::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..:::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.::::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	:::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581

360	380	UGGAGAAGC	::.:::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. ::::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.::::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: :::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.::::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.::::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	:::::::.:..:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.::.::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.:::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. ::::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.::::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: :::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661

1651	1671	UGGAGAAGC	:::.: :..:::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.:::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: :::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: :::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. ::::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:..::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : .::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.:::::::::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..:::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.:::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: :::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620

1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. ::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: :::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..:::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: :::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: :::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: :.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: :.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::.:::::::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. :::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .:::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. ::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: :::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..:::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: :::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: :::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627

1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: :::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..::::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.:::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.::::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	::::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	::::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::....::.::.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	::::.: :...::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.::::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.::::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: :::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..::::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.:::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721

1996	2015	UGGAGAAGC	::::.: :.::::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: ::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: :::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: ..:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: ::::::. :::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	:::: : .:::::::.::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: :::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	:::: : ::.: :::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.::::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: ::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: :::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424

391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.:::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: :::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..:::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: :::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..:::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: :::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.::::.::.:::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.::::.::.:::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.:::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: :::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..:::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: :::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640

322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGCC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: :::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. ::::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: ::.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:....:::::.::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : :::.: ::::::::	UGCACCUUCC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.::::::::.:::.:	UGCAUG-GUC	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: ::::::.::.::.:::.	AGCAAGUGCC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGCC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602

622	642 UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41 UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521 UGGAGAAGC	:::.::: :::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452 UGGAGAAGC	:..:::::. ::::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198 UGGAGAAGC	:.::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426 UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545 UGGAGAAGC	::::: : ::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015 UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918 UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149 UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149 UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451 UGGAGAAGC	::::.: :.:.::::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342 UGGAGAAGC	::::.: :.:.::::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794 UGGAGAAGC	: :::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671 UGGAGAAGC	::::.: :..:::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536 UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86 UGGAGAAGC	:.::::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170 UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031 UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457 UGGAGAAGC	:::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116 UGGAGAAGC	..:::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434 UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437 UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411 UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411 UGGAGAAGC	..:::: ::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258 UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380 UGGAGAAGC	::.::::: : ::::::.::	AUCAUGUGC	Translation	pacid=371680
112	132 UGGAGAAGC	:::: .:.::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358 UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642 UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41 UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521 UGGAGAAGC	:::.::: :::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452 UGGAGAAGC	:..:::::. ::::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198 UGGAGAAGC	:.::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426 UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545 UGGAGAAGC	::::: : ::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015 UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918 UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149 UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149 UGGAGAAGC	:.:::..:::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451 UGGAGAAGC	::::.: :.:.::::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342 UGGAGAAGC	::::.: :.:.::::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794 UGGAGAAGC	: :::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671 UGGAGAAGC	::::.: :..:::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536 UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86 UGGAGAAGC	:.::::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692

2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	::::: : ::.: ::::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.::::::::.::.:	UGCAUG-GUC	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: :::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::.::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::.::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..:::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: ::::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	::::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	::::: : .::::::::.:::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: ::::::::	CGUACGUGG	Cleavage	pacid=371566

406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	:::: : ::.: :::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: ::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: :::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	:::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	...::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: :::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : ::::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. :::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.::::::. :::	UUCUUGUGC	Cleavage	pacid=371502
21	41	UGGAGAAGC	:::: : .::::::::::	UGCACUUCU	Cleavage	pacid=371620
1501	1521	UGGAGAAGC	:::.::: ::::::: .::	GGCAUGUGG	Cleavage	pacid=371757
432	452	UGGAGAAGC	:..:::::. :::::::.:.	GGUGCGUGC	Translation	pacid=371502
1178	1198	UGGAGAAGC	:.::::: :.: :::::::	CGUACGUGG	Cleavage	pacid=371566
406	426	UGGAGAAGC	:...::::..::::::: ::	GGUGUGUGC	Cleavage	pacid=371737
525	545	UGGAGAAGC	:::: : ::.: :::::::	UGCACCUUC	Cleavage	pacid=371721
1996	2015	UGGAGAAGC	::::.: :.:::::::.::.:	UGCAUG-GU	Cleavage	pacid=371696
898	918	UGGAGAAGC	::: ::::.::.::.::.	AGCAAGUGC	Cleavage	pacid=371646
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
129	149	UGGAGAAGC	:.:::..::::::::.:	GAGAUGUGU	Cleavage	pacid=371632
431	451	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371640
322	342	UGGAGAAGC	:::.: :.:.:::::::...	AGCAUGGGU	Cleavage	pacid=371664
1774	1794	UGGAGAAGC	: ::::::...::.::.:.:	UUCACGUGU	Cleavage	pacid=371661
1651	1671	UGGAGAAGC	:::.: :..::::::::...	AGCAUGGGU	Cleavage	pacid=371610
1516	1536	UGGAGAAGC	::::.::: :::::::	UUUUCGUGU	Cleavage	pacid=371543
66	86	UGGAGAAGC	:.:::::.: :::.::::	GAGAUGUGC	Cleavage	pacid=371692
2150	2170	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
2011	2031	UGGAGAAGC	:.:::::.::.::::: :	AAAAUGUGC	Cleavage	pacid=371627
1437	1457	UGGAGAAGC	:::::::.::.:: :.:	CUCACGUGC	Cleavage	pacid=371647
96	116	UGGAGAAGC	...::::.:::.:::::.	GUUGUGUGC	Cleavage	pacid=371508
1414	1434	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727

1417	1437	UGGAGAAGC	: .:.::::..::.::.:..:	UUUAUGUGC	Cleavage	pacid=371727
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
391	411	UGGAGAAGC	..:::: :::::::::.:	CAUGCGUGG	Cleavage	pacid=371424
238	258	UGGAGAAGC	: ::.:::...:::: ::.:	UUCAUGUGU	Cleavage	pacid=371581
360	380	UGGAGAAGC	::.::::: : :::::.::	AUCAUGUGC	Translation	pacid=371680
112	132	UGGAGAAGC	:::: .:.:::::::::	UUGACGUAU	Cleavage	pacid=371766
1338	1358	UGGAGAAGC	: :: :::::::. ::::::	AGGACAUGC	Cleavage	pacid=371602
622	642	UGGAGAAGC	: : .::::.:::::. :::	UUCUUGUGC	Cleavage	pacid=371502
1773	1794	UGGAGAAGC	:: :::::::...::.::.:.:	UUUCACGUG	Cleavage	pacid=371661
1177	1198	UGGAGAAGC	: :.::::: :.: ::::::::	UCGUACGUG	Cleavage	pacid=371566
1413	1434	UGGAGAAGC	:: .:.::::..::.::.:..:	UUUUAUGUG	Cleavage	pacid=371727
1416	1437	UGGAGAAGC	:: .:.::::..::.::.:..:	UUUUAUGUG	Cleavage	pacid=371727
405	426	UGGAGAAGC	: :...::::..::::::: ::	UGGUGUGUG	Cleavage	pacid=371737
20	41	UGGAGAAGC	::::: : .::::::::.:::	GUGCACUUC	Cleavage	pacid=371620
1500	1521	UGGAGAAGC	:::.::: :::::::: .::	AGGCAUGUG	Cleavage	pacid=371757
431	452	UGGAGAAGC	:..:::::. :::::::.:.	AGGUGCGUG	Translation	pacid=371502
524	545	UGGAGAAGC	::::: : ::.: ::::::::	GUGCACCUU	Cleavage	pacid=371721
1995	2015	UGGAGAAGC	::::.: :.::::::::.::.:	GUGCAUG-G	Cleavage	pacid=371696
621	642	UGGAGAAGC	:: : .::::.::::::. :::	UUUCUUGUG	Cleavage	pacid=371502
2679	2700	UGGAGAAGC	:: : .:::.:.::.::.:::.	UUUCUUGUG	Cleavage	pacid=371518
2675	2696	UGGAGAAGC	:: : .:::.:.::.::.:::.	UUUCUUGUG	Cleavage	pacid=371518
430	451	UGGAGAAGC	: :::.: :.:::::::::...	UAGCAUGGG	Cleavage	pacid=371640
321	342	UGGAGAAGC	: ::::. :.::::::::...	UAGCAUGGG	Cleavage	pacid=371664
1650	1671	UGGAGAAGC	: :::.: :.:::::::::...	UAGCAUGGG	Cleavage	pacid=371610
897	918	UGGAGAAGC	::: :::::.::.::.::.	AAGCAAGUG	Cleavage	pacid=371646
128	149	UGGAGAAGC	:.:::..::::::::.:	UGAGAUGUG	Cleavage	pacid=371632
128	149	UGGAGAAGC	:.:::..::::::::.:	UGAGAUGUG	Cleavage	pacid=371632
1515	1536	UGGAGAAGC	::::.::: ::::::::	AUUUUCGUG	Cleavage	pacid=371543
65	86	UGGAGAAGC	:.:::::.: :::.::::	UGAGAUGUG	Cleavage	pacid=371692
2149	2170	UGGAGAAGC	:.:::::.::.::::: :	GAAAAUGUG	Cleavage	pacid=371627
2010	2031	UGGAGAAGC	:.:::::.::.::::: :	GAAAAUGUG	Cleavage	pacid=371627
111	132	UGGAGAAGC	:: :::: .:.::::::::::	UUUGACGUA	Cleavage	pacid=371766
1436	1457	UGGAGAAGC	:::::::::.::.:: :.:	ACUCACGUG	Cleavage	pacid=371647
95	116	UGGAGAAGC	...::::.:::.:::::.	UGUUGUGUG	Cleavage	pacid=371508
390	411	UGGAGAAGC	..:::: :::::::::.:	ACAUGCGUG	Cleavage	pacid=371424
390	411	UGGAGAAGC	..:::: :::::::::.:	ACAUGCGUG	Cleavage	pacid=371424
237	258	UGGAGAAGC	: ::.:::...:::: ::.:	GUUCAUGUG	Cleavage	pacid=371581
230	251	UGGAGAAGC	:: : ::: ..::::::.:.::	UUACUCGUU	Cleavage	pacid=371668
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: :::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500

210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: ::::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: ::::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	:::.. ::::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: :::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::..:::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::....	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	:::::::::::: ::::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: ::::::.::	GGUACAUGU	Cleavage	pacid=371422

49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	:::::::::: ::::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :..:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: ::::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..::::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742

879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: :::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...::::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..::::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	:::.:.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::...: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::...: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. ::::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	::::::.::: :::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. ::::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: :::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...::::::::.::	UGCGAGGGU	Cleavage	pacid=371516

1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. ::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. ::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.:::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: ::::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724

372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: :::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. ::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.:::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	:::::::::: :::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : ..:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::.:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::..:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..::::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: ::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: ::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-UC	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: :::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. ::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577

526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.::::::::	ACCACGUGCL	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	:::::::::: ::::::.:	CGCACGUGCC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGCC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...::::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: :::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.::::::.:: ::::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..::::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.::::::.::..:	UGCAUGU-UC	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::...:: ::::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::...:: ::::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGCL	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGCL	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGCL	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGCC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.::::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.::::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.::::::::	ACCACGUGCL	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	:::::::::: ::::::.:	CGCACGUGCC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGCC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...::::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764

876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: :::::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.:::.:::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.:::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: ::::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...::::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530

2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGCU	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGCU	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: ::::::	CGCAUCUGCC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.:::::::	ACCACGUGCU	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: ::::..:	CGCACGUGCC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGCC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: ::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: ::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-UC	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGCU	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGCU	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGCU	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: ::::::	CGCAUCUGCC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.:::::::	ACCACGUGCU	Cleavage	pacid=371515

1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: ::::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: ::::.: :::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: ::::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..::::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: ::::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-UC	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: ::::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: ::::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	:::.. ::::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::::: :::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: ..::::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: ..::::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. :::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.::::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.::::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: ::::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: ::::.: :::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: ::::::.:	AGCAUGUGC	Cleavage	pacid=371566

1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-UC	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGCC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	:::::::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::::::::::	ACCACGUGCU	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..::::.::.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: ::::::.:	CGCACGUGCC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGCC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...::::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: :::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-UC	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: ::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461

151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. :::::: ::.:::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	::::::::::: ::::::.:	CGCACGUGC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .:::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	:::::::::: ::::: ...	AGCACGUGC	Translation	pacid=371623
676	696	UGGAGAAGC	::::. : :...::::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..:::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..::::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: ::::.: :::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.::::::: ::::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::.: : ::.:::::::...:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::..:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::...:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::...:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.:::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. ::::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	::::::.::: :::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	::::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487

1237	1257	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	:::::::::: :::::.:	CGCACGUGCC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	::::::::: :::: ...	AGCACGUGCC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..:::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::..: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGCC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-UC	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. ::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	::::::.::: :::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.::::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. :::::: ::::::	CGCAUCUGCC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.:::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
526	546	UGGAGAAGC	::::.::::..::: :::...	UGCAUGUGC	Cleavage	pacid=371422
220	240	UGGAGAAGC	:::::::.::::::::	ACCACGUGC	Cleavage	pacid=371515
1359	1379	UGGAGAAGC	::::: :: ::: :::::::.	UGCACUUGG	Cleavage	pacid=371586
1415	1435	UGGAGAAGC	::. .:::..:::.::.:.::	UGUUUGUGU	Cleavage	pacid=371487
1237	1257	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
1208	1228	UGGAGAAGC	::. ::::: ::.::::..:	UGUUCGUGC	Translation	pacid=371708
238	257	UGGAGAAGC	:::::::::: :::::.:	CGCACGUGCC	Cleavage	pacid=371484
182	202	UGGAGAAGC	:.:.:::: :: .::::::	GGUAUGUGC	Cleavage	pacid=371500
210	230	UGGAGAAGC	::::::::: :::: ...	AGCACGUGCC	Translation	pacid=371623
676	696	UGGAGAAGC	:::. : :...:::::::.::	UGCGAGGGU	Cleavage	pacid=371516
1409	1429	UGGAGAAGC	::: ::::..::::: :::	UGCUGGUGC	Cleavage	pacid=371770
480	500	UGGAGAAGC	:::: :: ..:::::: :::	UGCAAGUUU	Cleavage	pacid=371764
876	896	UGGAGAAGC	:::: :::.: ::::::.::	UGCAGUUGC	Translation	pacid=371754
1302	1321	UGGAGAAGC	:::.:::::.:: :::::.:	AGCAUGUGC	Cleavage	pacid=371566
1139	1159	UGGAGAAGC	::::: ::::::::: ..:	UGCACUGGC	Cleavage	pacid=371699
998	1018	UGGAGAAGC	::..: : ::..:::::::..:	UGUAGGAGC	Cleavage	pacid=371749

564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
564	584	UGGAGAAGC	: :::::::.:::::: :.	CGAACGUGC	Cleavage	pacid=371759
78	97	UGGAGAAGC	::::.:: .:.:::::.::.:	UGCAUGU-U	Cleavage	pacid=371675
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
49	69	UGGAGAAGC	:.:: ::..:: :::::.::	GGUACAUGU	Cleavage	pacid=371422
3477	3497	UGGAGAAGC	.::::::::.: :::::	GGGCUGUGC	Cleavage	pacid=371724
372	392	UGGAGAAGC	::.. :::::::.: ::::.	AGCGUUUGC	Cleavage	pacid=371721
304	324	UGGAGAAGC	:::::.::: :::::.::	UCUCCGUGC	Cleavage	pacid=371530
2017	2037	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1749	1769	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
151	171	UGGAGAAGC	:.: :::.:::::::::	GCCGCUUGC	Cleavage	pacid=371589
1700	1720	UGGAGAAGC	:::.:: .:.:::::. :::	GGCAUGUCU	Cleavage	pacid=371461
1369	1389	UGGAGAAGC	:::. ::::::: ::::::	CGCAUCUGC	Cleavage	pacid=371646
775	795	UGGAGAAGC	:. ::::.. :::::::::.	AGUUCGUGU	Translation	pacid=371518
1011	1031	UGGAGAAGC	:.::: :: :::.::::::..	AGUACGGGC	Cleavage	pacid=371742
879	899	UGGAGAAGC	:.::: :: :::.::::::..	AGUACGGGC	Cleavage	pacid=371742
772	792	UGGAGAAGC	:..: ::::.::.:::: ::	AGUGCAUGC	Cleavage	pacid=371577
525	546	UGGAGAAGC	::::.::::..::: :::...	AUGCAUGUG	Cleavage	pacid=371422
675	696	UGGAGAAGC	::::. : :...::::::::.::	UUGCGAGGG	Cleavage	pacid=371516
219	240	UGGAGAAGC	:::::::.::::::::	AACCACGUG	Cleavage	pacid=371515
77	97	UGGAGAAGC	:::::.:: .:.:::::.::.:	UUGCAUGU-	Cleavage	pacid=371675
1358	1379	UGGAGAAGC	::::: :: ::: ::::::.	CUGCACUUG	Cleavage	pacid=371586
1414	1435	UGGAGAAGC	::. .:::.:::.::.::.::	CUGUUUGUG	Cleavage	pacid=371487
1236	1257	UGGAGAAGC	::. :::::: :::::::..:	AUGUUCGUG	Translation	pacid=371708
1207	1228	UGGAGAAGC	::. :::::: ::.::::...:	AUGUUCGUG	Translation	pacid=371708
784	805	UGGAGAAGC	:: ::::::..: : ::::.::	UUCCACGUG	Translation	pacid=371513
237	257	UGGAGAAGC	::::::::::: :::::.:	ACGCACGUG	Cleavage	pacid=371484
819	839	UGGAGAAGC	:::::: : : ::::::::::	UUGCACCU-C	Cleavage	pacid=371743
819	839	UGGAGAAGC	:::::: : : ::::::::::	UUGCACCU-C	Cleavage	pacid=371743
181	202	UGGAGAAGC	:.:.:::: :: .:::::::	CGGUAUGUG	Cleavage	pacid=371500
209	230	UGGAGAAGC	:::::::::: ::::: ...	AAGCACGUG	Translation	pacid=371623
1408	1429	UGGAGAAGC	::: ::::..::::: :::	CUGCUGGUG	Cleavage	pacid=371770
479	500	UGGAGAAGC	:::: :: ..::::::: :::	CUGCAAGUU	Cleavage	pacid=371764
875	896	UGGAGAAGC	:::: :::.: ::::::.::	GUGCAGUUG	Translation	pacid=371754
1301	1321	UGGAGAAGC	:::.:::::.:: :::::.:	CAGCAUGUG	Cleavage	pacid=371566
1222	1243	UGGAGAAGC	:. :::.:.:::::.: ::	AACCGGGUG	Cleavage	pacid=371718
1138	1159	UGGAGAAGC	::::: :::::::::: ..:	CUGCACUGG	Cleavage	pacid=371699
997	1018	UGGAGAAGC	::.: : ::..::::::::..:	CUGUAGGAG	Cleavage	pacid=371749
48	69	UGGAGAAGC	: :.:: ::..:: :::::.::	UGGUACAUG	Cleavage	pacid=371422
48	69	UGGAGAAGC	: :.:: ::..:: :::::.::	UGGUACAUG	Cleavage	pacid=371422
3461	3482	UGGAGAAGC	:: .:. ::: .::::::::.:	UUCUAUCUG	Cleavage	pacid=371775
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483

81	100	UGGAGAAGC	::::.:::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.:::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: ::::. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.:::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...::::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.:::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622

1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: :::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: :::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: ::::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	:::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656

819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::....:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: :::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: :::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::.....::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .::::.. :::::::..::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	::::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656

331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.:::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: ::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::.:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .::::::::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	:::::: :::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. ::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.:::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.:::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756

3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. .::::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.:::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	:::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	:::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	:::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ..::::::::	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: ::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656

393	413	UGGAGAAGC	::. .:::...::.:::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: :::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: :::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.:::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: :::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: ::::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.:::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...::::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: ::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622

890	911	UGGAGAAGC	::::: :::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::....:::. ::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.:::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.:::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:..::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::...:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::..::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::..::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: ::::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457

4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: :::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: :::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .::::.. ::::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.:::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::...	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::...	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.::::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.:::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.:::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740

249	269	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::....::: :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::...:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777

444	464	UGGAGAAGC	::.:::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.:::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: :::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::...:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468

1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...::::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: ::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445

210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...:::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : ::::.. :.:::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	:.:::::: ::::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::::: ::::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: ::::.	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: ::::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	:::::::.:::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: ::::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: ::::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: ::::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...::::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.:::::.:: . ::::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.::::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .::::::.::::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .::::::.::::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .::::::.::::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::...::::.::::...	UGAACAUGU	Cleavage	pacid=371514

2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.:::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: :::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: :::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: :::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	:::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528

501	521	UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	:::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::::::...:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: :::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: :::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.:::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: ::::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656

1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::...:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	:: .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::....:::. ::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::...:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.::::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCCC	Cleavage	pacid=371647

729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.:::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	::::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . ::::::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	::::: ::::.:::::.	ACCACGUGAC	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGCC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738

1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	::::::..:::.::::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.:::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.:::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: ::::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	:::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...::::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.:::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747

894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::..:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: :::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: ::::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.:::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	:::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : ::::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.::::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...::::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: ::::::::: ::	UGAACAUGA	Cleavage	pacid=371579

1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	::...:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	::::.:::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.:::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.:::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::...:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.:::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.:::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663
417	437	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120	UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298	UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCC	Cleavage	pacid=371740
249	269	UGGAGAAGC	::::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656

420	440	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181	UGGAGAAGC	::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839	UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305	UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521	UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631	UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225	UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200	UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286	UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910	UGGAGAAGC	::. .: :..:::.::.::::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681	UGGAGAAGC	:: :: ::..:::.::::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244	UGGAGAAGC	:::: ::: .:::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
890	911	UGGAGAAGC	::::: ::::: :::::::::	UGCACCUGC	Translation	pacid=371489
273	293	UGGAGAAGC	:.....:::. :::::::::.	UGUGUGUGU	Cleavage	pacid=371747
894	914	UGGAGAAGC	:::.::::.: ::.::.::.	UGCAUGUGU	Translation	pacid=371531
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
81	100	UGGAGAAGC	::::.::::: ::::::::.	UGCAUGUGC	Translation	pacid=371483
210	229	UGGAGAAGC	::::::::::: .:::::.	UGCACGUGC	Cleavage	pacid=371445
210	229	UGGAGAAGC	::::::::::: ::::::.	UGCACGUGC	Cleavage	pacid=371445
67	88	UGGAGAAGC	:::: ::::...::::::::.	UGCAACGUG	Cleavage	pacid=371715
2692	2712	UGGAGAAGC	::::. ::.:::::::: :.	UGCAUCUGU	Cleavage	pacid=371592
1441	1461	UGGAGAAGC	::: .:::.. :::::.:.::	UGCUUGUGU	Translation	pacid=371656
393	413	UGGAGAAGC	::. .:::...::.::::...:	UGUCUGUGU	Cleavage	pacid=371678
1867	1887	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
1795	1815	UGGAGAAGC	::.:. ::: ::::::.::..	UGUAUUUGC	Cleavage	pacid=371738
2809	2829	UGGAGAAGC	:::::::::: .::.:::	GGCACGUGC	Translation	pacid=371462
639	659	UGGAGAAGC	:::::..:::.:::::	UAGACGUGU	Cleavage	pacid=371520
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1429	1450	UGGAGAAGC	::: : :::::.::.::.::.:	UGCUCAGUG	Cleavage	pacid=371468
1946	1966	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
1712	1732	UGGAGAAGC	:::: ::::::::::. ::	UGCAGUUGC	Cleavage	pacid=371764
4127	4147	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
3713	3733	UGGAGAAGC	::.:::::.: ::::::	ACCAUGUGC	Cleavage	pacid=371756
2142	2165	UGGAGAAGC	:::::: ::.:::::::::	GGCACGUCC	Cleavage	pacid=371647
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
729	749	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371776
1576	1596	UGGAGAAGC	: : : :::.. :.::::::	UUCUCUUGC	Translation	pacid=371530
549	569	UGGAGAAGC	:::.:::.::: :: ::..:	AGCAUGUGU	Cleavage	pacid=371777
444	464	UGGAGAAGC	::.::::: :::::.::	GACAUGUGC	Translation	pacid=371607
449	469	UGGAGAAGC	:::.::::.:: :::.:. :	AGCAUGUGC	Cleavage	pacid=371663

417	437 UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
1075	1095 UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
331	351 UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
989	1009 UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
1100	1120 UGGAGAAGC	::::::.::::.:: ::	AACACGUGU	Cleavage	pacid=371470
99	119 UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
977	997 UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
278	298 UGGAGAAGC	::::: : :::::.::.:..	UGCACCUCCC	Cleavage	pacid=371740
249	269 UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
907	927 UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
420	440 UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371532
161	181 UGGAGAAGC	:::::::.:.:: :::.:.	AGCACGUGU	Cleavage	pacid=371656
819	839 UGGAGAAGC	::::::..::.: :::..	ACAACGUGC	Cleavage	pacid=371656
285	305 UGGAGAAGC	::: : :::::::::: .:	UGCUCCUGC	Cleavage	pacid=371528
501	521 UGGAGAAGC	:::.:::::.::. ::: .:	AGCAUGUGC	Cleavage	pacid=371779
611	631 UGGAGAAGC	:::: :: ...:::::::.:	UGCAAGUCU	Cleavage	pacid=371590
205	225 UGGAGAAGC	:::.::::.:: . :::.::	AGCAUGUGC	Cleavage	pacid=371599
179	200 UGGAGAAGC	:::::: :::::.:::::.	ACCACGUGA	Cleavage	pacid=371457
4269	4289 UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
4266	4286 UGGAGAAGC	:: :: :: :::::::: ::	UGAACAUGA	Cleavage	pacid=371579
1610	1630 UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1571	1591 UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
1531	1551 UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
3830	3850 UGGAGAAGC	:: :: ::..:::.:::...	UGAACAUGU	Cleavage	pacid=371514
2950	2970 UGGAGAAGC	::. .: :..:::.::.:::	UGUUUGGGU	Cleavage	pacid=371537
2890	2910 UGGAGAAGC	::. .: :..:::.::.:::	UGUUUGGGU	Cleavage	pacid=371537
3661	3681 UGGAGAAGC	:: :: ::..:::.:::...	UGAACAUGU	Cleavage	pacid=371514
1224	1244 UGGAGAAGC	:::: ::: .::::::.:::.	UGCAGCUGC	Cleavage	pacid=371622
66	88 UGGAGAAGC	::::: ::::...::::::::.	UUGCAACGU	Cleavage	pacid=371715
2691	2712 UGGAGAAGC	:::::. ::.:::::::: :.	UUGCAUCUG	Cleavage	pacid=371592
1866	1887 UGGAGAAGC	:::.:. ::: ::::::.::..	UUGUAUUUG	Cleavage	pacid=371738
889	911 UGGAGAAGC	::::: :::: ::::::::	AUGCACCUG	Translation	pacid=371489
1794	1815 UGGAGAAGC	:::.:. ::: ::::::.::..	UUGUAUUUG	Cleavage	pacid=371738
272	293 UGGAGAAGC	::...:::. :::::::::.	CUGUGUGUG	Cleavage	pacid=371747
893	914 UGGAGAAGC	::::.:::.: ::.::.::.	CUGCAUGUG	Translation	pacid=371531
80	100 UGGAGAAGC	::::.::::: ::::::::.	CUGCAUGUG	Translation	pacid=371483
80	100 UGGAGAAGC	::::.::::: ::::::::.	CUGCAUGUG	Translation	pacid=371483
209	229 UGGAGAAGC	::::::::::: .:::::.	CUGCACGUG	Cleavage	pacid=371445
209	229 UGGAGAAGC	::::::::::: .:::::.	CUGCACGUG	Cleavage	pacid=371445
419	440 UGGAGAAGC	:::: : :::::::::: .:	UUGCUCCUG	Cleavage	pacid=371532
284	305 UGGAGAAGC	:::: : :::::::::: .:	UUGCUCCUG	Cleavage	pacid=371528
4268	4289 UGGAGAAGC	::: :: :: :::::::: ::	UUGAACAUG	Cleavage	pacid=371579
4265	4286 UGGAGAAGC	::: :: :: :::::::: ::	UUGAACAUG	Cleavage	pacid=371579
3829	3850 UGGAGAAGC	::: :: ::..:::.:::...	UUGAACAUG	Cleavage	pacid=371514
2949	2970 UGGAGAAGC	:::. .: :..:::.::.:::	UUGUUUGGG	Cleavage	pacid=371537
2889	2910 UGGAGAAGC	:::. .: :..:::.::.:::	UUGUUUGGG	Cleavage	pacid=371537

3660	3681	UGGAGAAGC	::: :: ::..:::.::::...	UUGAACAUG	Cleavage	pacid=371514
2779	2800	UGGAGAAGC	:::. .: :..:::.::.::::	UUGUUUGGG	Cleavage	pacid=371537
2112	2133	UGGAGAAGC	::: .. :::::::.:::: :	UUGGGUCUG	Cleavage	pacid=371504
604	625	UGGAGAAGC	::::. : . :::.::::::	UUGCAUCUC	Cleavage	pacid=371453
1105	1126	UGGAGAAGC	:::: . ::.:.: :::::::	UUGCUUUUG	Cleavage	pacid=371761
1105	1126	UGGAGAAGC	:::: . ::.:.: :::::::	UUGCUUUUG	Cleavage	pacid=371761
1095	1116	UGGAGAAGC	:::: . ::.:.: :::::::	UUGCUUUUG	Cleavage	pacid=371761
3835	3856	UGGAGAAGC	:: : :::::::::.::.:.	UUUCUCGUG	Cleavage	pacid=371477
817	837	UGGAGAAGC	::::: ::::..:: ::::.::	UUGCA-GUG	Cleavage	pacid=371560
375	395	UGGAGAAGC	:::::: :: ..::::::::.::	UUGCAC-UGG	Cleavage	pacid=371469
1440	1461	UGGAGAAGC	::: .:::.. :::::.:.::	GUGCUUGUG	Translation	pacid=371656
2808	2829	UGGAGAAGC	: ::::::::: .::.:::	UGGCACGUG	Translation	pacid=371462
392	413	UGGAGAAGC	::. .:::...::.::::...:	GUGUCUGUG	Cleavage	pacid=371678
530	551	UGGAGAAGC	:: :..:::::: :.::.::.	UUCCGUGUG	Translation	pacid=371703
1601	1623	UGGAG-AAGC	:: ::.:: .:::::: ::::	UUCCAUGUU	Cleavage	pacid=371718
121	142	UGGAGAAGC	:: ::.::: :::: :::.:	UUCCAUGUG	Cleavage	pacid=371593

Multiplicity	peptideName	locusName	Pfam	Panther	KOG
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1	Phvul.003G189000	Phvul.003G189000	PF02365	PTHR31744,P	0
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1	Phvul.009G186000	Phvul.009G186000	PF02365	PTHR31744,P	0
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1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P	0
1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P	KOG1663
1	Phvul.006G169300	Phvul.006G169300	PF00657	PTHR22835,P	0
1	Phvul.007G164800	Phvul.007G164800	0	PTHR33448,P	0
1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P	0
1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P	0
1	Phvul.011G065700	Phvul.011G065700	PF01073	PTHR10366,P	0
1	Phvul.004G172600	Phvul.004G172600	PF13578	PTHR10509,P	KOG1663
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0

1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0

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1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
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1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
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1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.006G086200	Phvul.006G086200	0	PTHR32133	0
1	Phvul.010G128500	Phvul.010G128500	PF01699	PTHR12266,P	KOG2399
1	Phvul.010G089100	Phvul.010G089100	PF03634	PTHR31072,P	0
1	Phvul.002G325300	Phvul.002G325300	PF03033,PF04	PTHR21015,P	0
1	Phvul.004G139200	Phvul.004G139200	PF13355	PTHR33925,P	0
1	Phvul.005G001200	Phvul.005G001200	PF00657	PTHR22835,P	0
1	Phvul.008G147100	Phvul.008G147100	0	0	0
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1	Phvul.008G147100	Phvul.008G147100	0	0	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0C	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0

1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769	
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P		0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546	
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P		0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P		0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014	
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P		0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P		0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187	
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P		0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099		0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P		0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750	
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P		0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769	
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P		0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546	
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P		0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P		0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014	
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P		0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P		0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187	
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P		0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099		0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P		0
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1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P		0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769	
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P		0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546	
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P		0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P		0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014	
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P		0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P		0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187	

1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
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1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0

1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0

1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0C	PTHR11071,P	KOG0546	
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P		0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P		0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0C	PTHR11945,P	KOG0014	
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P		0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0C	PTHR23069		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P		0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187	
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P		0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099		0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0C	PTHR11689,P		0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750	
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P		0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769	
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P		0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0C	PTHR11071,P	KOG0546	
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P		0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P		0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0C	PTHR11945,P	KOG0014	
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P		0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0C	PTHR23069		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P		0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187	
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P		0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099		0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0C	PTHR11689,P		0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750	
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P		0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769	
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P		0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0C	PTHR11071,P	KOG0546	
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P		0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P		0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0C	PTHR11945,P	KOG0014	
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P		0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0C	PTHR23069		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P		0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P		0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187	
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P		0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099		0

1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0

1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0

1	Phvul.005G087600	Phvul.005G087600	0	PTHR34379,P	0
1	Phvul.009G130000	Phvul.009G130000	PF01486,PF0	PTHR11945,P	KOG0014
1	Phvul.011G108000	Phvul.011G108000	PF08241	PTHR10108,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.007G083500	Phvul.007G083500	0	PTHR36319,P	0
1	Phvul.011G079800	Phvul.011G079800	PF00046,PF08	PTHR24326,P	0
1	Phvul.011G054900	Phvul.011G054900	PF01695,PF0	PTHR23069	0
1	Phvul.008G077800	Phvul.008G077800	PF01657,PF07	PTHR27002	KOG1187
1	Phvul.011G110300	Phvul.011G110300	0	PTHR34056,P	0
1	Phvul.008G077700	Phvul.008G077700	PF01657	PTHR32099	0
1	Phvul.005G005200	Phvul.005G005200	PF00571,PF0	PTHR11689,P	0
1	Phvul.002G073200	Phvul.002G073200	PF00892	PTHR31218,P	KOG4510
1	Phvul.002G073100	Phvul.002G073100	PF00892	PTHR31218,P	KOG4510
1	Phvul.002G073100	Phvul.002G073100	PF00892	PTHR31218,P	KOG4510
1	Phvul.008G277800	Phvul.008G277800	PF00132,PF06	PTHR23416,P	KOG4750
1	Phvul.003G067000	Phvul.003G067000	0	PTHR34222,P	0
1	Phvul.001G240500	Phvul.001G240500	PF00153	PTHR24089,P	KOG0769
1	Phvul.008G061000	Phvul.008G061000	PF04851,PF08	PTHR10799,P	0
1	Phvul.003G246400	Phvul.003G246400	PF07719,PF0	PTHR11071,P	KOG0546
1	Phvul.009G132000	Phvul.009G132000	PF03141	PTHR10108,P	0
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0

1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
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1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0

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1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P		0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223	
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.008G127800	Phvul.008G127800	0	0		0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P		0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339	
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P		0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187	
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472	
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P		0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476	
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254	
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P		0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339	
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P		0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181	
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187	
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187	
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P		0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P		0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P		0
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1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P		0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223	
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.008G127800	Phvul.008G127800	0	0		0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P		0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339	
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P		0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187	
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472	

1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF0	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0

1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
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1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF0	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF0	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339

1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0

1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0

1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P		0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P		0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P		0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P		0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223	
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.008G127800	Phvul.008G127800	0	0		0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P		0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339	
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P		0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF0	PTHR27000	KOG1187	
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472	
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P		0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476	
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254	
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P		0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339	
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P		0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181	
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187	
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187	
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P		0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P		0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P		0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P		0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P		0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631		0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223	
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P		0
1	Phvul.008G127800	Phvul.008G127800	0	0		0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P		0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339	
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P		0

1	Phvul.009G244600	Phvul.009G244600	PF08263,PF0	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF0	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0

1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254

1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF0	PTHR27000	KOG1187
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF0	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF0	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF0	PTHR27000,P	KOG1187
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF0	PTHR21499,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0

1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.001G038000	Phvul.001G038000	PF01843	PTHR13140,P	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.008G032900	Phvul.008G032900	PF07897,PF16	PTHR31413,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.007G105700	Phvul.007G105700	PF13837,PF00	PTHR21499,P	0
1	Phvul.011G046800	Phvul.011G046800	PF00083	PTHR23500,P	KOG0254
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G102900	Phvul.006G102900	PF06886	PTHR31358,P	0
1	Phvul.006G023000	Phvul.006G023000	PF00657	PTHR22835,P	0
1	Phvul.004G099100	Phvul.004G099100	PF08263,PF00	PTHR27004,P	KOG0472
1	Phvul.002G157300	Phvul.002G157300	PF03479	PTHR31500,P	0
1	Phvul.009G146400	Phvul.009G146400	PF03360	PTHR10896,P	KOG1476
1	Phvul.006G093600	Phvul.006G093600	PF00026	PTHR13683,P	KOG1339
1	Phvul.001G151600	Phvul.001G151600	0	PTHR34798,P	0
1	Phvul.009G244600	Phvul.009G244600	PF08263,PF00	PTHR27000	KOG1187
1	Phvul.009G121200	Phvul.009G121200	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.009G121200	Phvul.009G121200	PF02493,PF01	PTHR23086,P	KOG0229
1	Phvul.007G156900	Phvul.007G156900	0	PTHR33981,P	0
1	Phvul.007G157000	Phvul.007G157000	0	PTHR33981,P	0
1	Phvul.008G159000	Phvul.008G159000	PF10250	PTHR31741,P	0
1	Phvul.007G231200	Phvul.007G231200	PF07650,PF00	PTHR11760,P	KOG3181
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.004G037600	Phvul.004G037600	PF00560,PF00	PTHR27000,P	KOG1187
1	Phvul.005G114000	Phvul.005G114000	PF05634	PTHR10388,P	0
1	Phvul.001G031000	Phvul.001G031000	PF08880,PF08	PTHR31602,P	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.004G041500	Phvul.004G041500	PF02005	PTHR10631	0
1	Phvul.002G105200	Phvul.002G105200	PF00026	PTHR13683,P	KOG1339
1	Phvul.007G084000	Phvul.007G084000	PF00230	PTHR19139,P	KOG0223
1	Phvul.009G119100	Phvul.009G119100	PF13386	PTHR33876,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.010G079200	Phvul.010G079200	PF04690	PTHR31675,P	0
1	Phvul.008G127800	Phvul.008G127800	0	0	0
1	Phvul.007G029900	Phvul.007G029900	PF00560,PF08	PTHR27008,P	KOG1187
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0

1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0

1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
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1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0

1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0

1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0

1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P		0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P		0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243		0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243		0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383	
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383	
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243		0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156	
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P		0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401		0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401		0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473	
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600	
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P		0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P		0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329		0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064		0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064		0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P		0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P		0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541	
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193		0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P		0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P		0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P		0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906		0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594	
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130		0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P		0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P		0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P		0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P		0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P		0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P		0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P		0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P		0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243		0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243		0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383	
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383	
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243		0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156	
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P		0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401		0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401		0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473	

1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF00	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF00	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0

1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0

1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0

1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
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1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0

1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0

1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0C	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0C	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0

1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
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1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0	PTHR10906	0
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0

1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.002G017700	Phvul.002G017700	PF00069	PTHR27001,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.006G154900	Phvul.006G154900	0	PTHR33739,P	0
1	Phvul.006G047000	Phvul.006G047000	PF02922,PF0C	PTHR10357,P	0
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.008G017200	Phvul.008G017200	PF00282	PTHR11999,P	KOG1383
1	Phvul.003G056900	Phvul.003G056900	0	PTHR37243	0
1	Phvul.007G106300	Phvul.007G106300	PF00067	PTHR24298,P	KOG0156
1	Phvul.009G034400	Phvul.009G034400	PF16913	PTHR31376,P	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.L002444	Phvul.L002444	0	PTHR33401	0
1	Phvul.008G070000	Phvul.008G070000	PF01988	PTHR31851,P	KOG4473
1	Phvul.010G156200	Phvul.010G156200	PF00487	PTHR11351,P	KOG1600
1	Phvul.009G160200	Phvul.009G160200	PF13414	PTHR16193	0
1	Phvul.009G217000	Phvul.009G217000	PF04783,PF04	PTHR21450,P	0
1	Phvul.007G022500	Phvul.007G022500	PF00111	PTHR19370,P	0
1	Phvul.008G043500	Phvul.008G043500	PF00847	PTHR32467,P	0
1	Phvul.009G079400	Phvul.009G079400	PF05254	PTHR21329	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.001G193000	Phvul.001G193000	0	PTHR36064	0
1	Phvul.009G167700	Phvul.009G167700	PF13193,PF0C	PTHR24096,P	KOG1176
1	Phvul.003G154400	Phvul.003G154400	PF12854,PF14	PTHR24015,P	0
1	Phvul.L003746	Phvul.L003746	PF01823	PTHR33199,P	0
1	Phvul.L003746	Phvul.L003746	PF01823	PTHR33199,P	0
1	Phvul.009G030200	Phvul.009G030200	PF08241	PTHR10108,P	0
1	Phvul.004G166100	Phvul.004G166100	PF00578	PTHR10430	KOG0541
1	Phvul.002G119600	Phvul.002G119600	PF11443	PTHR31373,P	0
1	Phvul.002G150800	Phvul.002G150800	PF00155	PTHR11751,P	0
1	Phvul.002G271400	Phvul.002G271400	PF00266	PTHR11601,P	0
1	Phvul.011G166200	Phvul.011G166200	PF10559,PF0C	PTHR10906	0
2	Phvul.006G067900	Phvul.006G067900	PF01699	PTHR31503,P	KOG1397
1	Phvul.001G110100	Phvul.001G110100	0	PTHR11122,P	KOG1594
1	Phvul.002G037500	Phvul.002G037500	0	PTHR17130	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.010G115000	Phvul.010G115000	PF00400,PF12	PTHR13950,P	0
1	Phvul.002G157000	Phvul.002G157000	PF08372,PF0C	PTHR10024,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0

1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0

1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0

2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0

2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0

1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0

1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0

1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P		0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P		0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P		0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P		0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P		0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P		0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P		0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P		0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P		0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P		0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P		0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764	
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764	
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381	
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993		0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P		0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P		0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P		0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P		0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P		0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P		0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P		0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172	
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172	
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P		0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172	
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P		0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773	
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P		0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551	
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P		0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P		0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P		0

1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
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1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0

2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172

1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0

1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0

1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P		0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P		0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P		0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P		0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P		0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764	
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764	
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381	
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993		0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P		0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P		0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P		0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P		0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P		0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P		0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P		0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172	
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172	
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P		0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172	
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P		0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773	
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
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1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P		0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P		0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551	
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P		0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P		0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P		0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658	
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658	
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P		0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P		0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P		0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P		0

1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0

1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0

1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0

1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764

1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0

1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF0C	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF0C	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658

1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.006G164800	Phvul.006G164800	PF04765	PTHR12956,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0

1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
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1	Phvul.005G059500	Phvul.005G059500	PF00141	PTHR31235,P	0
1	Phvul.002G116800	Phvul.002G116800	PF10181	PTHR15231,P	KOG4551
1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
1	Phvul.003G262800	Phvul.003G262800	PF02519	PTHR31374,P	0
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
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1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
1	Phvul.005G099500	Phvul.005G099500	PF02469	PTHR32077,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
1	Phvul.006G075600	Phvul.006G075600	PF00141	PTHR31388,P	0
1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P	0
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
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1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381
1	Phvul.009G007300	Phvul.009G007300	0	PTHR35993	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.003G100200	Phvul.003G100200	PF04851,PF00	PTHR10799,P	0
1	Phvul.002G262600	Phvul.002G262600	PF00168,PF00	PTHR23315,P	0
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1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.002G299004	Phvul.002G299004	PF01137,PF05	PTHR11096,P	0
1	Phvul.007G156200	Phvul.007G156200	PF00010	PTHR12565,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
2	Phvul.005G001000	Phvul.005G001000	PF03552	PTHR13301,P	0
1	Phvul.002G006400	Phvul.002G006400	PF13920	PTHR10044,P	KOG4172
1	Phvul.008G243700	Phvul.008G243700	PF01764	PTHR21493,P	0
1	Phvul.007G201400	Phvul.007G201400	PF03789,PF05	PTHR11850,P	KOG0773

2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
1	Phvul.003G181600	Phvul.003G181600	PF13639	PTHR22763,P	0
2	Phvul.007G157500	Phvul.007G157500	0	PTHR24320,P	0
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1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
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1	Phvul.008G103100	Phvul.008G103100	PF00249,PF14	PTHR31314,P	0
1	Phvul.008G075300	Phvul.008G075300	0	PTHR33601,P	0
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1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
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1	Phvul.004G088300	Phvul.004G088300	0	PTHR36319,P	0
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1	Phvul.008G284900	Phvul.008G284900	PF08801	PTHR13405,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.009G222600	Phvul.009G222600	PF04043,PF01	PTHR31707,P	0
1	Phvul.006G091100	Phvul.006G091100	PF00571,PF16	PTHR13780,P	KOG1764
1	Phvul.002G106900	Phvul.002G106900	PF04783,PF04	PTHR21450,P	0
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1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G181900	Phvul.003G181900	PF00010	PTHR12565,P	0
1	Phvul.003G121200	Phvul.003G121200	PF03151	PTHR11132,P	0
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1	Phvul.005G059700	Phvul.005G059700	PF00141	PTHR31235,P	0
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1	Phvul.008G072300	Phvul.008G072300	PF00931	PTHR23155,P	KOG4658
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1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P	0
1	Phvul.005G155100	Phvul.005G155100	PF00564,PF02	PTHR32002,P	0
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1	Phvul.009G201600	Phvul.009G201600	PF00122,PF12	PTHR24092,P		0
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1	Phvul.009G114400	Phvul.009G114400	PF00069	PTHR27000,P	KOG1187	
1	Phvul.003G240100	Phvul.003G240100	PF12710,PF00	PTHR24093,P		0
1	Phvul.002G283000	Phvul.002G283000	PF12627,PF01	PTHR13734,P		0
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1	Phvul.003G170100	Phvul.003G170100	PF00862,PF05	PTHR12526,P	KOG0853	
1	Phvul.011G173600	Phvul.011G173600	PF01535,PF13	PTHR24015,P		0
1	Phvul.003G283500	Phvul.003G283500	PF07297	PTHR15039,P	KOG3488	
1	Phvul.007G163400	Phvul.007G163400	PF00632	PTHR11254,P		0
1	Phvul.003G037500	Phvul.003G037500	PF00454	PTHR15245,P	KOG2381	
1	Phvul.001G266600	Phvul.001G266600	PF00464	PTHR11680,P		0
1	Phvul.001G243500	Phvul.001G243500	PF00069	PTHR27003,P	KOG1187	
2	Phvul.006G067900	Phvul.006G067900	PF01699	PTHR31503,P	KOG1397	
1	Phvul.008G140600	Phvul.008G140600	PF00201	PTHR11926,P		0

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4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6	

0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	
0	K00588	GO:0008171	AT4G26220.1		0
3.1.1.3	0	GO:0016788	AT1G29670.1		0
0	0	0	AT2G37100.1		0
4.1.1.35	K08678	GO:0055114,(	AT2G28760.3	UXS6	

4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
0	K00588	GO:0008171	AT4G26220.1	0
3.1.1.3	0	GO:0016788	AT1G29670.1	0
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4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
0	K00588	GO:0008171	AT4G26220.1	0
3.1.1.3	0	GO:0016788	AT1G29670.1	0
0	0	0	AT2G37100.1	0
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
4.1.1.35	K08678	GO:0055114,	AT2G28760.3	UXS6
0	K00588	GO:0008171	AT4G26220.1	0
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1	0
0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6
3.1.1.3	0	GO:0016788	AT1G33811.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	0	0
0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1	0
0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6
3.1.1.3	0	GO:0016788	AT1G33811.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	0	0
0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1	0
0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6
3.1.1.3	0	GO:0016788	AT1G33811.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	0	0
0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1	0
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3.1.1.3	0	GO:0016788	AT1G33811.1	0

	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	0		0
	0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
	0	0	0	AT2G45680.1		0
2.4.1.227		K02563	GO:0030259,	AT1G73740.1		0
	0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0	GO:0016788	AT1G33811.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	0		0
	0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
	0	0	0	AT2G45680.1		0
2.4.1.227		K02563	GO:0030259,	AT1G73740.1		0
	0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0	GO:0016788	AT1G33811.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	0		0
	0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
	0	0	0	AT2G45680.1		0
2.4.1.227		K02563	GO:0030259,	AT1G73740.1		0
	0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3		0	GO:0016788	AT1G33811.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	0		0
	0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
	0	0	0	AT2G45680.1		0
2.4.1.227		K02563	GO:0030259,	AT1G73740.1		0
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3.1.1.3		0	GO:0016788	AT1G33811.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	AT5G40600.1		0
	0	0	0	0		0
	0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
	0	0	0	AT2G45680.1		0
2.4.1.227		K02563	GO:0030259,	AT1G73740.1		0
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3.1.1.3		0	GO:0016788	AT1G33811.1		0
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0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0
0	0	0	0		0
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0	0	0	AT2G45680.1		0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1		0
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3.1.1.3	0	GO:0016788	AT1G33811.1		0
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0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0
0	0	0	0		0
0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
0	0	0	AT2G45680.1		0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1		0
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3.1.1.3	0	GO:0016788	AT1G33811.1		0
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0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0
0	0	0	0		0
0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
0	0	0	AT2G45680.1		0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1		0
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3.1.1.3	0	GO:0016788	AT1G33811.1		0
0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0
0	0	0	0		0
0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
0	0	0	AT2G45680.1		0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1		0
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3.1.1.3	0	GO:0016788	AT1G33811.1		0
0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0
0	0	0	0		0
0	K13754	GO:0055085,	AT1G54115.1	ATCCX4,CCX4	
0	0	0	AT2G45680.1		0
2.4.1.227	K02563	GO:0030259,	AT1G73740.1		0
0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6	
3.1.1.3	0	GO:0016788	AT1G33811.1		0
0	0	0	AT5G40600.1		0
0	0	0	AT5G40600.1		0

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0	K13754	GO:0055085,(	AT1G54115.1	ATCCX4,CCX4
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(	AT1G73740.1	0
0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6
3.1.1.3	0	GO:0016788	AT1G33811.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	0	0
0	K13754	GO:0055085,(	AT1G54115.1	ATCCX4,CCX4
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(	AT1G73740.1	0
0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6
3.1.1.3	0	GO:0016788	AT1G33811.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	0	0
0	K13754	GO:0055085,(	AT1G54115.1	ATCCX4,CCX4
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(	AT1G73740.1	0
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3.1.1.3	0	GO:0016788	AT1G33811.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	0	0
0	K13754	GO:0055085,(	AT1G54115.1	ATCCX4,CCX4
0	0	0	AT2G45680.1	0
2.4.1.227	K02563	GO:0030259,(	AT1G73740.1	0
0	0	0	AT3G19180.1	ARC6H,ATCDP1,CDP1,PARC6
3.1.1.3	0	GO:0016788	AT1G33811.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	0	0	AT5G40600.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0

0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25

0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,	AT5G20240.1	PI
0	0	GO:0008168,	AT2G16030.1	0
0	0	GO:0005524,	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,	AT5G20240.1	PI
0	0	GO:0008168,	AT2G16030.1	0
0	0	GO:0005524,	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,	AT5G20240.1	PI
0	0	GO:0008168,	AT2G16030.1	0

0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2

5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25

0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI

0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0

0	0	0	0	0
0	K09264	GO:0006355,(	AT5G20240.1	PI
0	0	GO:0008168,(	AT2G16030.1	0
0	0	GO:0005524,(	AT1G05910.1	0
0	K12124	0	AT1G22770.1	FB,GI
0	K12124	0	AT1G22770.1	FB,GI
0	K09338	GO:0003677,(	AT5G60690.1	IFL,IFL1,REV
0	0	GO:0005524,(	AT1G05910.1	0
2.7.11.1	0	GO:0006468,(	AT4G05200.1	CRK25
0	0	0	AT4G28100.1	0
0	0	0	AT4G05200.1	CRK25
0	0	GO:0055085,(	AT1G55620.2	ATCLC-F,CLC-F,CLCF
0	0	GO:0016021,(	AT5G40240.1	0
0	0	GO:0016021,(	AT5G40240.1	0
0	0	GO:0016021,(	AT5G40240.1	0
2.3.1.30	K00640	GO:0009001,(	AT3G13110.1	ATSERAT2;2,SAT-1,SAT-A,SAT-M
0	0	0	0	0
0	K13354	0	AT2G39970.1	0
3.6.4.12	K11647	GO:0016787,(	AT2G46020.2	ATBRM,BRM,CHA2,CHR2
5.2.1.8	K05864	GO:0005515,(	AT2G15790.1	CYP40,SQN
0	0	GO:0008168	AT5G64030.1	0
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7
0	0	0	AT1G63470.1	0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5
3.1.1.3	0	GO:0016788	AT4G26790.1	0
3.4.23.12	0	GO:0006508,(	AT1G03220.1	0
0	0	0	AT3G63180.1	ATTKL,TKL
0	K02985	GO:0003723	AT5G35530.1	0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2
0	0	0	AT2G37570.1	SLT1
0	0	0	AT2G37570.1	SLT1
2.7.4.22	K09903	0	AT3G10030.1	0
0	0	0	AT3G02250.1	0
0	0	GO:0003723	AT3G21740.1	APO4
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8
0	0	0	AT2G16800.1	0
0	0	0	AT3G04630.1	WDL1
0	0	0	AT3G04630.1	WDL1
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1
0	0	0	0	0

0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0

0	0	0	AT3G02250.1	0
0	0	GO:0003723	AT3G21740.1	APO4
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8
0	0	0	AT2G16800.1	0
0	0	0	AT3G04630.1	WDL1
0	0	0	AT3G04630.1	WDL1
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1
0	0	0	0	0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I
3.4.23.12	0	GO:0006508,(	AT2G17760.1	0
0	0	GO:0007165	AT3G29575.3	AFP3
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7
0	0	0	AT1G63470.1	0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5
3.1.1.3	0	GO:0016788	AT4G26790.1	0
3.4.23.12	0	GO:0006508,(	AT1G03220.1	0
0	0	0	AT3G63180.1	ATTKL,TKL
0	K02985	GO:0003723	AT5G35530.1	0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2
0	0	0	AT2G37570.1	SLT1
0	0	0	AT2G37570.1	SLT1
2.7.4.22	K09903	0	AT3G10030.1	0
0	0	0	AT3G02250.1	0
0	0	GO:0003723	AT3G21740.1	APO4
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1	0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8
0	0	0	AT2G16800.1	0
0	0	0	AT3G04630.1	WDL1
0	0	0	AT3G04630.1	WDL1
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1
0	0	0	0	0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I
3.4.23.12	0	GO:0006508,(	AT2G17760.1	0
0	0	GO:0007165	AT3G29575.3	AFP3
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7

0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0

0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0

0	0	0	AT3G63180.1	ATTKL,TKL		
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	

0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	

	0		0		0	AT2G37570.1	SLT1	
2.7.4.22		K09903			0	AT3G10030.1		0
	0		0		0	AT3G02250.1		0
	0		0	GO:0003723		AT3G21740.1	APO4	
	0		0	GO:0006355,(		AT2G22840.1	AtGRF1,GRF1	
2.1.1.216		K00555		GO:0008033,(		AT5G15810.1		0
2.1.1.216		K00555		GO:0008033,(		AT5G15810.1		0
	0	K09874		GO:0016020,(		AT4G10380.1	NIP5;1,NLM6,NLM8	
	0		0		0	AT2G16800.1		0
	0		0		0	AT3G04630.1	WDL1	
	0		0		0	AT3G04630.1	WDL1	
	0		0	GO:0007275		AT2G45190.1	AFO,FIL,YAB1	
	0		0	GO:0007275		AT2G45190.1	AFO,FIL,YAB1	
	0		0		0	0		0
	0		0		0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12			0	GO:0006508,(		AT2G17760.1		0
	0		0	GO:0007165		AT3G29575.3	AFP3	
2.7.11.1			0	GO:0005515,(		AT4G20140.1	GSO1	
2.7.11.1			0	GO:0005515		AT1G47890.1	AtRLP7,RLP7	
	0		0		0	AT1G63470.1		0
2.4.2.24			0	GO:0016020,(		AT1G27600.2	I9H,IRX9-L	
	0		0	GO:0055085,(		AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3			0	GO:0016788		AT4G26790.1		0
3.4.23.12			0	GO:0006508,(		AT1G03220.1		0
	0		0		0	AT3G63180.1	ATTKL,TKL	
	0	K02985		GO:0003723		AT5G35530.1		0
2.7.11.1			0	GO:0005515,(		AT3G02130.1	RPK2,TOAD2	
2.7.11.1			0	GO:0005515,(		AT3G02130.1	RPK2,TOAD2	
	0		0		0	AT2G37570.1	SLT1	
	0		0		0	AT2G37570.1	SLT1	
2.7.4.22		K09903			0	AT3G10030.1		0
	0		0		0	AT3G02250.1		0
	0		0	GO:0003723		AT3G21740.1	APO4	
	0		0	GO:0006355,(		AT2G22840.1	AtGRF1,GRF1	
2.1.1.216		K00555		GO:0008033,(		AT5G15810.1		0
2.1.1.216		K00555		GO:0008033,(		AT5G15810.1		0
	0	K09874		GO:0016020,(		AT4G10380.1	NIP5;1,NLM6,NLM8	
	0		0		0	AT2G16800.1		0
	0		0		0	AT3G04630.1	WDL1	
	0		0		0	AT3G04630.1	WDL1	
	0		0	GO:0007275		AT2G45190.1	AFO,FIL,YAB1	
	0		0	GO:0007275		AT2G45190.1	AFO,FIL,YAB1	
	0		0		0	0		0
	0		0		0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12			0	GO:0006508,(		AT2G17760.1		0
	0		0	GO:0007165		AT3G29575.3	AFP3	

2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	

2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	0	AT3G02250.1		0
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	

3.1.1.3		0	GO:0016788	AT4G26790.1		0
3.4.23.12		0	GO:0006508,(	AT1G03220.1		0
	0	0	0	AT3G63180.1	ATTKL,TKL	
	0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1		0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1		0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
	0	0	0	AT2G37570.1	SLT1	
	0	0	0	AT2G37570.1	SLT1	
2.7.4.22		K09903	0	AT3G10030.1		0
	0	0	0	AT3G02250.1		0
	0	0	GO:0003723	AT3G21740.1	APO4	
	0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216		K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216		K00555	GO:0008033,(	AT5G15810.1		0
	0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
	0	0	0	AT2G16800.1		0
	0	0	0	AT3G04630.1	WDL1	
	0	0	0	AT3G04630.1	WDL1	
	0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
	0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
	0	0	0	0		0
	0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12		0	GO:0006508,(	AT2G17760.1		0
	0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1		0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.11.1		0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
	0	0	0	AT1G63470.1		0
2.4.2.24		0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
	0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
3.1.1.3		0	GO:0016788	AT4G26790.1		0
3.4.23.12		0	GO:0006508,(	AT1G03220.1		0
	0	0	0	AT3G63180.1	ATTKL,TKL	
	0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1		0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1		0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
	0	0	0	AT2G37570.1	SLT1	
	0	0	0	AT2G37570.1	SLT1	
2.7.4.22		K09903	0	AT3G10030.1		0
	0	0	0	AT3G02250.1		0
	0	0	GO:0003723	AT3G21740.1	APO4	
	0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216		K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216		K00555	GO:0008033,(	AT5G15810.1		0
	0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
	0	0	0	AT2G16800.1		0
	0	0	0	AT3G04630.1	WDL1	

0	0	0	AT3G04630.1	WDL1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
0	0	0	AT4G33200.1	ATXI-I,XI-15,XI-I	
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	0	GO:0007165	AT3G29575.3	AFP3	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.4.22	K09903	0	AT3G10030.1		0
0	0	GO:0055085,(	AT3G18830.1	ATPLT5,ATPMT5,PMT5	
0	0	0	AT3G04630.1	WDL1	
0	0	0	AT3G04630.1	WDL1	
3.1.1.3	0	GO:0016788	AT4G26790.1		0
2.7.11.1	0	GO:0005515	AT1G47890.1	AtRLP7,RLP7	
0	0	0	AT1G63470.1		0
2.4.2.24	0	GO:0016020,(	AT1G27600.2	I9H,IRX9-L	
3.4.23.12	0	GO:0006508,(	AT1G03220.1		0
0	0	0	AT3G63180.1	ATTKL,TKL	
2.7.11.1	0	GO:0005515,(	AT4G20140.1	GSO1	
2.7.1.68	K00889	GO:0046488,(	AT1G77740.1	PIP5K2	
2.7.1.68	K00889	GO:0046488,(	AT1G77740.1	PIP5K2	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT2G37570.1	SLT1	
0	0	0	AT3G02250.1		0
0	K02985	GO:0003723	AT5G35530.1		0
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
2.7.11.1	0	GO:0005515,(	AT3G02130.1	RPK2,TOAD2	
0	0	GO:0003723	AT3G21740.1	APO4	
0	0	GO:0006355,(	AT2G22840.1	AtGRF1,GRF1	
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
2.1.1.216	K00555	GO:0008033,(	AT5G15810.1		0
3.4.23.12	0	GO:0006508,(	AT2G17760.1		0
0	K09874	GO:0016020,(	AT4G10380.1	NIP5;1,NLM6,NLM8	
0	0	0	AT2G16800.1		0
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	GO:0007275	AT2G45190.1	AFO,FIL,YAB1	
0	0	0	0		0
2.7.11.1	0	GO:0005515,(	AT1G68400.1		0
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0

1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1
0	0	0	AT5G17270.1	0
0	0	0	AT5G13210.1	0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF
0	K10956	GO:0016020,(	AT2G34250.1	0
0	0	0	AT1G64770.1	NDF2,NDH45
0	0	0	AT5G17170.1	ENH1
2.7.11.1	0	GO:0006468,(	AT4G02630.1	0
2.7.11.1	0	GO:0006468,(	AT4G02630.1	0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3
0	0	GO:0005515	AT2G46560.1	0
0	0	GO:0005515	AT2G46560.1	0
0	0	0	AT3G23590.1	MED33A,RFR1
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1
0	0	0	AT4G18470.1	SNI1
0	0	0	AT4G18470.1	SNI1
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1
0	0	0	AT4G18470.1	SNI1
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1
0	0	0	AT2G33390.1	0
0	0	0	AT2G33390.1	0
0	0	0	AT2G01770.1	ATVIT1,VIT1
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67
0	0	0	AT2G34670.2	0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1
0	K17968	0	AT4G33100.1	0
0	0	0	AT5G06240.1	emb2735
0	0	0	AT5G06240.1	emb2735
0	0	0	AT4G30700.1	0
2.1.1.163	0	GO:0008168,(	AT1G78140.1	0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1
0	0	0	AT5G17270.1	0
0	0	0	AT5G13210.1	0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF
0	K10956	GO:0016020,(	AT2G34250.1	0
0	0	0	AT1G64770.1	NDF2,NDH45
0	0	0	AT5G17170.1	ENH1
2.7.11.1	0	GO:0006468,(	AT4G02630.1	0
2.7.11.1	0	GO:0006468,(	AT4G02630.1	0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3
0	0	GO:0005515	AT2G46560.1	0

0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,	AT1G78140.1		0
1.11.1.15	0	GO:0055114,	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
0	K02639	GO:0051536,	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0

0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,	AT1G78140.1		0
1.11.1.15	0	GO:0055114,	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
0	K02639	GO:0051536,	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,	AT1G78140.1		0
1.11.1.15	0	GO:0055114,	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0

0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
0	K02639	GO:0051536,	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,	AT1G78140.1		0
1.11.1.15	0	GO:0055114,	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
0	K02639	GO:0051536,	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	

2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
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0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	

0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	

2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	

0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
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0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,	AT1G78140.1		0
1.11.1.15	0	GO:0055114,	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.	K14272	GO:0030170,	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNI	
0	K10956	GO:0016020,	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
0	K02639	GO:0051536,	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0

0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0

0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	

4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,	AT1G78140.1		0
1.11.1.15	0	GO:0055114,	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
2.7.11.1	0	GO:0006468,	AT4G02630.1		0
0	K02639	GO:0051536,	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,	AT2G45550.1	CYP76C4	
0	0	GO:0016021,	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0

0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT2G34670.2		0
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT4G30700.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G17270.1		0
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	

2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
2.7.11.1	0	GO:0006468,(	AT4G02630.1		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	0	AT3G23590.1	MED33A,RFR1	
2.4.1.18	K00700	GO:0005975,(	AT3G20440.2	BE1,EMB2729	
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT4G18470.1	SNI1	
0	0	0	AT4G18470.1	SNI1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
4.1.2.27	0	GO:0030170,(	AT1G27980.1	ATDPL1,DPL1	
0	0	0	AT4G18470.1	SNI1	
1.14.13.152	0	GO:0055114,(	AT2G45550.1	CYP76C4	
0	0	GO:0016021,(	AT1G28230.1	ATPUP1,PUP1	
0	0	0	AT2G33390.1		0
0	0	0	AT2G33390.1		0
0	0	0	AT2G01770.1	ATVIT1,VIT1	
0	K00507	GO:0006629	AT3G15850.1	ADS3,FAD5,FADB,JB67	
0	0	0	AT5G17270.1		0
0	0	0	AT2G34670.2		0
0	K02639	GO:0051536,(	AT2G27510.1	ATFD3,FD3	
0	0	GO:0006355,(	AT3G54320.1	ASML1,ATWRI1,WRI,WRI1	
0	K17968	0	AT4G33100.1		0
0	0	0	AT5G06240.1	emb2735	
0	0	0	AT5G06240.1	emb2735	
0	0	GO:0008152,(	AT5G63380.1		0
0	0	0	AT4G30700.1		0
0	0	0	AT1G14780.1		0
0	0	0	AT1G14780.1		0
2.1.1.163	0	GO:0008168,(	AT1G78140.1		0
1.11.1.15	0	GO:0055114,(	AT1G65980.1	TPX1	
0	0	0	AT5G13210.1		0
2.3.2.2,2.6.1.4	K14272	GO:0030170,(	AT1G70580.2	AOAT2,GGT2	
2.8.1.7,4.4.1.1	0	0	AT1G08490.1	ATCPNIFS,ATNFS2,ATSUFS,CPNIF	
0	K10956	GO:0016020,(	AT2G34250.1		0
0	K07300	GO:0055085,(	AT2G38170.3	ATCAX1,CAX1,RCI4	
0	0	0	AT1G64770.1	NDF2,NDH45	
0	0	0	AT5G17170.1	ENH1	
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT2G46560.1		0
0	0	GO:0005515	AT4G11610.1		0
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	

0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	

0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0

1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0

1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0

6.5.1.4	0	GO:0006396	AT5G22100.1	0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5
0	0	0	AT2G35330.1	0
0	0	0	AT2G35330.1	0
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1
0	0	0	AT2G35330.1	0
0	0	GO:0006629	AT4G16070.1	0
0	0	GO:0003677,	AT1G70510.1	ATK1,KNAT2
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
6.3.2.19	0	GO:0008270,	AT5G60820.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
0	0	0	AT5G46220.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1	0
2.4.1.198	K03858	GO:0017176	AT4G35530.1	0
0	0	0	AT2G01060.1	0
0	0	0	AT3G60890.2	ZPR2
0	K14488	GO:0009733	AT4G34760.1	0
0	0	GO:0043531	AT1G63350.1	0
0	0	GO:0043531	AT1G63350.1	0
0	0	0	AT1G22770.1	FB,GI
0	0	0	AT1G22770.1	FB,GI
0	0	0	AT1G22770.1	FB,GI
3.6.3.1	0	GO:0046872,	AT1G68710.1	0
0	0	GO:0005515	AT2G43500.1	0
0	0	GO:0005515	AT2G43500.1	0
3.6.3.1	0	GO:0046872,	AT1G68710.1	0
0	0	0	AT1G22770.1	FB,GI
3.1.1.11	K01051	GO:0004857,	AT4G33230.1	0
0	0	0	AT3G51290.2	0
0	0	0	AT1G03870.1	FLA9
0	0	GO:0046983	AT5G08130.5	BIM1
0	0	GO:0046983	AT5G08130.5	BIM1
0	0	0	AT3G17430.1	0
0	0	0	AT3G17430.1	0
1.11.1.7	K00430	GO:0055114,	AT5G05340.1	0
0	K14300	0	AT2G05120.1	0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4

2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4
0	0	0	AT1G09020.1	ATSNF4,SNF4
0	0	0	AT1G09020.1	ATSNF4,SNF4
2.7.1.67	0	GO:0016773	AT1G26270.1	0
0	0	0	AT1G76405.2	0
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD
0	0	GO:0005515	AT2G22125.1	CSI1
0	0	GO:0005515	AT2G22125.1	CSI1
6.5.1.4	0	GO:0006396	AT5G22100.1	0
6.5.1.4	0	GO:0006396	AT5G22100.1	0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5
0	0	0	AT2G35330.1	0
0	0	0	AT2G35330.1	0
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1
0	0	0	AT2G35330.1	0
0	0	GO:0006629	AT4G16070.1	0
0	0	GO:0003677,	AT1G70510.1	ATK1,KNAT2
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
6.3.2.19	0	GO:0008270,	AT5G60820.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
0	0	0	AT5G46220.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1	0
2.4.1.198	K03858	GO:0017176	AT4G35530.1	0
0	0	0	AT2G01060.1	0
0	0	0	AT3G60890.2	ZPR2
0	K14488	GO:0009733	AT4G34760.1	0
0	0	GO:0043531	AT1G63350.1	0
0	0	GO:0043531	AT1G63350.1	0
0	0	0	AT1G22770.1	FB,GI
0	0	0	AT1G22770.1	FB,GI
0	0	0	AT1G22770.1	FB,GI
3.6.3.1	0	GO:0046872,	AT1G68710.1	0
0	0	GO:0005515	AT2G43500.1	0
0	0	GO:0005515	AT2G43500.1	0
3.6.3.1	0	GO:0046872,	AT1G68710.1	0
0	0	0	AT1G22770.1	FB,GI

3.1.1.11	K01051	GO:0004857,	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0

0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0

1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0

0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	

3.6.4.12		0	GO:0016787,	AT2G28290.1	CHR3,SYD	
	0	0	GO:0005515	AT2G22125.1	CSI1	
	0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4		0	GO:0006396	AT5G22100.1		0
6.5.1.4		0	GO:0006396	AT5G22100.1		0
	0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
	0	0	0	AT2G35330.1		0
	0	0	0	AT2G35330.1		0
2.4.1.12		0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
	0	0	0	AT2G35330.1		0
	0	0	GO:0006629	AT4G16070.1		0
	0	0	GO:0003677,	AT1G70510.1	ATK1,KNAT2	
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
6.3.2.19		0	GO:0008270,	AT5G60820.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
	0	0	0	AT5G46220.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.11.1.7		K00430	GO:0055114,	AT4G33870.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.11.1.7		K00430	GO:0055114,	AT4G33870.1		0
2.4.1.198		K03858	GO:0017176	AT4G35530.1		0
	0	0	0	AT2G01060.1		0
	0	0	0	AT3G60890.2	ZPR2	
	0	K14488	GO:0009733	AT4G34760.1		0
	0	0	GO:0043531	AT1G63350.1		0
	0	0	GO:0043531	AT1G63350.1		0
	0	0	0	AT1G22770.1	FB,GI	
	0	0	0	AT1G22770.1	FB,GI	
	0	0	0	AT1G22770.1	FB,GI	
3.6.3.1		0	GO:0046872,	AT1G68710.1		0
	0	0	GO:0005515	AT2G43500.1		0
	0	0	GO:0005515	AT2G43500.1		0
3.6.3.1		0	GO:0046872,	AT1G68710.1		0
	0	0	0	AT1G22770.1	FB,GI	
3.1.1.11		K01051	GO:0004857,	AT4G33230.1		0
	0	0	0	AT3G51290.2		0
	0	0	0	AT1G03870.1	FLA9	
	0	0	GO:0046983	AT5G08130.5	BIM1	
	0	0	GO:0046983	AT5G08130.5	BIM1	
	0	0	0	AT3G17430.1		0

0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,	AT1G68710.1		0

0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0

2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0

6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	

0	0	0	AT2G35330.1	0
0	0	0	AT2G35330.1	0
2.4.1.12	0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1
0	0	0	AT2G35330.1	0
0	0	GO:0006629	AT4G16070.1	0
0	0	GO:0003677,	AT1G70510.1	ATK1,KNAT2
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
6.3.2.19	0	GO:0008270,	AT5G60820.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
0	0	0	AT5G46220.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.1.1.330	0	0	AT5G02540.1	0
1.11.1.7	K00430	GO:0055114,	AT4G33870.1	0
2.4.1.198	K03858	GO:0017176	AT4G35530.1	0
0	0	0	AT2G01060.1	0
0	0	0	AT3G60890.2	ZPR2
0	K14488	GO:0009733	AT4G34760.1	0
0	0	GO:0043531	AT1G63350.1	0
0	0	GO:0043531	AT1G63350.1	0
0	0	0	AT1G22770.1	FB,GI
0	0	0	AT1G22770.1	FB,GI
0	0	0	AT1G22770.1	FB,GI
3.6.3.1	0	GO:0046872,	AT1G68710.1	0
0	0	GO:0005515	AT2G43500.1	0
0	0	GO:0005515	AT2G43500.1	0
3.6.3.1	0	GO:0046872,	AT1G68710.1	0
0	0	0	AT1G22770.1	FB,GI
3.1.1.11	K01051	GO:0004857,	AT4G33230.1	0
0	0	0	AT3G51290.2	0
0	0	0	AT1G03870.1	FLA9
0	0	GO:0046983	AT5G08130.5	BIM1
0	0	GO:0046983	AT5G08130.5	BIM1
0	0	0	AT3G17430.1	0
0	0	0	AT3G17430.1	0
1.11.1.7	K00430	GO:0055114,	AT5G05340.1	0
0	K14300	0	AT2G05120.1	0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4
0	0	0	AT1G09020.1	ATSNF4,SNF4

	0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67		0	GO:0016773	AT1G26270.1		0
	0	0	0	AT1G76405.2		0
3.6.4.12		0	GO:0016787,	AT2G28290.1	CHR3,SYD	
3.6.4.12		0	GO:0016787,	AT2G28290.1	CHR3,SYD	
	0	0	GO:0005515	AT2G22125.1	CSI1	
	0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4		0	GO:0006396	AT5G22100.1		0
6.5.1.4		0	GO:0006396	AT5G22100.1		0
	0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
	0	0	0	AT2G35330.1		0
	0	0	0	AT2G35330.1		0
2.4.1.12		0	GO:0030244,	AT4G24010.1	ATCSLG1,CSLG1	
	0	0	0	AT2G35330.1		0
	0	0	GO:0006629	AT4G16070.1		0
	0	0	GO:0003677,	AT1G70510.1	ATK1,KNAT2	
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
6.3.2.19		0	GO:0008270,	AT5G60820.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
	0	0	0	AT5G46220.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.11.1.7		K00430	GO:0055114,	AT4G33870.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.1.1.330		0	0	AT5G02540.1		0
1.11.1.7		K00430	GO:0055114,	AT4G33870.1		0
2.4.1.198		K03858	GO:0017176	AT4G35530.1		0
	0	0	0	AT2G01060.1		0
	0	0	0	AT3G60890.2	ZPR2	
	0	K14488	GO:0009733	AT4G34760.1		0
	0	0	GO:0043531	AT1G63350.1		0
	0	0	GO:0043531	AT1G63350.1		0
	0	0	0	AT1G22770.1	FB,GI	
	0	0	0	AT1G22770.1	FB,GI	
	0	0	0	AT1G22770.1	FB,GI	
3.6.3.1		0	GO:0046872,	AT1G68710.1		0
	0	0	GO:0005515	AT2G43500.1		0
	0	0	GO:0005515	AT2G43500.1		0
3.6.3.1		0	GO:0046872,	AT1G68710.1		0
	0	0	0	AT1G22770.1	FB,GI	
3.1.1.11		K01051	GO:0004857,	AT4G33230.1		0
	0	0	0	AT3G51290.2		0

0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
0	0	0	AT2G35330.1		0
0	0	0	AT2G35330.1		0
2.4.1.12	0	GO:0030244,(	AT4G24010.1	ATCSLG1,CSLG1	
0	0	0	AT2G35330.1		0
0	0	GO:0006629	AT4G16070.1		0
0	0	GO:0003677,(	AT1G70510.1	ATK1,KNAT2	
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
6.3.2.19	0	GO:0008270,(	AT5G60820.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
0	0	0	AT5G46220.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.1.1.330	0	0	AT5G02540.1		0
1.11.1.7	K00430	GO:0055114,(	AT4G33870.1		0
2.4.1.198	K03858	GO:0017176	AT4G35530.1		0
0	0	0	AT2G01060.1		0
0	0	0	AT3G60890.2	ZPR2	
0	K14488	GO:0009733	AT4G34760.1		0
0	0	GO:0043531	AT1G63350.1		0
0	0	GO:0043531	AT1G63350.1		0

0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
0	0	0	AT1G22770.1	FB,GI	
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	GO:0005515	AT2G43500.1		0
0	0	GO:0005515	AT2G43500.1		0
3.6.3.1	0	GO:0046872,(	AT1G68710.1		0
0	0	0	AT1G22770.1	FB,GI	
3.1.1.11	K01051	GO:0004857,(	AT4G33230.1		0
0	0	0	AT3G51290.2		0
0	0	0	AT1G03870.1	FLA9	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	GO:0046983	AT5G08130.5	BIM1	
0	0	0	AT3G17430.1		0
0	0	0	AT3G17430.1		0
1.11.1.7	K00430	GO:0055114,(	AT5G05340.1		0
0	K14300	0	AT2G05120.1		0
6.3.2.19	K10590	GO:0004842	AT5G02880.1	UPL4	
2.1.2.1	K00600	GO:0016740	AT4G13930.1	SHM4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
0	0	0	AT1G09020.1	ATSNF4,SNF4	
2.7.1.67	0	GO:0016773	AT1G26270.1		0
0	0	0	AT1G76405.2		0
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
3.6.4.12	0	GO:0016787,(	AT2G28290.1	CHR3,SYD	
0	0	GO:0005515	AT2G22125.1	CSI1	
0	0	GO:0005515	AT2G22125.1	CSI1	
6.5.1.4	0	GO:0006396	AT5G22100.1		0
6.5.1.4	0	GO:0006396	AT5G22100.1		0
0	0	GO:0046983	AT2G20180.2	PIF1,PIL5	
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0	0	0	AT2G35330.1		0
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NAC (No Apical Meristem) domain transcriptional regul	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
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NAC (No Apical Meristem) domain transcriptional regul	Phvul.011G16	PTHR31744:S	Phvul.011G16
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NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
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NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
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NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
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NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
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NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
NAC (No Apical Meristem) domain transcriptional regu	Phvul.005G07	PTHR31744:S	Phvul.005G07
NAC (No Apical Meristem) domain transcriptional regu	Phvul.011G16	PTHR31744:S	Phvul.011G16
NAC domain containing protein 1	Phvul.005G05	PTHR31744:S	Phvul.005G05
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16

protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//	Phvul.011G06

S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:S	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06

UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:SI	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G16	PTHR22835//I	Phvul.006G16
protamine P1 family protein	Phvul.007G16	PTHR33448:SI	Phvul.007G16
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
UDP-XYL synthase 6	Phvul.011G06	PTHR10366//I	Phvul.011G06
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.004G17	PTHR10509//I	Phvul.004G17
TCP family transcription factor	Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//I	Phvul.005G00
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	0	0	Phvul.006G08
cation calcium exchanger 4	Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor	Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//I	Phvul.005G00
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	0	0	Phvul.006G08
cation calcium exchanger 4	Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor	Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//I	Phvul.005G00
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	0	0	Phvul.006G08
cation calcium exchanger 4	Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor	Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//I	Phvul.005G00

	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//I	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//I	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//I	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//I	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:SI	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:SI	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:SI	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//I	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14

	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	0	0	Phvul.006G08
cation calcium exchanger 4		Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor		Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein		Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6		Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein		Phvul.005G00	PTHR22835//	Phvul.005G00
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
	0	Phvul.008G14	PF17035 - Bro	Phvul.008G14

0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	0	0	Phvul.006G08
cation calcium exchanger 4	Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor	Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//	Phvul.005G00
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	0	0	Phvul.006G08
cation calcium exchanger 4	Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor	Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//	Phvul.005G00
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	0	0	Phvul.006G08
cation calcium exchanger 4	Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor	Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//	Phvul.005G00
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	0	0	Phvul.006G08
cation calcium exchanger 4	Phvul.010G12	PTHR12266:S	Phvul.010G12
TCP family transcription factor	Phvul.010G08	PTHR31072:S	Phvul.010G08
UDP-Glycosyltransferase superfamily protein	Phvul.002G32	2.4.1.227 - Un	Phvul.002G32
paralog of ARC6	Phvul.004G13	PTHR33925:S	Phvul.004G13
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.005G00	PTHR22835//	Phvul.005G00
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
0	Phvul.008G14	PF17035 - Bro	Phvul.008G14
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
0	0	0	Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 - (	Phvul.008G07
chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:S	Phvul.008G27
0	0	0	Phvul.003G06

Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI/	Phvul.008G06
peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CY	Phvul.003G24	K05864 - pept	Phvul.003G24
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
0	0	0	Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 -	Phvul.008G07
chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:S	Phvul.008G27
0	0	0	Phvul.003G06
Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI/	Phvul.008G06
peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CY	Phvul.003G24	K05864 - pept	Phvul.003G24
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
0	0	0	Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 -	Phvul.008G07
chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:S	Phvul.008G27
0	0	0	Phvul.003G06
Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI/	Phvul.008G06
peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CY	Phvul.003G24	K05864 - pept	Phvul.003G24
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07

0	0	0	Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 - (	Phvul.008G07
chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:S	Phvul.008G27
0	0	0	Phvul.003G06
Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI/	Phvul.008G06
peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CY	Phvul.003G24	K05864 - pept	Phvul.003G24
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
0	0	0	Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 - (	Phvul.008G07
chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:S	Phvul.008G27
0	0	0	Phvul.003G06
Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
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S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
0	0	0	Phvul.011G11
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chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
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S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10

cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
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cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
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cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
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K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
0	0	0	Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 -	Phvul.008G07

chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:S	Phvul.008G27
0	0	0	Phvul.003G06
Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI	Phvul.008G06
peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CY	Phvul.003G24	K05864 - pept	Phvul.003G24
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
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Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
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0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
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cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 -	Phvul.008G07
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0	0	0	Phvul.003G06
Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI	Phvul.008G06
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S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
0	0	0	Phvul.005G08
K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08

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K-box region and MADS-box transcription factor family	Phvul.009G13	PTHR11945:S	Phvul.009G13
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
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S-adenosyl-L-methionine-dependent methyltransferas	Phvul.011G10	PTHR10108//	Phvul.011G10
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gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
gigantea protein (GI)	Phvul.007G08	K12124 - GIG	Phvul.007G08
Homeobox-leucine zipper family protein / lipid-binding	Phvul.011G07	PF08670 - ME	Phvul.011G07
cell division cycle protein 48-related / CDC48-related	Phvul.011G05	PTHR23069 -	Phvul.011G05
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PF01657//PF	Phvul.008G07
0	0	0	Phvul.011G11
cysteine-rich RLK (RECEPTOR-like protein kinase) 25	Phvul.008G07	PTHR32099 -	Phvul.008G07
chloride channel F	Phvul.005G00	PTHR11689:S	Phvul.005G00
nodulin MtN21 /EamA-like transporter family protein	Phvul.002G07	KOG4510 - Pe	Phvul.002G07
nodulin MtN21 /EamA-like transporter family protein	Phvul.002G07	KOG4510 - Pe	Phvul.002G07
nodulin MtN21 /EamA-like transporter family protein	Phvul.002G07	KOG4510 - Pe	Phvul.002G07
serine acetyltransferase 2;2	Phvul.008G27	PTHR23416:S	Phvul.008G27
0	0	0	Phvul.003G06
Mitochondrial substrate carrier family protein	Phvul.001G24	K13354 - solu	Phvul.001G24
transcription regulatory protein SNF2, putative	Phvul.008G06	K11647 - SWI	Phvul.008G06
peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CY	Phvul.003G24	K05864 - pept	Phvul.003G24
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G13	PTHR10108:S	Phvul.009G13
receptor like protein 7	Phvul.004G09	PF00560//PF	Phvul.004G09
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WVD2-like 1	Phvul.006G10	PTHR31358:S	Phvul.006G10
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Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:S	Phvul.010G07
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0	0	0	Phvul.008G12
myosin, putative	Phvul.001G03	PTHR13140:S	Phvul.001G03
Eukaryotic aspartyl protease family protein	Phvul.002G10	PTHR13683:S	Phvul.002G10
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Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14	PTHR10896:S	Phvul.009G14
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myosin, putative	Phvul.001G03	PTHR13140:SI	Phvul.001G03
Eukaryotic aspartyl protease family protein	Phvul.002G10	PTHR13683:SI	Phvul.002G10
ABI five binding protein 3	Phvul.008G03	PTHR31413:SI	Phvul.008G03
Leucine-rich repeat transmembrane protein kinase	Phvul.009G24	PF00069//PFC	Phvul.009G24
receptor like protein 7	Phvul.004G09	PF00560//PFC	Phvul.004G09
AT hook motif DNA-binding family protein	Phvul.002G15	PTHR31500:SI	Phvul.002G15
Nucleotide-diphospho-sugar transferases superfamily p	Phvul.009G14	PTHR10896:SI	Phvul.009G14
polyol/monosaccharide transporter 5	Phvul.011G04	PTHR23500:SI	Phvul.011G04
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02	PTHR22835//I	Phvul.006G02
Eukaryotic aspartyl protease family protein	Phvul.006G09	PTHR13683:SI	Phvul.006G09
TIC-like	Phvul.001G15	PTHR34798:SI	Phvul.001G15
Ribosomal protein S3 family protein	Phvul.007G23	K02985 - smal	Phvul.007G23
receptor-like protein kinase 2	Phvul.004G03	PTHR27000:SI	Phvul.004G03
receptor-like protein kinase 2	Phvul.004G03	PTHR27000:SI	Phvul.004G03
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:SI	Phvul.007G15
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:SI	Phvul.007G15
aspartate/glutamate/uridylate kinase family protein	Phvul.007G10	PTHR21499//I	Phvul.007G10
O-fucosyltransferase family protein	Phvul.008G15	PF10250 - GDI	Phvul.008G15
Arabidopsis thaliana protein of unknown function (DUI	Phvul.005G11	PTHR10388:SI	Phvul.005G11
growth-regulating factor 1	Phvul.001G03	PTHR31602:SI	Phvul.001G03
N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tRI	Phvul.004G04
N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tRI	Phvul.004G04
NOD26-like intrinsic protein 5;1	Phvul.007G08	PTHR19139:SI	Phvul.007G08
high-affinity nickel-transport family protein	Phvul.009G11	PTHR33876:SI	Phvul.009G11
WVD2-like 1	Phvul.006G10	PTHR31358:SI	Phvul.006G10

WVD2-like 1	Phvul.006G10	PTHR31358:S	Phvul.006G10
Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:S	Phvul.010G07
Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:S	Phvul.010G07
0	0	0	Phvul.008G12
myosin, putative	Phvul.001G03	PTHR13140:S	Phvul.001G03
Eukaryotic aspartyl protease family protein	Phvul.002G10	PTHR13683:S	Phvul.002G10
ABI five binding protein 3	Phvul.008G03	PTHR31413:S	Phvul.008G03
Leucine-rich repeat transmembrane protein kinase	Phvul.009G24	PF00069//PF	Phvul.009G24
aspartate/glutamate/uridylate kinase family protein	Phvul.007G10	PTHR21499//	Phvul.007G10
polyol/monosaccharide transporter 5	Phvul.011G04	PTHR23500:S	Phvul.011G04
WVD2-like 1	Phvul.006G10	PTHR31358:S	Phvul.006G10
WVD2-like 1	Phvul.006G10	PTHR31358:S	Phvul.006G10
GDSL-like Lipase/Acylhydrolase superfamily protein	Phvul.006G02	PTHR22835//	Phvul.006G02
receptor like protein 7	Phvul.004G09	PF00560//PF	Phvul.004G09
AT hook motif DNA-binding family protein	Phvul.002G15	PTHR31500:S	Phvul.002G15
Nucleotide-diphospho-sugar transferases superfamily	Phvul.009G14	PTHR10896:S	Phvul.009G14
Eukaryotic aspartyl protease family protein	Phvul.006G09	PTHR13683:S	Phvul.006G09
TIC-like	Phvul.001G15	PTHR34798:S	Phvul.001G15
Leucine-rich repeat transmembrane protein kinase	Phvul.009G24	PF00069//PF	Phvul.009G24
phosphatidylinositol-4-phosphate 5-kinase 2	Phvul.009G12	PTHR23086:S	Phvul.009G12
phosphatidylinositol-4-phosphate 5-kinase 2	Phvul.009G12	PTHR23086:S	Phvul.009G12
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:S	Phvul.007G15
HSP20-like chaperones superfamily protein	Phvul.007G15	PTHR33981:S	Phvul.007G15
O-fucosyltransferase family protein	Phvul.008G15	PF10250 - GD	Phvul.008G15
Ribosomal protein S3 family protein	Phvul.007G23	K02985 - smal	Phvul.007G23
receptor-like protein kinase 2	Phvul.004G03	PTHR27000:S	Phvul.004G03
receptor-like protein kinase 2	Phvul.004G03	PTHR27000:S	Phvul.004G03
Arabidopsis thaliana protein of unknown function (DU	Phvul.005G11	PTHR10388:S	Phvul.005G11
growth-regulating factor 1	Phvul.001G03	PTHR31602:S	Phvul.001G03
N2,N2-dimethylguanosine tRNA methyltransferase	Phvul.004G04	2.1.1.216 - tR	Phvul.004G04
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Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:S	Phvul.010G07
Plant-specific transcription factor YABBY family protein	Phvul.010G07	PTHR31675:S	Phvul.010G07
0	0	0	Phvul.008G12
leucine-rich repeat transmembrane protein kinase fam	Phvul.007G02	PF00560//PF	Phvul.007G02
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03

thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 - I	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TPF	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:SI	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:SI	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 - I	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:SI	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:SI	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:SI	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//I	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:SI	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
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chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:SI	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 - I	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:SI	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11

transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:SI	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:SI	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//I	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:SI	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//I	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 - I	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:SI	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:SI	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 - I	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:SI	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:SI	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:SI	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//I	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:SI	Phvul.009G03
0	0	0	Phvul.L00244

0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
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ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
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dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
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0	0	0	Phvul.L00244
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vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
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embryo defective 2735	0	0	Phvul.001G19
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Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
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Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16

Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
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SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
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transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
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REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
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cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SN	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SN	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SN	0	0	Phvul.003G05
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purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L0024
0	0	0	Phvul.L0024
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ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15

Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07

fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
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ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
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REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
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cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SN	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SN	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SN	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L0024
0	0	0	Phvul.L0024
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
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0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
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dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SN	0	0	Phvul.003G05
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purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L0244
0	0	0	Phvul.L0244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
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Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
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chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//I	Phvul.005G00

negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:SI	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//I	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 - I	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:SI	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:SI	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 - I	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
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ferredoxin 3	Phvul.007G02	PTHR19370:SI	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:SI	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:SI	Phvul.006G04
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dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:SI	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21

Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP2	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransfera	Phvul.009G03	PTHR10108//I	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 - I	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
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chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
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NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 - I	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
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ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 - I	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
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dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
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Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
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ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
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REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
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embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05

dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L0024
0	0	0	Phvul.L0024
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L0024
0	0	0	Phvul.L0024
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07

embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03

Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
Protein kinase superfamily protein	Phvul.002G01	2.7.11.1 - Non	Phvul.002G01
ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
REF4-related 1	Phvul.006G15	PTHR33739:S	Phvul.006G15
Alpha amylase family protein	Phvul.006G04	PTHR10357:S	Phvul.006G04
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
dihydrosphingosine phosphate lyase	Phvul.008G01	4.1.2.27 - Sph	Phvul.008G01
negative regulator of systemic acquired resistance (SNI	0	0	Phvul.003G05
cytochrome P450, family 76, subfamily C, polypeptide	Phvul.007G10	1.14.13.152 -	Phvul.007G10
purine permease 1	Phvul.009G03	PTHR31376:S	Phvul.009G03
0	0	0	Phvul.L00244
0	0	0	Phvul.L00244
vacuolar iron transporter 1	Phvul.008G07	KOG4473 - Un	Phvul.008G07
fatty acid desaturase 5	Phvul.010G15	K00507 - stea	Phvul.010G15
Protein prenylyltransferase superfamily protein	Phvul.009G16	PF13414 - TP	Phvul.009G16
Protein of unknown function (DUF630 and DUF632)	Phvul.009G21	PF04782 - Pro	Phvul.009G21
ferredoxin 3	Phvul.007G02	PTHR19370:S	Phvul.007G02
Integrase-type DNA-binding superfamily protein	Phvul.008G04	PF00847 - AP	Phvul.008G04
0	Phvul.009G07	K17968 - TRIA	Phvul.009G07
embryo defective 2735	0	0	Phvul.001G19
embryo defective 2735	0	0	Phvul.001G19
AMP-dependent synthetase and ligase family protein	Phvul.009G16	PTHR24096:S	Phvul.009G16
Pentatricopeptide repeat (PPR) superfamily protein	Phvul.003G15	PF01535//PF1	Phvul.003G15
MAC/Perforin domain-containing protein	Phvul.L00374	PF01823 - MA	Phvul.L00374
MAC/Perforin domain-containing protein	Phvul.L00374	PF01823 - MA	Phvul.L00374
S-adenosyl-L-methionine-dependent methyltransferas	Phvul.009G03	PTHR10108//	Phvul.009G03
thioredoxin-dependent peroxidase 1	Phvul.004G16	PTHR10430 -	Phvul.004G16
Uncharacterised conserved protein UCP015417, vWA	Phvul.002G11	PTHR31373:S	Phvul.002G11
alanine-2-oxoglutarate aminotransferase 2	Phvul.002G15	2.6.1.4 - Glyci	Phvul.002G15
chloroplastic NIFS-like cysteine desulfurase	Phvul.002G27	4.4.1.16 - Sele	Phvul.002G27
SecY protein transport family protein	Phvul.011G16	K10956 - prot	Phvul.011G16
cation exchanger 1	Phvul.006G06	K07300 - Ca2	Phvul.006G06
NDH-dependent cyclic electron flow 1	Phvul.001G11	PTHR11122:S	Phvul.001G11
rubredoxin family protein	Phvul.002G03	PTHR17130 -	Phvul.002G03
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
transducin family protein / WD-40 repeat family protei	Phvul.010G11	PTHR13950 -	Phvul.010G11
C2 calcium/lipid-binding plant phosphoribosyltransfera	Phvul.002G15	PTHR10024:S	Phvul.002G15
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18

basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08

gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15

NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Perc	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:SI	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:SI	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//I	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//I	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:SI	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:SI	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:SI	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:SI	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:SI	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:SI	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//I	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//I	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Perc	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:SI	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//I	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:SI	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:SI	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:SI	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//I	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//I	Phvul.003G10
binding	Phvul.002G26	PTHR23315:SI	Phvul.002G26
binding	Phvul.002G26	PTHR23315:SI	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:SI	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//I	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//I	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//I	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
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Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29

RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:SF	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SF	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SF	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SF	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:SF	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SF	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
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SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:SF	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:SF	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:SF	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superf	Phvul.009G22	PTHR31707:SF	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:SF	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:SF	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:SF	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:SF	Phvul.007G16

serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
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gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
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ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - pho	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
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gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08

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Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
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ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
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P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
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RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26

Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
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Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
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Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
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Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16

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Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
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Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
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gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
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ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
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RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
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cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
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RING/U-box superfamily protein	Phvul.003G18	PTHR22763:SI	Phvul.003G18
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//I	Phvul.006G16
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Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
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gigantea protein (GI)	Phvul.004G08	K12124 - GIG/	Phvul.004G08
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ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
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Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//I	Phvul.003G12
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Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:SI	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//I	Phvul.001G26
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Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:SI	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//I	Phvul.003G10

P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//I	Phvul.003G10
binding	Phvul.002G26	PTHR23315:SI	Phvul.002G26
binding	Phvul.002G26	PTHR23315:SI	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA :	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA :	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:SI	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//I	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//I	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//I	Phvul.007G20
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Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20

Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:SI	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:SI	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG/	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:SI	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unkr	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:SI	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:SI	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:SI	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//I	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//I	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:SI	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//I	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:SI	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:SI	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:SI	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//I	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//I	Phvul.003G10
binding	Phvul.002G26	PTHR23315:SI	Phvul.002G26
binding	Phvul.002G26	PTHR23315:SI	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA :	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA :	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:SI	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//I	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:SI	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//I	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//I	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:SI	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//I	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:SI	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05

phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
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Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases s	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15

RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
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Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15

RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
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gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
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ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
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Plant invertase/pectin methylesterase inhibitor superf	Phvul.009G22	PTHR31707:S	Phvul.009G22
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Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
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Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09

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cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
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NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
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Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10

FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07

gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
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Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15

Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
myb-like HTH transcriptional regulator family protein	Phvul.008G10	PF14379 - MY	Phvul.008G10
protein binding	Phvul.008G07	PTHR33601:S	Phvul.008G07
SAUR-like auxin-responsive protein family	Phvul.003G26	PTHR31374:S	Phvul.003G26
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Plant invertase/pectin methylesterase inhibitor superf	Phvul.009G22	PTHR31707:S	Phvul.009G22
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
FASCICLIN-like arabinoogalactan 9	Phvul.005G09	PTHR32077:S	Phvul.005G09
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
basic helix-loop-helix (bHLH) DNA-binding superfamily	Phvul.003G18	PTHR12565:S	Phvul.003G18
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
0	0	0	Phvul.009G00
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
P-loop containing nucleoside triphosphate hydrolases	Phvul.003G10	PTHR10799//	Phvul.003G10
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
binding	Phvul.002G26	PTHR23315:S	Phvul.002G26
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
RNA cyclase family protein	Phvul.002G29	6.5.1.4 - RNA	Phvul.002G29
phytochrome interacting factor 3-like 5	Phvul.007G15	PTHR12565:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
cellulose synthase like G1	Phvul.005G00	PTHR13301//	Phvul.005G00
RING/U-box superfamily protein	Phvul.002G00	PTHR10044:S	Phvul.002G00
Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3	Phvul.008G24	PTHR21493//	Phvul.008G24
KNOTTED-like from Arabidopsis thaliana 2	Phvul.007G20	PTHR11850//	Phvul.007G20

NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
RING/U-box superfamily protein	Phvul.003G18	PTHR22763:S	Phvul.003G18
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Protein of unknown function (DUF616)	Phvul.006G16	PTHR12956//	Phvul.006G16
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
NAD(P)-binding Rossmann-fold superfamily protein	Phvul.007G15	PTHR24320:S	Phvul.007G15
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Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
phosphatidylinositolglycan-related	Phvul.002G11	K03858 - phos	Phvul.002G11
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Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
gigantea protein (GI)	Phvul.004G08	K12124 - GIG	Phvul.004G08
Peroxidase superfamily protein	Phvul.006G07	1.11.1.7 - Per	Phvul.006G07
Nucleoporin, Nup133/Nup155-like	Phvul.008G28	K14300 - nucl	Phvul.008G28
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Plant invertase/pectin methylesterase inhibitor superfa	Phvul.009G22	PTHR31707:S	Phvul.009G22
homolog of yeast sucrose nonfermenting 4	Phvul.006G09	PTHR13780:S	Phvul.006G09
Protein of unknown function (DUF630) ;Protein of unk	Phvul.002G10	PF04782 - Pro	Phvul.002G10
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Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Nucleotide-sugar transporter family protein	Phvul.003G12	PTHR11132//	Phvul.003G12
Peroxidase superfamily protein	Phvul.005G05	1.11.1.7 - Per	Phvul.005G05
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Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
Disease resistance protein (CC-NBS-LRR class) family	Phvul.008G07	PTHR23155//	Phvul.008G07
ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15

ATPase E1-E2 type family protein / haloacid dehalogen	Phvul.009G20	K01530 - phos	Phvul.009G20
Plant regulator RWP-RK family protein	Phvul.005G15	PTHR32002:S	Phvul.005G15
Leucine-rich repeat transmembrane protein kinase fam	Phvul.009G11	2.7.11.1 - Non	Phvul.009G11
heavy metal atpase 1	Phvul.003G24	PTHR24093:S	Phvul.003G24
Polynucleotide adenylyltransferase family protein	Phvul.002G28	PTHR13734:S	Phvul.002G28
Polynucleotide adenylyltransferase family protein	Phvul.002G28	PTHR13734:S	Phvul.002G28
Polynucleotide adenylyltransferase family protein	Phvul.002G28	PTHR13734:S	Phvul.002G28
sucrose phosphate synthase 1F	Phvul.003G17	PTHR12526//	Phvul.003G17
Tetratricopeptide repeat (TPR)-like superfamily protein	Phvul.011G17	PF01535//PF1	Phvul.011G17
dolichol phosphate-mannose biosynthesis regulatory p	Phvul.003G28	K09658 - dolic	Phvul.003G28
ubiquitin-protein ligase 4	Phvul.007G16	PTHR11254:S	Phvul.007G16
Phosphatidylinositol 3- and 4-kinase family protein	Phvul.003G03	PTHR15245:S	Phvul.003G03
serine hydroxymethyltransferase 4	Phvul.001G26	PTHR11680//	Phvul.001G26
CRINKLY4 related 3	Phvul.001G24	PTHR27003:S	Phvul.001G24
cation exchanger 1	Phvul.006G06	K07300 - Ca2	Phvul.006G06
UDP-Glycosyltransferase superfamily protein	Phvul.008G14	PTHR11926:S	Phvul.008G14

NAME	DESCRIPTION
RNA biosynth	transcription factor (NAC) (original description: pacid=37145328 transcript=Phvul.00
RNA biosynth	transcription factor (NAC) (original description: pacid=37148955 transcript=Phvul.00
RNA biosynth	transcription factor (NAC) (original description: pacid=37145328 transcript=Phvul.00
RNA biosynth	transcription factor (NAC) (original description: pacid=37148955 transcript=Phvul.00
RNA biosynth	transcription factor (NAC) (original description: pacid=37145328 transcript=Phvul.00
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RNA biosynth	transcription factor (NAC) (original description: pacid=37145328 transcript=Phvul.00
RNA biosynth	transcription factor (NAC) (original description: pacid=37148955 transcript=Phvul.00
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Carbohydrate	UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
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Carbohydrate	UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
Cell wall orga	caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=37162
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Cell wall orga	caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=37162
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Cell wall orga	caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=37162
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Carbohydrate	UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
Cell wall orga	caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629
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Carbohydrate	UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
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Carbohydrate	UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
Cell wall orga	caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629
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Carbohydrate	UDP-D-glucuronic acid decarboxylase (original description: pacid=37157441 transcrip
Cell wall orga	caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) (original description: pacid=371629
RNA biosynth	transcription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01
not assigned.n	no hits & (original description: pacid=37176752 transcript=Phvul.002G325300.2 locu
Cell cycle orga	PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
not assigned.a	(original description: pacid=37154217 transcript=Phvul.005G001200.1 locus=Phvul.0
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Solute transp	cation:calcium cation exchanger (CCX) (original description: pacid=37143954 transcri
RNA biosynth	transcription factor (TCP) (original description: pacid=37143823 transcript=Phvul.01
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Cell cycle orga	PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
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Cell cycle orga	PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
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Cell cycle orga	PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
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Cell cycle orga	PARC6 plastid division FtsZ assembly regulator (original description: pacid=37161971
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Protein modif	protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
not assigned.a	(original description: pacid=37148894 transcript=Phvul.009G132000.1 locus=Phvul.0
not assigned.n	no hits & (original description: pacid=37152409 transcript=Phvul.005G087600.1 locu
RNA biosynth	transcription factor (MADS/AGL) (original description: pacid=37150879 transcript=Ph
not assigned.n	no hits & (original description: pacid=37155288 transcript=Phvul.011G108000.1 locu
not assigned.a	(original description: pacid=37156031 transcript=Phvul.011G054900.1 locus=Phvul.0
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
Protein modif	protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
not assigned.a	(original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.0
not assigned.a	(original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.0
Solute transp	anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
Amino acid m	serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
not assigned.n	no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
Solute transp	solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
Protein modif	protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
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Solute transp	solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
Protein modif	protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
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External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
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RNA biosynth	transcription factor (HD-ZIP III) (original description: pacid=37156981 transcript=Phv
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Protein modif	protein kinase (SD-1) (original description: pacid=37159724 transcript=Phvul.008G07
not assigned.a	(original description: pacid=37156499 transcript=Phvul.011G110300.1 locus=Phvul.0
not assigned.a	(original description: pacid=37160936 transcript=Phvul.008G077700.1 locus=Phvul.0
Solute transp	anion channel / anion:proton antiporter (CLC) (original description: pacid=37154317
Solute transp	solute transporter (UmamiT) (original description: pacid=37178271 transcript=Phvul.
Solute transp	solute transporter (UmamiT) (original description: pacid=37174567 transcript=Phvul.
Solute transp	solute transporter (UmamiT) (original description: pacid=37174567 transcript=Phvul.
Amino acid m	serine O-acetyltransferase (SAT) (original description: pacid=37158626 transcript=Ph
not assigned.r	no hits & (original description: pacid=37147013 transcript=Phvul.003G067000.1 locu
Solute transp	solute transporter (MTCC) (original description: pacid=37170431 transcript=Phvul.00
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37159472 transcript=
Protein modif	protein folding catalyst (original description: pacid=37147261 transcript=Phvul.003G
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not assigned.a	(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.0
Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transp	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
not assigned.a	(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosy	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
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not assigned.r	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.r	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
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RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
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Solute transp	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcri
Solute transp	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
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not assigned.a	(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
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Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transp	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
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Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosy	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
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Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosy	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
not assigned.	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
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not assigned.	(original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.
RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Solute transp	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcri
Solute transp	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.
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not assigned.	(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
not assigned.	(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.

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Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transp	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
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Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosy	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
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RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
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RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=371
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Solute transp	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcri
Solute transp	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.
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not assigned.	no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 loc
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Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
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Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
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Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
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Cell wall orgar	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transpo	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 trans
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Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosyr	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
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RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
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Solute transpo	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
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Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
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Solute transp	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
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Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans

Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
not assigned.a	(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.0
not assigned.a	(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.0
Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transpo	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 trans
not assigned.a	(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosyn	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
not assigned.n	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.n	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
not assigned.a	(original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.0
not assigned.a	(original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.0
RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Solute transpo	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
Solute transpo	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
not assigned.n	no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
not assigned.a	(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
not assigned.a	(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.0
not assigned.a	(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.0
Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transpo	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 trans
not assigned.a	(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G09
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosyn	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
not assigned.n	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.n	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
not assigned.a	(original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.0
not assigned.a	(original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.0
RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716

RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Solute transp	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcri
Solute transp	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.
not assigned.	no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
not assigned.	(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
not assigned.	(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.
not assigned.	(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.
Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transp	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran
not assigned.	(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.
Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosy	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
not assigned.	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
not assigned.	(original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.
not assigned.	(original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.
RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processi	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Solute transp	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcri
Solute transp	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.
not assigned.	no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
not assigned.	(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G1
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G
not assigned.	(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.
not assigned.	(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.
Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transp	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 tran

not assigned.a	(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosy	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
not assigned.n	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.n	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
not assigned.a	(original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.0
not assigned.a	(original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.0
RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Solute transpo	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
Solute transpo	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
RNA biosynth	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
not assigned.n	no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
not assigned.a	(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
RNA biosynth	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
not assigned.a	(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.0
not assigned.a	(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.0
Cell wall orga	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Solute transpo	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 trans
not assigned.a	(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein biosy	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
not assigned.n	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.n	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
RNA biosynth	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
not assigned.a	(original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.0
not assigned.a	(original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.0
RNA biosynth	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Solute transpo	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
Solute transpo	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.00
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript

Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
RNA biosynthe	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
RNA biosynthe	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
not assigned.n	no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
not assigned.a	(original description: pacid=37168048 transcript=Phvul.001G038000.1 locus=Phvul.0
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
RNA biosynthe	transcriptional co-repressor (AFP/NINJA) (original description: pacid=37160240 trans
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
RNA biosynthe	transcription factor (Trihelix) (original description: pacid=37166116 transcript=Phvul.
Solute transpo	polyol/monosaccharide transporter (PLT) (original description: pacid=37156602 trans
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
Cytoskeleton	microtubule-stabilizing factor (WDL) (original description: pacid=37172717 transcript
not assigned.a	(original description: pacid=37173711 transcript=Phvul.006G023000.2 locus=Phvul.0
not assigned.a	(original description: pacid=37162042 transcript=Phvul.004G099100.1 locus=Phvul.0
not assigned.a	(original description: pacid=37175742 transcript=Phvul.002G157300.1 locus=Phvul.0
Cell wall organ	xylosyltransferase (IRX9) (original description: pacid=37150289 transcript=Phvul.009
Protein home	pepsin-type protease (original description: pacid=37172152 transcript=Phvul.006G0
Multi-process	circadian clock regulator (TIC) (original description: pacid=37169653 transcript=Phvu
Protein modif	protein kinase (LRR-XI) (original description: pacid=37150216 transcript=Phvul.009G2
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37151
Multi-process	phosphatidylinositol 4/5-phosphate kinase (PIP5K) (original description: pacid=37151
not assigned.n	no hits & (original description: pacid=37164025 transcript=Phvul.007G156900.1 locu
not assigned.n	no hits & (original description: pacid=37166494 transcript=Phvul.007G157000.1 locu
not assigned.a	(original description: pacid=37161093 transcript=Phvul.008G159000.1 locus=Phvul.0
Protein biosyn	component RPS3 of SSU proteome (original description: pacid=37164640 transcript=
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
Protein modif	protein kinase (LRR-XV) (original description: pacid=37163248 transcript=Phvul.004G
not assigned.a	(original description: pacid=37154385 transcript=Phvul.005G114000.1 locus=Phvul.0
RNA biosynthe	component GRF of GRF-GIF transcriptional complex (original description: pacid=3716
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
RNA processin	tRNA guanosine-methyltransferase (TRM1) (original description: pacid=37162701 tra
Protein home	pepsin-type protease (original description: pacid=37176606 transcript=Phvul.002G10
Solute transpo	Nodulin-26-like intrinsic protein (NIP) (original description: pacid=37164775 transcrip
Solute transpo	transport protein (NiCoT) (original description: pacid=37150843 transcript=Phvul.009
RNA biosynthe	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
RNA biosynthe	transcription factor (YABBY) (original description: pacid=37142427 transcript=Phvul.0
not assigned.n	no hits & (original description: pacid=37158153 transcript=Phvul.008G127800.1 locu
Protein modif	protein kinase (LRR-III) (original description: pacid=37166830 transcript=Phvul.007G0
Lipid metaboli	delta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
not assigned.a	(original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.0
External stimu	RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
Lipid metaboli	component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
not assigned.n	no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
not assigned.n	no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
not assigned.a	(original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.0
not assigned.a	(original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.0

Redox homeo	type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
not assigned.r	no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
not assigned.r	no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
Photosynthesi	glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
not assigned.r	no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
Protein transl	subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
Photosynthesi	component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
not assigned.r	no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
Enzyme classi	Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q3
Enzyme classi	Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q3
Photosynthesi	ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.00
not assigned.r	no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
not assigned.r	no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
RNA biosynth	component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
Carbohydrate	starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
not assigned.a	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.0
External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
Lipid metaboli	sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
Lipid metaboli	sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
Enzyme classi	Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
Solute transp	organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
not assigned.r	no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=P
not assigned.r	no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=P
Nutrient upta	iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
Lipid metaboli	delta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
not assigned.a	(original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.0
External stimu	RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695
Lipid metaboli	component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
not assigned.r	no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
not assigned.r	no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
not assigned.a	(original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.0
not assigned.a	(original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.0
Redox homeo	type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
not assigned.r	no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
not assigned.r	no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
Photosynthesi	glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
not assigned.r	no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
Protein transl	subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
Photosynthesi	component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=3716998
not assigned.r	no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
Enzyme classi	Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q3
Enzyme classi	Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q3
Photosynthesi	ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.00
not assigned.r	no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu

not assigned.r	no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
RNA biosynth	component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
Carbohydrate	starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
not assigned.a	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.0
External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
Lipid metaboli	sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
Lipid metaboli	sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
Enzyme classi	Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
Solute transpo	organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
not assigned.r	no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
not assigned.r	no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl
Nutrient uptal	iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
Lipid metaboli	delta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
not assigned.a	(original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.0
External stimu	RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
Lipid metaboli	component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
not assigned.r	no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
not assigned.r	no hits & (original description: pacid=37170810 transcript=Phvul.001G193000.4 locu
not assigned.a	(original description: pacid=37148412 transcript=Phvul.003G154400.1 locus=Phvul.0
not assigned.a	(original description: pacid=37150067 transcript=Phvul.009G030200.1 locus=Phvul.0
Redox homeo	type-2 peroxiredoxin (PrxII) (original description: pacid=37162348 transcript=Phvul.0
not assigned.r	no hits & (original description: pacid=37151606 transcript=Phvul.009G160200.1 locu
not assigned.r	no hits & (original description: pacid=37177090 transcript=Phvul.002G119600.1 locu
Photosynthesi	glutamate-glyoxylate transaminase (original description: pacid=37176429 transcript=
not assigned.r	no hits & (original description: pacid=37175432 transcript=Phvul.002G271400.1 locu
Protein transl	subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
Photosynthesi	component PnsB2/NDF2 of NDH subcomplex B (original description: pacid=37169988
not assigned.r	no hits & (original description: pacid=37174983 transcript=Phvul.002G037500.1 locu
Enzyme classi	Probable serine/threonine-protein kinase At1g01540 OS=Arabidopsis thaliana (sp|q3
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Photosynthesi	ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.00
not assigned.r	no hits & (original description: pacid=37142224 transcript=Phvul.010G115000.2 locu
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RNA biosynth	component MED5/MED24/MED33 of tail module of MEDIATOR transcription co-activ
Carbohydrate	starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
not assigned.a	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.0
External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
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Lipid metaboli	sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
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Enzyme classi	Geraniol 8-hydroxylase OS=Catharanthus roseus (sp|q8vwz7|c76b6_catro : 434.0) &
Solute transpo	organic cation transporter (PUP) (original description: pacid=37151850 transcript=Ph
not assigned.r	no hits & (original description: pacid=37174268 transcript=Phvul.L002444.2 locus=Pl

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Nutrient uptal	iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G07
Lipid metaboli	delta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
not assigned.a	(original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.0
External stimu	RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695 t
Lipid metaboli	component Mdm35 of UPS2-Mdm35 phospholipid transfer complex (original descrip
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Carbohydrate	starch branching enzyme (original description: pacid=37172123 transcript=Phvul.006
not assigned.a	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.0

External stimu	SNI1 systemic acquired resistance regulator protein (original description: pacid=3714
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Lipid metaboli	sphingosine-1-phosphate lyase (original description: pacid=37158983 transcript=Phv
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Nutrient uptal	iron transporter (VIT) (original description: pacid=37157783 transcript=Phvul.008G0
Lipid metaboli	delta-7/delta-9 fatty acid desaturase (original description: pacid=37142215 transcrip
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not assigned.a	(original description: pacid=37151584 transcript=Phvul.009G217000.3 locus=Phvul.0
Photosynthesi	ferredoxin electron carrier (original description: pacid=37167516 transcript=Phvul.00
External stimu	RAM1-dependent transcription factor (WRI5) (original description: pacid=37158695
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Protein transl	subunit alpha of co-translational insertion system Sec61 subcomplex (original descrip
Solute transp	cation antiporter (CAX) (original description: pacid=37171893 transcript=Phvul.006G
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Cell wall orga	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00

RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=P
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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External stim	PIF red/far-red light perception transcriptional regulator (original description: pacid=
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not assigned.	no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 loc
RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
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not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
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not assigned.	(original description: pacid=37147019 transcript=Phvul.003G181600.1 locus=Phvul.
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not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.
Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
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not assigned.	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio

External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
Cell wall orgar	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
not assigned.a	(original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.0
Cell wall orgar	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
not assigned.a	(original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.0
Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=P
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transpo	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
not assigned.a	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.0
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External stimu	PIF red/far-red light perception transcriptional regulator (original description: pacid=
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not assigned.a	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.0
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not assigned.r	no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
not assigned.r	no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
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External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
Cell wall orgar	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
not assigned.a	(original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.0
Cell wall orgar	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transpo	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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External stimu	PIF red/far-red light perception transcriptional regulator (original description: pacid=
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RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
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not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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not assigned.a	(original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.0
Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
not assigned.n	no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
not assigned.a	(original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.0
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External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
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Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
Cell wall orga	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
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Cell wall orga	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=P
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transpo	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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External stimu	PIF red/far-red light perception transcriptional regulator (original description: pacid=
not assigned.a	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.0
not assigned.a	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.0
not assigned.a	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.0
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RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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not assigned.r	no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 locu
not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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not assigned.a	(original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.0
Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
not assigned.r	no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
not assigned.a	(original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.0
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not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
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Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
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not assigned.a	(original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.0
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RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri

Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transpo	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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External stimu	PIF red/far-red light perception transcriptional regulator (original description: pacid=
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RNA biosynthe	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
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Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynthe	G2-like GARP transcription factor (original description: pacid=37159020 transcript=Pl
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External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
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Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
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Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
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Cell wall orga	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
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Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
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Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
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Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
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Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
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Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transpo	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
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Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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External stimu	PIF red/far-red light perception transcriptional regulator (original description: pacid=
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RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
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not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
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Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
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not assigned.	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
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Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
External stim	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
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Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
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Cell wall orga	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
not assigned.	(original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.
Cell wall orga	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
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Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
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Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
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Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
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Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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not assigned.	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.
not assigned.	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.
External stim	PIF red/far-red light perception transcriptional regulator (original description: pacid=
not assigned.	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.
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RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
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External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
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Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
Cell wall orga	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
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RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
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Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=P
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Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
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Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
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Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=Ph
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Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Ph
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transpo	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
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Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
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External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
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Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descripti
External stim	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
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Cell wall orga	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
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RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
not assigned.a	(original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.0
Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=

Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
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not assigned.	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.
External stim	PIF red/far-red light perception transcriptional regulator (original description: pacid=
not assigned.	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.
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not assigned.	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.
not assigned.	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.
not assigned.	no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 loc
RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
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not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
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not assigned.	no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 loc
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not assigned.	(original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.
Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
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not assigned.	(original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.
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not assigned.	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descripti
External stim	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stim	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descripti
External stim	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
Cell wall orga	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
not assigned.	(original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.

Cell wall orga	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=P
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
Chromatin or	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
not assigned.	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.
not assigned.	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.
External stim	PIF red/far-red light perception transcriptional regulator (original description: pacid=
not assigned.	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.
not assigned.	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.
not assigned.	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.
not assigned.	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.
not assigned.	no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 loc
RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
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not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
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not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	no hits & (original description: pacid=37174067 transcript=Phvul.006G164800.1 loc
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
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not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.
not assigned.	(original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.
Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
not assigned.	no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 loc
not assigned.	(original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.
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not assigned.	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.

External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transp	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
Cell wall orgar	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
not assigned.a	(original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.0
Cell wall orgar	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transp	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
not assigned.a	(original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.0
Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=P
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transp	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Ph
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orgar	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
not assigned.a	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.0
not assigned.a	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.0
External stimu	PIF red/far-red light perception transcriptional regulator (original description: pacid=
not assigned.a	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.0
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not assigned.n	no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0
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not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
not assigned.a	(original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.0
Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=Ph
not assigned.n	no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
not assigned.a	(original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptio
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptio
Cell wall orga	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
not assigned.a	(original description: pacid=37174751 transcript=Phvul.002G106900.1 locus=Phvul.0
Cell wall orga	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.00
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript=
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript=
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Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Ph
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Solute transpo	outer membrane porin (OEP21) (original description: pacid=37152022 transcript=Phv
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Chromatin org	chromatin remodeling factor (Snf2) (original description: pacid=37146853 transcript=
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
Cell wall orga	CSI-type cellulose synthase CSC-interactive protein (original description: pacid=3717
not assigned.a	(original description: pacid=37175691 transcript=Phvul.002G299004.3 locus=Phvul.0
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External stimu	PIF red/far-red light perception transcriptional regulator (original description: pacid=
not assigned.a	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.0
not assigned.a	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.0
not assigned.a	(original description: pacid=37153092 transcript=Phvul.005G001000.1 locus=Phvul.0
not assigned.a	(original description: pacid=37177698 transcript=Phvul.002G006400.3 locus=Phvul.0
not assigned.n	no hits & (original description: pacid=37160747 transcript=Phvul.008G243700.1 locu
RNA biosynth	transcription factor (KNOX) (original description: pacid=37166363 transcript=Phvul.0

not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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not assigned.a	(original description: pacid=37165612 transcript=Phvul.007G157500.5 locus=Phvul.0
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Protein modif	component PIG-H of GPI N-acetylglucosamine transferase complex (original descripti
RNA biosynth	G2-like GARP transcription factor (original description: pacid=37159020 transcript=P
not assigned.n	no hits & (original description: pacid=37159999 transcript=Phvul.008G075300.1 locu
not assigned.a	(original description: pacid=37145750 transcript=Phvul.003G262800.1 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
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External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
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External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	GIGANTEA zeitlupe-mediated photoperception regulator protein (original descriptior
not assigned.a	(original description: pacid=37171583 transcript=Phvul.006G075600.1 locus=Phvul.0
Protein transl	NUP133 scaffold nucleoporin of nuclear pore complex (original description: pacid=37
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
Cell wall orgar	pectin methylesterase (original description: pacid=37148958 transcript=Phvul.009G2
Multi-process	regulatory subunit betagamma of SnRK1 kinase complex (original description: pacid=
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Cell wall orgar	fasciclin-type arabinogalactan protein (original description: pacid=37153107 transcri
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
RNA biosynth	transcription factor (bHLH) (original description: pacid=37148325 transcript=Phvul.0
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
Solute transpo	nucleotide sugar transporter (UAfT) (original description: pacid=37144593 transcript
not assigned.a	(original description: pacid=37153288 transcript=Phvul.005G059700.1 locus=Phvul.0
not assigned.a	(original description: pacid=37152887 transcript=Phvul.005G059500.1 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
not assigned.a	(original description: pacid=37157933 transcript=Phvul.008G072300.2 locus=Phvul.0
Solute transpo	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005

Solute transpc	P4-type ATPase component ALA of phospholipid flippase complex (original descriptic
External stimu	transcription factor (NIN) (original description: pacid=37153734 transcript=Phvul.005
Nutrient uptal	CEPR systemic nitrogen signalling CEP-receptor kinase (original description: pacid=37
Solute transpc	P1B-type heavy metal cation-transporting ATPase (HMA) (original description: pacid=
not assigned.r	no hits & (original description: pacid=37176152 transcript=Phvul.002G283000.4 locu
not assigned.r	no hits & (original description: pacid=37176152 transcript=Phvul.002G283000.4 locu
not assigned.r	no hits & (original description: pacid=37176152 transcript=Phvul.002G283000.4 locu
Carbohydrate	sucrose-phosphate synthase (original description: pacid=37147754 transcript=Phvul.
not assigned.a	(original description: pacid=37156011 transcript=Phvul.011G173600.1 locus=Phvul.0
Protein modif	membrane-anchor component DPMS2 of DPMS dolichol-phosphate-mannose syntha
Protein home	monomeric E3 ubiquitin ligase (HECT) (original description: pacid=37165600 transcri
Multi-process	phosphatidylinositol 4-kinase (PI4K-gamma) (original description: pacid=37146293 tr
Amino acid m	serine hydroxymethyltransferase (original description: pacid=37167850 transcript=Pl
Enzyme classi	Putative serine/threonine-protein kinase-like protein CCR3 OS=Arabidopsis thaliana (
Solute transpc	cation antiporter (CAX) (original description: pacid=37171893 transcript=Phvul.006G
Enzyme classi	Hydroquinone glucosyltransferase OS=Rauvolfia serpentina (sp|q9ar73|hqgt_rause :

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006G169300 ID=Phvul.006G169300.1.v2.1 annot-version=v2.1) & GDSL esterase/lipase At1g29670 (

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008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
vul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
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09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT
s=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
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11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350
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11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
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09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT
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11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
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7800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
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s=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
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11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350
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011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr

008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei

transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers

hvul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &

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us=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)

hvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &

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011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai

n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350

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011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr

008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei

transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers

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011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr

008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei

transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers

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011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
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01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
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009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
us=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
hvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
us=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350
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77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
hvul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
us=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
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G246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &
009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT2
us=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)
hvul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &
us=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)
011G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai
n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350
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77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers
hvul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &
us=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)
01G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &
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246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &

09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT

us=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)

vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &

us=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)

11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai

n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350

n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350

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7800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &

11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr

08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei

transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers

vul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &

us=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)

1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &

=Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1)

246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &

09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT

us=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)

vul.009G130000.1 locus=Phvul.009G130000 ID=Phvul.009G130000.1.v2.1 annot-version=v2.1) &

us=Phvul.011G108000 ID=Phvul.011G108000.1.v2.1 annot-version=v2.1)

11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai

n: pacid=37167230 transcript=Phvul.007G083500.2 locus=Phvul.007G083500 ID=Phvul.007G08350

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7800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &

11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr

08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei

transcript=Phvul.005G005200.1 locus=Phvul.005G005200 ID=Phvul.005G005200.1.v2.1 annot-vers

vul.008G277800.1 locus=Phvul.008G277800 ID=Phvul.008G277800.1.v2.1 annot-version=v2.1) &

us=Phvul.003G067000 ID=Phvul.003G067000.1.v2.1 annot-version=v2.1)

1G240500.1 locus=Phvul.001G240500 ID=Phvul.001G240500.1.v2.1 annot-version=v2.1) &

=Phvul.008G061000.1 locus=Phvul.008G061000 ID=Phvul.008G061000.1.v2.1 annot-version=v2.1)

246400.1 locus=Phvul.003G246400 ID=Phvul.003G246400.1.v2.1 annot-version=v2.1) &

09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT

us=Phvul.005G087600 ID=Phvul.005G087600.1.v2.1 annot-version=v2.1)

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11G054900 ID=Phvul.011G054900.1.v2.1 annot-version=v2.1) & ATPase family AAA domain-contai

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7800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &

11G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr

08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei

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09G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT
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08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
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08G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
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008G077700 ID=Phvul.008G077700.1.v2.1 annot-version=v2.1) & Cysteine-rich receptor-like protei
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77800.1 locus=Phvul.008G077800 ID=Phvul.008G077800.1.v2.1 annot-version=v2.1) &
011G110300 ID=Phvul.011G110300.1.v2.1 annot-version=v2.1) & Uncharacterized GPI-anchored pr
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009G132000 ID=Phvul.009G132000.1.v2.1 annot-version=v2.1) & Probable methyltransferase PMT
004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990
93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
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Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
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008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v3
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anscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
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010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
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5200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
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02G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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06G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990
3600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
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G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
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08G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v3

05G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=

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anscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version

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pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1

9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &

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010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &

us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)

01G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thalia

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244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &

04G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol

02G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p

G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &

script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=

06G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990

93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &

l.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &

Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &

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us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)

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08G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v3

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anscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version

anscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version

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9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &

t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)

t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)

010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &

010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &

us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)

01G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thalia

05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &

script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=

244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &

04G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol

002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
l.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
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us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
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005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
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t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
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010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)
001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thalian
05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
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002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
l.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
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005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
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t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)
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001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thalian
05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
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002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990
93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
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us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)
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008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
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pt=Phvul.007G084000.1 locus=Phvul.007G084000 ID=Phvul.007G084000.1.v2.1 annot-version=v2.1
9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
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010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
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001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thalian
05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
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244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=
006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990
93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &

l.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &

Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &

037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &

037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &

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us=Phvul.007G157000 ID=Phvul.007G157000.1.v2.1 annot-version=v2.1)

.007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &

008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v3

005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=

59263 transcript=Phvul.001G031000.1 locus=Phvul.001G031000 ID=Phvul.001G031000.1.v2.1 anno

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9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &

t=Phvul.006G102900.2 locus=Phvul.006G102900 ID=Phvul.006G102900.2.v2.1 annot-version=v2.1)

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010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &

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us=Phvul.008G127800 ID=Phvul.008G127800.1.v2.1 annot-version=v2.1)

001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thalia

05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &

script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v

244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &

004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol

002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p

G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &

script=Phvul.011G046800.1 locus=Phvul.011G046800 ID=Phvul.011G046800.1.v2.1 annot-version=

006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990

93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &

l.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &

Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &

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anscript=Phvul.004G041500.2 locus=Phvul.004G041500 ID=Phvul.004G041500.2.v2.1 annot-version
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script=Phvul.008G032900.1 locus=Phvul.008G032900 ID=Phvul.008G032900.1.v2.1 annot-version=v
244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
l.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
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005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
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9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
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010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
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001G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thalian
05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
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244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
004G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
002G157300 ID=Phvul.002G157300.1.v2.1 annot-version=v2.1) & AT-hook motif nuclear-localized p
G146400.1 locus=Phvul.009G146400 ID=Phvul.009G146400.1.v2.1 annot-version=v2.1) &
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006G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990 (
93600.1 locus=Phvul.006G093600 ID=Phvul.006G093600.1.v2.1 annot-version=v2.1) &
l.001G151600.1 locus=Phvul.001G151600 ID=Phvul.001G151600.1.v2.1 annot-version=v2.1) &
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.007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
008G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
005G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
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9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
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010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
010G079200.2 locus=Phvul.010G079200 ID=Phvul.010G079200.2.v2.1 annot-version=v2.1) &
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01G038000 ID=Phvul.001G038000.1.v2.1 annot-version=v2.1) & Myosin-15 OS=Arabidopsis thaliar
05200.1 locus=Phvul.002G105200 ID=Phvul.002G105200.1.v2.1 annot-version=v2.1) &
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244600.1 locus=Phvul.009G244600 ID=Phvul.009G244600.1.v2.1 annot-version=v2.1) &
.007G105700.1 locus=Phvul.007G105700 ID=Phvul.007G105700.1.v2.1 annot-version=v2.1) &
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06G023000 ID=Phvul.006G023000.2.v2.1 annot-version=v2.1) & GDSL esterase/lipase At2g42990
04G099100 ID=Phvul.004G099100.1.v2.1 annot-version=v2.1) & Receptor-like protein EIX2 OS=Sol
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08G159000 ID=Phvul.008G159000.1.v2.1 annot-version=v2.1) & no description available(sp|q4v39
Phvul.007G231200.1 locus=Phvul.007G231200 ID=Phvul.007G231200.1.v2.1 annot-version=v2.1) &
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037600.3 locus=Phvul.004G037600 ID=Phvul.004G037600.3.v2.1 annot-version=v2.1) &
05G114000 ID=Phvul.005G114000.1.v2.1 annot-version=v2.1) & APO protein 4, mitochondrial OS=
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9G119100.1 locus=Phvul.009G119100 ID=Phvul.009G119100.1.v2.1 annot-version=v2.1) &
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09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07
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s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas

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us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
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us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
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05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
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Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
hvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
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09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
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us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransfera
04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
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ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16
8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
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005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
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vul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
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Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
hvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
ption: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07
us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
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3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
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46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
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46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
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hvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
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009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
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003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
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8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
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8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
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Bedl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
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8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
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3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
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07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
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46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
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09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07
s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransfera
04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
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=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)

us=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16
8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
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5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
vul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
vul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
ivul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
ption: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07
us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransfera
004G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)
us=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16
8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
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07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
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5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07
s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
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03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransfera
04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)
s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16
8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi

ption: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07

us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)

us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)

03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransfera

04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &

us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)

us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)

=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)

us=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)

ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16

8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver

us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)

3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri

3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri

07G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &

us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)

us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)

vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0

G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &

05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i

hvul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &

t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)

09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi

ption: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07

us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)

us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)

03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransfera

04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &

us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)

us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)

=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)

us=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)

ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16

8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver

us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)

3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri

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7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &

us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)

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vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0

G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &

05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i

vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &

t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)

09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi

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03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas

04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &

us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)

us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)

=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)

us=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)

ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16

8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver

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7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &

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vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0

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46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i

vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &

t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)

09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi

tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07

s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)

s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)

03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain

09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas

04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &

s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)

s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)

=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)

s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)

tion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16

8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver

s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)

3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri

3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri

7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &

s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)

s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)

vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0

G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &

05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &

46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno

Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i

vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)

70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &

t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)

09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi

tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07

s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)
s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
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8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
s=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
vator complex (original description: pacid=37172497 transcript=Phvul.006G154900.1 locus=Phvul.0
G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
6122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
6122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
6122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with
vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
09G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07
s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
s=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
03G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
09G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
s=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
s=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1)
s=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
ption: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16
8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
s=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)

3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
3edl4|y1154_arath : 415.0) & Enzyme classification.EC_2 transferases.EC_2.7 transferase transferri
)7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
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5G047000.1 locus=Phvul.006G047000 ID=Phvul.006G047000.1.v2.1 annot-version=v2.1) &
005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
ul.008G017200.2 locus=Phvul.008G017200 ID=Phvul.008G017200.2.v2.1 annot-version=v2.1) &
46122 transcript=Phvul.003G056900.3 locus=Phvul.003G056900 ID=Phvul.003G056900.3.v2.1 anno
Enzyme classification.EC_1 oxidoreductases.EC_1.14 oxidoreductase acting on paired donor with i
vul.009G034400.1 locus=Phvul.009G034400 ID=Phvul.009G034400.1.v2.1 annot-version=v2.1) &
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
hvul.L002444 ID=Phvul.L002444.2.v2.1 annot-version=v2.1)
70000.1 locus=Phvul.008G070000 ID=Phvul.008G070000.1.v2.1 annot-version=v2.1) &
t=Phvul.010G156200.1 locus=Phvul.010G156200 ID=Phvul.010G156200.1.v2.1 annot-version=v2.1)
us=Phvul.009G160200 ID=Phvul.009G160200.1.v2.1 annot-version=v2.1)
009G217000 ID=Phvul.009G217000.3.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
)7G022500.3 locus=Phvul.007G022500 ID=Phvul.007G022500.3.v2.1 annot-version=v2.1) &
transcript=Phvul.008G043500.1 locus=Phvul.008G043500 ID=Phvul.008G043500.1.v2.1 annot-versi
tion: pacid=37148775 transcript=Phvul.009G079400.3 locus=Phvul.009G079400 ID=Phvul.009G07
us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
us=Phvul.001G193000 ID=Phvul.001G193000.4.v2.1 annot-version=v2.1)
009G167700 ID=Phvul.009G167700.2.v2.1 annot-version=v2.1) & 4-coumarate--CoA ligase-like 9 OS
003G154400 ID=Phvul.003G154400.1.v2.1 annot-version=v2.1) & Pentatricopeptide repeat-contain
746 ID=Phvul.L003746.2.v2.1 annot-version=v2.1) & MACPF domain-containing protein At1g14780
746 ID=Phvul.L003746.2.v2.1 annot-version=v2.1) & MACPF domain-containing protein At1g14780
009G030200 ID=Phvul.009G030200.1.v2.1 annot-version=v2.1) & Uncharacterized methyltransferas
)04G166100.1 locus=Phvul.004G166100 ID=Phvul.004G166100.1.v2.1 annot-version=v2.1) &
us=Phvul.002G119600 ID=Phvul.002G119600.1.v2.1 annot-version=v2.1)
=Phvul.002G150800.1 locus=Phvul.002G150800 ID=Phvul.002G150800.1.v2.1 annot-version=v2.1) &
us=Phvul.002G271400 ID=Phvul.002G271400.1.v2.1 annot-version=v2.1)
otion: pacid=37156653 transcript=Phvul.011G166200.1 locus=Phvul.011G166200 ID=Phvul.011G16
067900.1 locus=Phvul.006G067900 ID=Phvul.006G067900.1.v2.1 annot-version=v2.1) &
8 transcript=Phvul.001G110100.1 locus=Phvul.001G110100 ID=Phvul.001G110100.1.v2.1 annot-ver
us=Phvul.002G037500 ID=Phvul.002G037500.1.v2.1 annot-version=v2.1)
us=Phvul.010G115000 ID=Phvul.010G115000.2.v2.1 annot-version=v2.1)
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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
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06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1
002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
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007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
s=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
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s=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830

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02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
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03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
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=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
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06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
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pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
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=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosph
02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosph
=37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1
02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
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07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
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08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
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=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosph
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03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
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07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
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03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
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=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
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06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
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hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
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ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
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02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
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n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G2016
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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &

37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

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02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

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05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

s=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)

07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

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07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

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05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

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03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50

08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
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=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
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vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
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07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50

08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
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06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
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vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
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02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
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02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
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02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
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07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
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006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
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ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
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007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein (
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03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
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006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
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vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
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002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
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007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis

7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an

pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &

37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio

vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot

002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1

002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)

007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

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us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32

005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid

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hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &

us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)

003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50

008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160

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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &

002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis

7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an

pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &

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anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio

vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot

6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot

002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosph

002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosph

=37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1

002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)

07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

005G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid

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hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &

s=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)

03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50

08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830

n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830

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n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160

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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &

02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis

159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an

pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &

37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio

vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &

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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot

02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

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07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
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006G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
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ranscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
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02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
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02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
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07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G1168
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us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
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G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
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06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

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vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1) &
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002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
002G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha
=37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1 a
002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
005G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
002G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
us=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
007G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
003G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
us=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)
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007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
005G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
007G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 32
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hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
us=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
003G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
008G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
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on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
on: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
002G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis

7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an

pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &

37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio

vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot

6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot

02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

s=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)

07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

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07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid

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hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &

s=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)

03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50

08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote

n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830

n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830

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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &

02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein

pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)

06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis

7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an

pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &

=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1

anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio

vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)

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6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot

02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phospha

=37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1

02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A

s=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)

07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

s=Phvul.006G164800 ID=Phvul.006G164800.1.v2.1 annot-version=v2.1)

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3

05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G116
hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
s=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
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G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
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22600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.
hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &
37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
anscript=Phvul.003G037500.1 locus=Phvul.003G037500 ID=Phvul.003G037500.1.v2.1 annot-versio
vul.009G007300.1 locus=Phvul.009G007300 ID=Phvul.009G007300.1.v2.1 annot-version=v2.1) &
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
=Phvul.003G100200.2 locus=Phvul.003G100200 ID=Phvul.003G100200.2.v2.1 annot-version=v2.1)
6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
6498 transcript=Phvul.002G262600.2 locus=Phvul.002G262600 ID=Phvul.002G262600.2.v2.1 annot
02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosph
02G299004 ID=Phvul.002G299004.3.v2.1 annot-version=v2.1) & Probable RNA 3-terminal phosph
37164783 transcript=Phvul.007G156200.3 locus=Phvul.007G156200 ID=Phvul.007G156200.3.v2.1
02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
05G001000 ID=Phvul.005G001000.1.v2.1 annot-version=v2.1) & Cellulose synthase-like protein G1
02G006400 ID=Phvul.002G006400.3.v2.1 annot-version=v2.1) & MND1-interacting protein 1 OS=A
s=Phvul.008G243700 ID=Phvul.008G243700.1.v2.1 annot-version=v2.1)
07G201400.1 locus=Phvul.007G201400 ID=Phvul.007G201400.1.v2.1 annot-version=v2.1) &

07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
03G181600 ID=Phvul.003G181600.1.v2.1 annot-version=v2.1) & E3 ubiquitin-protein ligase RING1
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
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07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
07G157500 ID=Phvul.007G157500.5.v2.1 annot-version=v2.1) & Short-chain dehydrogenase TIC 3
05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
ion: pacid=37177981 transcript=Phvul.002G116800.1 locus=Phvul.002G116800 ID=Phvul.002G116
hvul.008G103100.1 locus=Phvul.008G103100 ID=Phvul.008G103100.1.v2.1 annot-version=v2.1) &
s=Phvul.008G075300 ID=Phvul.008G075300.1.v2.1 annot-version=v2.1)
03G262800 ID=Phvul.003G262800.1.v2.1 annot-version=v2.1) & Auxin-responsive protein SAUR50
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
n: pacid=37162284 transcript=Phvul.004G088300.4 locus=Phvul.004G088300 ID=Phvul.004G08830
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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
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06G075600 ID=Phvul.006G075600.1.v2.1 annot-version=v2.1) & Cationic peroxidase 1 OS=Arachis
7159281 transcript=Phvul.008G284900.1 locus=Phvul.008G284900 ID=Phvul.008G284900.1.v2.1 an
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222600.1 locus=Phvul.009G222600 ID=Phvul.009G222600.1.v2.1 annot-version=v2.1) &
=37173827 transcript=Phvul.006G091100.2 locus=Phvul.006G091100 ID=Phvul.006G091100.2.v2.1
02G106900 ID=Phvul.002G106900.1.v2.1 annot-version=v2.1) & Nitrate regulatory gene2 protein
pt=Phvul.005G099500.1 locus=Phvul.005G099500 ID=Phvul.005G099500.1.v2.1 annot-version=v2.1
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
03G181900.2 locus=Phvul.003G181900 ID=Phvul.003G181900.2.v2.1 annot-version=v2.1) &
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
=Phvul.003G121200.3 locus=Phvul.003G121200 ID=Phvul.003G121200.3.v2.1 annot-version=v2.1)
05G059700 ID=Phvul.005G059700.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
05G059500 ID=Phvul.005G059500.1.v2.1 annot-version=v2.1) & Putative Peroxidase 48 OS=Arabid
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
08G072300 ID=Phvul.008G072300.2.v2.1 annot-version=v2.1) & Probable disease resistance prote
n: pacid=37151425 transcript=Phvul.009G201600.2 locus=Phvul.009G201600 ID=Phvul.009G20160
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &
5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

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5G155100.3 locus=Phvul.005G155100 ID=Phvul.005G155100.3.v2.1 annot-version=v2.1) &

7150436 transcript=Phvul.009G114400.1 locus=Phvul.009G114400 ID=Phvul.009G114400.1.v2.1 an

=37145343 transcript=Phvul.003G240100.1 locus=Phvul.003G240100 ID=Phvul.003G240100.1.v2.1

us=Phvul.002G283000 ID=Phvul.002G283000.4.v2.1 annot-version=v2.1)

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ase complex (original description: pacid=37146956 transcript=Phvul.003G283500.1 locus=Phvul.003

pt=Phvul.007G163400.1 locus=Phvul.007G163400 ID=Phvul.007G163400.1.v2.1 annot-version=v2.1

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hvul.001G266600.1 locus=Phvul.001G266600 ID=Phvul.001G266600.1.v2.1 annot-version=v2.1) &

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067900.1 locus=Phvul.006G067900 ID=Phvul.006G067900.1.v2.1 annot-version=v2.1) &

: 481.0) & Enzyme classification.EC_2 transferases.EC_2.4 glycosyltransferase(50.2.4 : 410.0) (origin

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=Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
t-version=v2.1) &
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1) &

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na (sp|q0wpu1|myo15_arath : 357.0)

v2.1) &

lanum lycopersicum (sp|q6jn46|eix2_sollc : 491.0)
rotein 5 OS=Arabidopsis thaliana (sp|q8gxb3|ahl5_arath : 201.0)

v2.1) &
OS=Arabidopsis thaliana (sp|q67zi9|gdl48_arath : 413.0)

&

98|rrt1_arath : 178.0)
=Arabidopsis thaliana (sp|q9lsz0|apo4_arath : 369.0)
t-version=v2.1) &
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ion=v2.1) &
9400.3.v2.1 annot-version=v2.1) &

ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

&

6200.1.v2.1 annot-version=v2.1) &
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ng phosphorus-containing group(50.2.7 : 93.6) (original description: pacid=37175990 transcript=Ph
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)06G154900 ID=Phvul.006G154900.1.v2.1 annot-version=v2.1) &

L OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
)t-version=v2.1) &
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ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

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OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)
ion=v2.1) &
)400.3.v2.1 annot-version=v2.1) &

ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

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OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
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ncorporation or reduction of molecular oxygen(50.1.13 : 325.4) (original description: pacid=371646

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OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 155.0)

ion=v2.1) &
400.3.v2.1 annot-version=v2.1) &

=Arabidopsis thaliana (sp|q84p23|4cll9_arath : 619.0)
ing protein At4g30700 OS=Arabidopsis thaliana (sp|q9suh6|pp341_arath : 1019.0)
OS=Arabidopsis thaliana (sp|q8l612|macp1_arath : 346.0)
OS=Arabidopsis thaliana (sp|q8l612|macp1_arath : 346.0)
se At1g78140, chloroplastic OS=Arabidopsis thaliana (sp|q8lbv4|y1814_arath : 425.0)

&

6200.1.v2.1 annot-version=v2.1) &

sion=v2.1) &

r0|ftip3_arath : 1142.0)

OS=Arabidopsis thaliana (sp|q93yu8|nrg2_arath : 254.0)
1) &

&
&
hypogaea (sp|p22195|per1_arahy : 381.0)
not-version=v2.1) &
1) &

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

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-version=v2.1) &
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ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
ate cyclase-like protein OS=Arabidopsis thaliana (sp|q9c578|rcl1_arath : 219.0)
annot-version=v2.1) &
rabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
rabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)
1 OS=Arabidopsis thaliana (sp|q570s7|cslg1_arath : 409.0)
rabidopsis thaliana (sp|q8rx22|mip1_arath : 389.0)

2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
2, chloroplastic OS=Pisum sativum (sp|q6rvv4|tic32_pea : 207.0)
OS=Gossypium hirsutum (sp|p0ch30|ring1_goshi : 103.0)
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OS=Arabidopsis thaliana (sp|o65695|sau50_arath : 159.0)
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sferring phosphorus-containing group(50.2.7 : 89.3) (original description: pacid=37170327 transcrip

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Supplementary Table 4: Primers used for qPCR experiments

cDNA	**Gene reference no.**	**Function**	**Primer sequence**
UBI	CV543388	Ubiquitin	GAGGATGGTCGCACCCTGGCT
			CCCTCCTTGTCCTGAATCTTA
EF1-α	GI151368189	Elongation factor 1α	CAAGGATCTCAAGCGTGGTTTCG
			TGGGAGGTGTGGCAATCAAGC
WRK72	Phvul.003G068700	WRKY72 TF	CCATTCCTGGGGCATCTTTG
			TGATTGCTTTGGTTGCAGCT