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## Data Article

# Dataset on phenotypic characterization, on protein and genome analysis of three fluorescent *Pseudomonas* strains from mid-mountain water



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## ABSTRACT

The identification of non-fermentative Gram negative bacilli from run-off and spring water, including fluorescent *Pseudomonas* is very complex and investigations are needed to contribute to the systematic of these bacteria. In this dataset, the phenotypical profiles of three strains isolated from Vosges mountains first identified as *Pseudomonas fluorescens* were determined using API® 50 CH galleries. Then, the identification of their proteins released directly into water was carried out using tandem/mass spectrometry after separating proteins on native two-dimensional polyacrylamide gels. Finally, genotypic analysis data is presented, that illustrates biodiversity in this fluorescent bacterial group.

*Abbreviations:* ANI, average nucleotide identity; MALDI, matrix assisted laser desorption ionization; MS, mass spectrometry; MS/MS, tandem mass spectrometry; MW, molecular weight; Nb, number of experimental peptides recognized; NCBI, National Center for Biotechnology Information; NR, not reviewed; P., *Pseudomonas*; PFF, peptide fragment fingerprinting; PMF, peptide mass fingerprinting; ppm, parts per million; R, reviewed; Spot no., spot number; TCS, tetra correlation search; TOF/TOF, time-of-flight/time-of-flight.

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This data is referred by a research article entitled “Fluorescent *Pseudomonas* strains from mid-mountain water able to release antioxidant proteins directly into water”.

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## Specifications table

Subject	Microbiology
Specific subject area	Identification of three fluorescent <i>Pseudomonas</i> strains isolated from mid-mountain run-off water (France)
Type of data	Figure
How data were acquired	API® 50 CH galleries (bioMérieux Diagnostics, Marcy-l'Étoile, France). Average nucleotide identity (ANI) and tetra correlation search (TCS) analyzes with JSpecies software (Ribocon GmbH). Alignment of the 3 bacterial draft genome sequences versus the complete genomes of the nearest bacterial species was performed using MAUVE algorithm. Protein identification by mass spectrometry (MS) and/or tandem mass spectrometry (MS/MS) using an Autoflex Speed™ matrix assisted laser desorption ionization (MALDI) time-of-flight/time-of-flight (TOF/TOF) mass spectrometer (Bruker, Bremen, Germany). Molecular mass measurement was performed in automatic mode using FlexControl™ 3.4 software in reflectron mode for MALDI-TOF peptide mass fingerprinting (PMF, MS mode) or LIFT mode for MALDI-TOF/TOF peptide fragment fingerprinting (PFF, MS/MS mode). Peak lists were generated from MS and MS/MS spectra using FlexAnalysis™ 3.4 software. Database search using PMF or PFF datasets was performed in the UniProt/SwissProt and National center for biotechnology information (NCBI) databases via Mascot 2.2 (Matrix Science Ltd, London, UK) or PEAKS Studio 7.0 (Bioinformatics Solutions).
Data format	Raw Analyzed
Parameters for data collection	Three strains of fluorescent <i>Pseudomonas</i> were collected from water and first identified as <i>Pseudomonas fluorescens</i> using optical microscopy, oxidase test and micro gallery API® 20 NE (bioMérieux) before to be tested. They were stored at -32 °C before to be aerobically cultured at 25 °C, either in broth medium and then recovered after spinning and placed into distilled water to produce the proteins analyzed, or on plate count agar to analyze their genomes. Total deoxyribonucleic acid (DNA) was extracted using the Wizard genomic purification DNA kit (Promega Corp., Madison, WI, USA) and sequenced at MicrobesNG ( <a href="http://www.microbesng.uk">http://www.microbesng.uk</a> ) using Illumina MiSeq and HiSeq 2500 technology platforms.
Description of data collection	API® 50 CH galleries were inoculated with F14BN1, F14BN2 and F15BN2 fluorescent strains and positive characters were collected and compared. Genome was extracted using the Wizard genomic purification DNA kit before to be sequenced and analyzed using TCS and ANI indices. An alignment of the sequences was performed that compared the three draft genomes with the genomes of the nearest bacterial species. The proteins released directly into distilled water by the three strains were then separated in native 2D-gels after washing and desalting using filter with 10-kDa cut-off. Trypsin hydrolysis was then performed on the proteins contained in the spots of interest in the colored gels, before to be analyzed for their mass using MS and MS/MS and database search above mentioned.
Data source location	Charles Viollette Institute Lille, France North latitude 50°36' and east longitude 3°8'

(continued on next page)

Data accessibility	<ol style="list-style-type: none"> <li>1. With the article</li> <li>2. Accession numbers of the three genomes deposited in NCBI database: (SUBID BioProject BioSample Accession Organism) - SUB6805363 PRJNA601118 SAMN13831441 JAAARL000000000 <i>Pseudomonas</i> sp. F15BN2 <a href="https://www.ncbi.nlm.nih.gov/nuccore/JAAARL000000000">https://www.ncbi.nlm.nih.gov/nuccore/JAAARL000000000</a> — <a href="https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARL01?display=contigs">https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARL01?display=contigs</a> - SUB6805363 PRJNA601118 SAMN13831440 JAAARM000000000 <i>Pseudomonas</i> sp. F14BN1 <a href="https://www.ncbi.nlm.nih.gov/nuccore/JAAARM000000000">https://www.ncbi.nlm.nih.gov/nuccore/JAAARM000000000</a> — <a href="https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARM01?display=contigs">https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARM01?display=contigs</a> - SUB6805363 PRJNA601118 SAMN13831439 JAAARN000000000 <i>Pseudomonas</i> sp. F14BN2 <a href="https://www.ncbi.nlm.nih.gov/nuccore/JAAARN000000000">https://www.ncbi.nlm.nih.gov/nuccore/JAAARN000000000</a> — <a href="https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARN01?display=contigs">https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARN01?display=contigs</a></li> </ol>
Related research article	<p>3. Repository name : Mendeley Data          Data identification number : DOI: <a href="https://doi.org/10.17632/p5kt4dvmxt.1">10.17632/p5kt4dvmxt.1</a>          Direct URL to Data : <a href="https://data.mendeley.com/datasets/p5kt4dvmxt/1">https://data.mendeley.com/datasets/p5kt4dvmxt/1</a>          Elodie Dussert<sup>1</sup>, Mélissa Tourret<sup>1</sup>, Barbara Deracinois<sup>1</sup>, Matthieu Duban<sup>1</sup>, Valérie Leclère<sup>1</sup>, Benoit Cudennec<sup>1</sup>, Rozenn Ravallec<sup>1</sup>, Josette Behra-Miellat<sup>1</sup>.          Fluorescent <i>Pseudomonas</i> strains from mid-mountain water able to release antioxidant proteins directly into water          Journal: Microbiological Research</p>

## Value of the data

- The data shows the complexity of the identification of fluorescent *Pseudomonas* strains, isolated from water.
- The data could be valuable for researchers working on the systematics of non-pathogenic bacteria from water, especially to compare *Pseudomonas* genomes with TCS and ANI.
- The data could be useful for researches on antioxidant proteins released into water by non-pathogenic bacteria.
- The data could contribute to the bacterial systematics of non-fermentative fluorescent Gram-negative bacilli.

## 1. Data description

Table 1 shows the data related to API<sup>®</sup> 50 CH micro galleries for the three strains studied: F14BN1, F14BN2 and F15BN2. For each substrate, oxidation and assimilation are specified. Table 2 describes TCS or tetra-nucleotide signature data for F14BN1, F14BN2 and F15BN2. Draft genomes of F14BN1 and F15BN2 were found very close to *Pseudomonas batumici* UCM B-321 strain and *Pseudomonas protegens* Cab57 strain, with Z-scores of 0.98989 and 0.98953 for F14BN1 and 0.98945 and 0.98938 for F15BN2, respectively whereas F14BN2 was identified as *Pseudomonas fragi* P121 and *Pseudomonas* sp. Lz4W with Z-scores of 0.99969 and 0.99949, respectively. Pair-wise genome comparison was performed using JSpecies to measure the probability that genomes belonged to the same species with their ANI: data are described in Tables 3 and 4 for ANIb and ANIm respectively. ANIb and ANIm analyzes of F14BN2 genome sequence versus 12 strains defined as having the genomes closest to those of F14BN1, F14BN2 and F15BN2 using TCS test revealed that this strain could belong to *Pseudomonas fragi* or *Pseudomonas* sp. Lz4W species with ANI higher than 98%. Both analyzes showed that F14BN1 and F15BN2 belonged to the same species with 99.28% ANIm (Table 4) and an ANIb higher than 98.94% (Table 3). Fig. 1 shows alignments of the bacterial draft genomes with the complete genomes of the nearest species determined by average nucleotide identity (JSpecies) (*Pseudomonas* sp. Lz4W and *P. fragi* P121 for F14BN2 and *Pseudomonas protegens* CHA0 for F14BN1 and F15BN2), performed using the Progressive MAUVE algorithm. Tables 5–11 summarize the raw data obtained from proteomic searches and available in Mendeley Data (deposited as Raw data of the article: “Dataset on phenotypic

**Table 1**

Data obtained using API® 50 CH micro gallery.

Test (active ingredients)	F14BN1	F14BN2	F15BN2
Glycerol	A-	O+/A+	A-
Erythritol	-	-	-
D-arabinose	-	A-	-
L-arabinose	-	A-	-
D-ribose	A-	A-	A-
D-xylose	O+	A-	O+
L-xylose	-	-	-
D-adonitol	-	-	-
Methyl-βD-xylopyranoside	-	-	-
D-galactose	O+	O+/A-	O+
D-glucose	A-	O-/A-	A+
D-fructose	A-	O+/A+	A-
D-mannose	-	O+	A-
L-sorbose	-	-	-
L-rhamnose	-	-	-
Dulcitol	-	-	-
Inositol	A+	A+	A-
D-mannitol	A+	-	A+
D-sorbitol	-	-	-
Methyl-αD-mannopyranoside	-	-	-
Methyl-αD-glucopyranoside	-	-	-
N-acetylglucosamine	A+	-	A-
Amygdalin	-	-	-
Arbutin	-	-	-
Esculin (ferric citrate)	-	-	-
Salicin	-	-	-
D-cellobiose	-	-	-
D-maltose	-	-	-
D-lactose (bovine origin)	-	-	-
D-melibiose	-	-	-
D-saccharose (sucrose)	-	-	-
D-trehalose	A+	A+	A-
Inuline	-	-	-
D-melezitose	-	-	-
D-raffinose	-	-	-
Amidon (starch)	-	-	-
Glycogen	-	-	A-
Xylitol	-	-	-
Gentiobiose	-	-	-
D-turanose	-	-	-
D-lyxose	-	-	-
D-tagatose	-	-	-
D-fucose	F+	O+	F-
L-fucose	-	A+	-
D-arabitol	A+	A+	A-
L-arabitol	-	-	-
Potassium gluconate	A+	A+	A+
Potassium 2-ketogluconate	A+	A+	A+
Potassium 5-ketogluconate	-	-	-

F+ = strong fermentation, F- = weak fermentation, O+ = strong oxidation, O- = weak oxidation, A+ = strong assimilation (strong growth of microorganism when the substrate used is the only source of carbon), A- = weak assimilation (weak growth of microorganism when the substrate used is the only source of carbon).

characterization, on protein and genome analysis of three fluorescent *Pseudomonas* strains from mid-mountain water”). Table 5 is related to the raw data contained in folder “MS” of Mendeley Data and describes identification of the proteins released by the three strains. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by the mass through the “Mascot” search algorithm. These proteins were

**Table 2**

TCS data for F14BN1, F14BN2 and F15BN2. \*\* above cut-off (&gt; 0.999), \* in range (&gt; 0.989), below cut-off (&lt; 0.989).

	Pos.	Species	Strain	Domain	Phylum	Class	Order	Family	Z-Score
<b>F14BN1</b>	1	<i>Pseudomonas batumici</i> UCM B-321	UCM B-321	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98989*
	2	<i>Pseudomonas protegens</i> Cab57	null	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98953*
	3	<i>Pseudomonas protegens</i> Pf-5	Pf-5	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.9888
	4	<i>Pseudomonas protegens</i> CHA0	CHA0	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98873
	5	<i>Pseudomonas</i> sp. Os17	Os17	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98751
	6	<i>Pseudomonas</i> sp. GM17	GM17	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98536
	7	<i>Pseudomonas chlororaphis</i> subsp. piscium PCL1391	PCL1391	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98517
	8	<i>Pseudomonas chlororaphis</i> O6	O6	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98456
	9	<i>Pseudomonas putida</i> (GCA_001006135) CBB5	CBB5	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.9845
	10	<i>Pseudomonas chlororaphis</i> subsp. aurantiaca str. JD37	JD37	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.9844
	11	<i>Pseudomonas chlororaphis</i> subsp. aureofaciens 30-84	30-84	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98435
	12	<i>Pseudomonas chlororaphis</i> PA23	PA23	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.9842
	13	<i>Pseudomonas</i> sp. GM78	GM78	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98399
	14	<i>Pseudomonas</i> sp. CF161	CF161	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98383
	15	<i>Pseudomonas chlororaphis</i> subsp. aurantiaca PB-St2	PB-St2	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98265
	16	<i>Pseudomonas</i> sp. G5(2012) G5	G5	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98165
	17	<i>Pseudomonas</i> sp. ABAC61	ABAC61	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98138
	18	<i>Pseudomonas fluorescens</i> (GCA_000836415) UM270	UM270	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98084
	19	<i>Pseudomonas fuscovaginae</i> IRRI 6609	IRRI 6609	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98083
	20	<i>Pseudomonas putida</i> (GCA_000729805) MC4-5222	MC4-5222	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98053
<b>F14BN2</b>	1	<i>Pseudomonas fragi</i> P121	P121	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.99969**
	2	<i>Pseudomonas</i> sp. Lz4W	Lz4W	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.99949**
	3	<i>Pseudomonas</i> sp. L10.10	L10.10	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.9944 *
	4	<i>Pseudomonas deceptionensis</i> DSM 26,521	DSM 26,521	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.97569
	5	<i>Pseudomonas taetrolensis</i> DSM 21,104	DSM 21,104	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.97146
	6	<i>Pseudomonas</i> sp. CF149	CF149	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.967
	7	<i>Pseudomonas psychrophila</i> DSM 17,535	DSM 17,535	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.96683
	8	<i>Pseudomonas fluorescens</i> str. S613	S613	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.95446
	9	<i>Pseudomonas</i> sp. GM55	GM55	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.95355

(continued on next page)

Table 2 (continued)

	Pos.	Species	Strain	Domain	Phylum	Class	Order	Family	Z-Score
	10	<i>Pseudomonas</i> sp. GM48	GM48	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.95245
	11	<i>Pseudomonas</i> sp. UW4	UW4	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.95237
	12	<i>Pseudomonas</i> sp. Leaf48	Leaf48	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.95231
	13	<i>Pseudomonas</i> sp. GM49	GM49	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.95209
	14	<i>Pseudomonas</i> sp. GM74	GM74	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.94993
	15	<i>Pseudomonas</i> sp. GM33	GM33	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.94968
	16	<i>Pseudomonas alkylphenolia</i> KL28	KL28	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.94814
	17	<i>Pseudomonas</i> sp. Root71	Root71	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.94767
	18	<i>Pseudomonas</i> sp. Root68	Root68	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.94755
	19	<i>Pseudomonas fluorescens</i> (GCA_000967965) C8	C8	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.94607
	20	<i>Pseudomonas</i> sp. StFLB209	StFLB209	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.94582
F15BN2	1	<i>Pseudomonas batumici</i> UCM B-321	UCM B-321	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98945*
	2	<i>Pseudomonas protegens</i> Cab57	null	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98938*
	3	<i>Pseudomonas protegens</i> PF-5	PF-5	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98866
	4	<i>Pseudomonas protegens</i> CHA0	CHA0	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98857
	5	<i>Pseudomonas</i> sp. Os17	Os17	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98698
	6	<i>Pseudomonas</i> sp. GM17	GM17	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98467
	7	<i>Pseudomonas chlororaphis</i> subsp. <i>piscium</i> PCL1391	PCL1391	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98443
	8	<i>Pseudomonas putida</i> (GCA_001006135) CBB5	CBB5	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98435
	9	<i>Pseudomonas chlororaphis</i> O6	O6	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98381
	10	<i>Pseudomonas</i> sp. GM78	GM78	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98373
	11	<i>Pseudomonas chlororaphis</i> subsp. <i>aurantiaca</i> str. JD37	JD37	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98369
	12	<i>Pseudomonas chlororaphis</i> subsp. <i>aureofaciens</i> 30–84	30–84	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98367
	13	<i>Pseudomonas chlororaphis</i> PA23	PA23	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98345
	14	<i>Pseudomonas</i> sp. CF161	CF161	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98329
	15	<i>Pseudomonas chlororaphis</i> subsp. <i>aurantiaca</i> PB-St2	PB-St2	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98191
	16	<i>Pseudomonas</i> sp. G5(2012) G5	G5	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98152
	17	<i>Pseudomonas</i> sp. ABAC61	ABAC61	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98117
	18	<i>Pseudomonas putida</i> (GCA_000729805) MC4-5222	MC4-5222	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98042
	19	<i>Pseudomonas fluorescens</i> (GCA_000836415) UM270	UM270	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98028
	20	<i>Pseudomonas fuscovaginae</i> IRR1 6609	IRRI 6609	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	0.98026

**Table 3**  
ANIB data for F14BN1, F14BN2 and F15BN2. The values represent scores (%). In bold values > 95%: identification of species.

	F14BN1 _92_ctg.fas	F14BN2 _181ctg.fas	F15BN2 _59_ctg.fas	<i>Pseudomonas</i> <i>batumici</i>	<i>Pseudomonas</i> <i>protegens</i> Cab57	<i>Pseudomonas</i> <i>protegens</i> CHA0	<i>Pseudomonas</i> <i>protegens</i> PF-5	<i>Pseudomonas</i> sp. Os17	<i>Pseudomonas</i> sp. GM17	<i>Pseudomonas</i> <i>fragi</i> P121	<i>Pseudomonas</i> sp. Lz4W	<i>Pseudomonas</i> sp. L10.10	<i>Pseudomonas</i> <i>deceptionensis</i> DSM 26,521	<i>Pseudomonas</i> <i>taetrolens</i> DSM 21,104	<i>Pseudomonas</i> sp. CF149
F14BN1_92_ctg.fas	*	77.48	<b>98.94</b>	79.62	87.50	87.55	87.48	87.11	82.62	77.44	77.49	77.22	77.82	77.15	77.23
F14BN2_181ctg.fas	78.38	*	78.40	78.70	78.56	78.56	78.51	78.58	78.93	<b>98.95</b>	<b>99.00</b>	90.53	84.80	83.06	83.93
F15BN2_59_ctg.fas	<b>99.03</b>	77.56	*	79.78	87.53	87.60	87.54	87.07	82.58	77.49	77.50	77.30	77.78	77.11	77.24
<i>Pseudomonas batumici</i>	80.06	78.21	80.12	*	80.67	80.71	80.63	80.67	81.22	78.16	78.21	77.95	78.48	77.71	77.77
UCM B-321															
<i>Pseudomonas protegens</i> Cab57	87.64	77.91	87.61	80.45	*	<b>98.36</b>	<b>98.06</b>	89.15	83.53	77.88	77.88	77.40	78.04	77.47	77.55
<i>Pseudomonas protegens</i> CHA0	87.69	77.79	87.70	80.58	<b>98.40</b>	*	<b>98.65</b>	89.11	83.57	77.75	77.80	77.46	78.09	77.49	77.51
<i>Pseudomonas protegens</i> PF-5	87.62	77.88	87.61	80.41	<b>98.03</b>	<b>98.55</b>	*	88.89	83.48	77.90	77.90	77.48	78.14	77.52	77.48
<i>Pseudomonas</i> sp. Os17	87.40	78.11	87.39	80.68	89.43	89.30	89.18	*	83.62	78.09	78.15	77.67	78.25	77.75	77.59
<i>Pseudomonas</i> sp. GM17	82.98	78.28	82.97	81.02	83.75	83.79	83.75	83.59	*	78.32	78.36	78.07	78.66	78.01	78.05
<i>Pseudomonas fragi</i> P121	78.39	<b>99.19</b>	78.40	78.85	78.71	78.66	78.65	78.70	79.09	*	<b>99.14</b>	90.71	85.00	83.22	84.37
<i>Pseudomonas</i> sp. Lz4W	78.30	<b>99.25</b>	78.30	78.79	78.67	78.62	78.63	78.66	79.02	<b>99.21</b>	*	90.76	84.99	83.24	84.22
<i>Pseudomonas</i> sp. L10.10	78.14	90.67	78.17	78.40	78.31	78.31	78.27	78.30	78.80	90.69	90.65	*	84.75	83.08	83.92
<i>Pseudomonas</i> <i>deceptionensis</i> DSM 26,521	78.38	84.93	78.39	78.89	78.69	78.76	78.76	78.71	79.16	84.98	84.91	84.63	*	83.68	87.99
<i>Pseudomonas taetrolens</i> DSM 21,104	77.77	83.11	77.74	78.30	78.03	78.08	78.04	78.15	78.58	83.10	83.16	82.94	83.57	*	83.02
<i>Pseudomonas</i> sp. CF149	77.81	84.09	77.82	78.07	78.07	78.08	78.08	78.11	78.49	84.29	84.15	83.80	87.97	83.03	*



**Table 4**  
ANIm data for F14BN1, F14BN2 and F15BN2. The values represent scores (%). In bold, values > 95%: identification of species.

	F14Bn1 _92_ctg.fas	F14Bn2 _181ctg.fas	F15Bn2 _59_ctg.fas	<i>Pseudomonas</i> <i>batumici</i> UCM B-321	<i>Pseudomonas</i> <i>protegens</i> Cab57	<i>Pseudomonas</i> <i>protegens</i> CHA0	<i>Pseudomonas</i> <i>protegens</i> Pf-5	<i>Pseudomonas</i> sp. Os17	<i>Pseudomonas</i> sp. GM17	<i>Pseudomonas</i> <i>fragi</i> P121	<i>Pseudomonas</i> sp. Lz4W	<i>Pseudomonas</i> sp. L10.10	<i>Pseudomonas</i> <i>deceptionensis</i> DSM 26,521	<i>Pseudomonas</i> <i>taetrolens</i> DSM 21,104	<i>Pseudomonas</i> sp. CF149
F14Bn1_92_ctg.fas	*	84.79	<b>99.28</b>	85.96	89.17	89.24	89.20	89.05	86.89	84.74	84.73	84.67	84.75	84.61	84.53
F14Bn2_181ctg.fas	84.79	*	84.80	84.80	84.86	84.83	84.82	84.81	84.93	<b>99.15</b>	<b>99.30</b>	91.37	87.06	86.24	86.54
F15Bn2_59_ctg.fas	<b>99.28</b>	84.80	*	85.93	89.16	89.24	89.19	89.06	86.89	84.77	84.75	84.66	84.71	84.63	84.54
<i>Pseudomonas</i> <i>batumici</i> UCM B-321	85.95	84.80	85.93	*	86.24	86.27	86.25	86.26	86.57	84.89	84.84	84.84	84.82	84.84	84.69
<i>Pseudomonas</i> <i>protegens</i> Cab57	89.16	84.86	89.16	86.24	*	<b>98.58</b>	<b>98.38</b>	90.66	87.40	84.93	84.88	84.87	84.85	84.68	84.68
<i>Pseudomonas</i> <i>protegens</i> CHA0	89.24	84.84	89.24	86.27	<b>98.60</b>	*	<b>98.87</b>	90.64	87.45	84.96	84.84	84.78	84.85	84.72	84.68
<i>Pseudomonas</i> <i>protegens</i> Pf-5	89.21	84.83	89.19	86.25	<b>98.38</b>	<b>98.87</b>	*	90.53	87.49	84.89	84.83	84.77	84.82	84.76	84.65
<i>Pseudomonas</i> sp. Os17	89.05	84.80	89.06	86.25	90.66	90.64	90.53	*	87.42	84.88	84.86	84.69	84.92	84.78	84.66
<i>Pseudomonas</i> sp. GM17	86.88	84.91	86.88	86.57	87.40	87.44	87.48	87.42	*	84.96	84.97	84.79	84.96	84.92	84.77
<i>Pseudomonas</i> <i>fragi</i> P121	84.74	<b>99.14</b>	84.76	84.89	84.93	84.95	84.88	84.88	84.97	*	<b>99.28</b>	91.35	87.05	86.23	86.77
<i>Pseudomonas</i> sp. Lz4W	84.74	<b>99.30</b>	84.75	84.84	84.87	84.84	84.82	84.87	84.98	99.29	*	91.36	87.07	86.27	86.62
<i>Pseudomonas</i> sp. L10.10	84.67	91.37	84.66	84.84	84.87	84.77	84.77	84.70	84.79	91.35	91.36	*	87.00	86.16	86.53
<i>Pseudomonas</i> <i>deceptionensis</i> DSM 26,521	84.75	87.06	84.71	84.82	84.85	84.86	84.83	84.92	84.96	87.04	87.07	87.00	*	86.46	89.41
<i>Pseudomonas</i> <i>taetrolens</i> DSM 21,104	84.61	86.24	84.62	84.83	84.69	84.73	84.77	84.78	84.92	86.23	86.27	86.16	86.46	*	86.12
<i>Pseudomonas</i> sp. CF149	84.54	86.53	84.55	84.69	84.68	84.68	84.66	84.66	84.77	86.76	86.62	86.53	89.40	86.11	*

**Table 5**

Identification of the proteins released by F14BN1, F14BN2 and F15BN2. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by mass through the "Mascot" search algorithm. ([http://www.matrixscience.com/cgi/search\\_form.pl?FORMVER=2&SEARCH=PMF](http://www.matrixscience.com/cgi/search_form.pl?FORMVER=2&SEARCH=PMF)). In the algorithm Mascot with the SwissProt and NCBI "National Center for Biotechnology Information" databases, protein identification was "significant" if the probability MOWSE score was greater than the signification threshold where P was the probability that the observed match was a random event. (Spot no.) spot number. (MW) molecular weight. (Nb) number of experimental peptides recognized. Maximum  $\neq$  between theoretical/experimental masses = maximum difference between theoretical peptide masses and experimental ones, expressed in ppm (parts per million).

Strain	Protein family	Spot no.	Data Definition	Research algorithm: Mascot								
				Sequence coverage (%)	Theoretical pl	Theoretical MW (kDa)	Nb	Rank	Probability MOWSE score (signification threshold)	ppm	-10lgP	Database
F14BN1	Proteins counteracting oxidative stress and/or ensuring redox balance	o3	ILVC_PSEF5, Ketol-acid reductoisomerase (NADP(+))	34	5.48	36.441	10	1	81 (68)	44.5	0.0029	SwissProt
			OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477/NRRL B-23,932/Pf-5) GN=ilvC									
	Chaperonin proteins	o4	WP_003212997.1, MULTISPECIES: superoxide dismutase [ <i>Pseudomonas</i> ]	46	5.56	22.078	8	1	107 (93)	43.4	0.0021	NCBIprot
			SODF_PSEPK, Superoxide dismutase [Fe]	36	5.55	22.096	6	1	76 (68)	31.8	0.0086	SwissProt
		OS= <i>Pseudomonas putida</i> (strain ATCC 47,054/DSM 6125/NCIMB 11,950/KT2440) GN=sodB										
		c2	HTPG_PSEPF, Chaperone protein HtpG	27	5.13	71.241	17	1	90 (68)	48.9	0.00033	SwissProt
		OS= <i>Pseudomonas fluorescens</i> (strain Pf0-1) GN=htpG										
		c4	WP_025126505.1, trigger factor [ <i>Pseudomonas</i> sp. PH1b]	46	4.82	48.500	18	1	117 (93)	37.5	0.00021	NCBIprot
			WP_015636350.1, trigger factor [ <i>Pseudomonas protegens</i> ]	40	4.81	48.481	16	2	94 (93)	32.8	0.039	NCBIprot
			WP_047337326.1, trigger factor [ <i>Pseudomonas fluorescens</i> ]	40	4.78	48.567	16	2	94 (93)	32.8	0.039	NCBIprot
			WP_011062275.1, MULTISPECIES: trigger factor [ <i>Pseudomonas</i> ]	40	4.78	48.539	16	2	94 (93)	32.8	0.039	NCBIprot
		c5	TIG_PSEF5, Trigger factor OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477/NRRL B-23,932/Pf-5) GN=tig	40	4.78	48.539	16	1	102 (68)	32.8	2.1E-05	SwissProt
	SURA_PSEF5, Chaperone SurA OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477/NRRL B-23,932/Pf-5) GN=surA		34	5.3	47.375	15	1	85 (68)	22.8	0.0011	SwissProt	
	c7	WP_047301678.1, MULTISPECIES: nucleotide exchange factor GrpE [ <i>Pseudomonas</i> ]	52	4.67	20.853	14	1	116 (93)	32	0.00026	NCBIprot	
WP_047283881.1, nucleotide exchange factor GrpE [ <i>Pseudomonas fluorescens</i> ]		52	4.65	20.782	14	1	116 (93)	32	0.00026	NCBIprot		
WP_011059187.1, MULTISPECIES: nucleotide exchange factor GrpE [ <i>Pseudomonas</i> ]		52	4.65	20.810	14	1	116 (93)	32	0.00026	NCBIprot		
GRPE_PSEF5, Protein GrpE OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477/NRRL B-23,932/Pf-5) GN=grpE		52	5.5	20.810	14	1	116 (68)	32	8.4E-07	SwissProt		
Other proteins involved in stress response	p2	CAPB_PSEFR, Cold shock protein CapB	69	6.54	7.722	6	1	77 (68)	56.5	0.0071	SwissProt	
		OS= <i>Pseudomonas fragi</i> GN=capB										

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Table 5 (continued)

Strain	Protein family	Spot no.	Data Definition	Research algorithm: Mascot								
				Sequence coverage (%)	Theoretical pI	Theoretical MW (kDa)	Nb	Rank	Probability MOWSE score (signification threshold)	ppm	-10lgP	Database
F14BN2	Chaperonin proteins	c1	WP_019410411.1, molecular chaperone DnaK [ <i>Pseudomonas psychrophila</i> ]	34	4.84	68.449	19	1	124 (93)	39.5	4.1E-05	NCBIprot
			DNAK_PSEA7, Chaperone protein DnaK OS= <i>Pseudomonas aeruginosa</i> (strain PA7) GN=dnaK	28	4.81	68.405	14	1	91 (68)	49.9	0.00026	SwissProt
		c2	WP_003439583.1, MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	38	4.84	68.265	21	1	150 (93)	32.3	1.0E-07	NCBIprot
		c3	WP_019410411.1, molecular chaperone DnaK [ <i>Pseudomonas psychrophila</i> ]	36	4.84	68.449	17	1	109 (93)	39.8	0.0013	NCBIprot
		c4	WP_003439583.1, MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	44	4.84	68.265	22	1	135 (93)	47.9	3.3E-06	NCBIprot
		c5	WP_003439583.1, MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	42	4.84	68.265	24	1	170 (93)	36.7	1.0E-09	NCBIprot
			DNAK_PSEA7, Chaperone protein DnaK OS= <i>Pseudomonas aeruginosa</i> (strain PA7) GN=dnaK	28	4.81	68.405	16	1	115 (68)	38.7	1.1E-06	SwissProt
		c6	WP_003439583.1, MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	40	4.84	68.265	20	1	133 (93)	48	5.2E-06	NCBIprot
			DNAK_PSEA7, Chaperone protein DnaK OS= <i>Pseudomonas aeruginosa</i> (strain PA7) GN=dnaK	30	4.81	68.405	15	1	93 (68)	48	0.00017	SwissProt
		c7	WP_003446928.1, MULTISPECIES: molecular chaperone HtpG [ <i>Pseudomonas</i> ]	45	5.18	71.200	23	1	153 (93)	49.9	5.2E-08	NCBIprot
		c9	WP_010655838.1, trigger factor [ <i>Pseudomonas fragi</i> ]	47	4.77	48.560	17	1	175 (93)	49.5	3.3E-10	NCBIprot
c10	WP_010655838.1, trigger factor [ <i>Pseudomonas fragi</i> ]	40	4.77	48.560	14	1	126 (93)	47.5	2.6E-05	NCBIprot		
c11	WP_003441361.1, trigger factor [ <i>Pseudomonas</i> sp. Lz4W]	57	4.77	48.530	22	1	164 (93)	48.1	4.1E-09	NCBIprot		
	Other proteins involved in stress response	p2	WP_074811207.1, cold-shock protein [ <i>Pseudomonas syringae</i> ]	81	6.54	7.836	8	1	100 (93)	23.6	0.011	NCBIprot
			CAPB_PSEFR, Cold shock protein CapB OS= <i>Pseudomonas fragi</i> GN=capB	66	6.54	7.722	6	1	83 (68)	18.1	0.0017	SwissProt

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Table 5 (continued)

Strain	Protein family	Spot no.	Data Definition	Research algorithm: Mascot				Rank	Probability MOWSE score (signification threshold)	ppm	-10lgP	Database
				Sequence coverage (%)	Theoretical pl	Theoretical MW (kDa)	Nb					
F15BN2	Proteins counteracting oxidative stress and/or ensuring redox balance	o3	WP_05739798.L1, dihydrolioyl dehydrogenase [ <i>Pseudomonas fluorescens</i> ]	36	5.93	50.091	12	1	98 (93)	23.3	0.016	NCBIprot
		o4	WP_008049689.1, dihydrolioyl dehydrogenase [ <i>Pseudomonas</i> sp. GM74]	35	6.03	50.104	12	1	103 (93)	48.7	0.0052	NCBIprot
	Chaperonin proteins	o5	WP_016966196.1, MULTISPECIES: superoxide dismutase [ <i>Pseudomonas</i> ]	53	5.55	22.089	11	1	104 (93)	49.4	0.0041	NCBIprot
		c2	WP_041119683.1, chaperonin GroEL [ <i>Pseudomonas protegens</i> ]	46	4.99	56.841	17	1	116 (93)	42.6	0.00026	NCBIprot
		c4	CH60_PSEF5, 60kDa chaperonin OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477/INRRL B-23.932/PF-5) GN=grl.	46	4.99	57.086	17	1	115 (68)	42.6	1.1e-06	SwissProt
				WP_025126505.1, trigger factor [ <i>Pseudomonas</i> sp. PH1b]	63	4.82	48.500	21	1	199 (93)	41.7	1.3E-12
		c5	TIG_PSEF5, Trigger factor OS= <i>Pseudomonas fluorescens</i> 57 (strain ATCC BAA-477/INRRL B-23.932/PF-5) GN=tig	57	4.78	48.539	16	1	164 (68)	41.7	1.3E-11	SwissProt
				WP_011063825.1, MULTISPECIES: molecular chaperone SurA [ <i>Pseudomonas</i> ]	53	5.30	47.375	22	1	174 (93)	48.2	4.1E-10
	Other proteins involved in stress response	p1	SURA_PSEF5, Chaperone SurA OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477/INRRL B-23.932/PF-5) GN=surA	53	5.30	47.375	22	1	174 (68)	48.2	1.3E-12	SwissProt
				SEB63063.1, C-terminal processing peptidase-1, Serine 29 peptidase, MEROPS family S41A [ <i>Pseudomonas saponiphila</i> ]	29	5.97	77.543	18	1	114 (93)	45	0.00041
		p4	WP_074811207.1, cold-shock protein [ <i>Pseudomonas syringae</i> ]	85	6.54	7.836	8	1	109 (93)	43.1	0.0013	NCBIprot
			CAPB_PSEFR, Cold shock protein CapB OS= <i>Pseudomonas fragi</i> GN=capB	71	6.54	7.722	7	1	91 (68)	43.1	0.00028	SwissProt

**Table 6**

Identification of the proteins released by Fl4BN1. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by mass through the "PEAKS studio" search algorithm, NCBI database. In the algorithm of PEAKS studio with the SwissProt and NCBI "National Center for Biotechnology Information" databases, protein identification was "significant" if the (-10lgP) score was greater than the peptide hit threshold (30.0). P was the probability that the observed match was a random event. (Spot no.) spot number. (MW) molecular weight. (R) reviewed. (NR) not reviewed. (*P. protegens*) *Pseudomonas protegens*.

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Proteins counteracting oxidative stress and/or ensuring redox balance	o1	dihydrolipoyl dehydrogenase [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332918899</a>	49.831	5	61.76	NCBI_ <i>P. protegens</i>
	o2	MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">gi 499375533</a>	21.787	6	96.79	NCBI_ <i>P. protegens</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">gi 495197643</a>	21.773	6	96.79	NCBI_ <i>P. protegens</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003178707.1</a>	21.856	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003231418.1</a>	21.938	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003188979.1</a>	21.947	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003254945.1</a>	21.730	6	65.14	NCBI_ <i>Bacteria_NR</i>
		peroxiredoxin [ <i>Pseudomonas putida</i> KT2440]	<a href="#">NP_743245.1</a>	21.730	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003172097.1</a>	21.933	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003204949.1</a>	21.929	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003227723.1</a>	21.765	6	65.14	NCBI_ <i>Bacteria_NR</i>

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**Table 6** (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Chaperonin proteins	c1	MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">gi 499371610</a>	68.476	7	45.69	NCBI_P. protegens
	c2	MULTISPECIES: molecular chaperone HtpG [ <i>Pseudomonas</i> ]	<a href="#">gi 499372481</a>	71.349	5	63.50	NCBI_P. protegens
		molecular chaperone HtpG [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332903508</a>	71.349	5	63.50	NCBI_P. protegens
		molecular chaperone HtpG [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332919100</a>	71.336	5	63.50	NCBI_P. protegens
	c3	chaperonin GroEL [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 751652819</a>	56.819	17	139.15	NCBI_P. protegens
		MULTISPECIES: molecular chaperone GroEL [ <i>Pseudomonas</i> ]	<a href="#">gi 499375514</a>	57.065	17	139.15	NCBI_P. protegens
		chaperonin GroEL [ <i>Beggiatoa alba</i> ]	<a href="#">WP_002686219.1</a>	57.692	3	35.32	NCBI_Bacteria_NR
		60 kDa chaperonin GroEL [ <i>Shewanella oneidensis</i> MR-1]	<a href="#">NP_716,337.1</a>	57.080	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Thauera linaloolentis</i> ]	<a href="#">WP_004339041.1</a>	56.684	3	35.32	NCBI_Bacteria_NR
		MULTISPECIES: molecular chaperone GroEL [ <i>Bordetella</i> ]	<a href="#">WP_003808619.1</a>	57.483	3	35.32	NCBI_Bacteria_NR
		molecular chaperone GroEL [ <i>Bordetella pertussis</i> Tohama I]	<a href="#">NP_882014.1</a>	57.482	3	35.32	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [ <i>Pseudomonas</i> ]	<a href="#">WP_003238874.1</a>	56.883	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003175873.1</a>	56.927	3	35.32	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [ <i>Pseudomonas</i> ]	<a href="#">WP_003178748.1</a>	56.843	3	35.32	NCBI_Bacteria_NR
	c6	MULTISPECIES: chaperonin GroEL [ <i>Pseudomonas</i> ]	<a href="#">WP_003227683.1</a>	56.905	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003193939.1</a>	56.882	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Cystobacter fuscus</i> ]	<a href="#">WP_002624037.1</a>	58.167	3	35.32	NCBI_Bacteria_NR
		molecular chaperone GroEL [ <i>Coxiella burnetii</i> RSA 493]	<a href="#">NP_820699.1</a>	58.284	3	35.32	NCBI_Bacteria_NR
		molecular chaperone GroEL [ <i>Nitrosococcus oceanii</i> ]	<a href="#">WP_002813030.1</a>	58.284	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 751652819</a>	56.819	17	139.15	NCBI_P. protegens
MULTISPECIES: molecular chaperone GroEL [ <i>Pseudomonas</i> ]		<a href="#">gi 499375514</a>	57.065	17	139.15	NCBI_P. protegens	

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Table 6 (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Other proteins involved in stress response	p1	tail-specific protease [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 499375085</a>	79.065	2	66.15	NCBI_P. protegens
		peptidase S41 [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1043219129</a>	79.051	2	66.15	NCBI_P. protegens
		MULTISPECIES: tail-specific protease [ <i>Pseudomonas</i> ]	<a href="#">gi 829054598</a>	79.040	2	66.15	NCBI_P. protegens
		tail-specific protease [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 505449515</a>	79.066	2	66.15	NCBI_P. protegens
		tail-specific protease [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 751652595</a>	79.024	2	66.15	NCBI_P. protegens
		MULTISPECIES: tail-specific protease [ <i>Pseudomonas fluorescens group</i> ]	<a href="#">gi 517923405</a>	79.026	2	66.15	NCBI_P. protegens
		tail-specific protease [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332920536</a>	79.022	2	66.15	NCBI_P. protegens
		tail-specific protease [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332900179</a>	79.008	2	66.15	NCBI_P. protegens
		MULTISPECIES: tail-specific protease [ <i>Pseudomonas</i> ]	<a href="#">WP_003179086.1</a>	78.994	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: tail-specific protease [ <i>Pseudomonas</i> ]	<a href="#">WP_003204565.1</a>	79.144	2	45.61	NCBI_Bacteria_NR
		peptidase S41 [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003172944.1</a>	79.122	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: peptidase S41 [ <i>Pseudomonas</i> ]	<a href="#">WP_003190141.1</a>	79.102	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: peptidase S41 [ <i>Pseudomonas</i> ]	<a href="#">WP_003211110.1</a>	79.101	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: tail-specific protease [ <i>Pseudomonas</i> ]	<a href="#">WP_003231887.1</a>	79.074	2	45.61	NCBI_Bacteria_NR
		tail-specific protease Prc [ <i>Pseudomonas putida</i> KT2440]	<a href="#">NP_743876.1</a>	79.097	2	45.61	NCBI_Bacteria_NR
		S41 family peptidase [ <i>Pseudomonas</i> sp. Lz4W]	<a href="#">WP_003446856.1</a>	79.047	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: cold-shock protein [ <i>Pseudomonas</i> ]	<a href="#">gi 495252543</a>	7.736	14	43.15	NCBI_P. protegens

**Table 7**

Identification of the proteins released by Fl4BN1. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by mass through the "PEAKS studio" search algorithm, SwissProt database. In the algorithm of PEAKS studio with the SwissProt and NCBI "National Center for Biotechnology Information" databases, protein identification was "significant" if the (-10lgP) score was greater than the peptide hit threshold (30.0). P was the probability that the observed match was a random event. (Spot no.) spot number. (MW) molecular weight. (R) reviewed. (NR) not reviewed. (*P. protegens*) *Pseudomonas protegens*.

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Proteins counteracting oxidative stress and/or ensuring redox balance	o1	Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> (strain DSM 19,095/LMG 27,888 / CHA0) GN=lpdG	<a href="#">A0A2C9EIR1_PSEPH</a>	49.874	5	47.56	SwissP_ <i>P. protegens</i>
	o2	Putative peroxiredoxin TsaA OS= <i>Pseudomonas protegens</i> (strain DSM 19,095/LMG 27,888 / CHA0) GN=tsaA	<a href="#">A0A2C9ESU7_PSEPH</a>	21.787	6	80.76	SwissP_ <i>P. protegens</i>
		Antioxidant, AhpC/TSA family OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477/NRRL B-23,932 / Pf-5) OX=220,664 GN=PFL_4857	<a href="#">Q4K745_PSEF5</a>	21.787	6	80.76	SwissP_ <i>P. protegens</i>
Chaperonin proteins	c1	Alkyl hydroperoxide reductase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_15,140	<a href="#">A0A2J7U847_9PSED</a>	21.773	6	80.76	SwissP_ <i>P. protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=dnaK	<a href="#">DNAK_PSEFS</a>	68.200	11	90.38	SwissP_ <i>Bacteria_R</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) GN=dnaK	<a href="#">A0A2C9EG81_PSEPH</a>	68.476	3	28.43	SwissP_ <i>P. protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	<a href="#">A0A2T6GM17_9PSED</a>	68.433	3	28.43	SwissP_ <i>P. protegens</i>
	c2	Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=dnaK	<a href="#">DNAK_PSEF5</a>	68.476	3	28.43	SwissP_ <i>P. protegens</i>
		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> OX=380,021 GN=htpG	<a href="#">A0A2T6GQG4_9PSED</a>	71.363	5	82.38	SwissP_ <i>P. protegens</i>
		Chaperone protein HtpG OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=htpG	<a href="#">HTPG_PSEF5</a>	71.349	5	82.38	SwissP_ <i>P. protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	<a href="#">A0A2J7UMP6_9PSED</a>	68.476	3	82.43	SwissP_ <i>P. protegens</i>
		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=htpG	<a href="#">A0A2C9EIV4_PSEPH</a>	71.581	5	82.38	SwissP_ <i>P. protegens</i>

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Table 7 (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Other proteins involved in stress response	c3	60 kDa chaperonin OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=groL	<a href="#">A0A2C9ESJ4_PSEPH</a>	57.065	15	165.11	SwissP_P. protegens
		60 kDa chaperonin OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=groL	<a href="#">CH60_PSEF5</a>	57.065	15	117.99	SwissP_Bacteria_R
	c4	Trigger factor OS= <i>Pseudomonas protegens</i> OX=380,021 GN=tig PE=3 SV=1	<a href="#">A0A2T6GBS8_9PSED</a>	48.484	2	31.70	SwissP_P. protegens
		Trigger factor OS= <i>Pseudomonas mendocina</i> (strain ymp) GN=tig	<a href="#">TIG_PSEMY</a>	48.330	2	24.02	SwissP_Bacteria_R
		Trigger factor OS= <i>Pseudomonas fluorescens</i> (strain Pf0-1) GN=tig	<a href="#">TIG_PSEPF</a>	48.485	2	24.02	SwissP_Bacteria_R
	c5	Elongation factor Tu OS= <i>Escherichia coli</i> O6:H1 (strain CFT073 / ATCC 700,928 / UPEC) GN=tufA	<a href="#">EFTU_ECOL6</a>	43.314	2	25.24	SwissP_Bacteria_R
	p1	Peptidase, S41 family OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=prc	<a href="#">Q4K8E7_PSEF5</a>	79.065	2	70.45	SwissP_P. protegens
		Tail-specific protease Prc OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=prc	<a href="#">A0A2C9ERC3_PSEPH</a>	79.066	2	70.45	SwissP_P. protegens
		Temperature acclimation protein B OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=tapB	<a href="#">A0A2C9ES32_PSEPH</a>	7.736	40	34.43	SwissP_P. protegens
		/Temperature acclimation protein B OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=tapB	<a href="#">Q4K7Q5_PSEF5</a>	7.736	40	34.43	SwissP_P. protegens
	p3	Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_14,565	<a href="#">A0A2K4M1K2_9PSED</a>	7.736	40	34.43	SwissP_P. protegens

**Table 8**

Identification of the proteins released by F14BN2 culture. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by mass through the "PEAKS studio" search algorithm, NCBI database. In the algorithm of PEAKS studio with the SwissProt and NCBI "National Center for Biotechnology Information" databases, protein identification was "significant" if the (-10lgP) score was greater than the peptide hit threshold (30.0). P was the probability that the observed match was a random event. (Spot no.) spot number. (MW) molecular weight. (R) reviewed. (NR) not reviewed. (*P. protegens*) *Pseudomonas protegens*.

Protein family	Spot no.	Data Definition	Research algorithm: PEAKS				
			Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Proteins counteracting oxidative stress and/or ensuring redox balance	o1	MULTISPECIES: monothiol glutaredoxin, Grx4 family [ <i>Pseudomonas</i> ]	<a href="#">gi 1125808736</a>	12.108	12	136.77	NCBI_ <i>P. protegens</i>
		MULTISPECIES: monothiol glutaredoxin, Grx4 family [ <i>Pseudomonas</i> ]	<a href="#">gi 499375536</a>	12.050	12	136.77	NCBI_ <i>P. protegens</i>
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003246056.1</a>	11.793	12	94.59	NCBI_Bacteria_NR
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas aeruginosa</i> ]	<a href="#">WP_003110008.1</a>	11.871	12	94.59	NCBI_Bacteria_NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003188975.1</a>	11.545	12	94.59	NCBI_Bacteria_NR
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas syringae</i> ]	<a href="#">WP_003405440.1</a>	11.649	12	94.59	NCBI_Bacteria_NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_002554852.1</a>	11.677	12	94.59	NCBI_Bacteria_NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003092082.1</a>	11.843	12	94.59	NCBI_Bacteria_NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_004396490.1</a>	11.650	12	94.59	NCBI_Bacteria_NR
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas aeruginosa</i> ]	<a href="#">WP_003130081.1</a>	11.843	12	94.59	NCBI_Bacteria_NR
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas stutzeri</i> ]	<a href="#">WP_003295894.1</a>	11.820	12	94.59	NCBI_Bacteria_NR
		hypothetical protein PA3533 [ <i>Pseudomonas aeruginosa</i> PAO1]	<a href="#">NP_252223.1</a>	11.843	12	94.59	NCBI_Bacteria_NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003299217.1</a>	11.817	12	94.59	NCBI_Bacteria_NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003453456.1</a>	11.819	12	94.59	NCBI_Bacteria_NR

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**Table 8** (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS						
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database		
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas stutzeri</i> ]	<a href="#">WP_003289286.1</a>	11.833	12	94.59	NCBI_Bacteria_NR		
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas syringae</i> ]	<a href="#">WP_004393736.1</a>	11.676	12	94.59	NCBI_Bacteria_NR		
		glutaredoxin-like protein [[ <i>Pseudomonas syringae</i> ] pv. <i>tomato</i> str. DC3000]	<a href="#">NP_793922.1</a>	11.650	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003284603.1</a>	11.857	12	94.59	NCBI_Bacteria_NR		
		monothiol glutaredoxin [ <i>Pseudomonas putida</i> KT2440]	<a href="#">NP_743242.1</a>	12.123	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003254949.1</a>	12.137	12	94.59	NCBI_Bacteria_NR		
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003178700.1</a>	12.050	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003208710.1</a>	12.000	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003231422.1</a>	11.874	12	94.59	NCBI_Bacteria_NR		
		Grx4 family monothiol glutaredoxin [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003172092.1</a>	12.015	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003204956.1</a>	12.135	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003443184.1</a>	12.080	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [ <i>Pseudomonas</i> ]	<a href="#">WP_003227729.1</a>	12.109	12	94.59	NCBI_Bacteria_NR		
		Chaperonin proteins	c1	MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">WP_003439583.1</a>	68.193	20	351.06	NCBI_Bacteria_NR
				molecular chaperone DnaK [ <i>Pseudomonas stutzeri</i> ]	<a href="#">WP_003298038.1</a>	68.696	7	262.60	NCBI_Bacteria_NR
molecular chaperone DnaK [ <i>Pseudomonas stutzeri</i> ]	<a href="#">WP_003293240.1</a>			68.628	7	262.60	NCBI_Bacteria_NR		
c3	molecular chaperone DnaK [ <i>Pseudomonas protegens</i> ]		<a href="#">gi 1332900475</a>	68.460	18	237.39	NCBI_P. protegens		
	molecular chaperone DnaK [ <i>Pseudomonas protegens</i> ]		<a href="#">gi 1332918337</a>	68.430	18	237.39	NCBI_P. protegens		
	MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]		<a href="#">gi 499371610</a>	68.476	17	204.77	NCBI_P. protegens		

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Table 8 (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
		molecular chaperone DnaK [ <i>Pseudomonas stutzeri</i> ]	<a href="#">WP_003293240.1</a>	68.628	7	262.60	NCBI_Bacteria_NR
		MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">WP_003439583.1</a>	68.193	20	351.06	NCBI_Bacteria_NR
c4		molecular chaperone DnaK [ <i>Pseudomonas stutzeri</i> ]	<a href="#">WP_003298038.1</a>	68.696	7	262.60	NCBI_Bacteria_NR
		molecular chaperone DnaK [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332900475</a>	68.460	18	237.39	NCBI_P. protegens
		molecular chaperone DnaK [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332918337</a>	68.430	18	237.39	NCBI_P. protegens
		MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">gi 499371610</a>	68.476	17	204.77	NCBI_P. protegens
		MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">WP_003439583.1</a>	68.193	20	351.06	NCBI_Bacteria_NR
c5		molecular chaperone DnaK [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332900475</a>	68.460	18	237.39	NCBI_P. protegens
		molecular chaperone DnaK [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332918337</a>	68.430	18	237.39	NCBI_P. protegens
		MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">gi 499371610</a>	68.476	17	204.77	NCBI_P. protegens
c6		MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">WP_003439583.1</a>	68.193	20	351.06	NCBI_Bacteria_NR
c8		MULTISPECIES: molecular chaperone HtpG [ <i>Pseudomonas</i> ]	<a href="#">gi 499372481</a>	71.349	13	153.49	NCBI_P. protegens
		molecular chaperone HtpG [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332903508</a>	71.349	13	153.49	NCBI_P. protegens
		molecular chaperone HtpG [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332919100</a>	71.336	13	153.49	NCBI_P. protegens
		MULTISPECIES: molecular chaperone HtpG [ <i>Pseudomonas</i> ]	<a href="#">WP_003446928.1</a>	71.244	13	190.80	NCBI_Bacteria_NR
c9		MULTISPECIES: trigger factor [ <i>Pseudomonas</i> ]	<a href="#">gi 499374697</a>	48.569	22	165.79	NCBI_P. protegens
c10		MULTISPECIES: trigger factor [ <i>Pseudomonas</i> ]	<a href="#">gi 499374697</a>	48.569	22	165.79	NCBI_P. protegens
c11		MULTISPECIES: trigger factor [ <i>Pseudomonas</i> ]	<a href="#">gi 499374697</a>	48.569	22	165.79	NCBI_P. protegens
c12		nucleotide exchange factor GrpE [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332900474</a>	20.837	25	116.18	NCBI_P. protegens

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Table 8 (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	−10lgP	Database
Other proteins involved in stress response	c13	MULTISPECIES: nucleotide exchange factor GrpE [ <i>Pseudomonas</i> ]	<a href="#">WP_003439582.1</a>	20.897	21	86.11	NCBI_Bacteria_NR
		nucleotide exchange factor GrpE [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332900474</a>	20.837	25	116.18	NCBI_P. protegens
		MULTISPECIES: nucleotide exchange factor GrpE [ <i>Pseudomonas</i> ]	<a href="#">WP_003439582.1</a>	20.897	21	86.11	NCBI_Bacteria_NR
		heat shock protein GrpE [ <i>Pseudomonas putida</i> KT2440]	<a href="#">NP_746836.1</a>	20.531	9	35.12	NCBI_Bacteria_NR
	c14	MULTISPECIES: nucleotide exchange factor GrpE [ <i>Pseudomonas</i> ]	<a href="#">WP_003249927.1</a>	20.501	9	35.12	NCBI_Bacteria_NR
		MULTISPECIES: cyclophilin [ <i>Pseudomonas</i> ]	<a href="#">gi 515532580</a>	18.283	7	44.00	NCBI_P. protegens
	p1	MULTISPECIES: cyclophilin [ <i>Pseudomonas</i> ]	<a href="#">gi 499374623</a>	18.269	7	44.00	NCBI_P. protegens
		MULTISPECIES: cold-shock protein CapB [ <i>Pseudomonas</i> ]	<a href="#">gi 488617988</a>	7.727	46	157.27	NCBI_P. protegens
		MULTISPECIES: nucleoid-associated protein, YbaB/EbfC family [ <i>Pseudomonas</i> ]	<a href="#">gi 505447677</a>	12.131	12	85.20	NCBI_P. protegens
		p2	MULTISPECIES: cold-shock protein CapB [ <i>Pseudomonas</i> ]	<a href="#">gi 488617988</a>	7.727	46	157.27
cold shock protein CapB [[ <i>Pseudomonas syringae</i> ] pv. <i>tomato</i> str. DC3000]	<a href="#">NP_793906.1</a>		7.727	46	116.65	NCBI_Bacteria_NR	
MULTISPECIES: cold-shock protein CapB [ <i>Pseudomonas</i> ]	<a href="#">WP_002554837.1</a>		7.727	46	116.65	NCBI_Bacteria_NR	

**Table 9**

Identification of the proteins released by Fl4BN2. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by mass through the "PEAKS studio" search algorithm, SwissProt database. In the algorithm of PEAKS studio with the SwissProt and NCBI "National Center for Biotechnology Information" databases, protein identification was "significant" if the (-10lgP) score was greater than the peptide hit threshold (30.0). P was the probability that the observed match was a random event. (Spot no.) spot number. (MW) molecular weight. (R) reviewed. (NR) not reviewed. (*P. protegens*) *Pseudomonas protegens*.

Protein family	Spot no.	Data		Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database	
Proteins counteracting oxidative stress and/or ensuring redox balance	o1	Glutaredoxin OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=grxD	<a href="#">Q4K742_PSEF5</a>	12.050	12	127.54	SwissP_ <i>P. protegens</i>	
		Glutaredoxin OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grxD	<a href="#">A0A2T6GIP8_9PSED</a>	12.050	12	127.54	SwissP_ <i>P. protegens</i>	
		Glutaredoxin OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_15,155	<a href="#">A0A2J7U865_9PSED</a>	12.108	12	127.54	SwissP_ <i>P. protegens</i>	
		Glutaredoxin OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=grxD	<a href="#">A0A2C9ESK9_PSEPH</a>	12.050	12	127.54	SwissP_ <i>P. protegens</i>	
Chaperonin proteins	c1	Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	<a href="#">A0A2J7UJG0_9PSED</a>	68.430	18	242.89	SwissP_ <i>P. protegens</i>	
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	<a href="#">A0A2C9EG81_PSEPH</a>	68.476	17	208.95	SwissP_ <i>P. protegens</i>	
	c2	Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	<a href="#">A0A2J7UJG0_9PSED</a>	68.430	18	242.89	SwissP_ <i>P. protegens</i>	
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	<a href="#">A0A2C9EG81_PSEPH</a>	68.476	17	208.95	SwissP_ <i>P. protegens</i>	
	c3	Chaperone protein DnaK OS= <i>Pseudomonas mendocina</i> (strain ymp) GN=dnaK	<a href="#">DNAK_PSEMY</a>	68.746	11	285.87	SwissP_ <i>Bacteria_R</i>	
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	<a href="#">A0A2J7UJG0_9PSED</a>	68.430	18	242.89	SwissP_ <i>P. protegens</i>	
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	<a href="#">A0A2C9EG81_PSEPH</a>	68.476	17	208.95	SwissP_ <i>P. protegens</i>	
			Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=dnaK	<a href="#">DNAK_PSEF5</a>	68.476	12	171.05	SwissP_ <i>Bacteria_R</i>

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Table 9 (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
c4		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	<a href="#">A0A2J7UJG0_9PSED</a>	68.430	18	242.89	SwissP_P. protegens
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	<a href="#">A0A2C9EG81_PSEPH</a>	68.476	17	208.95	SwissP_P. protegens
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=dnaK	<a href="#">DNAK_PSEF5</a>	68.476	12	171.05	SwissP_Bacteria_R
c6		Chaperone protein DnaK OS= <i>Pseudomonas mendocina</i> (strain ymp) GN=dnaK	<a href="#">DNAK_PSEMY</a>	68.476	11	285.87	SwissP_Bacteria_R
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=dnaK	<a href="#">DNAK_PSEF5</a>	68.476	12	171.05	SwissP_Bacteria_R
c8		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> OX=380,021 GN=htpG	<a href="#">A0A2T6GQG4_9PSED</a>	71.363	13	142.20	SwissP_P. protegens
		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> OX=380,021 GN=htpG	<a href="#">A0A2J7UMP6_9PSED</a>	71.336	13	142.20	SwissP_P. protegens
		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=htpG	<a href="#">A0A2C9EIV4_PSEPH</a>	71.581	13	142.20	SwissP_P. protegens
		Chaperone protein HtpG OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=htpG	<a href="#">HTPG_PSEF5</a>	71.349	13	137.93	SwissP_Bacteria_R
c9		Trigger factor OS= <i>Pseudomonas protegens</i> OX=380,021 GN=tig	<a href="#">A0A2J7U087_9PSED</a>	48.516	18	165.99	SwissP_P. protegens
		Trigger factor OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) GN=tig	<a href="#">A0A2C9EQ79_PSEPH</a>	48.511	17	165.98	SwissP_P. protegens
		Trigger factor OS= <i>Pseudomonas aeruginosa</i> (strain LESB58) GN=tig	<a href="#">TIG_PSEA8</a>	48.582	12	94.71	SwissP_Bacteria_R
		Trigger factor OS= <i>Pseudomonas aeruginosa</i> (strain ATCC 15,692 / DSM 22,644 / CIP 104,116 / JCM 14,847 / LMG 12,228 / 1C / PRS 101 / PAO1) GN=tig	<a href="#">TIG_PSEAE</a>	48.582	12	94.71	SwissP_Bacteria_R

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**Table 9** (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
		Trigger factor OS= <i>Pseudomonas aeruginosa</i> (strain PA7) GN=tig	<a href="#">TIG_PSEA7</a>	48.548	12	94.71	SwissP_Bacteria_R
		Trigger factor OS= <i>Pseudomonas aeruginosa</i> (strain UCBPP-PA14) GN=tig	<a href="#">TIG_PSEAB</a>	48.582	12	94.71	SwissP_Bacteria_R
	c11	Trigger factor OS= <i>Pseudomonas protegens</i> OX=380,021 GN=tig	<a href="#">A0A2J7U087_9PSED</a>	48.516	18	165.99	SwissP_P. protegens
		Trigger factor OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) GN=tig	<a href="#">A0A2C9EQ79_PSEPH</a>	48.511	17	165.98	SwissP_P. protegens
	c12	Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	<a href="#">A0A2J7UA71_9PSED</a>	20.837	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	<a href="#">A0A2T6GLZ5_9PSED</a>	10.865	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=grpE	<a href="#">A0A2C9EG73_PSEPH</a>	20.823	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=grpE	<a href="#">GRPE_PSEF5</a>	20.823	25	88.28	SwissP_Bacteria_R
	c13	Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	<a href="#">A0A2J7UA71_9PSED</a>	20.837	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	<a href="#">A0A2T6GLZ5_9PSED</a>	10.865	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=grpE	<a href="#">A0A2C9EG73_PSEPH</a>	20.823	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=grpE	<a href="#">GRPE_PSEF5</a>	20.823	25	88.28	SwissP_Bacteria_R

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Table 9 (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Other proteins involved in stress response	p1	Cold shock protein CapB OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=capB	<a href="#">A0A2C9EHH8_PSEPH</a>	7.727	46	271.99	SwissP_P. <i>protegens</i>
		Cold shock protein CapB OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=capB	<a href="#">Q4KH94_PSEF5</a>	7.727	46	271.99	SwissP_P. <i>protegens</i>
		Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_02635	<a href="#">A0A2J7UBE2_9PSED</a>	7.727	46	271.99	SwissP_P. <i>protegens</i>
		Nucleoid-associated protein PFL_1905 OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=PFL_1905	<a href="#">Y1905_PSEF5</a>	12	12	75.61	SwissP_P. <i>protegens</i>
		Nucleoid-associated protein A1395_05835 OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_05835	<a href="#">A0A2K4M432_9PSED</a>	12.131	12	75.61	SwissP_P. <i>protegens</i>
		Nucleoid-associated protein PFLCHA0_c19450 OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=PFLCHA0_c19450	<a href="#">A0A2C9EJ97_PSEPH</a>	12.131	12	75.61	SwissP_P. <i>protegens</i>
		Nucleoid-associated protein PFL_1905 OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=PFL_1905	<a href="#">Y1905_PSEF5</a>	12.000	12	84.97	SwissP_Bacteria_R
	p2	Cold shock protein CapB OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=capB	<a href="#">A0A2C9EHH8_PSEPH</a>	7.727	46	271.99	SwissP_P. <i>protegens</i>
		Cold shock protein CapB OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=capB	<a href="#">Q4KH94_PSEF5</a>	7.727	46	271.99	SwissP_P. <i>protegens</i>
		Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_02635	<a href="#">A0A2J7UBE2_9PSED</a>	7.727	46	271.99	SwissP_P. <i>protegens</i>
p3	Cold shock protein CapB OS= <i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000) GN=capB	<a href="#">CAPB_PSESM</a>	7.727	46	135.90	SwissP_Bacteria_R	

**Table 10**

Identification of the proteins released by F15BN2. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by mass through the "PEAKS studio" search algorithm, NCBI database. In the algorithm of PEAKS studio with the SwissProt and NCBI "National Center for Biotechnology Information" databases, protein identification was "significant" if the  $(-10\lg P)$  score was greater than the peptide hit threshold (30.0). P was the probability that the observed match was a random event. (Spot no.) spot number. (MW) molecular weight. (R) reviewed. (NR) not reviewed. (*P. protegens*) *Pseudomonas protegens*.

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	$-10\lg P$	Database
Proteins counteracting oxidative stress and/or ensuring redox balance	o2	Chain B, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	<a href="#">gi 1258501321</a>	50.185	8	108.72	NCBI_Bacteria_R
		Chain A, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	<a href="#">gi 1101274917</a>	50.185	8	108.72	NCBI_Bacteria_R
		Chain B, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	<a href="#">gi 1101274918</a>	50.185	8	108.72	NCBI_Bacteria_R
		Chain A, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	<a href="#">gi 1258501320</a>	50.185	8	108.72	NCBI_Bacteria_R
		dihydrolipoyl dehydrogenase [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332903368</a>	49.797	9	86.94	NCBI_P. protegens
		dihydrolipoyl dehydrogenase [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332918899</a>	49.831	9	86.94	NCBI_P. protegens
		MULTISPECIES: dihydrolipoyl dehydrogenase [ <i>Pseudomonas</i> ]	<a href="#">gi 499372476</a>	49.874	9	86.94	NCBI_P. protegens
		dihydrolipoyl dehydrogenase [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332903368</a>	49.797	9	86.94	NCBI_P. protegens
		MULTISPECIES: dihydrolipoyl dehydrogenase [ <i>Pseudomonas</i> ]	<a href="#">WP_003223013.1</a>	49.812	9	130.96	NCBI_Bacteria_NR
	o3	dihydrolipoyl dehydrogenase [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332903368</a>	49.797	9	86.94	NCBI_P. protegens
		dihydrolipoyl dehydrogenase [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 1332918899</a>	49.831	9	86.94	NCBI_P. protegens
		MULTISPECIES: dihydrolipoyl dehydrogenase [ <i>Pseudomonas</i> ]	<a href="#">gi 499372476</a>	49.874	9	86.94	NCBI_P. protegens
		MULTISPECIES: dihydrolipoyl dehydrogenase [ <i>Pseudomonas</i> ]	<a href="#">WP_003223013.1</a>	49.812	9	130.96	NCBI_Bacteria_NR

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Table 10 (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
	o5	MULTISPECIES: superoxide dismutase [ <i>Pseudomonas</i> ]	<a href="#">gi 499375502</a>	22.003	29	155.45	NCBI_ <i>P. protegens</i>
		Chain B, 1 Iron Superoxide Dismutase <i>Pseudomonas putida</i>	<a href="#">gi 349943</a>	21.530	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain A, 1 Iron Superoxide Dismutase <i>Pseudomonas putida</i>	<a href="#">gi 349942</a>	21.530	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain B, 1 SUPEROXIDE DISMUTASE <i>Pseudomonas putida</i>	<a href="#">gi 12084343</a>	21.890	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain C, 1 SUPEROXIDE DISMUTASE <i>Pseudomonas putida</i>	<a href="#">gi 12084344</a>	21.890	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain A, 1 SUPEROXIDE DISMUTASE <i>Pseudomonas putida</i>	<a href="#">gi 12084342</a>	21.890	14	138.13	NCBI_ <i>Bacteria_R</i>
		superoxide dismutase [ <i>Pseudomonas putida</i> KT2440]	<a href="#">NP_743076.1</a>	21.939	25	116.36	NCBI_ <i>Bacteria_NR</i>

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**Table 10** (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Chaperonin proteins	c2	MULTISPECIES: superoxide dismutase [Fe] [ <i>Pseudomonas</i> ]	<a href="#">WP_003255187.1</a>	21.939	25	116.36	NCBI_Bacteria_NR
		MULTISPECIES: superoxide dismutase [ <i>Pseudomonas</i> ]	<a href="#">WP_003212997.1</a>	21.978	25	116.36	NCBI_Bacteria_NR
		MULTISPECIES: superoxide dismutase [ <i>Pseudomonas</i> ]	<a href="#">WP_003175739.1</a>	22.005	25	116.36	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 751652819</a>	56.819	20	136.41	NCBI_P. protegens
		MULTISPECIES: molecular chaperone GroEL [ <i>Pseudomonas</i> ]	<a href="#">gi 499375514</a>	57.065	20	136.41	NCBI_P. protegens
		MULTISPECIES: chaperonin GroEL [ <i>Pseudomonas</i> ]	<a href="#">WP_003238874.1</a>	56.883	3	81.74	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003175873.1</a>	56.927	3	81.74	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [ <i>Pseudomonas</i> ]	<a href="#">WP_003178748.1</a>	56.843	3	81.74	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [ <i>Pseudomonas</i> ]	<a href="#">WP_003227683.1</a>	56.905	3	81.74	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003193939.1</a>	56.882	3	81.74	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas protegens</i> ]	<a href="#">gi 751652819</a>	56.819	11	131.03	NCBI_P. protegens
		MULTISPECIES: molecular chaperone GroEL [ <i>Pseudomonas</i> ]	<a href="#">gi 499375514</a>	57.065	11	131.03	NCBI_P. protegens
		MULTISPECIES: chaperonin GroEL [ <i>Pseudomonas</i> ]	<a href="#">WP_003238874.1</a>	56.883	7	77.38	NCBI_Bacteria_NR
		chaperonin GroEL [ <i>Pseudomonas fluorescens</i> ]	<a href="#">WP_003193939.1</a>	56.882	7	77.38	NCBI_Bacteria_NR

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Table 10 (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
	c6	MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">gi 499371610</a>	68.476	8	107.62	NCBI_ <i>P. protegens</i>
		MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">WP_003212222.1</a>	68.330	8	103.78	NCBI_ <i>Bacteria</i> _NR
	c7	MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">gi 499371610</a>	68.476	8	107.62	NCBI_ <i>P. protegens</i>
		MULTISPECIES: molecular chaperone DnaK [ <i>Pseudomonas</i> ]	<a href="#">WP_003212222.1</a>	68.330	8	103.78	NCBI_ <i>Bacteria</i> _NR
	c8	MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas</i> ]	<a href="#">gi 495199965</a>	21.678	18	217.97	NCBI_ <i>P. protegens</i>
		MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas</i> ]	<a href="#">WP_003194089.1</a>	21.675	9	124.62	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas</i> ]	<a href="#">WP_003230860.1</a>	21.718	9	124.62	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas</i> ]	<a href="#">WP_003176055.1</a>	21.689	9	124.62	NCBI_ <i>Bacteria</i> _NR

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Table 10 (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: NCBI reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	–10lgP	Database
	c9	MULTISPECIES: cyclophilin [ <i>Pseudomonas</i> ]	<a href="#">gi 515532580</a>	18.283	14	60.40	NCBI_P. protegens
		MULTISPECIES: cyclophilin [ <i>Pseudomonas</i> ]	<a href="#">gi 499374623</a>	18.269	14	60.40	NCBI_P. protegens
		peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas savastanoi</i> ]	<a href="#">WP_004664345.1</a>	18.176	7	20.50	NCBI_Bacteria_NR
		peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas syringae</i> ]	<a href="#">WP_003390678.1</a>	18.315	7	20.50	NCBI_Bacteria_NR
		peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas syringae</i> ]	<a href="#">WP_004418527.1</a>	18.328	7	20.50	NCBI_Bacteria_NR
		MULTISPECIES: peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas</i> ]	<a href="#">WP_003404493.1</a>	18.300	7	20.50	NCBI_Bacteria_NR
		MULTISPECIES: peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas syringae</i> group]	<a href="#">WP_004661308.1</a>	18.218	7	20.50	NCBI_Bacteria_NR
		MULTISPECIES: peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas</i> ]	<a href="#">WP_003441354.1</a>	18.288	7	20.50	NCBI_Bacteria_NR
		peptidyl-prolyl cis-trans isomerase [ <i>Pseudomonas syringae</i> ]	<a href="#">WP_003423206.1</a>	18.332	7	20.50	NCBI_Bacteria_NR
		Other proteins involved in stress response	p4	MULTISPECIES: cold-shock protein [ <i>Pseudomonas</i> ]	<a href="#">gi 489272243</a>	7.697	20
	p5	MULTISPECIES: cold-shock protein CapB [ <i>Pseudomonas</i> ]	<a href="#">gi 488617988</a>	7.727	46	140.69	NCBI_P. protegens
		cold shock protein CapB [[ <i>Pseudomonas syringae</i> ] pv. tomato str. DC3000]	<a href="#">NP_793906.1</a>	7.727	46	81.81	NCBI_Bacteria_NR
		MULTISPECIES: cold-shock protein CapB [ <i>Pseudomonas</i> ]	<a href="#">WP_002554837.1</a>	7.727	46	81.81	NCBI_Bacteria_NR

**Table 11**

Identification of the proteins released by F15BN2. They migrated in a gel with an isoelectric point gradient from 3 to 10 and were identified by the technique of peptide mapping by mass through the "PEAKS studio" search algorithm, SwissProt database. In the algorithm of PEAKS studio with the SwissProt and NCBI "National Center for Biotechnology Information" databases, protein identification was "significant" if the (-10lgP) score was greater than the peptide hit threshold (30.0). P was the probability that the observed match was a random event. (Spot no.) spot number. (MW) molecular weight. (R) reviewed. (NR) not reviewed. (*P. protegens*) *Pseudomonas protegens*.

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Proteins counteracting oxidative stress and/or ensuring redox balance	o1	Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas fluorescens</i> GN=lpd	<a href="#">DLDH_PSEFL</a>	50.151	4	88.73	SwissP_Bacteria_R
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas aeruginosa</i> (strain ATCC 15,692 / DSM 22,644 / CIP 104,116 / JCM 14,847 / LMG 12,228 / 1C / PRS 101 / PAO1) GN=lpdG	<a href="#">DLDH2_PSEAE</a>	50.165	4	88.73	SwissP_Bacteria_R
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas putida</i> GN=lpdG	<a href="#">DLDH2_PSEPU</a>	49.896	4	88.73	SwissP_Bacteria_R
	o2	Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=lpdA	<a href="#">A0A2T6GPH9_9PSED</a>	49.810	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=lpdA_1	<a href="#">Q4KFY7_PSEF5</a>	49.874	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=lpdG	<a href="#">A0A2C9EIR1_PSEPH</a>	49.874	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_04885	<a href="#">A0A2J7ULV5_9PSED</a>	49.831	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas fluorescens</i> GN=lpd	<a href="#">DLDH_PSEFL</a>	50.151	4	88.73	SwissP_Bacteria_R
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas aeruginosa</i> (strain ATCC 15,692 / DSM 22,644 / CIP 104,116 / JCM 14,847 / LMG 12,228 / 1C / PRS 101 / PAO1) GN=lpdG	<a href="#">DLDH2_PSEAE</a>	50.165	4	88.73	SwissP_Bacteria_R
Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas putida</i> GN=lpdG	<a href="#">DLDH2_PSEPU</a>	49.896	4	88.73	SwissP_Bacteria_R		

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**Table 11** (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas</i> sp. RIT-PI-r OX=1,699,620 GN=AK821_18,310	<a href="#">A0A0P6RYG8_9PSED</a>	49.840	4	63.95	SwissP_Bacteria_NR
	o3	Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=lpdA	<a href="#">A0A2T6GPH9_9PSED</a>	49.810	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=lpdA_1	<a href="#">Q4KFY7_PSEF5</a>	49.874	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=lpdG	<a href="#">A0A2C9EIR1_PSEPH</a>	49.874	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_04885	<a href="#">A0A2J7ULV5_9PSED</a>	49.831	9	95.34	SwissP_P. protegens
	o5	Superoxide dismutase OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=sodB	<a href="#">A0A2C9ESB6_PSEPH</a>	22.003	25	122.57	SwissP_P. protegens
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=sodB	<a href="#">Q4K776_PSEF5</a>	22.003	25	122.57	SwissP_P. protegens
		Superoxide dismutase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_14,980	<a href="#">A0A2J7U822_9PSED</a>	22.003	25	122.57	SwissP_P. protegens
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=A3L25_01085	<a href="#">A0A166M6_x6_PSEPU</a>	21.937	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=QV12_13,665	<a href="#">A0A0D1LV26_PSEPU</a>	21.994	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=sodB	<a href="#">A0A1B2F769_PSEPU</a>	21.969	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=A3K88_05175	<a href="#">A0A177YS39_PSEPU</a>	21.909	25	151.90	SwissP_Bacteria_NR

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Table 11 (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
		Superoxide dismutase OS= <i>Pseudomonas putida</i> B6-2 OX=1,081,940 GN=KKK_27,785	<a href="#">A0A168XBM6_PSEPU</a>	21.939	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> OX=294 GN=sodB_1	<a href="#">A0A0D0RQL4_PSEFL</a>	21.948	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. RIT-PI-r OX=1,699,620 GN=AK821_22,885	<a href="#">A0A0P6S377_9PSED</a>	21.992	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> OX=294 GN=sodB_1	<a href="#">A0A109L2F9_PSEFL</a>	22.005	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=AYO28_24,560	<a href="#">A0A177SFW3_PSEPU</a>	22.019	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. GM67 OX=1,144,335 GN=PMI33_04148	<a href="#">J2UAB6_9PSED</a>	22.021	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=AO269_03685	<a href="#">A0A0W0Q2E4_PSEPU</a>	22.007	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. GM21 OX=1,144,325 GN=PMI22_04575	<a href="#">J3EKI1_9PSED</a>	21.978	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> WH6 OX=746,360 GN=sodB	<a href="#">E2XX94_PSEFL</a>	22.005	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas plecoglossicida</i> NB2011 OX=1,330,531 GN=L321_24,006	<a href="#">S2JST8_9PSED</a>	21.952	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> BRIP34879 OX=1,205,750 GN=A986_21,285	<a href="#">L7H2T0_PSEFL</a>	21.950	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas trivialis</i> OX=200,450 GN=TU79_05835	<a href="#">A0A0R2ZL85_9PSED</a>	21.950	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. 22 E 5 OX=1,844,093 GN=sodB_1	<a href="#">A0A1B5EYJ2_9PSED</a>	22.005	25	151.90	SwissP_Bacteria_NR

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Table 11 (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
Chaperonin proteins	c1	Superoxide dismutase OS= <i>Pseudomonas monteilii</i> OX=76,759 GN=BC89_13,580	<a href="#">A0A136QIN6_9PSED</a>	21.937	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. Leaf58 OX=1,736,226 GN=ASF02_16,300	<a href="#">A0A0Q4N799_9PSED</a>	21.937	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. CMAA1215 OX=1,387,231 GN=P308_25,440	<a href="#">U7A3I6_9PSED</a>	21.989	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase [Fe] OS= <i>Pseudomonas putida</i> (strain ATCC 47,054 / DSM 6125 / NCIMB 11,950 / KT2440) GN=sodB	<a href="#">SODF_PSEPK</a>	21.939	25	113.96	SwissP_Bacteria_R
		Chaperone protein HtpG OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=htpG	<a href="#">HTPG_PSEFS</a>	71.633	2	36.92	SwissP_Bacteria_R
		60 kDa chaperonin OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=groL	<a href="#">A0A2C9ESJ4_PSEPH</a>	57.065	15	155.61	SwissP_P. protegens
		60 kDa chaperonin OS= <i>Pseudomonas</i> sp. GM18 OX=1,144,324 GN=groL	<a href="#">J2NZ80_9PSED</a>	57.053	7	135.04	SwissP_Bacteria_NR
		60 kDa chaperonin OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=groL	<a href="#">CH60_PSEF5</a>	57.065	15	123.35	SwissP_Bacteria_R
		60 kDa chaperonin OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=groL	<a href="#">A0A2C9ESJ4_PSEPH</a>	57.065	11	130.43	SwissP_P. protegens
		60 kDa chaperonin OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=groL	<a href="#">CH60_PSEF5</a>	57.065	11	113.92	SwissP_Bacteria_R

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Table 11 (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
c6		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	<a href="#">A0A2C9EG81_PSEPH</a>	68.476	8	146.02	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	<a href="#">A0A2J7UJG0_9PSED</a>	68.430	10	138.77	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=dnaK	<a href="#">DNAK_PSEFS</a>	68.200	6	95.25	SwissP_Bacteria_R
		Chaperone protein DnaK OS= <i>Pseudomonas</i> sp. ES3-33 OX=1,628,833 GN=dnaK	<a href="#">A0A0D9A6C8_9PSED</a>	68.415	6	92.03	SwissP_Bacteria_NR
c7		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	<a href="#">A0A2C9EG81_PSEPH</a>	68.476	8	146.02	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	<a href="#">A0A2J7UJG0_9PSED</a>	68.430	10	138.77	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=dnaK	<a href="#">DNAK_PSEFS</a>	68.200	6	95.25	SwissP_Bacteria_R
		Chaperone protein DnaK OS= <i>Pseudomonas</i> sp. ES3-33 OX=1,628,833 GN=dnaK	<a href="#">A0A0D9A6C8_9PSED</a>	68.415	6	92.03	SwissP_Bacteria_NR
c8		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / PF-5) OX=220,664 GN=flkB	<a href="#">Q4K5T2_PSEF5</a>	21.678	18	214.28	SwissP_P. <i>protegens</i>
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=flkB	<a href="#">A0A2C9ETR2_PSEPH</a>	21.678	18	214.28	SwissP_P. <i>protegens</i>
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_26,505	<a href="#">A0A2J7TS41_9PSED</a>	21.664	18	214.28	SwissP_P. <i>protegens</i>
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas fluorescens</i> OX=294 GN=flkB_1	<a href="#">A0A0D0SQ47_PSEFL</a>	21.675	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas batumici</i> OX=226,910 GN=UCMB321_4721	<a href="#">A0A0C2E6G3_9PSED</a>	21.586	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas synxantha</i> BG33R OX=96,901 GN=flkB	<a href="#">I4LAD2_9PSED</a>	21.645	18	209.04	SwissP_Bacteria_NR

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Table 11 (continued)

Protein family	Spot no.	Data Definition	Research algorithm: PEAKS				
			Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	–10lgP	Database
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> sp. CMAA1215 OX=1,387,231 GN=P308_28,130	<a href="#">U7A1W8_9PSED</a>	21.708	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> <i>fluorescens</i> OX=294 GN=A7317_24,270	<a href="#">A0A0W0HKFO_PSEFL</a>	21.689	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> <i>fluorescens</i> BRIP34879 OX=1,205,750 GN=A986_02186	<a href="#">L7HNG1_PSEFL</a>	21.718	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> <i>fluorescens</i> WH6 OX=746,360 GN=fkpA	<a href="#">E2XY02_PSEFL</a>	21.689	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> sp. 37 R 15 OX=1,844,104 GN=fklB_2	<a href="#">A0A1B5DMV2_9PSED</a>	21.675	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> sp. 22 E 5 OX=1,844,093 GN=fklB_3	<a href="#">A0A1B5ESY5_9PSED</a>	21.675	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> sp. 24 E 1 OX=1,844,094 GN=fklB_1	<a href="#">A0A1B5D261_9PSED</a>	21.689	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> sp. RIT357 OX=1,470,593 GN=BW43_01525	<a href="#">A0A031J4K3_9PSED</a>	21.648	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas</i> <i>trivialis</i> OX=200,450 GN=TU79_07195	<a href="#">A0A0R2ZUP9_9PSED</a>	21.746	18	209.04	SwissP_Bacteria_NR

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Table 11 (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
	c9	Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=CSU62_23,620	<a href="#">A0A2T6GHH3_9PSED</a>	18.267	7	46.63	SwissP_P. <i>protegens</i>
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=ppiB	<a href="#">Q4K9R9_PSEF5</a>	18.269	7	46.63	SwissP_P. <i>protegens</i>
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_23,035	<a href="#">A0A2J7U033_9PSED</a>	18.283	7	46.63	SwissP_P. <i>protegens</i>
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=cyp	<a href="#">A0A2C9EQ49_PSEPH</a>	18.269	7	46.63	SwissP_P. <i>protegens</i>
Other proteins involved in stress response	p2	Nucleoid protein HU beta subunit OS= <i>Pseudomonas amygdali</i> pv. <i>lachrymans</i> str. M302278 OX=629,267 GN=PLA106_24,593	<a href="#">F3IQ72_PSEAV</a>	9.106	23	72.47	SwissP_Bacteria_NR
		DNA-binding protein HU, beta subunit OS= <i>Pseudomonas fluorescens</i> WH6 OX=746,360 GN=hupB	<a href="#">E2XUJ9_PSEFL</a>	9.062	23	72.47	SwissP_Bacteria_NR
		Nucleoid protein HU beta subunit OS= <i>Pseudomonas syringae</i> pv. <i>papulans</i> OX=83,963 GN=ALO65_02562	<a href="#">A0A0P9ZVJ6_PSESX</a>	9.106	23	72.47	SwissP_Bacteria_NR
		DNA-binding protein HU, beta subunit OS= <i>Pseudomonas fluorescens</i> BRIP34879 OX=1,205,750 GN=A986_22,410	<a href="#">L7GXR8_PSEFL</a>	9.062	23	72.47	SwissP_Bacteria_NR
		Transcriptional regulator OS= <i>Pseudomonas</i> sp. CMAA1215 OX=1,387,231 GN=P308_20,875	<a href="#">U7A634_9PSED</a>	9.091	23	72.47	SwissP_Bacteria_NR
		DNA-binding protein HU, beta subunit OS= <i>Pseudomonas coronafaciens</i> pv. <i>zizaniae</i> OX=251,700 GN=ALO38_02514	<a href="#">A0A0QOHEI0_9PSED</a>	9.076	23	72.47	SwissP_Bacteria_NR

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**Table 11** (continued)

Protein family	Spot no.	Data		Research algorithm: PEAKS			
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
		DNA-binding protein HU OS= <i>Pseudomonas</i> sp. Root68 OX=1,736,585 GN=ASD91_22,695	<a href="#">A0A0Q8J0C7_9PSED</a>	9.106	23	72.47	SwissP_Bacteria_NR
		Nucleoid protein HU beta subunit OS= <i>Pseudomonas syringae</i> pv. <i>aceris</i> OX=199,198 GN=ALO91_03094	<a href="#">A0A0L8IW02_PSESX</a>	9.106	23	72.47	SwissP_Bacteria_NR
		Nucleoid protein HU beta subunit OS= <i>Pseudomonas savastanoi</i> pv. <i>phaseolicola</i> OX=319 GN=ALO55_00346	<a href="#">A0A0P9 × 6 × 9_PSESH</a>	9.106	23	72.47	SwissP_Bacteria_NR
		DNA-binding protein HU-beta OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=hupB	<a href="#">DBHB_PSEF5</a>	9.106	23	65.89	SwissP_Bacteria_R
	p3	DNA-binding protein HU-beta OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=hupB	<a href="#">A0A2C9EQC3_PSEPH</a>	9.106	23	80.95	SwissP_P. protegens
		DNA-binding protein HU-beta OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=hupB	<a href="#">Q9KHS6 DBHB_PSEF5</a>	9.106	23	80.95	SwissP_P. protegens
		DNA-binding protein HU OS= <i>Pseudomonas protegens</i> OX=380,021 GN=C5U62_31,250	<a href="#">A0A2T6GBS6_9PSED</a>	9.106	23	80.95	SwissP_P. protegens
	p4	Cold shock protein CapB OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=capB	<a href="#">A0A2C9EHH8_PSEPH</a>	7.727	46	146.74	SwissP_P. protegens
		Cold shock protein CapB OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) OX=220,664 GN=capB	<a href="#">Q4KH94_PSEF5</a>	7.727	46	146.74	SwissP_P. protegens
		Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_02635	<a href="#">A0A2J7UBE2_9PSED</a>	7.727	46	146.74	SwissP_P. protegens
		Cold shock protein CapB OS= <i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain ATCC BAA-871 / DC3000) GN=capB	<a href="#">CAPB_PSESM</a>	7.727	46	127.60	SwissP_Bacteria_R

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Table 11 (continued)

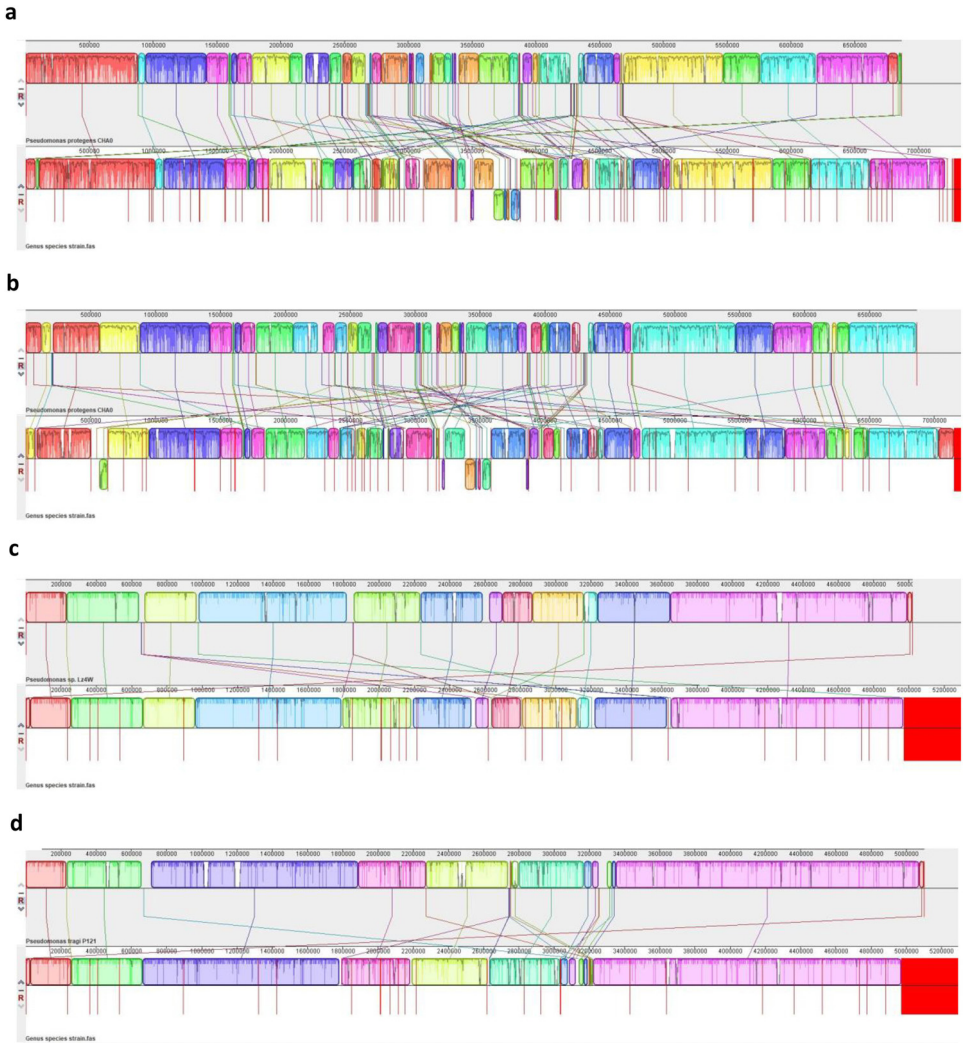
Protein family	Spot no.	Data Definition	Accession number: SwissProt reference sequence (version)	Research algorithm: PEAKS			
				Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
		Cold shock protein CapB OS= <i>Pseudomonas fragi</i> GN=capB	<a href="#">CAPB_PSEFR</a>	7.727	46	127.60	SwissP_Bacteria_R
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM49 OX=1,144,331 GN=PMI29_02448	<a href="#">J2SK38_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock DNA-binding protein family OS= <i>Pseudomonas deceptionensis</i> OX=882,211 GN=SAMN04489800_1852	<a href="#">A0A0J6GIW5_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas syringae</i> pv. <i>cerasicola</i> OX=264,451 GN=ALO50_03241	<a href="#">A0A0P9NMB0_PSESX</a>	7.727	46	123.98	SwissP_Bacteria_NR
		CapB_2 protein OS= <i>Pseudomonas fluorescens</i> OX=294 GN=capB_2	<a href="#">A0A075PGX5_PSEFL</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas tremae</i> OX=200,454 GN=ALO43_00013	<a href="#">A0A0Q0CHU5_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein CapB OS= <i>Pseudomonas fluorescens</i> BRIP34879 OX=1,205,750 GN=A986_0300	<a href="#">L7HLD3_PSEFL</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold acclimation protein B OS= <i>Pseudomonas</i> sp. 22 E 5 OX=1,844,093 GN=capB_2	<a href="#">A0A1B5EK52_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas putida</i> OX=303 GN=AO269_03090	<a href="#">A0A0W0P7R9_PSEPU</a>	7.697	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas brassicacearum</i> OX=930,166 GN=CD58_06475	<a href="#">W8PFF4_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas amygdali</i> pv. <i>eribotryae</i> OX=129,137 GN=ALO52_06405	<a href="#">A0A0P9QTI2_PSEA0</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas azotoformans</i> OX=47,878 GN=AYR47_13,715	<a href="#">A0A127HXU4_PSEAZ</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas fluorescens</i> (strain SBW25) OX=216,595 GN=capB	<a href="#">C3K709_PSEFS</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas amygdali</i> pv. <i>morsprunorum</i> OX=129,138 GN=AC509_2282	<a href="#">A0A0N0GLZ4_PSEA0</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas</i> sp. RIT-PI-r OX=1,699,620 GN=AK821_27,805	<a href="#">A0A0P6S0W4_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Uncharacterized protein OS= <i>Pseudomonas syringae</i> pv. <i>aceris</i> OX=199,198 GN=ALO91_01408	<a href="#">A0A0L8ITA8_PSESX</a>	7.727	46	123.98	SwissP_Bacteria_NR

(continued on next page)

**Table 11** (continued)

Protein family	Spot no.	Data	Research algorithm: PEAKS				
		Definition	Accession number: SwissProt reference sequence (version)	Theoretical MW (kDa)	Sequence coverage (%)	-10lgP	Database
		Cold-shock protein OS= <i>Pseudomonas</i> sp. Root68 OX=1,736,585 GN=ASD91_00740	<a href="#">A0A0Q8J556_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas syringae</i> pv. <i>syringae</i> OX=321 GN=AL062_19,410	<a href="#">A0A0M9H959_PSESY</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock DNA-binding protein family OS= <i>Pseudomonas fragi</i> OX=296 GN=AV641_05125	<a href="#">A0A0 × 8EWR3_PSEFR</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas weihenstephanensis</i> OX=1,608,994 GN=TU86_02400	<a href="#">A0A0J6IW85_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas amygdali</i> pv. <i>ciccaronei</i> OX=264,452 GN=ALO78_01383	<a href="#">A0A0P9Q5F3_PSEA0</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM18 OX=1,144,324 GN=PMI21_04449	<a href="#">J2NQX1_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas amygdali</i> pv. <i>lachrymans</i> str. M302278 OX=629,267 GN=PLA106_06845	<a href="#">F3IF92_PSEAV</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein CapB OS= <i>Pseudomonas antarctica</i> OX=219,572 GN=A7J50_1439	<a href="#">A0A172YYL9_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas coronafaciens</i> pv. <i>zizaniae</i> OX=251,700 GN=ALO38_04720	<a href="#">A0A0Q0F3Z6_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock DNA-binding protein family OS= <i>Pseudomonas kilonensis</i> OX=132,476 GN=SAMN04490188_3222	<a href="#">A0A0F4XHM9_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM21 OX=1,144,325 GN=PMI22_04135	<a href="#">J2NCS9_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM67 OX=1,144,335 GN=PMI33_02223	<a href="#">J2UA47_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock DNA-binding protein family OS= <i>Pseudomonas lini</i> OX=163,011 GN=SAMN04490191_5956	<a href="#">A0A0J6KCW5_9PSED</a>	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas amygdali</i> pv. <i>ulmi</i> OX=251,720 GN=AL065_17,960	<a href="#">A0A0Q0E2H2_PSEA0</a>	7.727	46	123.98	SwissP_Bacteria_NR





**Fig. 1.** Alignments of the bacterial draft genomes of F14BN1, F15BN2 and F14BN2 with the complete genomes of the nearest species determined by average nucleotide identity (JSpecies) performed using the Progressive MAUVE algorithm. **a.** Alignment of F14BN1 draft genome versus *Pseudomonas protegens* CHA0 genome (NCBI accession number: NC\_021237). **b.** Alignment of F15BN2 draft genome versus *P. protegens* CHA0 genome (NCBI accession number: NC\_021237). **c.** Alignment of F14BN2 draft genome versus *Pseudomonas sp.* Lz4W genome (NCBI accession number: CP017432.1). **d.** Alignment of F14BN2 draft genome versus *Pseudomonas fragi* P121 genome (NCBI accession number: NZ\_CP013861).

classified in three families: “Proteins counteracting oxidative stress and/or ensuring redox balance”, “Chaperonin proteins” and “Other proteins involved in stress response”. For each protein, sequence coverage (%), theoretical isoelectric point, theoretical molecular weight, number of experimental peptides recognized, rank, probability MOWSE score, maximum difference between theoretical peptide masses and experimental ones, score ( $-10 \lg P$ ) and database leading to the identification were presented. Only the significant data are described. [Tables 6, 8 and 10](#) are related to folder “MS-MS”/subfolder “NCBI” of Mendeley Data and contain the identification data of the proteins released by F14BN1, F14BN2 and F15BN2, respectively, by the technique of mapping by mass through the “PEAKS studio” search algorithm with NCBI database. [Tables](#)

7, 9 and 11 are related to folder “MS-MS”/subfolder “SwissProt” of Mendeley Data and include the identification data of the proteins produced by F14BN1, F14BN2 and F15BN2, respectively, by the technique of mapping by mass through the “PEAKS studio” search algorithm with SwissProt database. Only significant data (with score greater than the peptide hit threshold (30) obtained with “PEAKS studio” search algorithm was presented and classified in three families: “Proteins counteracting oxidative stress and/or ensuring redox balance”, “Chaperonin proteins” and “Other proteins involved in stress response”. Moreover, database research was carried out using different databases: bacteria database not reviewed (\_NR), bacteria database reviewed (\_R), and *Pseudomonas protegens* database (NCBI and SwissProt).

## 2. Experimental design, materials, and methods

### 2.1. Phenotypic identification of bacterial strains

*Pseudomonas* strains were isolated from water (of pH 5.5) taken on the granite soil of the Vosges mountains (France) using spraying water on plate count agar (PCA, Biokar Diagnostics, Beauvais, France). Colony forming units (CFUs) were first selected on the ultraviolet ray fluorescence criterion. They were then identified as *P. fluorescens* using phenotypic and biochemical tests such as bacillus morphology with Gram negative staining and oxidase and catalase research, followed by inoculating API<sup>®</sup> 50CH micro galleries (bioMérieux Diagnostics, Marcy-l’Etoile, France). The three strains to be analyzed were named F14BN1, F14BN2 and F15BN2.

### 2.2. Whole genome analysis

Total deoxyribonucleic acid (DNA) was extracted using the Wizard genomic purification DNA kit (Promega Corp., Madison, WI, USA) and sequenced at MicrobesNG (<http://www.microbesng.uk>) using Illumina MiSeq and HiSeq 2500 technology platforms, with  $2 \times 250$ -bp paired-end reads. The closest existing reference genome was determined using Kraken [1], and the reads were mapped using the Burrows-Wheeler aligner (BWA) MEM algorithm (<http://bio-bwa.sourceforge.net>) to assess data quality. The reads were assembled by de novo assembly using SPAdes (<http://cab.spbu.ru/software/spades/>). Gene function prediction was performed by the rapid annotations using subsystems technology (RAST) server (<http://rast.nmpdr.org>) [2] followed by an annotation using the SEED database [3]. The alignments of the bacterial draft genomes with the complete genomes of the nearest species determined by average nucleotide identity (JSpecies) (*Pseudomonas* sp. Lz4W and *P. fragi* P121 for F14BN2 and *Pseudomonas protegens* CHA0 for F14BN1 and F15BN2) were also performed using the Progressive MAUVE algorithm [4].

### 2.3. Average nucleotide identity and tetra correlation search analyzes

Bacteria draft genomes deposited in NCBI database were compared with indices based on the analysis of whole-genome sequences that had for species delineation, such as TCS based on the previously algorithm described [5] and ANI, as previously reported [6] using the JSpecies software (Ribocon GmbH) (<http://jspecies.ribohost.com/jspeciesws/>) [7]. TCS was performed between each assembled genome in the cart against the entire genomes reference database GenomesDB. Data is provided as a hit list (only the first 20/100 hits were presented in this dataset for each strain) for fast insights into the relationships of our organisms of interest (internal reference database GenomesDB: 47,489 entries, release date: 2018-03-14). The ANI was calculated based on the BLAST algorithm (ANiB) [6,8] and the MUMmer ultra-rapid aligning tool (ANIm) [9], between pairwise genomic comparisons with the 12 species frequently found for the three strains. The recommended species cut-off was 95% for the ANiB and ANIm indices, and higher than 0.99 for tetra-nucleotide signature analysis.

## 2.4. Proteomic characterization of the bacteria

The proteins directly produced into distilled water (DW) by the three strains, separated by two-dimensional polyacrylamide gel electrophoresis were analyzed for their mass after in-gel-trypsin-digestion, concentration and elution. The AnchorChip™ MALDI target plate was used to deposit the extracted peptides eluted from ZipTip C18 by an 80% acetonitrile (ACN), 0.1% trifluoroacetic acid (TFA) (vol/vol) solution and mixed with  $\alpha$ -cyano-4-hydroxy-cinnamic acid matrix (5 mg.ml<sup>-1</sup> in ACN:TFA, 85:0.1 vol/vol). The molecular mass measurements were performed in automatic mode using FlexControl™ 3.4 software in reflectron mode for MALDI-TOF peptide mass fingerprinting (PMF, MS mode) or LIFT mode for MALDI-TOF/TOF peptide fragment fingerprinting (PFF, MS/MS mode). External calibration was performed using a method previously described [10]. A maximum of ten precursor ions per sample were chosen for MS/MS analysis. Peak lists were generated from MS and MS/MS spectra using FlexAnalysis™ 3.4 software. Database search using PMF or PFF datasets was performed in the UniProt/SwissProt and NCBI databases via Mascot 2.2 (Matrix Science Ltd, London, UK) or PEAKS Studio 7.0 (Bioinformatics Solutions). A mass tolerance of 50 parts per million (ppm) and 1 missing cleavage site were generally admitted for PMF. All sequence recovery percentages were higher than 27%. A MS/MS tolerance of 150 ppm and 3 missing cleavage sites for MS/MS searching were allowed. Variable cysteine carbamidomethylation and methionine oxidation were also considered. The relevance of protein identities was judged according to their score in the research software ( $p$  value of 0.05 ( $p < 0.05$ ), False Discovery Rate < 1%).

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## Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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