



Data Article

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



Elodie Dussert, Mélissa Turret, Barbara Deracinois, Matthieu Duban, Valérie Leclère, Benoit Cudennec, Rozenn Ravallec, Josette Behra-Miellet*

Univ. Lille, INRA, ISA, Univ. Artois, Univ. Côte d'Opale, EA 7394 – ICV – Institut Charles Viollette, F-59000 Lille, France

ARTICLE INFO

Article history:

Received 9 March 2020

Accepted 17 March 2020

Available online 10 April 2020

Keywords:

Bacterial identification

Fluorescent *Pseudomonas*

Proteomics

Genome sequencing

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.

* Corresponding author.

E-mail address: josette.behra@univ-lille.fr (J. Behra-Miellet).

<https://doi.org/10.1016/j.dib.2020.105466>

2352-3409/© 2020 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license. (<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

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

© 2020 The Author(s). Published by Elsevier Inc.

This is an open access article under the CC BY-NC-ND license. (<http://creativecommons.org/licenses/by-nc-nd/4.0/>)

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 (http://www.microbesng.uk) 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"> 1. With the article 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 https://www.ncbi.nlm.nih.gov/nuccore/JAAARL000000000 — https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARL01?display=contigs - SUB6805363 PRJNA601118 SAMN13831440 JAAARM000000000 <i>Pseudomonas</i> sp. F14BN1 https://www.ncbi.nlm.nih.gov/nuccore/JAAARM000000000 — https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARM01?display=contigs - SUB6805363 PRJNA601118 SAMN13831439 JAAARN000000000 <i>Pseudomonas</i> sp. F14BN2 https://www.ncbi.nlm.nih.gov/nuccore/JAAARN000000000 — https://www.ncbi.nlm.nih.gov/Traces/wgs/JAAARN01?display=contigs
Related research article	<p>3. Repository name : Mendeley Data Data identification number : DOI: 10.17632/p5kt4dvmxt.1 Direct URL to Data : https://data.mendeley.com/datasets/p5kt4dvmxt/1 Elodie Dussert¹, Mélissa Tourret¹, Barbara Deracinois¹, Matthieu Duban¹, Valérie Leclère¹, Benoit Cudennec¹, Rozenn Ravallec¹, Josette Behra-Miellat¹. 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[®] 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 (> 0.999), * in range (> 0.989), below cut-off (< 0.989).

	Pos.	Species	Strain	Domain	Phylum	Class	Order	Family	Z-Score
F14BN1	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
F14BN2	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> 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	*	77.48	98.94	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	98.95	99.00	90.53	84.80	83.06	83.93
F15BN2_59_ctg.fas	99.03	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> UCM B-321	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
<i>Pseudomonas protegens</i> Cab57	87.64	77.91	87.61	80.45	*	98.36	98.06	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	98.40	*	98.65	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	98.03	98.55	*	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	99.19	78.40	78.85	78.71	78.66	78.65	78.70	79.09	*	99.14	90.71	85.00	83.22	84.37
<i>Pseudomonas</i> sp. Lz4W	78.30	99.25	78.30	78.79	78.67	78.62	78.63	78.66	79.02	99.21	*	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	99.28	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	99.15	99.30	91.37	87.06	86.24	86.54
F15Bn2_59_ctg.fas	99.28	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	*	98.58	98.38	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	98.60	*	98.87	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	98.38	98.87	*	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 fragi</i> P121	84.74	99.14	84.76	84.89	84.93	84.95	84.88	84.88	84.97	*	99.28	91.35	87.05	86.23	86.77
<i>Pseudomonas</i> sp. Lz4W	84.74	99.30	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). 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										
		o4	WP_003212997.1, MULTISPECIES: superoxide dismutase [<i>Pseudomonas</i>]	46	5.56	22.078	8	1	107 (93)	43.4	0.0021	NCBIprot	
	Chaperonin proteins		c2	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									
		c4	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										
			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	
			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	
		c5	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			
Other proteins involved in stress response	p2	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		
		CAPB_PSEFR, Cold shock protein CapB OS= <i>Pseudomonas fragi</i> GN=capB	69	6.54	7.722	6	1	77 (68)	56.5	0.0071	SwissProt		

(continued on next page)

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

(continued on next page)

Table 5 (continued)

Strain	Protein family	Spot no.	Data Definition	Research algorithm: Mascot					Database			
				Sequence coverage (%)	Theoretical pl	Theoretical MW (kDa)	Nb	Rank		Probability MOWSE score (signification threshold)	ppm	-10lgP
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
		o5	WP_016966196.1, MULTISPECIES: superoxide dismutase [<i>Pseudomonas</i>]	53	5.55	22.089	11	1	104 (93)	49.4	0.0041	NCBIprot
	Chaperonin proteins	c2	WP_04119683.1, 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=groL	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	NCBIprot
		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	NCBIprot
			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
	Other proteins involved in stress response	p1	SEB63063.1, C-terminal processing peptidase-1, Serine peptidase, MEROPS family S41A [<i>Pseudomonas saponiphila</i>]	29	5.97	77.543	18	1	114 (93)	45	0.00041	NCBIprot
		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>]	gi 1332918899	49.831	5	61.76	NCBI_ <i>P. protegens</i>
	o2	MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	gi 499375533	21.787	6	96.79	NCBI_ <i>P. protegens</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	gi 495197643	21.773	6	96.79	NCBI_ <i>P. protegens</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	WP_003178707.1	21.856	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	WP_003231418.1	21.938	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	WP_003188979.1	21.947	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	WP_003254945.1	21.730	6	65.14	NCBI_ <i>Bacteria_NR</i>
		peroxiredoxin [<i>Pseudomonas putida</i> KT2440]	NP_743245.1	21.730	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	WP_003172097.1	21.933	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	WP_003204949.1	21.929	6	65.14	NCBI_ <i>Bacteria_NR</i>
		MULTISPECIES: peroxiredoxin [<i>Pseudomonas</i>]	WP_003227723.1	21.765	6	65.14	NCBI_ <i>Bacteria_NR</i>

(continued on next page)

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>]	gi 499371610	68.476	7	45.69	NCBI_P. protegens
	c2	MULTISPECIES: molecular chaperone HtpG [<i>Pseudomonas</i>] molecular chaperone HtpG [<i>Pseudomonas protegens</i>] molecular chaperone HtpG [<i>Pseudomonas protegens</i>]	gi 499372481 gi 1332903508 gi 1332919100	71.349 71.349 71.336	5 5 5	63.50 63.50 63.50	NCBI_P. protegens NCBI_P. protegens NCBI_P. protegens
	c3	chaperonin GroEL [<i>Pseudomonas protegens</i>]	gi 751652819	56.819	17	139.15	NCBI_P. protegens
		MULTISPECIES: molecular chaperone GroEL [<i>Pseudomonas</i>]	gi 499375514	57.065	17	139.15	NCBI_P. protegens
		chaperonin GroEL [<i>Beggiatoa alba</i>]	WP_002686219.1	57.692	3	35.32	NCBI_Bacteria_NR
		60 kDa chaperonin GroEL [<i>Shewanella oneidensis</i> MR-1]	NP_716,337.1	57.080	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Thauera linaloolentis</i>]	WP_004339041.1	56.684	3	35.32	NCBI_Bacteria_NR
		MULTISPECIES: molecular chaperone GroEL [<i>Bordetella</i>]	WP_003808619.1	57.483	3	35.32	NCBI_Bacteria_NR
		molecular chaperone GroEL [<i>Bordetella pertussis</i> <i>Tohama I</i>]	NP_882014.1	57.482	3	35.32	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [<i>Pseudomonas</i>]	WP_003238874.1	56.883	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Pseudomonas fluorescens</i>]	WP_003175873.1	56.927	3	35.32	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [<i>Pseudomonas</i>]	WP_003178748.1	56.843	3	35.32	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [<i>Pseudomonas</i>]	WP_003227683.1	56.905	3	35.32	NCBI_Bacteria_NR
	chaperonin GroEL [<i>Pseudomonas fluorescens</i>]	WP_003193939.1	56.882	3	35.32	NCBI_Bacteria_NR	
	chaperonin GroEL [<i>Cystobacter fuscus</i>]	WP_002624037.1	58.167	3	35.32	NCBI_Bacteria_NR	
	molecular chaperone GroEL [<i>Coxiella burnetii</i> RSA 493]	NP_820699.1	58.284	3	35.32	NCBI_Bacteria_NR	
	c6	molecular chaperone GroEL [<i>Nitrosococcus oceanii</i>]	WP_002813030.1	58.284	3	35.32	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Pseudomonas protegens</i>]	gi 751652819	56.819	17	139.15	NCBI_P. protegens
		MULTISPECIES: molecular chaperone GroEL [<i>Pseudomonas</i>]	gi 499375514	57.065	17	139.15	NCBI_P. protegens

(continued on next page)

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>]	gi 499375085	79.065	2	66.15	NCBI_P. protegens
		peptidase S41 [<i>Pseudomonas protegens</i>]	gi 1043219129	79.051	2	66.15	NCBI_P. protegens
		MULTISPECIES: tail-specific protease [<i>Pseudomonas</i>]	gi 829054598	79.040	2	66.15	NCBI_P. protegens
		tail-specific protease [<i>Pseudomonas protegens</i>]	gi 505449515	79.066	2	66.15	NCBI_P. protegens
		tail-specific protease [<i>Pseudomonas protegens</i>]	gi 751652595	79.024	2	66.15	NCBI_P. protegens
		MULTISPECIES: tail-specific protease [<i>Pseudomonas fluorescens</i> group]	gi 517923405	79.026	2	66.15	NCBI_P. protegens
		tail-specific protease [<i>Pseudomonas protegens</i>]	gi 1332920536	79.022	2	66.15	NCBI_P. protegens
		tail-specific protease [<i>Pseudomonas protegens</i>]	gi 1332900179	79.008	2	66.15	NCBI_P. protegens
		MULTISPECIES: tail-specific protease [<i>Pseudomonas</i>]	WP_003179086.1	78.994	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: tail-specific protease [<i>Pseudomonas</i>]	WP_003204565.1	79.144	2	45.61	NCBI_Bacteria_NR
		peptidase S41 [<i>Pseudomonas fluorescens</i>]	WP_003172944.1	79.122	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: peptidase S41 [<i>Pseudomonas</i>]	WP_003190141.1	79.102	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: peptidase S41 [<i>Pseudomonas</i>]	WP_003211110.1	79.101	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: tail-specific protease [<i>Pseudomonas</i>]	WP_003231887.1	79.074	2	45.61	NCBI_Bacteria_NR
		tail-specific protease Prc [<i>Pseudomonas putida</i> KT2440]	NP_743876.1	79.097	2	45.61	NCBI_Bacteria_NR
		S41 family peptidase [<i>Pseudomonas</i> sp. Lz4W]	WP_003446856.1	79.047	2	45.61	NCBI_Bacteria_NR
		MULTISPECIES: cold-shock protein [<i>Pseudomonas</i>]	gi 495252543	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	Dihydropolyl dehydrogenase OS= <i>Pseudomonas protegens</i> (strain DSM 19,095/LMG 27,888 / CHA0) GN=lpdG	A0A2C9EIR1_PSEPH	49.874	5	47.56	SwissP_P. <i>protegens</i>
	o2	Putative peroxiredoxin TsaA OS= <i>Pseudomonas protegens</i> (strain DSM 19,095/LMG 27,888 / CHA0) GN=tsaA	A0A2C9ESU7_PSEPH	21.787	6	80.76	SwissP_P. <i>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	Q4K745_PSEF5	21.787	6	80.76	SwissP_P. <i>protegens</i>
		Alkyl hydroperoxide reductase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_15,140	A0A2J7U847_9PSED	21.773	6	80.76	SwissP_P. <i>protegens</i>
Chaperonin proteins	c1	Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=dnaK	DNAK_PSEFS	68.200	11	90.38	SwissP_Bacteria_R
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) GN=dnaK	A0A2C9EG81_PSEPH	68.476	3	28.43	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	A0A2T6GM17_9PSED	68.433	3	28.43	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=dnaK	DNAK_PSEF5	68.476	3	28.43	SwissP_P. <i>protegens</i>
	c2	Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> OX=380,021 GN=htpG	A0A2T6GQG4_9PSED	71.363	5	82.38	SwissP_P. <i>protegens</i>
		Chaperone protein HtpG OS= <i>Pseudomonas fluorescens</i> (strain ATCC BAA-477 / NRRL B-23,932 / Pf-5) GN=htpG	HTPG_PSEF5	71.349	5	82.38	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	A0A2J7UMP6_9PSED	68.476	3	82.43	SwissP_P. <i>protegens</i>
		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=htpG	A0A2C9EIV4_PSEPH	71.581	5	82.38	SwissP_P. <i>protegens</i>

(continued on next page)

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	A0A2C9ESJ4_PSEPH	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	CH60_PSEF5	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	A0A2T6GBS8_9PSED	48.484	2	31.70	SwissP_P. protegens
		Trigger factor OS= <i>Pseudomonas mendocina</i> (strain ymp) GN=tig	TIG_PSEMY	48.330	2	24.02	SwissP_Bacteria_R
		Trigger factor OS= <i>Pseudomonas fluorescens</i> (strain Pf0-1) GN=tig	TIG_PSEPF	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	EFTU_ECOL6	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	Q4K8E7_PSEF5	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	A0A2C9ERC3_PSEPH	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	A0A2C9ES32_PSEPH	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	Q4K7Q5_PSEF5	7.736	40	34.43	SwissP_P. protegens
	p3	Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_14,565	A0A2K4M1K2_9PSED	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>]	gi 1125808736	12.108	12	136.77	NCBI_ <i>P. protegens</i>
		MULTISPECIES: monothiol glutaredoxin, Grx4 family [<i>Pseudomonas</i>]	gi 499375536	12.050	12	136.77	NCBI_ <i>P. protegens</i>
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003246056.1	11.793	12	94.59	NCBI_ <i>Bacteria</i> _NR
		Grx4 family monothiol glutaredoxin [<i>Pseudomonas aeruginosa</i>]	WP_003110008.1	11.871	12	94.59	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003188975.1	11.545	12	94.59	NCBI_ <i>Bacteria</i> _NR
		Grx4 family monothiol glutaredoxin [<i>Pseudomonas syringae</i>]	WP_003405440.1	11.649	12	94.59	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_002554852.1	11.677	12	94.59	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003092082.1	11.843	12	94.59	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_004396490.1	11.650	12	94.59	NCBI_ <i>Bacteria</i> _NR
		Grx4 family monothiol glutaredoxin [<i>Pseudomonas aeruginosa</i>]	WP_003130081.1	11.843	12	94.59	NCBI_ <i>Bacteria</i> _NR
		Grx4 family monothiol glutaredoxin [<i>Pseudomonas stutzeri</i>]	WP_003295894.1	11.820	12	94.59	NCBI_ <i>Bacteria</i> _NR
		hypothetical protein PA3533 [<i>Pseudomonas aeruginosa</i> PAO1]	NP_252223.1	11.843	12	94.59	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003299217.1	11.817	12	94.59	NCBI_ <i>Bacteria</i> _NR
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003453456.1	11.819	12	94.59	NCBI_ <i>Bacteria</i> _NR

(continued on next page)

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>]	WP_003289286.1	11.833	12	94.59	NCBI_Bacteria_NR		
		Grx4 family monothiol glutaredoxin [<i>Pseudomonas syringae</i>]	WP_004393736.1	11.676	12	94.59	NCBI_Bacteria_NR		
		glutaredoxin-like protein [[<i>Pseudomonas syringae</i>] pv. <i>tomato</i> str. DC3000]	NP_793922.1	11.650	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003284603.1	11.857	12	94.59	NCBI_Bacteria_NR		
		monothiol glutaredoxin [<i>Pseudomonas putida</i> KT2440]	NP_743242.1	12.123	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003254949.1	12.137	12	94.59	NCBI_Bacteria_NR		
		Grx4 family monothiol glutaredoxin [<i>Pseudomonas fluorescens</i>]	WP_003178700.1	12.050	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003208710.1	12.000	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003231422.1	11.874	12	94.59	NCBI_Bacteria_NR		
		Grx4 family monothiol glutaredoxin [<i>Pseudomonas fluorescens</i>]	WP_003172092.1	12.015	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003204956.1	12.135	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003443184.1	12.080	12	94.59	NCBI_Bacteria_NR		
		MULTISPECIES: Grx4 family monothiol glutaredoxin [<i>Pseudomonas</i>]	WP_003227729.1	12.109	12	94.59	NCBI_Bacteria_NR		
		Chaperonin proteins	c1	MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	WP_003439583.1	68.193	20	351.06	NCBI_Bacteria_NR
				molecular chaperone DnaK [<i>Pseudomonas stutzeri</i>]	WP_003298038.1	68.696	7	262.60	NCBI_Bacteria_NR
molecular chaperone DnaK [<i>Pseudomonas stutzeri</i>]	WP_003293240.1			68.628	7	262.60	NCBI_Bacteria_NR		
c3	molecular chaperone DnaK [<i>Pseudomonas protegens</i>]		gi 1332900475	68.460	18	237.39	NCBI_P. protegens		
	molecular chaperone DnaK [<i>Pseudomonas protegens</i>]		gi 1332918337	68.430	18	237.39	NCBI_P. protegens		
	MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]		gi 499371610	68.476	17	204.77	NCBI_P. protegens		

(continued on next page)

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>]	WP_003293240.1	68.628	7	262.60	NCBI_Bacteria_NR
		MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	WP_003439583.1	68.193	20	351.06	NCBI_Bacteria_NR
c4		molecular chaperone DnaK [<i>Pseudomonas stutzeri</i>]	WP_003298038.1	68.696	7	262.60	NCBI_Bacteria_NR
		molecular chaperone DnaK [<i>Pseudomonas protegens</i>]	gi 1332900475	68.460	18	237.39	NCBI_P. protegens
		molecular chaperone DnaK [<i>Pseudomonas protegens</i>]	gi 1332918337	68.430	18	237.39	NCBI_P. protegens
		MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	gi 499371610	68.476	17	204.77	NCBI_P. protegens
		MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	WP_003439583.1	68.193	20	351.06	NCBI_Bacteria_NR
c5		molecular chaperone DnaK [<i>Pseudomonas protegens</i>]	gi 1332900475	68.460	18	237.39	NCBI_P. protegens
		molecular chaperone DnaK [<i>Pseudomonas protegens</i>]	gi 1332918337	68.430	18	237.39	NCBI_P. protegens
		MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	gi 499371610	68.476	17	204.77	NCBI_P. protegens
c6		MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	WP_003439583.1	68.193	20	351.06	NCBI_Bacteria_NR
c8		MULTISPECIES: molecular chaperone HtpG [<i>Pseudomonas</i>]	gi 499372481	71.349	13	153.49	NCBI_P. protegens
		molecular chaperone HtpG [<i>Pseudomonas protegens</i>]	gi 1332903508	71.349	13	153.49	NCBI_P. protegens
		molecular chaperone HtpG [<i>Pseudomonas protegens</i>]	gi 1332919100	71.336	13	153.49	NCBI_P. protegens
		MULTISPECIES: molecular chaperone HtpG [<i>Pseudomonas</i>]	WP_003446928.1	71.244	13	190.80	NCBI_Bacteria_NR
c9		MULTISPECIES: trigger factor [<i>Pseudomonas</i>]	gi 499374697	48.569	22	165.79	NCBI_P. protegens
c10		MULTISPECIES: trigger factor [<i>Pseudomonas</i>]	gi 499374697	48.569	22	165.79	NCBI_P. protegens
c11		MULTISPECIES: trigger factor [<i>Pseudomonas</i>]	gi 499374697	48.569	22	165.79	NCBI_P. protegens
c12		nucleotide exchange factor GrpE [<i>Pseudomonas protegens</i>]	gi 1332900474	20.837	25	116.18	NCBI_P. protegens

(continued on next page)

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>]	WP_003439582.1	20.897	21	86.11	NCBI_Bacteria_NR
		nucleotide exchange factor GrpE [<i>Pseudomonas protegens</i>]	gi 1332900474	20.837	25	116.18	NCBI_P. protegens
		MULTISPECIES: nucleotide exchange factor GrpE [<i>Pseudomonas</i>]	WP_003439582.1	20.897	21	86.11	NCBI_Bacteria_NR
		heat shock protein GrpE [<i>Pseudomonas putida</i> KT2440]	NP_746836.1	20.531	9	35.12	NCBI_Bacteria_NR
	c14	MULTISPECIES: nucleotide exchange factor GrpE [<i>Pseudomonas</i>]	WP_003249927.1	20.501	9	35.12	NCBI_Bacteria_NR
		MULTISPECIES: cyclophilin [<i>Pseudomonas</i>]	gi 515532580	18.283	7	44.00	NCBI_P. protegens
	p1	MULTISPECIES: cyclophilin [<i>Pseudomonas</i>]	gi 499374623	18.269	7	44.00	NCBI_P. protegens
		MULTISPECIES: cold-shock protein CapB [<i>Pseudomonas</i>]	gi 488617988	7.727	46	157.27	NCBI_P. protegens
		MULTISPECIES: nucleoid-associated protein, YbaB/EbfC family [<i>Pseudomonas</i>]	gi 505447677	12.131	12	85.20	NCBI_P. protegens
		p2	MULTISPECIES: cold-shock protein CapB [<i>Pseudomonas</i>]	gi 488617988	7.727	46	157.27
cold shock protein CapB [[<i>Pseudomonas syringae</i>] pv. <i>tomato</i> str. DC3000]	NP_793906.1		7.727	46	116.65	NCBI_Bacteria_NR	
MULTISPECIES: cold-shock protein CapB [<i>Pseudomonas</i>]	WP_002554837.1		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	Q4K742_PSEF5	12.050	12	127.54	SwissP_ <i>P. protegens</i>	
		Glutaredoxin OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grxD	A0A2T6GIP8_9PSED	12.050	12	127.54	SwissP_ <i>P. protegens</i>	
		Glutaredoxin OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_15,155	A0A2J7U865_9PSED	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	A0A2C9ESK9_PSEPH	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	A0A2J7UJG0_9PSED	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	A0A2C9EG81_PSEPH	68.476	17	208.95	SwissP_ <i>P. protegens</i>	
	c2	Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	A0A2J7UJG0_9PSED	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	A0A2C9EG81_PSEPH	68.476	17	208.95	SwissP_ <i>P. protegens</i>	
	c3	Chaperone protein DnaK OS= <i>Pseudomonas mendocina</i> (strain ymp) GN=dnaK	DNAK_PSEMY	68.746	11	285.87	SwissP_ <i>Bacteria_R</i>	
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	A0A2J7UJG0_9PSED	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	A0A2C9EG81_PSEPH	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	DNAK_PSEF5	68.476	12	171.05	SwissP_ <i>Bacteria_R</i>

(continued on next page)

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	A0A2J7UJG0_9PSED	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	A0A2C9EG81_PSEPH	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	DNAK_PSEF5	68.476	12	171.05	SwissP_Bacteria_R
c6		Chaperone protein DnaK OS= <i>Pseudomonas mendocina</i> (strain ymp) GN=dnaK	DNAK_PSEMY	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	DNAK_PSEF5	68.476	12	171.05	SwissP_Bacteria_R
c8		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> OX=380,021 GN=htpG	A0A2T6GQG4_9PSED	71.363	13	142.20	SwissP_P. protegens
		Chaperone protein HtpG OS= <i>Pseudomonas protegens</i> OX=380,021 GN=htpG	A0A2J7UMP6_9PSED	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	A0A2C9EIV4_PSEPH	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	HTPG_PSEF5	71.349	13	137.93	SwissP_Bacteria_R
c9		Trigger factor OS= <i>Pseudomonas protegens</i> OX=380,021 GN=tig	A0A2J7U087_9PSED	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	A0A2C9EQ79_PSEPH	48.511	17	165.98	SwissP_P. protegens
		Trigger factor OS= <i>Pseudomonas aeruginosa</i> (strain LESB58) GN=tig	TIG_PSEA8	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	TIG_PSEAE	48.582	12	94.71	SwissP_Bacteria_R

(continued on next page)

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	TIG_PSEA7	48.548	12	94.71	SwissP_Bacteria_R
		Trigger factor OS= <i>Pseudomonas aeruginosa</i> (strain UCBPP-PA14) GN=tig	TIG_PSEAB	48.582	12	94.71	SwissP_Bacteria_R
	c11	Trigger factor OS= <i>Pseudomonas protegens</i> OX=380,021 GN=tig	A0A2J7U087_9PSED	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	A0A2C9EQ79_PSEPH	48.511	17	165.98	SwissP_P. protegens
	c12	Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	A0A2J7UA71_9PSED	20.837	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	A0A2T6GLZ5_9PSED	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	A0A2C9EG73_PSEPH	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	GRPE_PSEF5	20.823	25	88.28	SwissP_Bacteria_R
	c13	Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	A0A2J7UA71_9PSED	20.837	25	153.06	SwissP_P. protegens
		Protein GrpE OS= <i>Pseudomonas protegens</i> OX=380,021 GN=grpE	A0A2T6GLZ5_9PSED	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	A0A2C9EG73_PSEPH	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	GRPE_PSEF5	20.823	25	88.28	SwissP_Bacteria_R

(continued on next page)

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	A0A2C9EHH8_PSEPH	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	Q4KH94_PSEF5	7.727	46	271.99	SwissP_P. <i>protegens</i>
		Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_02635	A0A2J7UBE2_9PSED	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	Y1905_PSEF5	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	A0A2K4M432_9PSED	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	A0A2C9EJ97_PSEPH	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	Y1905_PSEF5	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	A0A2C9EHH8_PSEPH	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	Q4KH94_PSEF5	7.727	46	271.99	SwissP_P. <i>protegens</i>
		Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_02635	A0A2J7UBE2_9PSED	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	CAPB_PSESM	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 (-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	o2	Chain B, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	gi 1258501321	50.185	8	108.72	NCBI_Bacteria_R
		Chain A, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	gi 1101274917	50.185	8	108.72	NCBI_Bacteria_R
		Chain B, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	gi 1101274918	50.185	8	108.72	NCBI_Bacteria_R
		Chain A, 1 Dihydrolipoyl Dehydrogenase <i>Pseudomonas putida</i> KT2440	gi 1258501320	50.185	8	108.72	NCBI_Bacteria_R
		dihydrolipoyl dehydrogenase [<i>Pseudomonas protegens</i>]	gi 1332903368	49.797	9	86.94	NCBI_P. protegens
		dihydrolipoyl dehydrogenase [<i>Pseudomonas protegens</i>]	gi 1332918899	49.831	9	86.94	NCBI_P. protegens
		MULTISPECIES: dihydrolipoyl dehydrogenase [<i>Pseudomonas</i>]	gi 499372476	49.874	9	86.94	NCBI_P. protegens
		dihydrolipoyl dehydrogenase [<i>Pseudomonas protegens</i>]	gi 1332903368	49.797	9	86.94	NCBI_P. protegens
	o3	MULTISPECIES: dihydrolipoyl dehydrogenase [<i>Pseudomonas</i>]	WP_003223013.1	49.812	9	130.96	NCBI_Bacteria_NR
		dihydrolipoyl dehydrogenase [<i>Pseudomonas protegens</i>]	gi 1332903368	49.797	9	86.94	NCBI_P. protegens
		dihydrolipoyl dehydrogenase [<i>Pseudomonas protegens</i>]	gi 1332918899	49.831	9	86.94	NCBI_P. protegens
		MULTISPECIES: dihydrolipoyl dehydrogenase [<i>Pseudomonas</i>]	gi 499372476	49.874	9	86.94	NCBI_P. protegens
		MULTISPECIES: dihydrolipoyl dehydrogenase [<i>Pseudomonas</i>]	WP_003223013.1	49.812	9	130.96	NCBI_Bacteria_NR
		dihydrolipoyl dehydrogenase [<i>Pseudomonas</i>]					

(continued on next page)

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>]	gi 499375502	22.003	29	155.45	NCBI_ <i>P. protegens</i>
		Chain B, 1 Iron Superoxide Dismutase <i>Pseudomonas putida</i>	gi 349943	21.530	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain A, 1 Iron Superoxide Dismutase <i>Pseudomonas putida</i>	gi 349942	21.530	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain B, 1 SUPEROXIDE DISMUTASE <i>Pseudomonas putida</i>	gi 12084343	21.890	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain C, 1 SUPEROXIDE DISMUTASE <i>Pseudomonas putida</i>	gi 12084344	21.890	14	138.13	NCBI_ <i>Bacteria_R</i>
		Chain A, 1 SUPEROXIDE DISMUTASE <i>Pseudomonas putida</i>	gi 12084342	21.890	14	138.13	NCBI_ <i>Bacteria_R</i>
		superoxide dismutase [<i>Pseudomonas putida</i> KT2440]	NP_743076.1	21.939	25	116.36	NCBI_ <i>Bacteria_NR</i>

(continued on next page)

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>]	WP_003255187.1	21.939	25	116.36	NCBI_Bacteria_NR
		MULTISPECIES: superoxide dismutase [<i>Pseudomonas</i>]	WP_003212997.1	21.978	25	116.36	NCBI_Bacteria_NR
		MULTISPECIES: superoxide dismutase [<i>Pseudomonas</i>]	WP_003175739.1	22.005	25	116.36	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Pseudomonas protegens</i>]	gi 751652819	56.819	20	136.41	NCBI_P. protegens
		MULTISPECIES: molecular chaperone GroEL [<i>Pseudomonas</i>]	gi 499375514	57.065	20	136.41	NCBI_P. protegens
		MULTISPECIES: chaperonin GroEL [<i>Pseudomonas</i>]	WP_003238874.1	56.883	3	81.74	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Pseudomonas fluorescens</i>]	WP_003175873.1	56.927	3	81.74	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [<i>Pseudomonas</i>]	WP_003178748.1	56.843	3	81.74	NCBI_Bacteria_NR
		MULTISPECIES: chaperonin GroEL [<i>Pseudomonas</i>]	WP_003227683.1	56.905	3	81.74	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Pseudomonas fluorescens</i>]	WP_003193939.1	56.882	3	81.74	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Pseudomonas protegens</i>]	gi 751652819	56.819	11	131.03	NCBI_P. protegens
		MULTISPECIES: molecular chaperone GroEL [<i>Pseudomonas</i>]	gi 499375514	57.065	11	131.03	NCBI_P. protegens
		MULTISPECIES: chaperonin GroEL [<i>Pseudomonas</i>]	WP_003238874.1	56.883	7	77.38	NCBI_Bacteria_NR
		chaperonin GroEL [<i>Pseudomonas fluorescens</i>]	WP_003193939.1	56.882	7	77.38	NCBI_Bacteria_NR

(continued on next page)

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>]	gi 499371610	68.476	8	107.62	NCBI_ <i>P. protegens</i>
		MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	WP_003212222.1	68.330	8	103.78	NCBI_Bacteria_NR
	c7	MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	gi 499371610	68.476	8	107.62	NCBI_ <i>P. protegens</i>
		MULTISPECIES: molecular chaperone DnaK [<i>Pseudomonas</i>]	WP_003212222.1	68.330	8	103.78	NCBI_Bacteria_NR
	c8	MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas</i>]	gi 495199965	21.678	18	217.97	NCBI_ <i>P. protegens</i>
		MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas</i>]	WP_003194089.1	21.675	9	124.62	NCBI_Bacteria_NR
		MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas</i>]	WP_003230860.1	21.718	9	124.62	NCBI_Bacteria_NR
		MULTISPECIES: FKBP-type peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas</i>]	WP_003176055.1	21.689	9	124.62	NCBI_Bacteria_NR

(continued on next page)

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>]	gi 515532580	18.283	14	60.40	NCBI_P. protegens
		MULTISPECIES: cyclophilin [<i>Pseudomonas</i>]	gi 499374623	18.269	14	60.40	NCBI_P. protegens
		peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas savastanoi</i>]	WP_004664345.1	18.176	7	20.50	NCBI_Bacteria_NR
		peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas syringae</i>]	WP_003390678.1	18.315	7	20.50	NCBI_Bacteria_NR
		peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas syringae</i>]	WP_004418527.1	18.328	7	20.50	NCBI_Bacteria_NR
		MULTISPECIES: peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas</i>]	WP_003404493.1	18.300	7	20.50	NCBI_Bacteria_NR
		MULTISPECIES: peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas syringae</i> group]	WP_004661308.1	18.218	7	20.50	NCBI_Bacteria_NR
		MULTISPECIES: peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas</i>]	WP_003441354.1	18.288	7	20.50	NCBI_Bacteria_NR
		peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas syringae</i>]	WP_003423206.1	18.332	7	20.50	NCBI_Bacteria_NR
		peptidyl-prolyl cis-trans isomerase [<i>Pseudomonas syringae</i>]	WP_003423206.1	18.332	7	20.50	NCBI_Bacteria_NR
Other proteins involved in stress response	p4	MULTISPECIES: cold-shock protein [<i>Pseudomonas</i>]	gi 489272243	7.697	20	38.71	NCBI_P. protegens
	p5	MULTISPECIES: cold-shock protein CapB [<i>Pseudomonas</i>]	gi 488617988	7.727	46	140.69	NCBI_P. protegens
		cold shock protein CapB [[<i>Pseudomonas syringae</i>] pv. tomato str. DC3000]	NP_793906.1	7.727	46	81.81	NCBI_Bacteria_NR
		MULTISPECIES: cold-shock protein CapB [<i>Pseudomonas</i>]	WP_002554837.1	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	DLDH_PSEFL	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	DLDH2_PSEAE	50.165	4	88.73	SwissP_Bacteria_R
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas putida</i> GN=lpdG	DLDH2_PSEPU	49.896	4	88.73	SwissP_Bacteria_R
	o2	Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=lpdA	A0A2T6GPH9_9PSED	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	Q4KFY7_PSEF5	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	A0A2C9EIR1_PSEPH	49.874	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_04885	A0A2J7ULV5_9PSED	49.831	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas fluorescens</i> GN=lpd	DLDH_PSEFL	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	DLDH2_PSEAE	50.165	4	88.73	SwissP_Bacteria_R
Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas putida</i> GN=lpdG	DLDH2_PSEPU	49.896	4	88.73	SwissP_Bacteria_R		

(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
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas</i> sp. RIT-PI-r OX=1,699,620 GN=AK821_18,310	A0A0P6RYG8_9PSED	49.840	4	63.95	SwissP_Bacteria_NR
	o3	Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=lpdA	A0A2T6GPH9_9PSED	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	Q4KFY7_PSEF5	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	A0A2C9EIR1_PSEPH	49.874	9	95.34	SwissP_P. protegens
		Dihydrolipoyl dehydrogenase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_04885	A0A2J7ULV5_9PSED	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	A0A2C9ESB6_PSEPH	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	Q4K776_PSEF5	22.003	25	122.57	SwissP_P. protegens
		Superoxide dismutase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_14,980	A0A2J7U822_9PSED	22.003	25	122.57	SwissP_P. protegens
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=A3L25_01085	A0A166M6_x6_PSEPU	21.937	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=QV12_13,665	A0A0D1LV26_PSEPU	21.994	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=sodB	A0A1B2F769_PSEPU	21.969	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=A3K88_05175	A0A177YS39_PSEPU	21.909	25	151.90	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
		Superoxide dismutase OS= <i>Pseudomonas putida</i> B6-2 OX=1,081,940 GN=KKK_27,785	A0A168XBM6_PSEPU	21.939	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> OX=294 GN=sodB_1	A0A0D0RQL4_PSEFL	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	A0A0P6S377_9PSED	21.992	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> OX=294 GN=sodB_1	A0A109L2F9_PSEFL	22.005	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=AYO28_24,560	A0A177SFW3_PSEPU	22.019	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. GM67 OX=1,144,335 GN=PMI33_04148	J2UAB6_9PSED	22.021	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas putida</i> OX=303 GN=AO269_03685	A0A0W0Q2E4_PSEPU	22.007	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. GM21 OX=1,144,325 GN=PMI22_04575	J3EKI1_9PSED	21.978	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> WH6 OX=746,360 GN=sodB	E2XX94_PSEFL	22.005	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas plecoglossicida</i> NB2011 OX=1,330,531 GN=L321_24,006	S2JST8_9PSED	21.952	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas fluorescens</i> BRIP34879 OX=1,205,750 GN=A986_21,285	L7H2T0_PSEFL	21.950	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas trivialis</i> OX=200,450 GN=TU79_05835	A0A0R2ZL85_9PSED	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	A0A1B5EYJ2_9PSED	22.005	25	151.90	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
Chaperonin proteins	c1	Superoxide dismutase OS= <i>Pseudomonas monteilii</i> OX=76,759 GN=BC89_13,580	A0A136QIN6_9PSED	21.937	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. Leaf58 OX=1,736,226 GN=ASF02_16,300	A0A0Q4N799_9PSED	21.937	25	151.90	SwissP_Bacteria_NR
		Superoxide dismutase OS= <i>Pseudomonas</i> sp. CMAA1215 OX=1,387,231 GN=P308_25,440	U7A3I6_9PSED	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	SODF_PSEPK	21.939	25	113.96	SwissP_Bacteria_R
		Chaperone protein HtpG OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=htpG	HTPG_PSEFS	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	A0A2C9ESJ4_PSEPH	57.065	15	155.61	SwissP_P. protegens
		60 kDa chaperonin OS= <i>Pseudomonas</i> sp. GM18 OX=1,144,324 GN=groL	J2NZ80_9PSED	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	CH60_PSEF5	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	A0A2C9ESJ4_PSEPH	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	CH60_PSEF5	57.065	11	113.92	SwissP_Bacteria_R

(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
c6		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> (strain DSM 19,095 / LMG 27,888 / CHA0) OX=1,124,983 GN=dnaK	A0A2C9EG81_PSEPH	68.476	8	146.02	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	A0A2J7UJG0_9PSED	68.430	10	138.77	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=dnaK	DNAK_PSEFS	68.200	6	95.25	SwissP_Bacteria_R
		Chaperone protein DnaK OS= <i>Pseudomonas</i> sp. ES3-33 OX=1,628,833 GN=dnaK	A0A0D9A6C8_9PSED	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	A0A2C9EG81_PSEPH	68.476	8	146.02	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas protegens</i> OX=380,021 GN=dnaK	A0A2J7UJG0_9PSED	68.430	10	138.77	SwissP_P. <i>protegens</i>
		Chaperone protein DnaK OS= <i>Pseudomonas fluorescens</i> (strain SBW25) GN=dnaK	DNAK_PSEFS	68.200	6	95.25	SwissP_Bacteria_R
		Chaperone protein DnaK OS= <i>Pseudomonas</i> sp. ES3-33 OX=1,628,833 GN=dnaK	A0A0D9A6C8_9PSED	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	Q4K5T2_PSEF5	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	A0A2C9ETR2_PSEPH	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	A0A2J7TS41_9PSED	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	A0A0D0SQ47_PSEFL	21.675	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas batumici</i> OX=226,910 GN=UCMB321_4721	A0A0C2E6G3_9PSED	21.586	18	209.04	SwissP_Bacteria_NR
		Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas synxantha</i> BG33R OX=96,901 GN=flkB	I4LAD2_9PSED	21.645	18	209.04	SwissP_Bacteria_NR

(continued on next page)

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	U7A1W8_9PSED	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	A0A0W0HKFO_PSEFL	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	L7HNG1_PSEFL	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	E2XY02_PSEFL	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	A0A1B5DMV2_9PSED	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	A0A1B5ESY5_9PSED	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	A0A1B5D261_9PSED	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	A0A031J4K3_9PSED	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	A0A0R2ZUP9_9PSED	21.746	18	209.04	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
	c9	Peptidyl-prolyl cis-trans isomerase OS= <i>Pseudomonas protegens</i> OX=380,021 GN=CSU62_23,620	A0A2T6GHH3_9PSED	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	Q4K9R9_PSEF5	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	A0A2J7U033_9PSED	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	A0A2C9EQ49_PSEPH	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	F3IQ72_PSEAV	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	E2XUJ9_PSEFL	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	A0A0P9ZVJ6_PSESX	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	L7GXR8_PSEFL	9.062	23	72.47	SwissP_Bacteria_NR
		Transcriptional regulator OS= <i>Pseudomonas</i> sp. CMAA1215 OX=1,387,231 GN=P308_20,875	U7A634_9PSED	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	A0A0QOHEI0_9PSED	9.076	23	72.47	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
		DNA-binding protein HU OS= <i>Pseudomonas</i> sp. Root68 OX=1,736,585 GN=ASD91_22,695	A0A0Q8JOC7_9PSED	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	A0A0L8IW02_PSESX	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	A0A0P9 × 6 × 9_PSESH	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	DBHB_PSEF5	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	A0A2C9EQC3_PSEPH	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	Q9KHS6 DBHB_PSEF5	9.106	23	80.95	SwissP_P. protegens
		DNA-binding protein HU OS= <i>Pseudomonas protegens</i> OX=380,021 GN=C5U62_31,250	A0A2T6GBS6_9PSED	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	A0A2C9EHH8_PSEPH	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	Q4KH94_PSEF5	7.727	46	146.74	SwissP_P. protegens
		Cold-shock protein OS= <i>Pseudomonas protegens</i> OX=380,021 GN=A1395_02635	A0A2J7UBE2_9PSED	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	CAPB_PSESM	7.727	46	127.60	SwissP_Bacteria_R

(continued on next page)

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	CAPB_PSEFR	7.727	46	127.60	SwissP_Bacteria_R
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM49 OX=1,144,331 GN=PMI29_02448	J2SK38_9PSED	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	A0A0J6GIW5_9PSED	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	A0A0P9NMB0_PSESX	7.727	46	123.98	SwissP_Bacteria_NR
		CapB_2 protein OS= <i>Pseudomonas fluorescens</i> OX=294 GN=capB_2	A0A075PGX5_PSEFL	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas tremae</i> OX=200,454 GN=ALO43_00013	A0A0Q0CHU5_9PSED	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	L7HLD3_PSEFL	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	A0A1B5EK52_9PSED	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas putida</i> OX=303 GN=AO269_03090	A0A0W0P7R9_PSEPU	7.697	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas brassicacearum</i> OX=930,166 GN=CD58_06475	W8PFF4_9PSED	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas amygdali</i> pv. <i>eribotryae</i> OX=129,137 GN=AL052_06405	A0A0P9QTI2_PSEA0	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas azotoformans</i> OX=47,878 GN=AYR47_13,715	A0A127HXU4_PSEAZ	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas fluorescens</i> (strain SBW25) OX=216,595 GN=capB	C3K709_PSEFS	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	A0A0N0GLZ4_PSEA0	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	A0A0P6SOW4_9PSED	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	A0A0L8ITA8_PSESX	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	A0A0Q8J556_9PSED	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	A0A0M9H959_PSESY	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock DNA-binding protein family OS= <i>Pseudomonas fragi</i> OX=296 GN=AV641_05125	A0A0 × 8EWR3_PSEFR	7.727	46	123.98	SwissP_Bacteria_NR
		Cold-shock protein OS= <i>Pseudomonas weihenstephanensis</i> OX=1,608,994 GN=TU86_02400	A0A0J6IW85_9PSED	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	A0A0P9Q5F3_PSEA0	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM18 OX=1,144,324 GN=PMI21_04449	J2NQX1_9PSED	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	F3IF92_PSEAV	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein CapB OS= <i>Pseudomonas antarctica</i> OX=219,572 GN=A7J50_1439	A0A172YYL9_9PSED	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	A0A0Q0F3Z6_9PSED	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	A0A0F4XHM9_9PSED	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM21 OX=1,144,325 GN=PMI22_04135	J2NCS9_9PSED	7.727	46	123.98	SwissP_Bacteria_NR
		Cold shock protein OS= <i>Pseudomonas</i> sp. GM67 OX=1,144,335 GN=PMI33_02223	J2UA47_9PSED	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	A0A0J6KCW5_9PSED	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	A0A0Q0E2H2_PSEA0	7.727	46	123.98	SwissP_Bacteria_NR

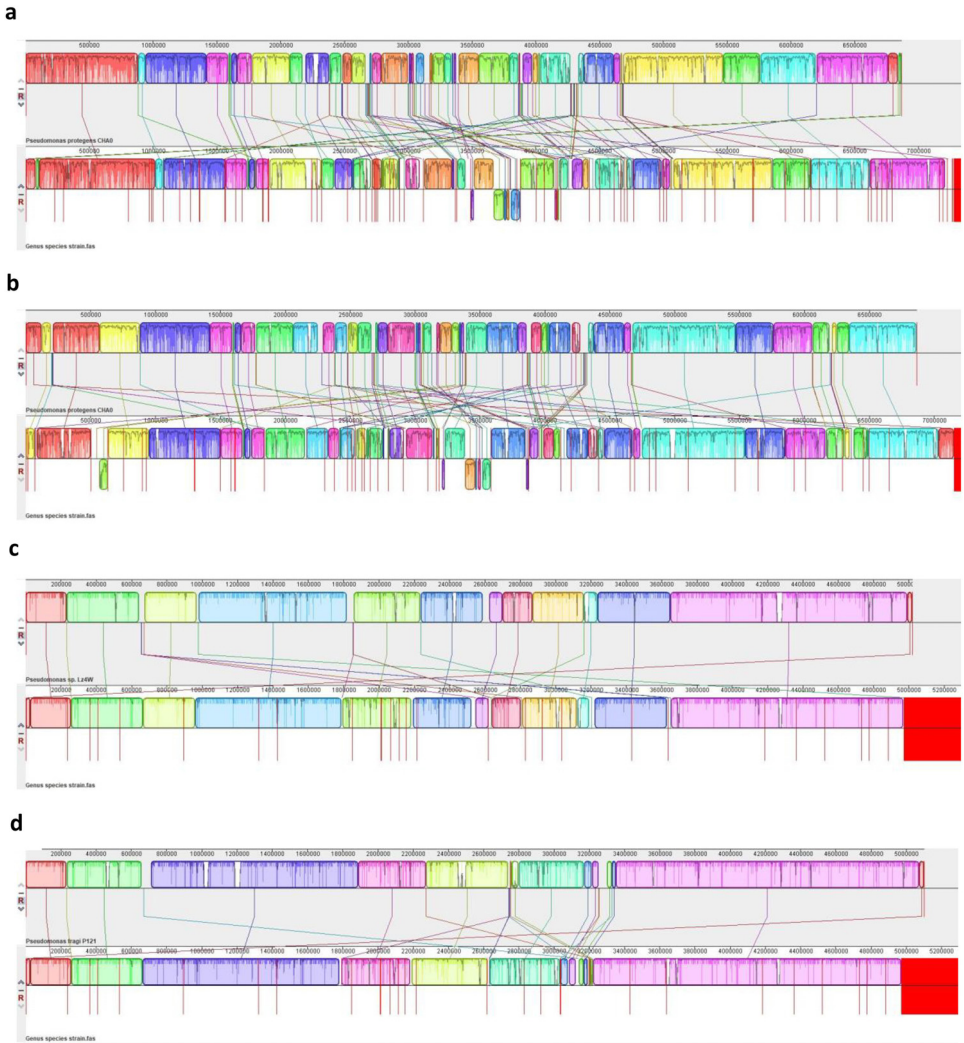


Fig. 1. Alignments of the bacterial draft genomes of F14BN1, F15BN2 and F14BN2 with the complete genomes of the nearest species determined by average nucleotide identity (JSpecies) performed using the Progressive MAUVE algorithm. **a.** Alignment of F14BN1 draft genome versus *Pseudomonas protegens* 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® 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 2×250 -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 α -cyano-4-hydroxy-cinnamic acid matrix (5 mg.ml⁻¹ 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%).

Acknowledgments

The authors thank all the bodies that contributed to the funding of this research. The REALCAT platform is benefiting from a state subsidy administrated by the French National Research Agency (ANR) within the frame of the 'future Investments' program (PIA), with the contractual reference 'ANR-11-EQPX-0037'. The European Union, through the ERDF funding administered by the Hauts-de-France Region, has co-financed the platform. Centrale Lille, the CNRS, and Lille University as well as the Centrale Initiative Foundation, are thanked for their financial contribution to the acquisition and implementation of the equipment of the REALCAT platform. The Hauts-de-France Region attributed the thesis Region Contract N°17007747 to Elodie Dussert for her studies that were also performed thanks to the 'Contrats de Plan ETAT-REGION' CPER PO 2015–2020 ALIBIOTECH.

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.

References

- [1] D.E. Wood, S.L. Salzberg, Kraken: ultrafast metagenomic sequence classification using exact alignments, *Genome Biol.* 15 (2014) R46, doi:[10.1186/gb-2014-15-3-r46](https://doi.org/10.1186/gb-2014-15-3-r46).
- [2] R.K. Aziz, D. Bartels, A.A. Best, M. DeJongh, T. Disz, R.A. Edwards, K. Formisano, S. Gerdes, E.M. Glass, M. Kubal, F. Meyer, G.J. Olsen, R. Olson, A.L. Osterman, R.A. Overbeek, L.K. McNeil, D. Paarmann, T. Paczian, B. Parrello, G.D. Pusch, C. Reich, R. Stevens, O. Vassieva, V. Vonstein, A. Wilke, O. Zagnitko, The RAST server: rapid annotations using subsystems technology, *BMC Genom.* 9 (2008) 75, doi:[10.1186/1471-2164-9-75](https://doi.org/10.1186/1471-2164-9-75).
- [3] T. Disz, S. Akhter, D. Cuevas, R. Olson, R. Overbeek, V. Vonstein, R. Stevens, R.A. Edwards, Accessing the SEED genome databases via Web services API: tools for programmers, *BMC Bioinform.* 11 (2010) 319, doi:[10.1186/1471-2105-11-319](https://doi.org/10.1186/1471-2105-11-319).
- [4] A.E. Darling, B. Mau, N.T. Perna, progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement, *PLoS ONE* 5 (2010) e11147, doi:[10.1371/journal.pone.0011147](https://doi.org/10.1371/journal.pone.0011147).

- [5] H. Teeling, A. Meyerdierks, M. Bauer, R. Amann, F.O. Glöckner, Application of tetranucleotide frequencies for the assignment of genomic fragments, *Environ. Microbiol.* 6 (2004) 938–947, doi:[10.1111/j.1462-2920.2004.00624.x](https://doi.org/10.1111/j.1462-2920.2004.00624.x).
- [6] J. Goris, K.T. Konstantinidis, J.A. Klappenbach, T. Coenye, P. Vandamme, J.M. Tiedje, DNA-DNA hybridization values and their relationship to whole-genome sequence similarities, *Int. J. Syst. Evol. Microbiol.* 57 (2007) 81–91, doi:[10.1099/ijs.0.64483-0](https://doi.org/10.1099/ijs.0.64483-0).
- [7] M. Richter, R. Rosselló-Móra, F. Oliver Glöckner, J. Peplies, JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison, *Bioinformatics* 32 (2016) 929–931, doi:[10.1093/bioinformatics/btv681](https://doi.org/10.1093/bioinformatics/btv681).
- [8] C. Camacho, G. Coulouris, V. Avagyan, N. Ma, J. Papadopoulos, K. Bealer, T.L. Madden, BLAST+: architecture and applications, *BMC Bioinform.* 10 (2009) 421, doi:[10.1186/1471-2105-10-421](https://doi.org/10.1186/1471-2105-10-421).
- [9] S. Kurtz, A. Phillippy, A.L. Delcher, M. Smoot, M. Shumway, C. Antonescu, S.L. Salzberg, Versatile and open software for comparing large genomes, *Genome Biol.* 5 (2004) R12, doi:[10.1186/gb-2004-5-2-r12](https://doi.org/10.1186/gb-2004-5-2-r12).
- [10] A. Ceugniz, M. Tourret, E. Dussert, F. Coucheney, B. Deracinois, P. Jacques, C. Flahaut, E. Heuson, D. Drider, J. Behra-Miellet, Interactions between *kluveromyces marxianus* from cheese origin and the intestinal symbiont *bacteroides thetaiotaomicron*: impressive antioxidative effects, *LWT Food Sci. Technol.* 81 (2017) 281–290, doi:[10.1016/j.lwt.2017.03.056](https://doi.org/10.1016/j.lwt.2017.03.056).