



PAT/*pat* PROTEIN
AMINO ACID SEQUENCE HOMOLOGY
SEARCH WITH KNOWN TOXINS

DATA REQUIREMENT
No applicable guidelines

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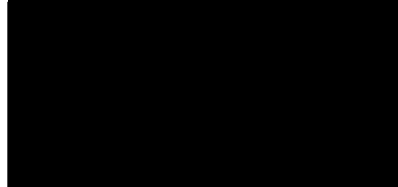
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PAT/*pat* Protein
Amino acid sequence homology search with known toxins

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APPROVALS PAGE

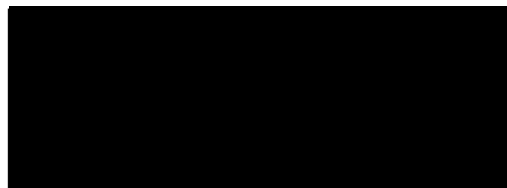
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SUMMARY

This study used an *in silico* approach to evaluate the potential amino acid sequence similarity of the PAT/*pat* protein with known toxins.

The amino acid sequence identity search was carried out by using FASTA algorithm, using the BLOSUM50 scoring matrix. Two approaches were used:

- An overall identity search with all protein sequences present in the following large public reference databases: Uniprot_Swissprot, Uniprot_TrEMBL, PDB, DAD and GenPept. The overconservative criterion for selecting similar proteins was an E-value threshold of 0.1.
- An overall identity search with all protein sequences present in the in-house Bayer Toxin database. The overconservative criterion for selecting similar proteins was an E-value threshold of 10.

Matched sequence proteins were further examined for potential toxicity records in literature in order to assess their biological relevance.

As expected, the results of the overall homology search with the PAT/*pat* protein showed only main similarities with other acetyltransferases from various bacterial origins. In addition, no significant similarities were found with any toxic protein from the Bayer Toxin database. Therefore, the PAT/*pat* protein does not show any evidence of potential toxic properties.

1. Material and methods

1.1. Amino acid query sequence

The 183 amino acid query sequence was coded using the one-letter code adopted by the Commission on Biochemical Nomenclature of the [IUPAC-IUB \(1984\)](#).

As described in the document number M-084188-01-1 ([De Beuckeleer, 2004](#)), the query sequence corresponding to the PAT/*pat* protein is as follows:

```
1  MSPERRPVEI  RPATAADMAA  VCDIVNHYIE  TSTVNFRTPE  QTPQEWIDDL  ERLQDRYPWL
61  VAEVEGVVAG  IAYAGPWKAR  NAYDWTVEST  VYVSHRHQRL  GLGSTLYTHL  LKSMEAQGFK
121  SVVAVIGLPN  DPSVRLHEAL  GYTARGTLRA  AGYKHGGWHD  VGFWRQDFEL  PAPPRPVRPV
181  TQI
```

Date of search: February 22, 2012

1.2. Search design

The complete query sequence was compared with all the sequences available in the databases using the FASTA program (version 35.04 Jan. 15, 2009).

The FASTA program is a sequence comparison algorithm that is used to search sequence databases for optimal local alignments with a query sequence. The FASTA algorithm, developed by the University of Virginia ([Pearson and Lipman, 1988](#)), provides a quick search and local alignment of sequences contained within specified databases.

Each comparison was given a score reflecting the degree of similarity between the query and the comparing sequence. The scoring matrix used was BLOSUM50.

Discrimination between real and artefactual matches is done by using the Expect (E)-value, which describes an estimate of probability that the match might occur by chance when searching a database of a particular size. An E-value threshold of 0.1 was used for the comparison against the general protein databases, and an E-value threshold of 10 was used for the comparison against the toxin database. If the statistical significance ascribed to a match was greater than the E-value threshold, the match was not reported.

Matched sequence proteins were further examined for potential toxicity records in literature in order to assess their biological relevance.

1.3. General protein databases

The sequence comparisons were carried out by using large publicly available protein databases as described below:

- Uniprot_Swissprot: Uniprot-Swissprot is a protein sequence database that strives to provide a high level of annotations (e.g. protein function, post-translational modification, etc.), a minimal level of redundancy and a high level of integration with other databases, notably the EMBL, PROSITE pattern and NRL-3D databases. Uniprot-Swissprot has been developed by SIB (Swiss Institute of Bioinformatics) and EBI (European Bioinformatics Institute).
- Uniprot TrEMBL: Uniprot-TrEMBL is a computer-annotated supplement of Uniprot_Swissprot that contains all the translations of EMBL nucleotide sequence entries not yet integrated in Uniprot-Swissprot. Uniprot-TrEMBL has been developed by SIB and EBI.
- PDB: The PDB (Protein Data Bank) is the single international repository for public data on the 3-dimensional structures of biological macromolecules. The contents are primarily experimental data derived from X-ray crystallography and NMR experiments. This database is constantly updated as new structures are deposited by the international scientific community. It is also called NRL-3D.
- DAD (DDBJ Amino acid sequence Database): The DAD is a protein database translated from the DDBJ (DNA Data Bank of Japan) which is officially certified to collect DNA sequences from researchers and to issue the internationally recognized accession number to data submitters. This database exchanges the collected data with EMBL/EBI and GenBank/NCBI on a daily basis.
- GenPept: The GenPept is an amino acid sequence database translated from the GenBank DNA sequence of the NCBI (National Center for Biotechnology Information) as a division of the National Library of Medicine (NLM) at the National Institutes of Health (NIH). The GenBank is built by individual laboratories and by data exchange with the international nucleotide sequence databases, EMBL and DDBJ. Arrangements with the U.S. Patent and Trademark Office enable the incorporation of patent sequence data. A powerful and unique feature of this database is the ability to retrieve references that are available through PubMed, a Web search interface that provides access to over 11 million journal citations in MEDLINE and contains links to full-text articles at participating publishers' Web sites.

1.4. Toxin database

Bayer toxin database (version 1.1) was set up by following a two-steps process.

First step consisted in using the following keyword(s): *calcin*, *channel*block*, *harmful*, *noxious*, *poison*, *venin*, *porin*, *lectin*, *toxic*, *knottin*, *toxin*, *venom*, *channel*inhibitor* to screen Uniprot_SwissProt and NCBI GenPept protein databases. After running this keyword search, 93 167 sequences were collected. In addition, the toxin database was completed with sequences present in the well-described Animal Toxin Database (ATDB; <http://protchem.hunnu.edu.cn/toxin>). ATDB is considered as the most comprehensive existing

repository of annotated animal toxins. A total of 3 844 sequences were present in ATDB. Among them, 3 163 were already present in the preliminary collection of sequences, extracted from Uniprot_SwissProt and GenPept databases. The other 681 sequences from ATDB were added to the toxin dataset. Overall, 93 848 sequences have been collected in the version 1.0 of the toxin database.

Second step consisted in reducing the number of false positive entries (estimated to be approximately 78% in the version 1.0). In order to optimize the database, a keyword selection refinement was performed on the version 1.0 dataset (93 848 sequences) to obtain the upgraded version 1.1 database. The refined selection keywords were: *calcine, *channel*block*, *channel*inhibitor*, *harmful*, *knottin*, *lectins*, *noxious*, *poison*, venom, poreforming, pore forming, pore-forming, *toxic* (but not nontoxic* or non-toxic*) and *toxin* (but not antitoxin* or anti-toxin*). Overall, 31 662 sequences have been kept in the version 1.1 of the database.

Importantly, Bayer toxin database has not been curated to ensure that only relevant toxin sequences were present and that non-relevant entries were excluded (e.g. misleading annotations, missing scientific justifications, etc). The false positive rate was estimated at circa 35% by performing an analysis on 100 sequences from the 31 662 sequences dataset (=manual annotation of toxins versus non-toxins). This means that only 65% of the dataset, corresponding to approximately 20 500 sequences, are very likely true toxins in the version 1.1 of the database.

Therefore, matched sequence proteins need further examination for their potential toxicity records in literature, to evaluate if they are toxins or not.

1.5. Summary of the public protein and allergen database releases

Name	Database type	Number of sequences	Version	Date of release
Uniprot_Swissprot	General database	534 242	2012.01	2012-02-22
Uniprot_TrEMBL	General database	19 434 245	2012.01	2012-02-22
PDB	General database	188 996	2011.11	2011-12-01
DAD	General database	20 972 337	57	2011-10-03
Genpept	General database	12 127 510	185	2011-10-03
Bayer Toxin database	Toxin database	31 662	1.1	2011-11-15

2. Results

2.1. General protein databases

The matching sequences for each of the protein databases are reported in [Tables 1 to 5](#).

Only the first 1000 matches were reported when more than 1000 matches were found.

Table number	Database Names	Number of matches with E-value <0.1
1	Uniprot_Swissprot	7
2	Uniprot_TrEMBL	> 1000
3	PDB	26
4	DAD	> 1000
5	Genpept	> 1000

As expected, only main similarities with other acetyltransferases from various origins were observed. Although some GCN5-related N-acetyltransferases (GNAT) are involved in toxin-antitoxin systems in some pathogenic bacteria, the acetyltransferase family proteins are not considered as toxins.

2.2. Toxin database

The matching sequences for the Bayer Toxin databases are reported in [Table 6](#).

Table number	Database Name	Number of matches with E-value <10
6	Bayer Toxin database	30

As expected based on the good safety profile of the PAT protein, none of the 30 sequences from the toxin database matching with the PAT/*pat* protein sequence were true toxins.

Several matched sequences were derived from complete genomes of various organisms, or from complete sequences of chromosomes, and did not correspond to an identified protein. In addition, several matched sequences were inaccurately included in the Bayer Toxin database because of the presence of specific keywords (see section 1.4) in their phylogeny. Therefore, these homologies are not relevant.

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Similarly, several matched sequences from non toxic proteins (e.g., sortase, Accession number GQ352402_11) were not true toxins and were unaccurately included in the toxin database because of the presence of specific keywords in their description.

Therefore, no significant similarities were found between the PAT/*pat* protein and any toxic proteins from the Toxin database.

3. Conclusion

The PAT/*pat* protein shows a high degree of homology with other proteins of its respective family. No records were found on potential hazard associated with this protein family. In addition, no biologically significant similarities were found with any toxic protein from the Bayer Toxin database. Therefore, the PAT/*pat* protein does not show any evidence of potential toxic properties.

4. References

DART #	References
M-135134-03-1	De Beuckeleer, M. 2004. Description of the amino acid sequence of the PAT protein encoded from the <i>pat</i> gene. Study Report pat/pat_aas/01. Unpublished. Bayer CropScience. Jan 19, 2004. 5 pages.
M-264607-01-1	IUPAC-IUB. 1984. Joint Commission on Biochemical Nomenclature (JCBN). Nomenclature and symbolism for amino acids and peptides. Recommendations 1983. Eur. J. Biochem. 138: 9-37. http://www.chem.gmw.ac.uk/iupac/AminoAcid/
M-303903-01-1	Pearson, W.R. and Lipman, D.J. 1988. Improved tools for biological sequence comparison. Proc. Natl. Acad. Sci. USA. 85:2444-2448.

5. Acronyms and Abbreviations

%	Percent(age)
aa	Amino acid(s)
ATDB	Animal toxin database
DAD	DDBJ Amino acid sequence Database
DDBJ	DNA Data Bank of Japan
DNA	Desoxyribonucleic acid
E-Value	Expect(ed) value
E.C.	Enzyme classification
EBI	European Bioinformatics Institute
EMBL	European Molecular Biology Laboratory sequence database
ID	Accession number
Ident.	Identity
JCBN.....	Joint Commission on Biochemical Nomenclature
MOL. NAME.....	Molecule name
NCBI	National Center for Biotechnology Information
NIH.....	National Institute of Health
NLM	National Library of Medicine
PAT	Phosphinothricin acetyltransferase
PDB.....	Protein Data Bank
PTC.....	Phosphinothricin
SIB	Swiss Institute of Bioinformatics
TrEMBL.....	Translated sequences from the EMBL nucleotide sequence database

6. Tables - FASTA sequence similarities of the PAT/*pat* protein

6.1. Table 1 - Uniprot_Swissprot database

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
1	PAT_STRVR	Q57146	<i>Streptomyces viridochromogenes</i> .	Phosphinothricin N-acetyltransferase. Short=PPT N-acetyltransferase. EC=2.3.1.183. Phosphinothricin-resistance protein.	183	1.4E-79	183	94.5
2	PAT_STRHY	P16426	<i>Streptomyces hygroscopicus</i> .	Phosphinothricin N-acetyltransferase. Short=PPT N-acetyltransferase. EC=2.3.1.183. Phosphinothricin-resistance protein.	183	3.7E-67	183	80.3
3	PAT_STRCO	P21861	<i>Streptomyces coelicolor</i> .	Phosphinothricin N-acetyltransferase. Short=PPT N-acetyltransferase. EC=2.3.1.183. Phosphinothricin-resistance protein.	171	1.7E-15	170	33.5
4	PAT_ALCFA	P31668	<i>Alcaligenes faecalis</i> .	Phosphinothricin N-acetyltransferase. Short=PPT N-acetyltransferase. EC=2.3.1.183. Phosphinothricin-resistance protein.	197	1.4E-10	174	28.7
5	YNCA_ECOLI	P76112	<i>Escherichia coli</i> (strain K12).	Uncharacterized N-acetyltransferase YncA. EC=2.3.1.-.	172	3.4E-10	169	29.6
6	NAT_STRGR	Q54225	<i>Streptomyces griseus</i> .	N-acetyltransferase. EC=2.3.1.-.	194	3.3E-9	179	26.8
7	YWNH_BACSU	P71043	<i>Bacillus subtilis</i> .	Putative phosphinothricin acetyltransferase YwnH. Short=PPT N-acetyltransferase. EC=2.3.1.183.	163	0.00004	161	26.1

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6.2. Table 2 - Uniprot_TREMBL database

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
1	Q5IW47_STRVR	Q5IW47	<i>Streptomyces viridochromogenes</i> .	Phosphinothricin N-acetyltransferase.	183	2.3E-77	183	94.5
2	Q285M3_9ZZZZ	Q285M3	<i>synthetic construct</i> .	Phosphinothricin acetyltransferase.	183	2.3E-77	183	94.5
3	D9XF32_STRVR	D9XF32	<i>Streptomyces viridochromogenes DSM 40736</i> .	Phosphinothricin-N-acetyltransferase.	183	2.3E-77	183	94.5
4	A0PG61_9ZZZZ	A0PG61	<i>synthetic construct</i> .	Phosphinothricin acetyl transferase.	183	1.1E-64	183	79.8
5	F4ZNF8_GOSHI	F4ZNF8	<i>Gossypium hirsutum (Upland cotton) (Gossypium mexicanum)</i> .	Phosphinothricin N-acetyltransferase.	183	1.1E-64	183	79.8
6	Q285M5_9ZZZZ	Q285M5	<i>synthetic construct</i> .	Phosphinothricin acetyltransferase. Flags: Fragment.	109	1.6E-46	109	100.0
7	A4X117_SALTO	A4X117	<i>Salinispora tropica (strain ATCC BAA-916 / DSM 44818 / CNB-440)</i> .	GCN5-related N-acetyltransferase.	192	1.4E-35	178	51.1
8	Q4ZWC2_PSEU2	Q4ZWC2	<i>Pseudomonas syringae pv. syringae (strain B728a)</i> .	GCN5-related N-acetyltransferase.	184	1.7E-24	174	38.5
9	Q7NHN9_GLOVI	Q7NHN9	<i>Gloeobacter violaceus (strain PCC 7421)</i> .	Phosphinothricin N-acetyltransferase.	212	1E-23	170	41.8
10	Q3IQH0_NATPD	Q3IQH0	<i>Natronomonas pharaonis (strain DSM 2160 / ATCC 35678)</i> .	Probable N-acetyltransferase.	206	1.2E-23	177	40.7
11	D0LNJ4_HALO1	D0LNJ4	<i>Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2)</i> .	Phosphinothricin acetyltransferase.	190	1.3E-23	179	39.1

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
12	D8J0P4_HERSS	D8J0P4	<i>Herbaspirillum seropedicae</i> (strain SmR1).	Phosphinothricin N-acetyltransferase (Sortase) protein. EC=2.3.1.-.	167	4.4E-23	156	41.0
13	A5V3M5_SPHWW	A5V3M5	<i>Sphingomonas wittichii</i> (strain RW1 / DSM 6014 / JCM 10273).	GCN5-related N-acetyltransferase.	182	4.7E-23	177	39.5
14	E6J7Z5_9ACTO	E6J7Z5	<i>Dietzia cinnamea</i> P4.	Phosphinothricin acetyltransferase, putative.	190	5.7E-23	171	41.5
15	D3SUX9_NATMM	D3SUX9	<i>Natrialba magadii</i> (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) (<i>Natronobacterium magadii</i>).	Phosphinothricin acetyltransferase.	198	7E-23	176	39.8
16	C7NMA1_HALUD	C7NMA1	<i>Halorhabdus utahensis</i> (strain DSM 12940 / JCM 11049 / AX-2).	GCN5-related N-acetyltransferase.	200	1.9E-22	173	38.7
17	F7PGA0_9EURY	F7PGA0	<i>Halorhabdus tiamateae</i> SARL4B.	GCN5-related N-acetyltransferase.	200	4.4E-22	176	38.6
18	F7NZS5_9GAMM	F7NZS5	<i>Rheinheimera</i> sp. A13L.	Sortase-like acyltransferase.	210	8.9E-22	165	41.2
19	F9TUA8_9VIBR	F9TUA8	<i>Vibrio nigripulchritudo</i> ATCC 27043.	Phosphinothricin N-acetyltransferase, putative.	164	1.2E-21	163	38.7
20	G4FTY3_9GAMM	G4FTY3	<i>Rhodanobacter</i> sp. 2APBS1.	Phosphinothricin acetyltransferase.	187	1.6E-21	173	41.0
21	F4CVA3_9PSEU	F4CVA3	<i>Pseudonocardia dioxanivorans</i> CB1190.	Phosphinothricin acetyltransferase.	193	1.9E-21	175	40.0
22	A9B643_HERA2	A9B643	<i>Herpetosiphon aurantiacus</i> (strain ATCC 23779 / DSM 785).	GCN5-related N-acetyltransferase.	198	1.9E-21	176	39.8
23	F3WZ78_9SPHN	F3WZ78	<i>Sphingomonas</i> sp. S17.	Acetyltransferase family protein.	196	2.3E-21	184	36.4

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
24	E7QSG0_9EURY	E7QSG0	<i>Haladaptatus paucihalophilus</i> DX253.	GCN5-related N-acetyltransferase.	196	3.7E-21	174	36.2
25	E3J1E4_FRASU	E3J1E4	<i>Frankia</i> sp. (strain <i>Eul1c</i>).	Phosphinothricin acetyltransferase.	180	6.8E-21	175	38.3
26	F8F387_SPICH	F8F387	<i>Spirochaeta caldaria</i> (strain ATCC 51460 / DSM 7334 / H1).	Phosphinothricin acetyltransferase. Flags: Precursor.	162	1E-20	156	40.4
27	Q2IND8_ANADE	Q2IND8	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-C).	GCN5-related N-acetyltransferase.	197	1.7E-20	172	40.1
28	D4GXV7_HALVD	D4GXV7	<i>Haloferax volcanii</i> (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) (<i>Halobacterium volcanii</i>).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	199	2.8E-20	174	36.8
29	D9VA56_9ACTO	D9VA56	<i>Streptomyces</i> sp. AA4.	Phosphinothricin N-acetyltransferase.	179	4.2E-20	170	36.5
30	F6ADP5_PSEF1	F6ADP5	<i>Pseudomonas fulva</i> (strain 12-X).	Phosphinothricin acetyltransferase.	187	4.3E-20	175	36.6
31	D2PUE1_KRIFD	D2PUE1	<i>Kribbella flavida</i> (strain DSM 17836 / JCM 10339 / NBRC 14399).	Phosphinothricin acetyltransferase.	178	4.9E-20	171	37.4
32	F9QN66_9MYCO	F9QN66	<i>Mycobacterium colombiense</i> CECT 3035.	Putative uncharacterized protein.	190	5.2E-20	167	37.1
33	B4UC03_ANASK	B4UC03	<i>Anaeromyxobacter</i> sp. (strain K).	GCN5-related N-acetyltransferase.	197	5.3E-20	172	39.5
34	G0AAQ9_COLFT	G0AAQ9	<i>Collimonas fungivorans</i> (strain Ter331).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	174	5.7E-20	157	39.5

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
35	A6WF10_KINRD	A6WF10	<i>Kineococcus radiotolerans</i> (strain ATCC BAA-149 / DSM 14245 / SRS30216).	GCN5-related N-acetyltransferase.	176	6.8E-20	170	38.2
36	G4GIK9_9EURY	G4GIK9	<i>Natrinema pellirubrum</i> DSM 15624.	Phosphinothricin acetyltransferase.	202	9E-20	177	37.3
37	E5XT18_9ACTO	E5XT18	<i>Segniliparus rugosus</i> ATCC BAA-974.	Acetyltransferase.	177	1.3E-19	170	36.5
38	G5HNL0_9CLOT	G5HNL0	<i>Clostridium citroniae</i> WAL-17108.	Putative uncharacterized protein.	181	2.2E-19	179	36.3
39	D2SGR4_GEOOG	D2SGR4	<i>Geodermatophilus obscurus</i> (strain ATCC 25078 / DSM 43160 / JCM 3152 / G-20).	Phosphinothricin acetyltransferase.	198	2.4E-19	171	39.2
40	Q11D00_MESSB	Q11D00	<i>Mesorhizobium</i> sp. (strain BNC1).	GCN5-related N-acetyltransferase.	186	2.7E-19	174	37.4
41	B8JC07_ANAD2	B8JC07	<i>Anaeromyxobacter dehalogenans</i> (strain 2CP-1 / ATCC BAA-258).	GCN5-related N-acetyltransferase.	197	4.6E-19	173	38.7
42	A6D5Q4_9VIBR	A6D5Q4	<i>Vibrio shilonii</i> AK1.	Phosphinothricin N-acetyltransferase, putative.	162	4.7E-19	158	38.0
43	D3FAB4_CONWI	D3FAB4	<i>Conexibacter woesei</i> (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577).	GCN5-related N-acetyltransferase.	176	5.9E-19	173	39.3
44	D5UCV6_CELFN	D5UCV6	<i>Cellulomonas flavigena</i> (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134).	Phosphinothricin acetyltransferase.	193	6.4E-19	184	35.9
45	F8DBW3_9EURY	F8DBW3	<i>Halopiger xanaduensis</i> SH-6.	Phosphinothricin acetyltransferase.	202	6.6E-19	169	37.3

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
46	A1S593_SHEAM	A1S593	<i>Shewanella amazonensis</i> (strain ATCC BAA-1098 / SB2B).	Phosphinothricin N-acetyltransferase, putative.	171	6.8E-19	161	37.9
47	A7HSK6_PARL1	A7HSK6	<i>Parvibaculum lavamentivorans</i> (strain DS-1 / DSM 13023 / NCIMB 13966).	GCN5-related N-acetyltransferase.	197	7.6E-19	174	35.6
48	D0X5S4_VIBHA	D0X5S4	<i>Vibrio harveyi</i> 1DA3.	Putative uncharacterized protein.	164	7.8E-19	166	36.7
49	E2MLV9_PSEUB	E2MLV9	<i>Pseudomonas syringae</i> pv. <i>tomato</i> T1.	Phosphinothricin N-acetyltransferase.	185	1E-18	171	36.3
50	A3TJ84_9MICO	A3TJ84	<i>Janibacter</i> sp. HTCC2649.	GCN5-related N-acetyltransferase.	164	1.1E-18	162	37.0
51	C9PDR8_VIBFU	C9PDR8	<i>Vibrio furnissii</i> CIP 102972.	Phosphinothricin N-acetyltransferase putative.	165	1.3E-18	166	34.9
52	G5L3G2_STRSU	G5L3G2	<i>Streptococcus suis</i> R61.	Sortase and related acyltransferase.	169	1.3E-18	161	36.0
53	Q1ZRV6_PHOAS	Q1ZRV6	<i>Photobacterium angustum</i> (strain S14 / CCUG 15956) (<i>Vibrio</i> sp. (strain S14 / CCUG 15956)).	Phosphinothricin N-acetyltransferase, putative.	166	1.5E-18	163	36.2
54	E6PKZ1_9ZZZZ	E6PKZ1	<i>mine drainage metagenome</i> .	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.-.	181	1.6E-18	173	38.7
55	E8LTH0_9VIBR	E8LTH0	<i>Vibrio brasiliensis</i> LMG 20546.	Phosphinothricin N-acetyltransferase, putative.	164	2.5E-18	166	36.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
56	C7NY05_HALMD	C7NY05	<i>Halomicrobium mukohataei</i> (strain ATCC 700874 / DSM 12286 / JCM 9738 / NCIMB 13541) (<i>Haloarcula mukohataei</i>).	GCN5-related N-acetyltransferase.	196	2.9E-18	174	34.5
57	G6X4M9_MYCAB	G6X4M9	<i>Mycobacterium abscessus</i> 47J26.	Phosphinothricin N-acetyltransferase.	177	3.1E-18	158	36.7
58	D2RU77_HALTV	D2RU77	<i>Haloterrigena turkmenica</i> (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (<i>Halococcus turkmenicus</i>).	GCN5-related N-acetyltransferase.	203	3.5E-18	172	36.6
59	E7SBD1_9STRE	E7SBD1	<i>Streptococcus australis</i> ATCC 700641.	FR47-like protein. Phosphinothricin acetyltransferase. EC=2.3.1.-.	170	3.6E-18	167	35.3
60	Q744X8_MYCPA	Q744X8	<i>Mycobacterium paratuberculosis</i> .	Putative uncharacterized protein.	192	3.9E-18	175	36.0
61	A4W0H2_STRS2	A4W0H2	<i>Streptococcus suis</i> (strain 98HAH33).	Sortase and related acyltransferase.	169	4.2E-18	161	35.4
62	G7RZ50_STRSU	G7RZ50	<i>Streptococcus suis</i> A7.	Sortase and related acyltransferase.	169	4.2E-18	161	35.4
63	C5VVG3_STRSE	C5VVG3	<i>Streptococcus suis</i> (strain P1/7).	Putative acetyltransferase.	169	4.2E-18	161	35.4
64	D5AH34_STRGZ	D5AH34	<i>Streptococcus suis</i> (strain GZ1).	GCN5-related N-acetyltransferase.	169	4.2E-18	161	35.4
65	E8UN02_STREJ	E8UN02	<i>Streptococcus suis</i> (strain JS14).	Sortase and related acyltransferase.	169	4.2E-18	161	35.4
66	G7S526_STRSU	G7S526	<i>Streptococcus suis</i> SS12.	Sortase and related acyltransferase.	169	4.2E-18	161	35.4
67	C6GS01_STRSX	C6GS01	<i>Streptococcus suis</i> (strain SC84).	Putative acetyltransferase.	169	4.2E-18	161	35.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
68	C6GTP1_STRS4	C6GTP1	<i>Streptococcus suis</i> (strain BM407).	Putative acetyltransferase.	169	4.2E-18	161	35.4
69	A4VU78_STRSY	A4VU78	<i>Streptococcus suis</i> (strain 05ZYH33).	Sortase and related acyltransferase.	169	4.2E-18	161	35.4
70	Q03K13_STRTD	Q03K13	<i>Streptococcus thermophilus</i> (strain ATCC BAA-491 / LMD-9).	Sortase or related acyltransferase.	170	4.2E-18	171	35.1
71	E6J2J9_STRAP	E6J2J9	<i>Streptococcus anginosus</i> F0211.	Acetyltransferase, GNAT family.	180	4.4E-18	171	34.5
72	A0Q906_MYCA1	A0Q906	<i>Mycobacterium avium</i> (strain 104).	Phosphinothricin N-acetyltransferase.	188	4.6E-18	172	36.6
73	F6ENU2_AMYSD	F6ENU2	<i>Amycolicoccus subflavus</i> (strain DSM 45089 / DQS3-9A1).	Phosphinothricin N-acetyltransferase.	172	5E-18	171	34.5
74	G7SH78_STRSU	G7SH78	<i>Streptococcus suis</i> D12.	Sortase and related acyltransferase.	169	5.8E-18	161	34.8
75	B1MCZ6_MYCA9	B1MCZ6	<i>Mycobacterium abscessus</i> (strain ATCC 19977 / DSM 44196).	Hypothetical phosphinothricin N-acetyltransferase.	177	6.1E-18	158	36.1
76	F3J3Y2_PSEAP	F3J3Y2	<i>Pseudomonas syringae</i> pv. <i>aptata</i> str. DSM 50252.	Phosphinothricin N-acetyltransferase, putative.	185	6.3E-18	171	35.1
77	D8J990_HALJB	D8J990	<i>Halalkalicoccus jeotgali</i> (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3).	Phosphinothricin N-acetyltransferase.	196	6.6E-18	171	36.3
78	E4LSH7_9CLOT	E4LSH7	<i>Clostridium</i> sp. HGF2.	Putative phosphinothricin N-acetyltransferase.	207	6.9E-18	172	36.0
79	A6T0T8_JANMA	A6T0T8	<i>Janthinobacterium</i> sp. (strain Marseille) (<i>Minibacterium massiliensis</i>).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	173	7E-18	156	37.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
80	E8KUE7_STRVE	E8KUE7	<i>Streptococcus vestibularis</i> ATCC 49124.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	177	7.1E-18	170	33.5
81	A8RP99_9CLOT	A8RP99	<i>Clostridium bolteae</i> ATCC BAA-613.	Putative uncharacterized protein.	182	8.6E-18	178	37.1
82	D7C1T0_STRBB	D7C1T0	<i>Streptomyces bingchenggensis</i> (strain BCW-1).	Phosphinothricin acetyltransferase.	185	8.7E-18	184	36.4
83	G2GT77_STRSL	G2GT77	<i>Streptococcus salivarius</i> M18.	Phosphinothricin N-acetyltransferase.	170	9.6E-18	162	34.0
84	D7B792_NOCDD	D7B792	<i>Nocardiopsis dassonvillei</i> (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (<i>Actinomadura dassonvillei</i>).	Phosphinothricin acetyltransferase.	175	9.9E-18	163	33.7
85	F7P936_MYCPA	F7P936	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> S397.	Sortase-like acyltransferase.	188	1E-17	172	36.0
86	Q5R129_IDILO	Q5R129	<i>Idiomarina loihiensis</i> (strain ATCC BAA-735 / DSM 15497 / L2-TR).	Phosphinothricin N-acetyltransferase, putative.	166	1.1E-17	157	36.3
87	G7SM47_STRSU	G7SM47	<i>Streptococcus suis</i> ST1.	Sortase and related acyltransferase.	169	1.1E-17	161	34.8
88	D1PRI9_9FIRM	D1PRI9	<i>Subdoligranulum variabile</i> DSM 15176.	Phosphinothricin N-acetyltransferase.	299	1.3E-17	176	35.8
89	C5BQQ3_TERTT	C5BQQ3	<i>Teredinibacter turnerae</i> (strain ATCC 39867 / T7901).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	204	1.3E-17	168	33.3
90	G7SCL0_STRSU	G7SCL0	<i>Streptococcus suis</i> D9.	GCN5-related N-acetyltransferase.	169	2.2E-17	161	34.2
91	B9WTB8_STRSU	B9WTB8	<i>Streptococcus suis</i> 89/1591.	GCN5-related N-acetyltransferase.	169	2.2E-17	161	34.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
92	E4SPZ4_STRTN	E4SPZ4	<i>Streptococcus thermophilus</i> (strain ND03).	Sortase acyltransferase-like protein.	170	2.6E-17	171	34.5
93	E3CQL3_STRVE	E3CQL3	<i>Streptococcus vestibularis</i> F0396.	Putative phosphinothricin N-acetyltransferase.	170	2.6E-17	162	34.0
94	F8LY68_STRTR	F8LY68	<i>Streptococcus thermophilus</i> JIM 8232.	GCN5-related N-acetyltransferase.	170	2.6E-17	171	34.5
95	C2LTF7_STRSL	C2LTF7	<i>Streptococcus salivarius</i> SK126.	Phosphinothricin N-acetyltransferase. EC=2.3.1.183.	170	2.6E-17	162	34.0
96	F2JVJ4_MARM1	F2JVJ4	<i>Marinomonas mediterranea</i> (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1).	Phosphinothricin acetyltransferase.	163	3E-17	157	34.4
97	F8HCJ0_STRE5	F8HCJ0	<i>Streptococcus salivarius</i> (strain 57.I).	Phosphinothricin acetyltransferase.	177	3.2E-17	170	33.5
98	C6BLE8_RALP1	C6BLE8	<i>Ralstonia pickettii</i> (strain 12D).	GCN5-related N-acetyltransferase.	182	3.3E-17	170	36.5
99	B2UJQ7_RALPJ	B2UJQ7	<i>Ralstonia pickettii</i> (strain 12J).	GCN5-related N-acetyltransferase.	182	3.3E-17	170	36.5
100	Q5LZ64_STRT1	Q5LZ64	<i>Streptococcus thermophilus</i> (strain CNRZ 1066).	Phosphinothricin acetyltransferase, putative.	193	3.4E-17	177	33.9
101	F3KNL1_9BURK	F3KNL1	<i>Hylemonella gracilis</i> ATCC 19624.	Phosphinothricin acetyltransferase.	161	3.5E-17	164	37.2
102	B2SJR5_XANOP	B2SJR5	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain PXO99A).	Phosphinothricin N-acetyltransferase.	170	3.6E-17	164	35.4
103	G1VKV8_9FIRM	G1VKV8	<i>Erysipelotrichaceae bacterium 2_2_44A</i> .	Putative uncharacterized protein.	219	3.8E-17	172	35.5
104	F8LQI8_STRE8	F8LQI8	<i>Streptococcus salivarius</i> (strain JIM8777).	Phosphinothricin acetyltransferase, putative, GNAT family acetyltransferase. EC=2.3.1.183.	170	4.3E-17	162	34.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
105	G8AXJ4_AZOBR	G8AXJ4	<i>Azospirillum brasilense</i> Sp245.	Putative phosphinothricin N-acetyltransferase.	189	4.7E-17	178	37.6
106	A6FCF9_9GAMM	A6FCF9	<i>Moritella</i> sp. PE36.	Phosphinothricin N-acetyltransferase, putative.	162	4.9E-17	158	35.4
107	A4U5I4_9PROT	A4U5I4	<i>Magnetospirillum gryphiswaldense</i> .	Phosphinothricin acetyltransferase.	176	5.2E-17	165	37.6
108	F9M128_STRPA	F9M128	<i>Streptococcus parasanguinis</i> SK236.	FR47-like protein.	169	6E-17	162	34.0
109	Q5M3R9_STRT2	Q5M3R9	<i>Streptococcus thermophilus</i> (strain ATCC BAA-250 / LMG 18311).	Phosphinothricin acetyltransferase, putative.	193	6.6E-17	177	33.3
110	E9UTM5_9ACTO	E9UTM5	<i>Nocardioideaceae</i> bacterium Broad-1.	Phosphinothricin N-acetyltransferase.	170	7.1E-17	159	34.6
111	F8LIC7_STREH	F8LIC7	<i>Streptococcus salivarius</i> (strain CCHSS3).	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.183.	170	7.1E-17	162	34.6
112	F5U2U0_STRAP	F5U2U0	<i>Streptococcus anginosus</i> SK52.	Putative phosphinothricin N-acetyltransferase.	180	7.4E-17	171	33.3
113	F4EF12_STRSU	F4EF12	<i>Streptococcus suis</i> .	GCN5-related N-acetyltransferase.	169	9.8E-17	161	33.5
114	C9AVE7_ENTCA	C9AVE7	<i>Enterococcus casseliflavus</i> EC30.	Putative uncharacterized protein.	177	1E-16	160	36.9
115	C9CJ38_ENTCA	C9CJ38	<i>Enterococcus casseliflavus</i> EC10.	Putative uncharacterized protein.	177	1E-16	160	36.9
116	B5ZH13_GLU DA	B5ZH13	<i>Gluconacetobacter diazotrophicus</i> (strain ATCC 49037 / DSM 5601 / PAI5).	GCN5-related N-acetyltransferase.	184	1.1E-16	182	36.8
117	E8TIT3_MESCW	E8TIT3	<i>Mesorhizobium ciceri</i> bv. <i>biserrulae</i> (strain HAMBI 2942 / LMG 23838 / WSM1271).	Phosphinothricin acetyltransferase.	190	1.1E-16	174	35.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
118	B1LZI2_METRJ	B1LZI2	<i>Methylobacterium radiotolerans</i> (strain ATCC 27329 / DSM 1819 / JCM 2831).	GCN5-related N-acetyltransferase.	176	1.2E-16	172	37.8
119	C9A7A9_ENTCA	C9A7A9	<i>Enterococcus casseliflavus</i> EC20.	Putative uncharacterized protein.	177	1.2E-16	160	36.9
120	A9HB40_GLU DA	A9HB40	<i>Gluconacetobacter diazotrophicus</i> (strain ATCC 49037 / DSM 5601 / PAI5).	Putative phosphinothricin N-acetyltransferase.	222	1.2E-16	182	36.8
121	F7YC15_MESOW	F7YC15	<i>Mesorhizobium opportunistum</i> (strain LMG 24607 / HAMBI 3007 / WSM2075).	Phosphinothricin acetyltransferase.	191	1.3E-16	174	35.6
122	G4K0E6_9RHIZ	G4K0E6	<i>Mesorhizobium australicum</i> WSM2073.	Phosphinothricin acetyltransferase.	192	1.8E-16	174	36.8
123	E1SWL3_FERBD	E1SWL3	<i>Ferrimonas balearica</i> (strain DSM 9799 / CCM 4581 / PAT).	Phosphinothricin acetyltransferase.	165	1.9E-16	159	36.5
124	G0FT75_AM YMD	G0FT75	<i>Amycolatopsis mediterranei</i> S699.	Acetyltransferase.	171	1.9E-16	159	35.8
125	D8HWU1_AM YMU	D8HWU1	<i>Amycolatopsis mediterranei</i> (strain U-32).	Acetyltransferase.	171	1.9E-16	159	35.8
126	Q0RK75_FRAAA	Q0RK75	<i>Frankia alni</i> (strain ACN14a).	Putative N-acetyltransferase. EC=2.3.1.-.	184	2E-16	177	36.2
127	C0B506_9FIRM	C0B506	<i>Coprococcus comes</i> ATCC 27758.	Putative uncharacterized protein.	189	2.1E-16	185	32.4
128	E4MGA4_9FIRM	E4MGA4	<i>Eubacterium cellulosolvens</i> 6.	Phosphinothricin acetyltransferase.	183	2.4E-16	162	33.3
129	G4F341_9GAMM	G4F341	<i>Halomonas</i> sp. HAL 1.	Phosphinothricin N-acetyltransferase.	174	2.7E-16	157	34.4
130	F0EKG4_ENTCA	F0EKG4	<i>Enterococcus casseliflavus</i> ATCC 12755.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	177	2.8E-16	160	36.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
131	A4C427_9GAMM	A4C427	<i>Pseudoalteromonas tunicata</i> D2.	Phosphinothricin N-acetyltransferase.	164	3.1E-16	158	36.1
132	E3CAV6_STRPA	E3CAV6	<i>Streptococcus parasanguinis</i> F0405.	Putative phosphinothricin N-acetyltransferase.	169	3.1E-16	162	32.7
133	F3LN29_9BURK	F3LN29	<i>Rubrivivax benzoatilyticus</i> JA2.	GCN5-like N-acetyltransferase.	177	3.3E-16	171	38.0
134	E8K4Y5_STRPA	E8K4Y5	<i>Streptococcus parasanguinis</i> ATCC 903.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	3.7E-16	162	32.1
135	B9JUA6_AGRVS	B9JUA6	<i>Agrobacterium vitis</i> (strain S4 / ATCC BAA-846) (<i>Rhizobium vitis</i> (strain S4)).	Acetyltransferase.	209	4.4E-16	162	34.6
136	D8MZB9_RALSL	D8MZB9	<i>Ralstonia solanacearum</i> PSI07.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.183.	183	4.7E-16	164	36.6
137	Q127E8_POLSJ	Q127E8	<i>Polaromonas</i> sp. (strain JS666 / ATCC BAA-500).	GCN5-related N-acetyltransferase.	226	4.7E-16	159	37.7
138	D0RV44_9STRE	D0RV44	<i>Streptococcus</i> sp. 2_1_36FAA.	Acyltransferase.	189	4.8E-16	167	34.7
139	F0FD97_STRSA	F0FD97	<i>Streptococcus sanguinis</i> SK353.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	207	5.2E-16	167	34.1
140	F0IMC3_STRSA	F0IMC3	<i>Streptococcus sanguinis</i> SK150.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	185	5.6E-16	167	34.1
141	D2QNC0_SPILD	D2QNC0	<i>Spirosoma linguale</i> (strain ATCC 33905 / DSM 74 / LMG 10896).	GCN5-related N-acetyltransferase.	185	5.6E-16	171	34.5
142	A1KBV2_AZOSB	A1KBV2	<i>Azoarcus</i> sp. (strain BH72).	Putative N-acetyltransferase.	188	5.6E-16	178	37.6
143	C0BWV6_9CLOT	C0BWV6	<i>Clostridium hylemonae</i> DSM 15053.	Putative uncharacterized protein.	193	5.8E-16	172	32.0
144	D5RJ76_9PROT	D5RJ76	<i>Roseomonas cervicalis</i> ATCC 49957.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	183	6.5E-16	185	36.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
145	F0I242_STRSA	F0I242	<i>Streptococcus sanguinis</i> SK72.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	207	7.2E-16	167	34.1
146	F2C623_STRSA	F2C623	<i>Streptococcus sanguinis</i> SK330.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	215	7.4E-16	167	33.5
147	D5CKF5_ENTCC	D5CKF5	<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> (strain ATCC 13047 / DSM 30054 / NBRC 13535 / NCDC 279-56).	Putative phosphinothricin N-acetyltransferase.	178	7.5E-16	155	35.5
148	B5RJY2_KLEP3	B5RJY2	<i>Klebsiella pneumoniae</i> (strain 342).	Putative phosphinothricin N-acetyltransferase.	178	7.5E-16	155	35.5
149	A8TRN6_9PROT	A8TRN6	<i>alpha proteobacterium</i> BAL 199.	GCN5-related N-acetyltransferase.	180	7.6E-16	178	35.4
150	G5HZ63_9CLOT	G5HZ63	<i>Clostridium clostridioforme</i> 2_1_49FAA.	Putative uncharacterized protein.	182	7.6E-16	178	34.3
151	D3CY62_9ACTO	D3CY62	<i>Frankia</i> sp. EUN1f.	Phosphinothricin acetyltransferase.	201	8.3E-16	177	33.3
152	E8KPG2_STRSA	E8KPG2	<i>Streptococcus sanguinis</i> VMC66.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	207	8.5E-16	167	34.1
153	A9N3V5_SALPB	A9N3V5	<i>Salmonella paratyphi</i> B (strain ATCC BAA-1250 / SPB7).	Putative uncharacterized protein.	171	8.6E-16	163	30.1
154	E9DNG5_9STRE	E9DNG5	<i>Streptococcus</i> sp. C150.	Phosphinothricin N-acetyltransferase.	172	8.6E-16	162	32.7
155	F0YW62_9CLOT	F0YW62	<i>Clostridium</i> sp. D5.	Phosphinothricin N-acetyltransferase.	190	9.3E-16	182	30.8
156	F9E0B0_STRSA	F9E0B0	<i>Streptococcus sanguinis</i> ATCC 29667.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	207	1E-15	167	32.9
157	F9E8S4_STRSA	F9E8S4	<i>Streptococcus sanguinis</i> SK340.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	207	1E-15	167	32.9
158	F3UHE7_STRSA	F3UHE7	<i>Streptococcus sanguinis</i> SK1059.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	207	1E-15	167	32.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
159	F0I7C8_STRSA	F0I7C8	<i>Streptococcus sanguinis</i> SK115.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	207	1E-15	167	32.9
160	D2BA97_STRRD	D2BA97	<i>Streptosporangium roseum</i> (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100).	Phosphinothricin acetyltransferase.	170	1E-15	167	37.1
161	B0UKJ7_METS4	B0UKJ7	<i>Methylobacterium</i> sp. (strain 4-46).	GCN5-related N-acetyltransferase.	180	1.1E-15	170	38.2
162	F7JWL1_9FIRM	F7JWL1	<i>Lachnospiraceae bacterium</i> 2_1_58FAA.	Putative uncharacterized protein.	183	1.1E-15	174	35.6
163	A7B2T0_RUMGN	A7B2T0	<i>Ruminococcus gnavus</i> ATCC 29149.	Putative uncharacterized protein.	183	1.1E-15	174	35.6
164	F6CW29_MARPP	F6CW29	<i>Marinomonas posidonica</i> (strain CECT 7376 / NCIMB 14433 / IVIA-Po-181).	Phosphinothricin acetyltransferase.	161	1.1E-15	157	35.0
165	A8HUK7_AZOC5	A8HUK7	<i>Azorhizobium caulinodans</i> (strain ATCC 43989 / DSM 5975 / ORS 571).	GCN5-related N-acetyltransferase.	174	1.2E-15	162	37.0
166	F0FTL7_STRSA	F0FTL7	<i>Streptococcus sanguinis</i> SK678.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	215	1.2E-15	167	33.5
167	F2CLB2_STRSA	F2CLB2	<i>Streptococcus sanguinis</i> SK1058.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	215	1.2E-15	167	33.5
168	F2BIK4_STRSA	F2BIK4	<i>Streptococcus sanguinis</i> SK1.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	215	1.2E-15	167	33.5
169	Q88LK7_PSEPK	Q88LK7	<i>Pseudomonas putida</i> (strain KT2440).	Phosphinothricin N-acetyltransferase, putative.	186	1.3E-15	178	33.1
170	G5ISB6_9ENTE	G5ISB6	<i>Enterococcus saccharolyticus</i> 30_1.	Putative uncharacterized protein.	178	1.7E-15	178	32.6
171	F0IV10_STRSA	F0IV10	<i>Streptococcus sanguinis</i> SK160.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	185	1.8E-15	167	33.5
172	F0FJG2_STRSA	F0FJG2	<i>Streptococcus sanguinis</i> SK405.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	215	2E-15	167	33.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
173	A4TUM8_9PROT	A4TUM8	<i>Magnetospirillum gryphiswaldense</i> .	GCN5-related N-acetyltransferase.	195	2.2E-15	181	36.5
174	D9XUL9_9ACTO	D9XUL9	<i>Streptomyces griseoflavus</i> Tu4000.	Phosphinothricin N-acetyltransferase.	172	2.3E-15	173	31.8
175	F3USC5_STRSA	F3USC5	<i>Streptococcus sanguinis</i> SK355.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	175	2.4E-15	167	32.9
176	C8ZY61_ENTGA	C8ZY61	<i>Enterococcus gallinarum</i> EG2.	Phosphinothricin N-acetyltransferase.	178	2.4E-15	178	32.0
177	E6UAE0_RUMA7	E6UAE0	<i>Ruminococcus albus</i> (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7).	Phosphinothricin acetyltransferase.	191	2.5E-15	186	31.2
178	E7H0B6_9BURK	E7H0B6	<i>Sutterella wadsworthensis</i> 3_1_45B.	Putative uncharacterized protein.	192	2.6E-15	171	33.9
179	F5YP84_TREPZ	F5YP84	<i>Treponema primitia</i> (strain ATCC BAA-887 / DSM 12427 / ZAS-2).	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.-.	169	2.7E-15	156	32.7
180	A3CN48_STRSV	A3CN48	<i>Streptococcus sanguinis</i> (strain SK36).	Phosphinothricin acetyltransferase, putative. EC=2.3.1.-.	215	2.8E-15	167	32.9
181	F2CD26_STRSA	F2CD26	<i>Streptococcus sanguinis</i> SK408.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	215	2.8E-15	167	32.9
182	A8AXI6_STRGC	A8AXI6	<i>Streptococcus gordonii</i> (strain Challis / ATCC 35105 / CH1 / DL1 / V288).	Acyltransferase. EC=2.3.1.-.	178	2.8E-15	173	32.4
183	G3A8R9_9RALS	G3A8R9	<i>Ralstonia syzygii</i> R24.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.183.	183	2.9E-15	162	36.4
184	G2ZRI9_9RALS	G2ZRI9	<i>blood disease bacterium</i> R229.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.183.	183	2.9E-15	164	36.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
185	F5J308_9PORP	F5J308	<i>Dysgonomonas gadei</i> ATCC BAA-286.	Putative uncharacterized protein.	307	3.2E-15	169	32.0
186	D6AKW1_STRFL	D6AKW1	<i>Streptomyces roseosporus</i> NRRL 15998.	Putative uncharacterized protein.	212	3.3E-15	169	35.5
187	F8DH80_STREP	F8DH80	<i>Streptococcus parasanguinis</i> (strain ATCC 15912 / DSM 6778 / CIP 104372 / LMG 14537).	Phosphinothricin acetyltransferase. EC=2.3.1.-.	174	3.3E-15	160	30.6
188	D9Y3X1_9BURK	D9Y3X1	<i>Burkholderiales bacterium</i> 1_1_47.	Phosphinothricin N-acetyltransferase.	176	3.3E-15	165	33.3
189	F3QMQ9_9BURK	F3QMQ9	<i>Parasutterella excrementihominis</i> YIT 11859.	Putative phosphinothricin N-acetyltransferase.	176	3.3E-15	165	33.3
190	Q07UW8_RHOP5	Q07UW8	<i>Rhodopseudomonas palustris</i> (strain BisA53).	GCN5-related N-acetyltransferase.	179	3.4E-15	176	35.2
191	Q13DS3_RHOPS	Q13DS3	<i>Rhodopseudomonas palustris</i> (strain BisB5).	GCN5-related N-acetyltransferase.	181	3.4E-15	159	37.7
192	Q8XSS0_RALSO	Q8XSS0	<i>Ralstonia solanacearum</i> (strain GM1000) (<i>Pseudomonas solanacearum</i>).	Probable phosphinothricin acetyltransferase protein. EC=2.3.1.-.	183	3.4E-15	162	36.4
193	G4KR44_9FIRM	G4KR44	<i>Oscillibacter valericigenes</i> Sjm18-20.	Acetyltransferase. EC=2.3.1.-.	195	3.6E-15	178	33.7
194	Q481I3_COLP3	Q481I3	<i>Colwellia psychrerythraea</i> (strain 34H / ATCC BAA-681) (<i>Vibrio psychroerythus</i>).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	169	3.8E-15	160	33.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
195	C5ELD2_9FIRM	C5ELD2	<i>Clostridiales bacterium 1_7_47FAA</i> .	Phosphinothricin N-acetyltransferase.	189	4.1E-15	178	32.6
196	G6YB36_9RHIZ	G6YB36	<i>Mesorhizobium amorphae</i> CCNWGS0123.	Phosphinothricin acetyltransferase.	191	4.2E-15	174	33.3
197	G7ZEX9_AZOLI	G7ZEX9	<i>Azospirillum lipoferum</i> 4B.	Putative phosphinothricin N-acetyltransferase.	206	4.4E-15	184	33.2
198	B8ILK1_METNO	B8ILK1	<i>Methylobacterium nodulans</i> (strain ORS2060 / LMG 21967).	GCN5-related N-acetyltransferase.	182	4.7E-15	171	36.3
199	C0D0D9_9CLOT	C0D0D9	<i>Clostridium asparagiforme</i> DSM 15981.	Putative uncharacterized protein.	214	5.4E-15	161	32.3
200	F9HEK4_9STRE	F9HEK4	<i>Streptococcus</i> sp. oral taxon 056 str. F0418.	Putative phosphinothricin N-acetyltransferase.	175	5.4E-15	165	32.7
201	A8GBH0_SERP5	A8GBH0	<i>Serratia proteamaculans</i> (strain 568).	GCN5-related N-acetyltransferase.	181	5.6E-15	163	34.4
202	F0RLD0_DEIPM	F0RLD0	<i>Deinococcus proteolyticus</i> (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703).	Phosphinothricin acetyltransferase.	178	6.5E-15	173	35.3
203	F3Q2G6_9ENTR	F3Q2G6	<i>Klebsiella</i> sp. MS 92-3.	Toxin-antitoxin system, toxin component, GNAT family.	178	7.7E-15	173	34.1
204	G7RUZ4_KLEPN	G7RUZ4	<i>Klebsiella pneumoniae</i> .	Putative acetyltransferase.	178	7.7E-15	173	34.1
205	A6TI81_KLEP7	A6TI81	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> (strain ATCC 700721 / MGH 78578).	Putative acetyltransferase.	178	7.7E-15	173	34.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
206	F3SHM1_STRSA	F3SHM1	<i>Streptococcus sanguinis</i> SK1087.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	185	7.9E-15	162	34.0
207	F2BRZ5_STRSA	F2BRZ5	<i>Streptococcus sanguinis</i> SK1057.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	185	7.9E-15	162	34.0
208	C0FZ16_9FIRM	C0FZ16	<i>Roseburia inulinivorans</i> DSM 16841.	Putative uncharacterized protein.	189	8.1E-15	166	34.3
209	D5RQQ2_9PROT	D5RQQ2	<i>Roseomonas cervicalis</i> ATCC 49957.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	190	8.1E-15	161	37.9
210	D5RL96_9PROT	D5RL96	<i>Roseomonas cervicalis</i> ATCC 49957.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	179	9.1E-15	174	36.8
211	D8KDC7_LACLN	D8KDC7	<i>Lactococcus lactis</i> subsp. <i>cremoris</i> (strain NZ9000).	Phosphinothricin N-acetyltransferase.	186	9.4E-15	157	32.5
212	A2RMJ4_LACLM	A2RMJ4	<i>Lactococcus lactis</i> subsp. <i>cremoris</i> (strain MG1363).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	186	9.4E-15	157	32.5
213	D4JZN4_9FIRM	D4JZN4	<i>Faecalibacterium prausnitzii</i> L2-6.	Sortase and related acyltransferases. EC=2.3.1.-.	186	9.4E-15	179	32.4
214	G5ICL0_9CLOT	G5ICL0	<i>Clostridium hathewayi</i> WAL-18680.	Putative uncharacterized protein.	188	9.5E-15	176	31.8
215	D3P6Y6_AZOS1	D3P6Y6	<i>Azospirillum</i> sp. (strain B510).	Acetyltransferase.	189	9.5E-15	161	36.6
216	Q98E99_RHILO	Q98E99	<i>Rhizobium loti</i> (strain MAFF303099) (<i>Mesorhizobium loti</i>).	Phosphinothricin acetyltransferase.	194	9.7E-15	172	35.5
217	E0Q0Y0_9STRE	E0Q0Y0	<i>Streptococcus</i> sp. oral taxon 071 str. 73H25AP.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	170	1E-14	170	31.2
218	F4X9K0_9FIRM	F4X9K0	<i>Ruminococcaceae</i> bacterium D16.	Phosphinothricin N-acetyltransferase.	187	1.1E-14	175	31.4
219	B4W7J2_9CAUL	B4W7J2	<i>Brevundimonas</i> sp. BAL3.	Acetyltransferase, GNAT family.	189	1.1E-14	177	35.0
220	F5VXC8_STROR	F5VXC8	<i>Streptococcus oralis</i> SK255.	FR47-like protein.	170	1.2E-14	170	30.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
221	C9XW28_CROTZ	C9XW28	<i>Cronobacter turicensis</i> (strain DSM 18703 / LMG 23827 / z3032).	Phosphinothricin N-acetyltransferase. EC=2.3.1.183.	181	1.3E-14	170	33.5
222	G1UX80_9DELT	G1UX80	<i>Desulfovibrio</i> sp. 6_1_46AFAA.	Putative uncharacterized protein.	189	1.3E-14	178	34.3
223	F0SXV1_SYNGF	F0SXV1	<i>Syntrophobotulus glycolicus</i> (strain DSM 8271 / FIGlyR).	Phosphinothricin acetyltransferase.	190	1.3E-14	156	32.1
224	D2RLZ5_ACIFV	D2RLZ5	<i>Acidaminococcus fermentans</i> (strain ATCC 25085 / DSM 20731 / VR4).	GCN5-related N-acetyltransferase.	191	1.3E-14	182	29.7
225	F8WXA6_9PORP	F8WXA6	<i>Dysgonomonas mossii</i> DSM 22836.	Putative uncharacterized protein.	161	1.4E-14	157	34.4
226	B0NLR6_BACSE	B0NLR6	<i>Bacteroides stercoris</i> ATCC 43183.	Putative uncharacterized protein.	161	1.4E-14	161	34.8
227	D2BU09_DICD5	D2BU09	<i>Dickeya dadantii</i> (strain Ech586).	Phosphinothricin acetyltransferase.	176	1.5E-14	163	33.7
228	C1MB43_9ENTR	C1MB43	<i>Citrobacter</i> sp. 30_2.	YceA.	178	1.5E-14	163	30.7
229	A9IDM3_BORPD	A9IDM3	<i>Bordetella petrii</i> (strain ATCC BAA-461 / DSM 12804 / CCUG 43448).	Acetyltransferase. EC=2.3.1.-.	183	1.5E-14	177	35.0
230	E2SH73_9FIRM	E2SH73	<i>Erysipelotrichaceae bacterium</i> 3_1_53.	Phosphinothricin N-acetyltransferase.	195	1.6E-14	166	33.1
231	Q2J3G1_RHOP2	Q2J3G1	<i>Rhodopseudomonas palustris</i> (strain HaA2).	GCN5-related N-acetyltransferase.	205	1.7E-14	159	37.1
232	C6WFY6_ACTMD	C6WFY6	<i>Actinosynnema mirum</i> (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971).	GCN5-related N-acetyltransferase.	169	1.7E-14	166	35.5
233	C2WNJ0_BACCE	C2WNJ0	<i>Bacillus cereus</i> Rock4-2.	Phosphinothricin N-acetyltransferase.	170	1.7E-14	169	33.1
234	C2R977_BACCE	C2R977	<i>Bacillus cereus</i> m1550.	Phosphinothricin N-acetyltransferase.	170	1.7E-14	169	33.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
235	C3ELQ5_BACTK	C3ELQ5	<i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> .	Phosphinothricin N-acetyltransferase.	170	1.7E-14	169	33.1
236	C2XCM2_BACCE	C2XCM2	<i>Bacillus cereus</i> F65185.	Phosphinothricin N-acetyltransferase.	170	1.7E-14	169	33.1
237	G2G1G8_9FIRM	G2G1G8	<i>Desulfosporosinus</i> sp. OT.	Putative antibiotic resistance protein.	170	1.7E-14	171	32.2
238	D4X3V5_9BURK	D4X3V5	<i>Achromobacter piechaudii</i> ATCC 43553.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	212	1.7E-14	184	35.3
239	C2YSL7_BACCE	C2YSL7	<i>Bacillus cereus</i> AH1271.	Phosphinothricin N-acetyltransferase.	179	1.8E-14	174	32.2
240	D2BL68_LACLK	D2BL68	<i>Lactococcus lactis</i> subsp. <i>lactis</i> (strain KF147).	Acetyltransferase, GNAT family. EC=2.3.1.-.	187	1.8E-14	176	29.0
241	Q02X91_LACLS	Q02X91	<i>Lactococcus lactis</i> subsp. <i>cremoris</i> (strain SK11).	Sortase related acyltransferase.	186	2.2E-14	157	32.5
242	E0QHM8_9FIRM	E0QHM8	<i>Eubacterium yurii</i> subsp. <i>margaretiae</i> ATCC 43715.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	365	2.3E-14	166	29.5
243	Q0G4Z0_9RHIZ	Q0G4Z0	<i>Fulvimarina pelagi</i> HTCC2506.	Putative phosphinothricin N-acetyltransferase (Antibiotic resistance) protein.	187	2.6E-14	162	34.6
244	C1I6E5_9CLOT	C1I6E5	<i>Clostridium</i> sp. 7_2_43FAA.	Phosphinothricin acetyltransferase.	197	2.7E-14	177	28.8
245	C3H1Z2_BACTU	C3H1Z2	<i>Bacillus thuringiensis</i> serovar <i>huazhongensis</i> BGSC 4BD1.	Phosphinothricin N-acetyltransferase.	170	2.8E-14	169	33.1
246	C2KJG1_LEUMC	C2KJG1	<i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> ATCC 19254.	Possible Phosphinothricin acetyltransferase. EC=2.3.1.183.	177	2.9E-14	177	28.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
247	Q03WJ3_LEUMM	Q03WJ3	<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> (strain ATCC 8293 / NCDO 523).	Sortase related acyltransferase.	177	2.9E-14	177	28.8
248	G7VNH7_LEUME	G7VNH7	<i>Leuconostoc mesenteroides</i> subsp. <i>mesenteroides</i> J18.	Sortase related acyltransferase.	177	2.9E-14	177	28.8
249	E0SCH6_DICD3	E0SCH6	<i>Dickeya dadantii</i> (strain 3937) (<i>Erwinia chrysanthemi</i> (strain 3937)).	Phosphinothricin N-acetyltransferase. EC=2.3.-.-.	187	3E-14	161	34.8
250	D9YCA9_9DELT	D9YCA9	<i>Desulfovibrio</i> sp. 3_1_syn3.	Phosphinothricin N-acetyltransferase.	189	3E-14	178	33.7
251	D6KCH6_9ACTO	D6KCH6	<i>Streptomyces</i> sp. e14.	GNAT family toxin-antitoxin system, toxin component.	168	3.3E-14	159	36.5
252	B3ZKC1_BACCE	B3ZKC1	<i>Bacillus cereus</i> 03BB108.	Acetyltransferase, GNAT family.	170	3.3E-14	169	32.5
253	B5V0Q9_BACCE	B5V0Q9	<i>Bacillus cereus</i> H3081.97.	Acetyltransferase, GNAT family.	170	3.3E-14	169	32.5
254	A4YKB8_BRASO	A4YKB8	<i>Bradyrhizobium</i> sp. (strain ORS278).	Phosphinothricin acetyltransferase (PPT N-acetyltransferase). EC=2.3.1.-.	175	3.4E-14	160	34.4
255	E5UH00_ALCXX	E5UH00	<i>Achromobacter xylosoxidans</i> C54.	Acetyltransferase.	181	3.5E-14	182	32.4
256	G6FBS5_LACLC	G6FBS5	<i>Lactococcus lactis</i> subsp. <i>cremoris</i> CNCM I-1631.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	187	3.6E-14	176	28.4
257	Q9CEQ9_LACLA	Q9CEQ9	<i>Lactococcus lactis</i> subsp. <i>lactis</i> (strain IL1403) (<i>Streptococcus lactis</i>).	Acyltransferase.	187	3.6E-14	176	28.4
258	F2HMY5_LACLV	F2HMY5	<i>Lactococcus lactis</i> subsp. <i>lactis</i> (strain CV56).	Phosphinothricin acetyltransferase. EC=2.3.1.183.	187	3.6E-14	176	28.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
259	Q2W593_MAGSA	Q2W593	<i>Magnetospirillum magneticum</i> (strain AMB-1 / ATCC 700264).	Phosphinothricin N-acetyltransferase.	197	3.7E-14	187	35.8
260	C2Z8Y7_BACCE	C2Z8Y7	<i>Bacillus cereus</i> AH1272.	Phosphinothricin N-acetyltransferase.	170	3.9E-14	169	32.5
261	C2ZQN0_BACCE	C2ZQN0	<i>Bacillus cereus</i> AH1273.	Phosphinothricin N-acetyltransferase.	170	3.9E-14	169	32.5
262	A9KS43_CLOPH	A9KS43	<i>Clostridium phytofermentans</i> (strain ATCC 700394 / DSM 18823 / ISDg).	GCN5-related N-acetyltransferase.	184	4.1E-14	176	30.1
263	C6SQJ8_STRMN	C6SQJ8	<i>Streptococcus mutans</i> serotype c (strain NN2025).	Putative acetyltransferase.	163	4.4E-14	159	28.9
264	G6H505_9ACTO	G6H505	<i>Frankia</i> sp. CN3.	GCN5-related N-acetyltransferase.	206	4.5E-14	177	33.3
265	C3E4C0_BACTU	C3E4C0	<i>Bacillus thuringiensis</i> serovar <i>pakistani</i> str. T13001.	Phosphinothricin N-acetyltransferase.	170	4.6E-14	169	33.1
266	C3DKT8_BACTS	C3DKT8	<i>Bacillus thuringiensis</i> subsp. <i>sotto</i> .	Phosphinothricin N-acetyltransferase.	170	4.6E-14	169	33.1
267	C3A6Y7_BACMY	C3A6Y7	<i>Bacillus mycoides</i> DSM 2048.	Phosphinothricin N-acetyltransferase.	170	4.6E-14	169	32.5
268	C2UEX4_BACCE	C2UEX4	<i>Bacillus cereus</i> Rock1-15.	Phosphinothricin N-acetyltransferase.	170	4.6E-14	169	33.1
269	D9XGY1_STRVR	D9XGY1	<i>Streptomyces viridochromogenes</i> DSM 40736.	Phosphinothricin N-acetyltransferase.	172	4.6E-14	171	32.2
270	G0BH40_9ENTR	G0BH40	<i>Serratia</i> sp. AS12.	Phosphinothricin acetyltransferase.	178	4.8E-14	173	32.9
271	G0BEE7_SERSA	G0BEE7	<i>Serratia</i> sp. (strain AS9).	Phosphinothricin acetyltransferase.	178	4.8E-14	173	32.9
272	G0BVX7_9ENTR	G0BVX7	<i>Serratia</i> sp. AS13.	Phosphinothricin acetyltransferase.	178	4.8E-14	173	32.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
273	B4RHU1_PHEZH	B4RHU1	<i>Phenylobacterium zucineum</i> (strain HLK1).	Phosphinothricin N-acetyltransferase.	179	4.8E-14	172	36.0
274	E3HJK4_ACHXA	E3HJK4	<i>Achromobacter xylosoxidans</i> (strain A8).	Acetyltransferase, GNAT family protein 28. EC=2.3.1.-.	181	4.8E-14	182	33.0
275	D5BQY4_PUNMI	D5BQY4	<i>Puniceispirillum marinum</i> (strain IMCC1322).	GCN5-related N-acetyltransferase. EC=2.3.1.-.	182	4.9E-14	163	35.6
276	E3HBF2_ILYPC	E3HBF2	<i>Ilyobacter polytropus</i> (strain DSM 2926 / CuHBU1).	Phosphinothricin acetyltransferase.	161	5.2E-14	156	28.8
277	A0ADA9_STRAM	A0ADA9	<i>Streptomyces ambofaciens</i> ATCC 23877.	Putative acetyltransferase.	200	5.2E-14	165	34.5
278	D1RN68_SEROD	D1RN68	<i>Serratia odorifera</i> 4Rx13.	Putative N-acetyltransferase.	178	5.6E-14	177	32.2
279	G3YHZ8_9RALS	G3YHZ8	<i>Ralstonia</i> sp. 5_2_56FAA.	Putative uncharacterized protein.	178	5.6E-14	166	34.9
280	F4QT47_9CAUL	F4QT47	<i>Asticcacaulis biprosthicum</i> C19.	Acetyltransferase GNAT family protein.	178	5.6E-14	170	32.9
281	E2SUR4_9RALS	E2SUR4	<i>Ralstonia</i> sp. 5_7_47FAA.	Toxin-antitoxin system, toxin component, GNAT family.	178	5.6E-14	166	34.9
282	A2WFF2_9BURK	A2WFF2	<i>Burkholderia dolosa</i> AUO158.	Putative uncharacterized protein.	191	6E-14	179	33.0
283	D6CPP1_THIS3	D6CPP1	<i>Thiomonas</i> sp. (strain 3As).	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.183.	175	6.6E-14	170	34.7
284	C4G7W3_9FIRM	C4G7W3	<i>Shuttleworthia satelles</i> DSM 14600.	Putative uncharacterized protein.	195	7.2E-14	164	33.5
285	D0TAH2_9BACE	D0TAH2	<i>Bacteroides</i> sp. 2_1_33B.	Putative uncharacterized protein.	165	7.4E-14	165	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
286	Q0B8B1_BURCM	Q0B8B1	<i>Burkholderia ambifaria</i> (strain ATCC BAA-244 / AMMD) (<i>Burkholderia cepacia</i> (strain AMMD)).	GCN5-related N-acetyltransferase. Flags: Precursor.	207	7.5E-14	179	33.0
287	C2T233_BACCE	C2T233	<i>Bacillus cereus</i> BDRD-Cer4.	Phosphinothricin N-acetyltransferase.	170	7.6E-14	169	33.1
288	B5UUQ3_BACCE	B5UUQ3	<i>Bacillus cereus</i> AH1134.	Acetyltransferase, GNAT family.	170	7.6E-14	169	32.5
289	Q81CF9_BACCR	Q81CF9	<i>Bacillus cereus</i> (strain ATCC 14579 / DSM 31).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	170	7.6E-14	169	33.1
290	C2RNS1_BACCE	C2RNS1	<i>Bacillus cereus</i> BDRD-ST24.	Phosphinothricin N-acetyltransferase.	170	7.6E-14	169	32.0
291	D5TMY3_BACT1	D5TMY3	<i>Bacillus thuringiensis</i> (strain BMB171).	Phosphinothricin N-acetyltransferase.	170	7.6E-14	169	32.0
292	C3I1T7_BACTU	C3I1T7	<i>Bacillus thuringiensis</i> IBL 200.	Phosphinothricin N-acetyltransferase.	170	7.6E-14	169	32.0
293	B6IX50_RHOCS	B6IX50	<i>Rhodospirillum centenum</i> (strain ATCC 51521 / SW).	Phosphinothricin N-acetyltransferase.	180	7.9E-14	155	38.7
294	F7KK45_9FIRM	F7KK45	<i>Lachnospiraceae</i> bacterium 3_1_57FAA_CT1.	Putative uncharacterized protein.	204	8.8E-14	178	29.2
295	A6L988_PARD8	A6L988	<i>Parabacteroides distasonis</i> (strain ATCC 8503 / DSM 20701 / NCTC 11152).	Phosphinothricin N-acetyltransferase, putative.	167	8.8E-14	165	33.3
296	C6W9P6_ACTMD	C6W9P6	<i>Actinosynnema mirum</i> (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971).	GCN5-related N-acetyltransferase.	168	8.8E-14	160	32.5
297	C3CJR8_BACTU	C3CJR8	<i>Bacillus thuringiensis</i> .	Phosphinothricin N-acetyltransferase.	170	8.9E-14	169	32.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
298	C3FL87_BACTB	C3FL87	<i>Bacillus thuringiensis</i> subsp. <i>berliner</i> .	Phosphinothricin N-acetyltransferase.	170	8.9E-14	169	32.5
299	F2H4A1_BACTU	F2H4A1	<i>Bacillus thuringiensis</i> serovar <i>chinensis</i> CT-43.	Phosphinothricin N-acetyltransferase.	170	8.9E-14	169	32.5
300	C3D2S0_BACTU	C3D2S0	<i>Bacillus thuringiensis</i> serovar <i>thuringiensis</i> str. T01001.	Phosphinothricin N-acetyltransferase.	170	8.9E-14	169	32.5
301	C2XV57_BACCE	C2XV57	<i>Bacillus cereus</i> AH603.	Phosphinothricin N-acetyltransferase.	170	8.9E-14	169	32.5
302	F9Q116_STROR	F9Q116	<i>Streptococcus oralis</i> SK313.	FR47-like protein.	170	8.9E-14	162	30.9
303	D6ETC2_STRLI	D6ETC2	<i>Streptomyces lividans</i> TK24.	Phosphorinothrycin n-acetyltransferase.	171	9E-14	170	33.5
304	G7DFC6_BRAJA	G7DFC6	<i>Bradyrhizobium japonicum</i> USDA 6.	Acetyltransferase.	175	9.1E-14	170	34.7
305	C6CBU6_DICDC	C6CBU6	<i>Dickeya dadantii</i> (strain Ech703).	Phosphinothricin acetyltransferase.	178	9.3E-14	175	32.6
306	C2PG19_BACCE	C2PG19	<i>Bacillus cereus</i> MM3.	Phosphinothricin N-acetyltransferase.	182	9.4E-14	174	31.6
307	B7IJN0_BACC2	B7IJN0	<i>Bacillus cereus</i> (strain G9842).	Acetyltransferase, GNAT family.	170	1.1E-13	169	32.5
308	Q3EKE3_BACTI	Q3EKE3	<i>Bacillus thuringiensis</i> serovar <i>israelensis</i> ATCC 35646.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	170	1.1E-13	169	32.5
309	C3IKD5_BACTU	C3IKD5	<i>Bacillus thuringiensis</i> IBL 4222.	Phosphinothricin N-acetyltransferase.	170	1.1E-13	169	32.5
310	C2MLS3_BACCE	C2MLS3	<i>Bacillus cereus</i> m1293.	Phosphinothricin N-acetyltransferase.	170	1.1E-13	169	32.0
311	B4SSU6_STRM5	B4SSU6	<i>Stenotrophomonas maltophilia</i> (strain R551-3).	GCN5-related N-acetyltransferase.	176	1.1E-13	171	33.9
312	D7IWC0_9BACE	D7IWC0	<i>Bacteroides</i> sp. 3_1_19.	Phosphinothricin N-acetyltransferase.	167	1.2E-13	165	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
313	C3HJK8_BACTU	C3HJK8	<i>Bacillus thuringiensis</i> serovar <i>pulsiensis</i> BGSC 4CC1.	Phosphinothricin N-acetyltransferase.	170	1.2E-13	169	31.4
314	C3LG41_BACAC	C3LG41	<i>Bacillus anthracis</i> (strain CDC 684 / NRRL 3495).	Acetyltransferase, GNAT family.	170	1.2E-13	169	32.0
315	B7HA24_BACC4	B7HA24	<i>Bacillus cereus</i> (strain B4264).	Acetyltransferase, GNAT family.	170	1.2E-13	169	32.5
316	B0QC74_BACAN	B0QC74	<i>Bacillus anthracis</i> str. A0442.	Acetyltransferase, GNAT family.	170	1.2E-13	169	32.0
317	B1GDZ4_BACAN	B1GDZ4	<i>Bacillus anthracis</i> str. A0465.	Acetyltransferase, GNAT family.	170	1.2E-13	169	32.0
318	B0AK43_BACAN	B0AK43	<i>Bacillus anthracis</i> str. A0488.	Acetyltransferase, GNAT family.	170	1.2E-13	169	32.0
319	A9VIF3_BACWK	A9VIF3	<i>Bacillus weihenstephanensis</i> (strain KBAB4).	GCN5-related N-acetyltransferase.	170	1.2E-13	169	33.1
320	Q82H51_STRAW	Q82H51	<i>Streptomyces avermitilis</i> .	Putative phosphinothricin N-acetyltransferase.	172	1.3E-13	174	33.3
321	B8L1S8_9GAMM	B8L1S8	<i>Stenotrophomonas</i> sp. SKA14.	Phosphinothricin N-acetyltransferase.	176	1.3E-13	171	33.9
322	E6VJT0_RHOPX	E6VJT0	<i>Rhodopseudomonas palustris</i> (strain DX-1).	Phosphinothricin acetyltransferase.	176	1.3E-13	161	35.4
323	D5T047_LEUKI	D5T047	<i>Leuconostoc kimchii</i> (strain IMSNU 11154 / KCTC 2386 / IH25).	Putative uncharacterized protein.	180	1.3E-13	178	31.5
324	F8HUE2_LEUS2	F8HUE2	<i>Leuconostoc</i> sp. (strain C2).	Putative uncharacterized protein.	180	1.3E-13	178	31.5
325	A9AQR6_BURM1	A9AQR6	<i>Burkholderia multivorans</i> (strain ATCC 17616 / 249).	Acetyltransferase. GCN5-related N-acetyltransferase.	186	1.3E-13	172	32.6
326	G5KCS9_9STRE	G5KCS9	<i>Streptococcus urinalis</i> 2285-97.	Acetyltransferase, GNAT family.	191	1.4E-13	185	29.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
327	F2LLL3_BURGS	F2LLL3	<i>Burkholderia gladioli</i> (strain BSR3).	GCN5-related N-acetyltransferase.	192	1.4E-13	182	34.1
328	B9E960_MACCJ	B9E960	<i>Macrococcus caseolyticus</i> (strain JCSC5402).	Acetyltransferase family protein.	162	1.4E-13	159	32.7
329	C2NIR0_BACCE	C2NIR0	<i>Bacillus cereus</i> .	Phosphinothricin N-acetyltransferase.	170	1.5E-13	169	32.0
330	C2THP2_BACCE	C2THP2	<i>Bacillus cereus</i> 95/8201.	Phosphinothricin N-acetyltransferase.	170	1.5E-13	169	32.0
331	A0RF14_BACAH	A0RF14	<i>Bacillus thuringiensis</i> (strain Al Hakam).	Phosphinothricin N-acetyltransferase, acetyltransferase, GNAT family. EC=2.3.1.-.	170	1.5E-13	169	32.0
332	C3F2P4_BACTU	C3F2P4	<i>Bacillus thuringiensis</i> serovar monterrey BGSC 4AJ1.	Phosphinothricin N-acetyltransferase.	170	1.5E-13	169	32.0
333	B7HUB7_BACC7	B7HUB7	<i>Bacillus cereus</i> (strain AH187).	Acetyltransferase, GNAT family.	170	1.5E-13	169	32.0
334	C2QU47_BACCE	C2QU47	<i>Bacillus cereus</i> ATCC 4342.	Phosphinothricin N-acetyltransferase.	170	1.5E-13	169	32.0
335	B7JRS8_BACC0	B7JRS8	<i>Bacillus cereus</i> (strain AH820).	Acetyltransferase, GNAT family.	170	1.5E-13	169	32.0
336	B3YP48_BACCE	B3YP48	<i>Bacillus cereus</i> W.	Acetyltransferase, GNAT family.	170	1.5E-13	169	32.0
337	C3C3F4_BACTU	C3C3F4	<i>Bacillus thuringiensis</i> serovar tochiensis BGSC 4Y1.	Phosphinothricin N-acetyltransferase.	170	1.5E-13	169	32.0
338	B3ZF32_BACCE	B3ZF32	<i>Bacillus cereus</i> NVH0597-99.	Acetyltransferase, GNAT family.	170	1.5E-13	169	32.0
339	C3GJY1_BACTU	C3GJY1	<i>Bacillus thuringiensis</i> serovar pondicheriensis BGSC 4BA1.	Phosphinothricin N-acetyltransferase.	170	1.5E-13	169	32.0
340	C1EXU0_BACC3	C1EXU0	<i>Bacillus cereus</i> (strain 03BB102).	Acetyltransferase, GNAT family.	170	1.5E-13	169	32.0
341	C2SLF1_BACCE	C2SLF1	<i>Bacillus cereus</i> BDRD-ST196.	Phosphinothricin N-acetyltransferase.	170	1.5E-13	169	31.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
342	B9J336_BACCQ	B9J336	<i>Bacillus cereus</i> (strain Q1).	Possible phosphinothricin N-acetyltransferase.	170	1.5E-13	169	32.0
343	F0PTU3_BACT0	F0PTU3	<i>Bacillus thuringiensis</i> subsp. <i>finitimus</i> (strain YBT-020).	Acetyltransferase, GNAT family protein.	170	1.5E-13	169	32.0
344	B2FN24_STRMK	B2FN24	<i>Stenotrophomonas maltophilia</i> (strain K279a).	Putative acetyltransferase.	176	1.5E-13	171	33.9
345	G5ZWC7_9PROT	G5ZWC7	SAR 116 cluster alpha proteobacterium HIMB100.	Sortase-like acyltransferase.	154	1.6E-13	151	37.7
346	D8GQ12_CLOLD	D8GQ12	<i>Clostridium ljungdahlii</i> (strain ATCC 55383 / DSM 13528 / PETC).	Predicted acetyltransferase.	194	1.6E-13	185	29.2
347	C2VUU7_BACCE	C2VUU7	<i>Bacillus cereus</i> Rock3-42.	Phosphinothricin N-acetyltransferase.	170	1.7E-13	169	32.0
348	D8H149_BACAI	D8H149	<i>Bacillus cereus</i> var. <i>anthracis</i> (strain CI).	Possible phosphinothricin N-acetyltransferase. EC=2.3.1.-.	170	1.7E-13	169	31.4
349	D2DXS0_9BACT	D2DXS0	uncultured <i>Verrucomicrobia</i> bacterium.	Putative acetyltransferase.	164	2E-13	152	34.2
350	G7W8S5_9FIRM	G7W8S5	<i>Desulfosporosinus orientis</i> DSM 765.	Sortase-like acyltransferase.	205	2E-13	175	29.1
351	Q6NDB0_RHOPA	Q6NDB0	<i>Rhodopseudomonas palustris</i> (strain ATCC BAA-98 / CGA009).	Putative phosphinothricin acetyltransferase.	176	2.1E-13	159	34.0
352	B3Q768_RHOPT	B3Q768	<i>Rhodopseudomonas palustris</i> (strain TIE-1).	GCN5-related N-acetyltransferase.	176	2.1E-13	159	34.0
353	C6CEN9_DICZE	C6CEN9	<i>Dickeya zeae</i> (strain Ech1591).	Phosphinothricin acetyltransferase.	176	2.1E-13	161	34.2
354	B1T650_9BURK	B1T650	<i>Burkholderia ambifaria</i> MEX-5.	GCN5-related N-acetyltransferase.	186	2.2E-13	179	32.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
355	G0ENH4_BRAIP	G0ENH4	<i>Brachyspira intermedia</i> (strain ATCC 51140 / PWS/A) (<i>Serpulina intermedia</i>).	Sortase related acyltransferase.	190	2.2E-13	178	27.5
356	B0G758_9FIRM	B0G758	<i>Dorea formicigenerans</i> ATCC 27755.	Putative uncharacterized protein.	195	2.3E-13	171	28.7
357	B6WY92_9DELT	B6WY92	<i>Desulfovibrio piger</i> ATCC 29098.	Putative uncharacterized protein.	195	2.3E-13	176	33.5
358	D4J7L5_9FIRM	D4J7L5	<i>Coprococcus catus</i> GD/7.	Sortase and related acyltransferases. EC=2.3.1.-.	197	2.3E-13	165	33.3
359	C2VCZ0_BACCE	C2VCZ0	<i>Bacillus cereus</i> Rock3-29.	Phosphinothricin N-acetyltransferase.	170	2.4E-13	169	32.0
360	C2TYL8_BACCE	C2TYL8	<i>Bacillus cereus</i> Rock1-3.	Phosphinothricin N-acetyltransferase.	170	2.4E-13	169	32.0
361	C2QCU9_BACCE	C2QCU9	<i>Bacillus cereus</i> R309803.	Phosphinothricin N-acetyltransferase.	170	2.4E-13	169	31.4
362	Q7W0D2_BORPE	Q7W0D2	<i>Bordetella pertussis</i> .	Putative acetyltransferase.	182	2.6E-13	182	35.7
363	A7VH30_9CLOT	A7VH30	<i>Clostridium</i> sp. L2-50.	Putative uncharacterized protein.	182	2.6E-13	164	30.5
364	Q7WQB1_BORBR	Q7WQB1	<i>Bordetella bronchiseptica</i> (strain ATCC BAA-588 / NCTC 13252 / RB50) (<i>Alcaligenes bronchisepticus</i>).	Putative acetyltransferase.	182	2.6E-13	182	35.7
365	Q7WCA7_BORPA	Q7WCA7	<i>Bordetella parapertussis</i> .	Putative acetyltransferase.	182	2.6E-13	182	35.7
366	F4L966_BORPC	F4L966	<i>Bordetella pertussis</i> (strain CS).	Putative acetyltransferase.	182	2.6E-13	182	35.7
367	G5JSU2_STRCG	G5JSU2	<i>Streptococcus criceti</i> HS-6.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	192	2.7E-13	179	28.5
368	B3JPC1_9BACE	B3JPC1	<i>Bacteroides coprocola</i> DSM 17136.	Putative uncharacterized protein.	160	2.7E-13	156	34.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
369	C7XA28_9PORP	C7XA28	<i>Parabacteroides</i> sp. D13.	Putative uncharacterized protein.	165	2.8E-13	165	32.7
370	E8SKE4_STAPH	E8SKE4	<i>Staphylococcus pseudintermedius</i> (strain HKU10-03).	Phosphinothricin N-acetyltransferase.	165	2.8E-13	163	31.9
371	F0P860_STAPE	F0P860	<i>Staphylococcus pseudintermedius</i> (strain ED99).	Phosphinothricin N-acetyltransferase, putative. EC=2.3.1.183.	165	2.8E-13	163	31.9
372	F9QMP6_9MYCO	F9QMP6	<i>Mycobacterium colombiense</i> CECT 3035.	Phosphinothricin acetyltransferase.	168	2.8E-13	151	31.1
373	F2F7E6_SOLSS	F2F7E6	<i>Solibacillus silvestris</i> (strain StLB046) (<i>Bacillus silvestris</i>).	Sortase.	170	2.9E-13	167	32.3
374	C2UWF2_BACCE	C2UWF2	<i>Bacillus cereus</i> Rock3-28.	Phosphinothricin N-acetyltransferase.	170	2.9E-13	169	31.4
375	Q736R3_BACC1	Q736R3	<i>Bacillus cereus</i> (strain ATCC 10987).	Acetyltransferase, GNAT family.	170	2.9E-13	169	31.4
376	C2YBI3_BACCE	C2YBI3	<i>Bacillus cereus</i> AH676.	Phosphinothricin N-acetyltransferase.	170	2.9E-13	169	31.4
377	E0LSH2_9ENTR	E0LSH2	<i>Pantoea</i> sp. aB.	Phosphinothricin acetyltransferase.	174	2.9E-13	161	33.5
378	Q8L251_SALTY	Q8L251	<i>Salmonella typhimurium</i> .	Sortase and related acyltransferases.	178	3E-13	163	28.2
379	B9AZN1_9BURK	B9AZN1	<i>Burkholderia multivorans</i> CGD1.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.-.	186	3.1E-13	172	32.0
380	B9C1H7_9BURK	B9C1H7	<i>Burkholderia multivorans</i> CGD2M.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.-.	186	3.1E-13	172	32.0
381	Q397U3_BURS3	Q397U3	<i>Burkholderia</i> sp. (strain 383) (<i>Burkholderia cepacia</i> (strain ATCC 17760 / NCIB 9086 / R18194)).	GCN5-related N-acetyltransferase.	186	3.1E-13	172	32.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
382	B9BHH3_9BURK	B9BHH3	<i>Burkholderia multivorans</i> CGD2.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.-.	186	3.1E-13	172	32.0
383	G0EZI9_CUPNE	G0EZI9	<i>Cupriavidus necator</i> N-1.	Phosphinothricin N-acetyltransferase Pat. EC=2.3.1.183.	193	3.2E-13	167	32.3
384	C7NE23_LEPBD	C7NE23	<i>Leptotrichia buccalis</i> (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249).	GCN5-related N-acetyltransferase.	197	3.2E-13	174	27.6
385	A7MHM0_CROS8	A7MHM0	<i>Cronobacter sakazakii</i> (strain ATCC BAA-894) (<i>Enterobacter sakazakii</i>).	Putative uncharacterized protein.	199	3.2E-13	170	32.9
386	F5VPF5_ENTSA	F5VPF5	<i>Cronobacter sakazakii</i> E899.	Putative uncharacterized protein.	199	3.2E-13	170	32.9
387	C0ERN9_9FIRM	C0ERN9	<i>Eubacterium hallii</i> DSM 3353.	Putative uncharacterized protein.	178	3.5E-13	159	30.8
388	C4ICF0_CLOBU	C4ICF0	<i>Clostridium butyricum</i> E4 str. BoNT E BL5262.	Acetyltransferase, GNAT family. EC=2.3.1.-.	179	3.5E-13	172	29.7
389	B1QUN2_CLOBU	B1QUN2	<i>Clostridium butyricum</i> 5521.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	179	3.5E-13	172	29.7
390	E9S8K5_RUMAL	E9S8K5	<i>Ruminococcus albus</i> 8.	Putative phosphinothricin N-acetyltransferase.	188	3.7E-13	186	30.1
391	Q0C1K4_HYPNA	Q0C1K4	<i>Hyphomonas neptunium</i> (strain ATCC 15444).	Acetyltransferase, GNAT family.	190	3.7E-13	159	35.2
392	E8YV54_9BURK	E8YV54	<i>Burkholderia</i> sp. CCGE1001.	Phosphinothricin acetyltransferase.	195	3.8E-13	181	33.7
393	F5JA34_9RHIZ	F5JA34	<i>Agrobacterium</i> sp. ATCC 31749.	Acetyltransferase.	206	3.9E-13	170	33.5
394	C2PW92_BACCE	C2PW92	<i>Bacillus cereus</i> AH621.	Phosphinothricin N-acetyltransferase.	170	4E-13	168	32.7
395	E2NSA4_9FIRM	E2NSA4	<i>Catenibacterium mitsuokai</i> DSM 15897.	Putative uncharacterized protein.	177	4.1E-13	167	28.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
396	F7X160_SINMM	F7X160	<i>Sinorhizobium meliloti</i> (strain SM11).	Acetyltransferase. EC=2.3.1.-.	183	4.2E-13	172	29.1
397	B0N1E4_9FIRM	B0N1E4	<i>Clostridium ramosum</i> DSM 1402.	Putative uncharacterized protein.	191	4.4E-13	178	29.8
398	D6HNP8_9FIRM	D6HNP8	<i>Erysipelotrichaceae bacterium 5_2_54FAA</i> .	Phosphinothricin N-acetyltransferase.	195	4.4E-13	171	32.7
399	G1WS32_9FIRM	G1WS32	<i>Dorea formicigenerans</i> 4_6_53AFAA.	Putative uncharacterized protein.	195	4.4E-13	171	28.7
400	B5D457_9BACE	B5D457	<i>Bacteroides plebeius</i> DSM 17135.	Putative uncharacterized protein.	160	4.5E-13	161	29.8
401	Q6HHT3_BACHK	Q6HHT3	<i>Bacillus thuringiensis</i> subsp. <i>konkukian</i> (strain 97-27).	Possible phosphinothricin N-acetyltransferase. EC=2.3.1.-.	170	4.7E-13	169	30.8
402	Q63AE3_BACCZ	Q63AE3	<i>Bacillus cereus</i> (strain ZK / E33L).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	170	4.7E-13	169	31.4
403	G1V2S3_9DELT	G1V2S3	<i>Bilophila</i> sp. 4_1_30.	Putative uncharacterized protein.	170	4.7E-13	168	30.4
404	G0JX55_STEMA	G0JX55	<i>Stenotrophomonas maltophilia</i> JV3.	Phosphinothricin acetyltransferase.	176	4.8E-13	171	33.3
405	D4K5Y8_9FIRM	D4K5Y8	<i>Faecalibacterium prausnitzii</i> SL3/3.	Sortase and related acyltransferases. EC=2.3.1.-.	184	5E-13	164	31.1
406	C3XAS2_OXAFO	C3XAS2	<i>Oxalobacter formigenes</i> OXCC13.	Putative uncharacterized protein.	188	5.1E-13	175	32.0
407	D7GVI8_9FIRM	D7GVI8	<i>butyrate-producing bacterium</i> SS3/4.	Sortase and related acyltransferases. EC=2.3.1.-.	189	5.1E-13	183	28.4
408	C0QYY8_BRAHW	C0QYY8	<i>Brachyspira hyodysenteriae</i> (strain ATCC 49526 / WA1).	Sortase related acyltransferase.	190	5.1E-13	178	28.1
409	Q0K5S7_CUPNH	Q0K5S7	<i>Cupriavidus necator</i> (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (<i>Ralstonia eutropha</i>).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	193	5.2E-13	177	31.1
410	C4FAB7_ACTN	C4FAB7	<i>Collinsella intestinalis</i> DSM 13280.	Putative uncharacterized protein.	198	5.3E-13	182	29.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
411	C4KZF3_EXISA	C4KZF3	<i>Exiguobacterium</i> sp. (strain ATCC BAA-1283 / AT1b).	GCN5-related N-acetyltransferase.	170	5.5E-13	168	33.3
412	D4BGN0_9ENTR	D4BGN0	<i>Citrobacter youngae</i> ATCC 29220.	Toxin-antitoxin system, toxin component, GNAT family.	174	5.6E-13	163	29.4
413	D5WZ80_THIK1	D5WZ80	<i>Thiomonas intermedia</i> (strain K12) (<i>Thiobacillus intermedius</i>).	Phosphinothricin acetyltransferase.	175	5.7E-13	170	33.5
414	A1VM96_POLNA	A1VM96	<i>Polaromonas naphthalenivorans</i> (strain CJ2).	GCN5-related N-acetyltransferase.	178	5.8E-13	173	33.5
415	Q92L60_RHIME	Q92L60	<i>Rhizobium meliloti</i> (strain 1021) (<i>Ensifer meliloti</i>) (<i>Sinorhizobium meliloti</i>).	Acetyltransferase. EC=2.3.1.-.	185	5.9E-13	173	28.9
416	F6BU31_SINMB	F6BU31	<i>Sinorhizobium meliloti</i> (strain BL225C).	Phosphinothricin acetyltransferase.	185	5.9E-13	173	28.9
417	B5ZTG1_RHILW	B5ZTG1	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> (strain WSM2304).	GCN5-related N-acetyltransferase.	185	5.9E-13	171	29.8
418	F6E4N4_SINMK	F6E4N4	<i>Sinorhizobium meliloti</i> (strain AK83).	Phosphinothricin acetyltransferase.	185	5.9E-13	173	28.9
419	C3RH74_9FIRM	C3RH74	<i>Coprobacillus</i> sp. D7.	Phosphinothricin N-acetyltransferase.	186	6E-13	178	29.8
420	B1FIS4_9BURK	B1FIS4	<i>Burkholderia ambifaria</i> IOP40-10.	GCN5-related N-acetyltransferase.	187	6E-13	179	31.8
421	D1AJ90_SEBTE	D1AJ90	<i>Sebaldella termitidis</i> (strain ATCC 33386 / NCTC 11300).	Phosphinothricin acetyltransferase.	165	6.4E-13	160	33.1
422	Q1LHR7_RALME	Q1LHR7	<i>Ralstonia metallidurans</i> (strain CH34 / ATCC 43123 / DSM 2839).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	206	6.5E-13	167	31.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
423	B9P8X3_POPTR	B9P8X3	<i>Populus trichocarpa</i> (Western balsam poplar) (<i>Populus balsamifera</i> subsp. <i>trichocarpa</i>).	Predicted protein.	206	6.5E-13	167	31.7
424	C3G3Z7_BACTU	C3G3Z7	<i>Bacillus thuringiensis</i> serovar <i>andalousiensis</i> BGSC 4AW1.	Phosphinothricin N-acetyltransferase.	170	6.5E-13	169	31.4
425	F0C9C2_9XANT	F0C9C2	<i>Xanthomonas gardneri</i> ATCC 19865.	Sortase-like acyltransferase.	175	6.7E-13	172	32.0
426	F4R272_BREDI	F4R272	<i>Brevundimonas diminuta</i> ATCC 11568.	Phosphinothricin N-acetyltransferase.	180	6.9E-13	169	36.1
427	E7G8F5_9FIRM	E7G8F5	<i>Coprobacillus</i> sp. 29_1.	Phosphinothricin N-acetyltransferase.	187	7.1E-13	157	31.2
428	B1YXB1_BURA4	B1YXB1	<i>Burkholderia ambifaria</i> (strain MC40-6).	GCN5-related N-acetyltransferase.	187	7.1E-13	175	32.0
429	B1C554_9FIRM	B1C554	<i>Clostridium spiroforme</i> DSM 1552.	Putative uncharacterized protein.	195	7.3E-13	173	28.9
430	B2UNN2_AKKM8	B2UNN2	<i>Akkermansia muciniphila</i> (strain ATCC BAA-835).	GCN5-related N-acetyltransferase.	199	7.4E-13	176	33.5
431	E7S2B3_STRAG	E7S2B3	<i>Streptococcus agalactiae</i> ATCC 13813.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	163	7.5E-13	157	29.3
432	E1YY63_9BACE	E1YY63	<i>Bacteroides</i> sp. 20_3.	Phosphinothricin N-acetyltransferase.	164	7.5E-13	161	32.9
433	G6Y0G9_RHIRD	G6Y0G9	<i>Agrobacterium tumefaciens</i> CCNWGS0286.	GCN5-related N-acetyltransferase.	206	7.7E-13	180	30.6
434	C2N1Z2_BACCE	C2N1Z2	<i>Bacillus cereus</i> ATCC 10876.	Phosphinothricin N-acetyltransferase.	170	7.7E-13	169	32.0
435	Q21CW0_RHOPB	Q21CW0	<i>Rhodopseudomonas palustris</i> (strain BisB18).	GCN5-related N-acetyltransferase.	174	7.9E-13	161	32.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
436	D6Z7D9_SEGRD	D6Z7D9	<i>Segniliparus rotundus</i> (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578).	GCN5-related N-acetyltransferase.	174	7.9E-13	159	33.3
437	Q89X52_BRAJA	Q89X52	<i>Bradyrhizobium japonicum</i> .	Acetyltransferase.	176	7.9E-13	170	33.5
438	B9JCJ9_AGRRK	B9JCJ9	<i>Agrobacterium radiobacter</i> (strain K84 / ATCC BAA-868).	Phosphinothricin N-acetyltransferase (Antibiotic resistance) protein.	185	8.3E-13	169	29.6
439	A5ZN30_9FIRM	A5ZN30	<i>Ruminococcus obeum</i> ATCC 29174.	Putative uncharacterized protein.	190	8.5E-13	182	27.5
440	F7U6L2_RHIRD	F7U6L2	<i>Agrobacterium tumefaciens</i> F2.	Acetyltransferase.	193	8.6E-13	159	32.7
441	G7M194_9CLOT	G7M194	<i>Clostridium</i> sp. DL-VIII.	GCN5-related N-acetyltransferase.	193	8.6E-13	186	30.6
442	Q8DU75_STRMU	Q8DU75	<i>Streptococcus mutans</i> .	Putative acetyltransferase.	163	8.8E-13	159	27.7
443	D9W602_9ACTO	D9W602	<i>Streptomyces himastatinicus</i> ATCC 53653.	GNAT family toxin-antitoxin system, toxin component.	172	9.2E-13	164	36.6
444	C7H1N5_9FIRM	C7H1N5	<i>Faecalibacterium prausnitzii</i> A2-165.	Phosphinothricin N-acetyltransferase.	282	9.9E-13	175	33.7
445	A5Z9M9_9FIRM	A5Z9M9	<i>Eubacterium ventriosum</i> ATCC 27560.	Putative uncharacterized protein.	192	1E-12	164	33.5
446	D0BJF9_9LACT	D0BJF9	<i>Granulicatella elegans</i> ATCC 700633.	Phosphinothricin N-acetyltransferase.	192	1E-12	162	27.8
447	B1M474_METRJ	B1M474	<i>Methylobacterium radiotolerans</i> (strain ATCC 27329 / DSM 1819 / JCM 2831).	GCN5-related N-acetyltransferase.	192	1E-12	184	33.7
448	B1G8U3_9BURK	B1G8U3	<i>Burkholderia graminis</i> C4D1M.	GCN5-related N-acetyltransferase.	193	1E-12	169	33.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
449	F8Y301_STRAG	F8Y301	<i>Streptococcus agalactiae</i> FSL S3-026.	Phosphinothricin N-acetyltransferase, putative.	163	1E-12	157	29.3
450	Q3DUR5_STRAG	Q3DUR5	<i>Streptococcus agalactiae</i> 18RS21.	Acyltransferase. EC=2.3.1.-.	163	1E-12	157	29.3
451	Q8E393_STRA3	Q8E393	<i>Streptococcus agalactiae</i> serotype III.	Putative uncharacterized protein gbs1868.	163	1E-12	157	29.3
452	Q8DXM3_STRA5	Q8DXM3	<i>Streptococcus agalactiae</i> serotype V.	Phosphinothricin N-acetyltransferase.	163	1E-12	157	29.3
453	Q3DK61_STRAG	Q3DK61	<i>Streptococcus agalactiae</i> 515.	Phosphinothricin N-acetyltransferase.	163	1E-12	157	29.3
454	E8NB23_MICTS	E8NB23	<i>Microbacterium testaceum</i> (strain StLB037).	Sortase.	203	1.1E-12	171	32.7
455	B6GAS2_9ACTN	B6GAS2	<i>Collinsella stercoris</i> DSM 13279.	Putative uncharacterized protein.	203	1.1E-12	186	31.7
456	A5E928_BRASB	A5E928	<i>Bradyrhizobium</i> sp. (strain BTAi1 / ATCC BAA-1182).	Phosphinothricin acetyltransferase (PPT N-acetyltransferase). EC=2.3.1.-.	176	1.1E-12	160	33.1
457	A1WPT8_VEREI	A1WPT8	<i>Verminephrobacter eiseniae</i> (strain EF01-2).	GCN5-related N-acetyltransferase.	181	1.1E-12	159	34.0
458	D4Z780_SPHJU	D4Z780	<i>Sphingobium japonicum</i> (strain NBRC 101211 / UT26S).	Putative acetyltransferase.	181	1.1E-12	159	34.6
459	E1TGF6_BURSG	E1TGF6	<i>Burkholderia</i> sp. (strain CCGE1003).	Phosphinothricin acetyltransferase.	184	1.1E-12	166	33.1
460	E3GC35_ENTCS	E3GC35	<i>Enterobacter cloacae</i> (strain SCF1).	Phosphinothricin acetyltransferase.	184	1.1E-12	172	32.0
461	G6E9P1_9SPHN	G6E9P1	<i>Novosphingobium pentaromativorans</i> US6-1.	Phosphinothricin acetyltransferase.	185	1.2E-12	166	35.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
462	E8W1M0_STRFA	E8W1M0	<i>Streptomyces flavogriseus</i> (strain ATCC 33331 / DSM 40990 / IAF-45CD).	Phosphinothricin acetyltransferase.	192	1.2E-12	187	32.6
463	B8ENW8_METSB	B8ENW8	<i>Methylocella silvestris</i> (strain BL2 / DSM 15510 / NCIMB 13906).	GCN5-related N-acetyltransferase.	193	1.2E-12	169	30.8
464	D8HR87_AMYMU	D8HR87	<i>Amycolatopsis mediterranei</i> (strain U-32).	Acetyltransferase.	162	1.2E-12	160	33.1
465	D7C7K3_STRBB	D7C7K3	<i>Streptomyces bingchenggensis</i> (strain BCW-1).	GCN5-related N-acetyltransferase.	162	1.2E-12	154	35.1
466	G0FQE0_AMYMD	G0FQE0	<i>Amycolatopsis mediterranei</i> S699.	Acetyltransferase.	162	1.2E-12	160	33.1
467	B7B8I1_9PORP	B7B8I1	<i>Parabacteroides johnsonii</i> DSM 18315.	Putative uncharacterized protein.	165	1.2E-12	165	31.5
468	F7VB03_9PROT	F7VB03	<i>Acetobacter tropicalis</i> NBRC 101654.	GCN5-related N-acetyltransferase.	169	1.3E-12	173	35.3
469	F7SY33_ALCXX	F7SY33	<i>Achromobacter xylosoxidans</i> AXX-A.	GNAT family acetyltransferase 28.	181	1.3E-12	175	32.0
470	A9CU55_9RHIZ	A9CU55	<i>Hoeflea phototrophica</i> DFL-43.	Putative phosphinothricin N-acetyltransferase (Antibiotic resistance) protein.	182	1.3E-12	178	29.8
471	F6DRU9_DESRL	F6DRU9	<i>Desulfotomaculum ruminis</i> (strain ATCC 23193 / DSM 2154 / NCIB 8452 / DL).	GCN5-related N-acetyltransferase.	191	1.4E-12	185	31.4
472	B0A9F5_9CLOT	B0A9F5	<i>Clostridium bartlettii</i> DSM 16795.	Putative uncharacterized protein.	208	1.5E-12	179	25.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
473	A6LS30_CLOB8	A6LS30	<i>Clostridium beijerinckii</i> (strain ATCC 51743 / NCIMB 8052) (<i>Clostridium acetobutylicum</i>).	GCN5-related N-acetyltransferase.	170	1.5E-12	168	31.5
474	C5T287_ACIDE	C5T287	<i>Acidovorax delafieldii</i> 2AN.	GCN5-related N-acetyltransferase.	173	1.5E-12	159	31.4
475	F3I4Q1_PSESF	F3I4Q1	<i>Pseudomonas syringae</i> pv. <i>actinidiae</i> str. M302091.	Phosphinothricin N-acetyltransferase.	179	1.6E-12	162	33.3
476	A7IB78_XANP2	A7IB78	<i>Xanthobacter autotrophicus</i> (strain ATCC BAA-1158 / Py2).	GCN5-related N-acetyltransferase.	180	1.6E-12	159	36.5
477	E6V2J8_VARPE	E6V2J8	<i>Variovorax paradoxus</i> (strain EPS).	Phosphinothricin acetyltransferase.	182	1.6E-12	161	34.8
478	D9QKW4_BRESC	D9QKW4	<i>Brevundimonas subvibrioides</i> (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (<i>Caulobacter subvibrioides</i>).	Phosphinothricin acetyltransferase.	182	1.6E-12	173	31.2
479	E6LCM2_9ENTE	E6LCM2	<i>Enterococcus italicus</i> DSM 15952.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	185	1.6E-12	172	30.2
480	F0K932_CLOAE	F0K932	<i>Clostridium acetobutylicum</i> (strain EA 2018).	Phosphinothricin acetyltransferase.	196	1.7E-12	175	26.3
481	Q97KQ9_CLOAB	Q97KQ9	<i>Clostridium acetobutylicum</i> .	Phosphinothricin acetyltransferase.	196	1.7E-12	175	26.3
482	F7ZM24_CLOAB	F7ZM24	<i>Clostridium acetobutylicum</i> DSM 1731.	Phosphinothricin acetyltransferase.	196	1.7E-12	175	26.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
483	F5IZW0_9PORP	F5IZW0	<i>Dysgonomonas gadei</i> ATCC BAA-286.	Putative uncharacterized protein.	161	1.7E-12	157	29.3
484	Q2BEU8_9BACI	Q2BEU8	<i>Bacillus</i> sp. NRRL B-14911.	Probable phosphinothricin acetyltransferase (Antibiotic resistance) protein.	163	1.7E-12	159	31.4
485	F6FPM1_ISOVS2	F6FPM1	<i>Isoptricola variabilis</i> (strain 225).	GCN5-related N-acetyltransferase.	206	1.8E-12	189	34.4
486	C9YWD9_STRSW	C9YWD9	<i>Streptomyces scabies</i> (strain 87.22) (<i>Streptomyces scabiei</i>).	Putative N-acetyltransferase.	172	1.8E-12	174	31.6
487	A6WV28_OCHA4	A6WV28	<i>Ochrobactrum anthropi</i> (strain ATCC 49188 / DSM 6882 / NCTC 12168).	GCN5-related N-acetyltransferase.	193	2E-12	177	31.6
488	D4M1R5_9FIRM	D4M1R5	<i>Ruminococcus torques</i> L2-14.	Sortase and related acyltransferases. EC=2.3.1.-.	196	2E-12	178	29.2
489	D4LV66_9FIRM	D4LV66	<i>Ruminococcus obeum</i> A2-162.	Sortase and related acyltransferases. EC=2.3.1.-.	202	2E-12	171	30.4
490	C7N8A5_SLAHD	C7N8A5	<i>Slackia heliotrinireducens</i> (strain ATCC 29202 / DSM 20476 / NCTC 11029 / RHS 1) (<i>Peptococcus heliotrinireducens</i>).	Sortase-like acyltransferase.	210	2.1E-12	183	31.7
491	Q87ZV1_PSESM	Q87ZV1	<i>Pseudomonas syringae</i> pv. <i>tomato</i> (strain DC3000).	Phosphinothricin N-acetyltransferase.	179	2.2E-12	168	33.3
492	A9CJT1_AGRT5	A9CJT1	<i>Agrobacterium tumefaciens</i> (strain C58 / ATCC 33970).	Acetyltransferase.	180	2.2E-12	170	32.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
493	A4JPE3_BURVG	A4JPE3	<i>Burkholderia vietnamiensis</i> (strain G4 / LMG 22486) (<i>Burkholderia cepacia</i> (strain R1808)).	GCN5-related N-acetyltransferase.	186	2.3E-12	179	31.3
494	Q89QF2_BRAJA	Q89QF2	<i>Bradyrhizobium japonicum</i> .	Acetyltransferase.	194	2.3E-12	179	31.3
495	A4XL16_CALS8	A4XL16	<i>Caldicellulosiruptor saccharolyticus</i> (strain ATCC 43494 / DSM 8903).	GCN5-related N-acetyltransferase.	162	2.4E-12	157	29.3
496	E5Y851_BILWA	E5Y851	<i>Bilophila wadsworthia</i> 3_1_6.	Acetyltransferase.	170	2.5E-12	168	29.8
497	Q46W53_CUPPJ	Q46W53	<i>Cupriavidus pinatubonensis</i> (strain JMP134 / LMG 1197) (<i>Alcaligenes eutrophus</i>) (<i>Ralstonia eutropha</i>).	GCN5-related N-acetyltransferase.	210	2.5E-12	172	32.6
498	Q7P142_CHRVO	Q7P142	<i>Chromobacterium violaceum</i> .	Probable resistance protein.	174	2.5E-12	174	32.2
499	E0DSI4_9RHIZ	E0DSI4	<i>Brucella</i> sp. BO1.	Phosphinothricin N-acetyltransferase.	179	2.6E-12	162	32.7
500	F3IJG7_PSESL	F3IJG7	<i>Pseudomonas syringae</i> pv. <i>lachrymans</i> str. M302278PT.	Phosphinothricin N-acetyltransferase.	179	2.6E-12	168	33.3
501	D5WGY3_BURSC	D5WGY3	<i>Burkholderia</i> sp. (strain CCGE1002).	Phosphinothricin acetyltransferase.	193	2.7E-12	181	30.9
502	D5NK58_9BURK	D5NK58	<i>Burkholderia</i> sp. Ch1-1.	Phosphinothricin acetyltransferase.	197	2.8E-12	178	33.7
503	Q3D2Q7_STRAG	Q3D2Q7	<i>Streptococcus agalactiae</i> H36B.	Phosphinothricin N-acetyltransferase.	163	2.8E-12	157	28.7
504	Q3JZ59_STRAI	Q3JZ59	<i>Streptococcus agalactiae</i> serotype Ia.	Phosphinothricin N-acetyltransferase, putative.	163	2.8E-12	157	28.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
505	Q3D9C8_STRAG	Q3D9C8	<i>Streptococcus agalactiae</i> COH1.	Phosphinothricin N-acetyltransferase.	163	2.8E-12	157	28.7
506	Q3DEN3_STRAG	Q3DEN3	<i>Streptococcus agalactiae</i> CJB111.	Phosphinothricin N-acetyltransferase.	163	2.8E-12	157	28.7
507	Q13P08_BURXL	Q13P08	<i>Burkholderia xenovorans</i> (strain LB400).	Putative phosphinothricin N-acetyltransferase. EC=2.3.1.-.	200	2.8E-12	178	33.7
508	B2H7D0_BURPS	B2H7D0	<i>Burkholderia pseudomallei</i> 1655.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	2.8E-12	163	33.1
509	C8WKG7_EGGLE	C8WKG7	<i>Eggerthella lenta</i> (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (<i>Eubacterium lentum</i>).	GCN5-related N-acetyltransferase.	213	3E-12	179	32.4
510	G7UJY3_PANAN	G7UJY3	<i>Pantoea ananatis</i> PA13.	Putative acetyltransferase.	175	3E-12	161	31.7
511	D1EPW7_9RHIZ	D1EPW7	<i>Brucella pinnipedialis</i> M292/94/1.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
512	B0CIK1_BRUSI	B0CIK1	<i>Brucella suis</i> (strain ATCC 23445 / NCTC 10510).	Phosphinothricin N-acetyltransferase.	179	3E-12	162	32.7
513	C9V7X2_BRUNE	C9V7X2	<i>Brucella neotomae</i> 5K33.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
514	D0RL86_9RHIZ	D0RL86	<i>Brucella</i> sp. F5/99.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
515	C7LFE7_BRUMC	C7LFE7	<i>Brucella microti</i> (strain CCM 4915).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	179	3E-12	162	32.7
516	C9TE00_9RHIZ	C9TE00	<i>Brucella ceti</i> M13/05/1.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
517	C9T2V3_9RHIZ	C9T2V3	<i>Brucella ceti</i> M644/93/1.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
518	D6LL28_9RHIZ	D6LL28	<i>Brucella</i> sp. NVSL 07-0026.	Acetyltransferase.	179	3E-12	162	32.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
519	D1F655_BRUML	D1F655	<i>Brucella melitensis</i> bv. 3 str. Ether.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
520	D0PN03_BRUSS	D0PN03	<i>Brucella suis</i> bv. 3 str. 686.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
521	D1F164_BRUML	D1F164	<i>Brucella melitensis</i> bv. 1 str. Rev.1.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
522	C9TXY1_9RHIZ	C9TXY1	<i>Brucella pinnipedialis</i> B2/94.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-. Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
523	D0PAC1_BRUSS	D0PAC1	<i>Brucella suis</i> bv. 5 str. 513.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
524	C0G3L6_9RHIZ	C0G3L6	<i>Brucella ceti</i> str. Cudo.	Phosphinothricin N-acetyltransferase.	179	3E-12	162	32.7
525	D0BDP3_BRUSS	D0BDP3	<i>Brucella suis</i> bv. 4 str. 40.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
526	Q8YEM0_BRUME	Q8YEM0	<i>Brucella melitensis</i> biotype 1 (strain 16M / ATCC 23456 / NCTC 10094).	Phosphinothricin n-acetyltransferase. EC=2.3.1.-. Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
527	C9TN42_9RHIZ	C9TN42	<i>Brucella pinnipedialis</i> M163/99/10.	Phosphinotricin acetyltransferase.	179	3E-12	162	32.7
528	Q8G363_BRUSU	Q8G363	<i>Brucella suis</i> biovar 1 (strain 1330).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	179	3E-12	162	32.7
529	E2PQL7_9RHIZ	E2PQL7	<i>Brucella</i> sp. BO2.	Phosphinothricin N-acetyltransferase.	179	3E-12	162	32.7
530	A9M6U1_BRUC2	A9M6U1	<i>Brucella canis</i> (strain ATCC 23365 / NCTC 10854).	Phosphinothricin N-acetyltransferase.	179	3E-12	162	32.7
531	A5VN33_BRUO2	A5VN33	<i>Brucella ovis</i> (strain ATCC 25840 / 63/290 / NCTC 10512).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	179	3E-12	162	32.7
532	E8RT62_ASTEC	E8RT62	<i>Asticcacaulis excentricus</i> (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48).	Phosphinothricin acetyltransferase.	180	3.1E-12	170	35.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
533	F2NYB6_TRES6	F2NYB6	<i>Treponema succinifaciens</i> (strain ATCC 33096 / DSM 2489 / 6091).	Phosphinothricin acetyltransferase.	184	3.1E-12	177	28.2
534	E5VP65_9FIRM	E5VP65	<i>Lachnospiraceae bacterium 5_1_63FAA</i> .	Acetyltransferase.	185	3.1E-12	169	32.5
535	G7ZB07_AZOLI	G7ZB07	<i>Azospirillum lipoferum</i> 4B.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	192	3.2E-12	179	31.8
536	C6AYZ0_RHILS	C6AYZ0	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> (strain WSM1325).	GCN5-related N-acetyltransferase.	200	3.3E-12	171	28.7
537	B7QLK8_IXOSC	B7QLK8	<i>Ixodes scapularis</i> (Black-legged tick) (Deer tick).	Phosphinothricin N-acetyltransferase, putative. Flags: Fragment.	164	3.3E-12	161	34.8
538	A7AHJ4_9PORP	A7AHJ4	<i>Parabacteroides merdae</i> ATCC 43184.	Putative uncharacterized protein.	165	3.4E-12	161	31.7
539	D4E9B7_SEROD	D4E9B7	<i>Serratia odorifera</i> DSM 4582.	Phosphinothricin acetyltransferase.	178	3.6E-12	160	33.8
540	F6IJD5_9SPHN	F6IJD5	<i>Novosphingobium</i> sp. PP1Y.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	181	3.6E-12	166	34.9
541	D5CJW7_ENTCC	D5CJW7	<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> (strain ATCC 13047 / DSM 30054 / NBRC 13535 / NCDC 279-56).	GCN5-related N-acetyltransferase.	184	3.7E-12	172	32.0
542	B0P0X2_9CLOT	B0P0X2	<i>Clostridium</i> sp. SS2/1.	Putative uncharacterized protein.	185	3.7E-12	169	32.5
543	B4ELW8_BURCJ	B4ELW8	<i>Burkholderia cepacia</i> (strain J2315 / LMG 16656) (<i>Burkholderia cenocepacia</i> (strain J2315)).	Putative acetyltransferase.	186	3.7E-12	172	30.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
544	B7RU71_9GAMM	B7RU71	<i>marine gamma proteobacterium HTCC2148.</i>	Acetyltransferase, GNAT family.	154	3.8E-12	147	34.0
545	D5UE50_CELFN	D5UE50	<i>Cellulomonas flavigena</i> (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134).	Phosphinothricin acetyltransferase.	168	4E-12	161	31.1
546	A6B860_VIBPA	A6B860	<i>Vibrio parahaemolyticus</i> AQ3810.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	169	4E-12	166	32.5
547	F8IS93_STREC	F8IS93	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> (strain ATCC 35246 / C74-63).	Phosphinothricin N-acetyltransferase.	212	4.1E-12	177	33.3
548	Q3BNL7_XANC5	Q3BNL7	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10).	N-acetyltransferase.	173	4.1E-12	162	32.1
549	D4T7F0_9XANT	D4T7F0	<i>Xanthomonas fuscans</i> subsp. <i>aurantifolii</i> str. ICPB 10535.	N-acetyltransferase.	173	4.1E-12	162	32.7
550	D4STE8_9XANT	D4STE8	<i>Xanthomonas fuscans</i> subsp. <i>aurantifolii</i> str. ICPB 11122.	N-acetyltransferase.	173	4.1E-12	162	32.7
551	Q8PG30_XANAC	Q8PG30	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (Citrus canker).	Phosphinothricin acetyltransferase.	173	4.1E-12	162	32.1
552	E5X7C1_9ACTN	E5X7C1	<i>Eggerthella</i> sp. 1_3_56FAA.	Acetyltransferase.	213	4.1E-12	179	32.4
553	D4J303_BUTFI	D4J303	<i>Butyrivibrio fibrisolvens</i> .	Sortase and related acyltransferases. EC=2.3.1.-.	175	4.2E-12	161	29.8
554	F7QGL9_9BRAD	F7QGL9	<i>Bradyrhizobiaceae bacterium</i> SG-6C.	GCN5-related N-acetyltransferase.	179	4.2E-12	176	32.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
555	B2VBV3_ERWT9	B2VBV3	<i>Erwinia tasmaniensis</i> (strain DSM 17950 / Et1/99).	Putative N-acetyltransferase.	179	4.2E-12	160	31.9
556	E1SBR2_PANVC	E1SBR2	<i>Pantoea vagans</i> (strain C9-1) (<i>Pantoea agglomerans</i> (strain C9-1)).	Putative acetyltransferase. EC=2.3.1.-.	222	4.3E-12	172	28.5
557	Q1QRK9_NITHX	Q1QRK9	<i>Nitrobacter hamburgensis</i> (strain X14 / DSM 10229).	GCN5-related N-acetyltransferase.	183	4.3E-12	161	33.5
558	C7MNV7_CRYCD	C7MNV7	<i>Cryptobacterium curtum</i> (strain ATCC 700683 / DSM 15641 / 12-3).	Sortase-like acyltransferase.	185	4.4E-12	175	30.9
559	B1K2D0_BURCC	B1K2D0	<i>Burkholderia cenocepacia</i> (strain MC0-3).	GCN5-related N-acetyltransferase.	186	4.4E-12	172	30.2
560	Q1BP64_BURCA	Q1BP64	<i>Burkholderia cenocepacia</i> (strain AU 1054).	GCN5-related N-acetyltransferase.	186	4.4E-12	172	30.2
561	A0B177_BURCH	A0B177	<i>Burkholderia cenocepacia</i> (strain HI2424).	GCN5-related N-acetyltransferase.	186	4.4E-12	172	30.2
562	G7DRS9_BRAJA	G7DRS9	<i>Bradyrhizobium japonicum</i> USDA 6.	Acetyltransferase.	192	4.5E-12	174	31.0
563	B3R7G3_CUPTR	B3R7G3	<i>Cupriavidus taiwanensis</i> (strain R1 / LMG 19424) (<i>Ralstonia taiwanensis</i> (strain LMG 19424)).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	197	4.6E-12	167	31.1
564	E3CMN5_STRDO	E3CMN5	<i>Streptococcus downei</i> F0415.	Acetyltransferase, GNAT family.	197	4.6E-12	178	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
565	Q4A096_STAS1	Q4A096	<i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i> (strain ATCC 15305 / DSM 20229).	Putative acetyltransferase.	163	4.6E-12	162	30.2
566	E6MK44_9FIRM	E6MK44	<i>Pseudoramibacter alactolyticus</i> ATCC 23263.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	204	4.7E-12	183	31.1
567	G5H9K4_9BACT	G5H9K4	<i>Alistipes indistinctus</i> YIT 12060.	Putative uncharacterized protein.	168	4.8E-12	169	31.4
568	G7M8H9_9CLOT	G7M8H9	<i>Clostridium</i> sp. DL-VIII.	GCN5-related N-acetyltransferase.	170	4.8E-12	168	30.4
569	D0IA19_VIBHO	D0IA19	<i>Grimontia hollisae</i> CIP 101886.	GCN5-related N-acetyltransferase.	171	4.8E-12	161	31.1
570	D6VAW9_9BRAD	D6VAW9	<i>Afipia</i> sp. 1NLS2.	Phosphinothricin acetyltransferase.	176	4.9E-12	157	32.5
571	B4D011_9BACT	B4D011	<i>Chthoniobacter flavus</i> Ellin428.	GCN5-related N-acetyltransferase.	177	5E-12	178	30.3
572	Q12CW7_POLSJ	Q12CW7	<i>Polaromonas</i> sp. (strain JS666 / ATCC BAA-500).	GCN5-related N-acetyltransferase.	178	5E-12	176	34.1
573	G7HK30_9BURK	G7HK30	<i>Burkholderia cenocepacia</i> H111.	Histone acetyltransferase HPA2 and related acetyltransferases.	178	5E-12	172	30.2
574	D5VMR9_CAUST	D5VMR9	<i>Caulobacter segnis</i> (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (<i>Mycoplana segnis</i>).	Phosphinothricin acetyltransferase.	185	5.1E-12	174	32.8
575	A2VY40_9BURK	A2VY40	<i>Burkholderia cenocepacia</i> PC184.	GCN5-related N-acetyltransferase.	186	5.2E-12	172	30.2
576	A7ICZ9_XANP2	A7ICZ9	<i>Xanthobacter autotrophicus</i> (strain ATCC BAA-1158 / Py2).	GCN5-related N-acetyltransferase.	186	5.2E-12	183	30.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
577	A2SES5_METPP	A2SES5	<i>Methylibium petroleiphilum</i> (strain PM1).	Putative phosphinothricin acetyltransferase. EC=2.3.1.-.	190	5.3E-12	176	32.4
578	B5WEJ4_9BURK	B5WEJ4	<i>Burkholderia</i> sp. H160.	GCN5-related N-acetyltransferase.	193	5.3E-12	180	31.7
579	Q5H5C1_XANOR	Q5H5C1	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> .	Phosphinothricin acetyltransferase.	201	5.5E-12	171	32.2
580	D3NZB6_AZOS1	D3NZB6	<i>Azospirillum</i> sp. (strain B510).	Acetyltransferase.	177	5.9E-12	155	32.9
581	D1CV28_9RHIZ	D1CV28	<i>Brucella</i> sp. 83/13.	Phosphinothricin acetyltransferase.	179	5.9E-12	162	32.1
582	E0DSN5_9RHIZ	E0DSN5	<i>Brucella</i> sp. NF 2653.	Phosphinothricin N-acetyltransferase.	179	5.9E-12	162	32.1
583	A6UE23_SINMW	A6UE23	<i>Sinorhizobium medicae</i> (strain WSM419) (<i>Ensifer medicae</i>).	GCN5-related N-acetyltransferase.	185	6.1E-12	177	29.9
584	B1Y0H4_LEPCP	B1Y0H4	<i>Leptothrix cholodnii</i> (strain ATCC 51168 / LMG 8142 / SP-6) (<i>Leptothrix discophora</i> (strain SP-6)).	GCN5-related N-acetyltransferase.	186	6.1E-12	171	33.9
585	C6U2I7_BURPS	C6U2I7	<i>Burkholderia pseudomallei</i> 1710a.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	188	6.2E-12	163	32.5
586	Q63LT2_BURPS	Q63LT2	<i>Burkholderia pseudomallei</i> (<i>Pseudomonas pseudomallei</i>).	Putative phosphinothricin N-acetyltransferase.	188	6.2E-12	163	32.5
587	D8I9U5_BRAP9	D8I9U5	<i>Brachyspira pilosicoli</i> (strain ATCC BAA-1826 / 95/1000).	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase.	189	6.2E-12	175	28.6
588	F5RZN6_9ENTR	F5RZN6	<i>Enterobacter hormaechei</i> ATCC 49162.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	190	6.2E-12	177	31.6
589	B5HKY1_9ACTO	B5HKY1	<i>Streptomyces sviveus</i> ATCC 29083.	Phosphinothricin N-acetyltransferase.	169	6.7E-12	169	30.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
590	B7CFC6_BURPS	B7CFC6	<i>Burkholderia pseudomallei</i> 576.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	210	6.7E-12	163	32.5
591	G0CFM5_XANCA	G0CFM5	<i>Xanthomonas campestris</i> pv. <i>raphani</i> 756C.	Phosphinothricin N-acetyltransferase.	175	6.9E-12	171	32.2
592	F3DVK2_9PSED	F3DVK2	<i>Pseudomonas syringae</i> pv. <i>morsprunorum</i> str. M302280PT.	Phosphinothricin N-acetyltransferase.	179	7E-12	162	32.7
593	B9JH00_AGRRK	B9JH00	<i>Agrobacterium radiobacter</i> (strain K84 / ATCC BAA-868).	Phosphinothricin acetyltransferase (Antibiotic resistance) protein.	183	7.1E-12	169	34.9
594	F0R0U7_BACSH	F0R0U7	<i>Bacteroides salanitronis</i> (strain DSM 18170 / JCM 13567 / BL78).	Phosphinothricin acetyltransferase.	160	7.5E-12	161	32.9
595	C4I2N6_BURPS	C4I2N6	<i>Burkholderia pseudomallei</i> MSHR346.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.183.	247	7.7E-12	163	32.5
596	A4LH07_BURPS	A4LH07	<i>Burkholderia pseudomallei</i> 305.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	7.7E-12	163	32.5
597	A3P4P9_BURP0	A3P4P9	<i>Burkholderia pseudomallei</i> (strain 1106a).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	7.7E-12	163	32.5
598	A3NJ28_BURP6	A3NJ28	<i>Burkholderia pseudomallei</i> (strain 668).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	7.7E-12	163	32.5
599	C5ZUC3_BURPS	C5ZUC3	<i>Burkholderia pseudomallei</i> 1106b.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	7.7E-12	163	32.5
600	Q3JFH3_BURP1	Q3JFH3	<i>Burkholderia pseudomallei</i> (strain 1710b).	Phosphinothricin N-acetyltransferase.	247	7.7E-12	163	32.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
601	A8KRS6_BURPS	A8KRS6	<i>Burkholderia pseudomallei</i> Pasteur 52237.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	7.7E-12	163	32.5
602	B1H5T0_BURPS	B1H5T0	<i>Burkholderia pseudomallei</i> S13.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	7.7E-12	163	32.5
603	A8EL92_BURPS	A8EL92	<i>Burkholderia pseudomallei</i> 406e.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	247	7.7E-12	163	32.5
604	B0RS98_XANCB	B0RS98	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain B100).	Putative phosphinothricin N-acetyltransferase. EC=2.3.1.-.	175	8.1E-12	172	32.6
605	C0Y9C0_BURPS	C0Y9C0	<i>Burkholderia pseudomallei</i> Pakistan 9.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	176	8.1E-12	163	32.5
606	C9VKI5_9RHIZ	C9VKI5	<i>Brucella ceti</i> B1/94.	Phosphinothricin acetyltransferase.	179	8.2E-12	162	32.1
607	D1FHC2_9RHIZ	D1FHC2	<i>Brucella ceti</i> M490/95/1.	Phosphinothricin acetyltransferase.	179	8.2E-12	162	32.1
608	F3UAW6_STRSA	F3UAW6	<i>Streptococcus sanguinis</i> SK1056.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	180	8.3E-12	147	33.3
609	Q2T586_BURTA	Q2T586	<i>Burkholderia thailandensis</i> (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301).	Phosphinothricin N-acetyltransferase.	188	8.6E-12	173	32.9
610	C6JH06_9FIRM	C6JH06	<i>Ruminococcus</i> sp. 5_1_39BFAA.	Putative uncharacterized protein.	194	8.8E-12	164	28.7
611	B4UZ55_9ACTO	B4UZ55	<i>Streptomyces</i> sp. Mg1.	Putative uncharacterized protein.	172	9.4E-12	168	34.5
612	E5V3N7_9BACL	E5V3N7	<i>Gemella moribillum</i> M424.	Acetyltransferase.	172	9.4E-12	158	28.5
613	D5UHA0_CELFN	D5UHA0	<i>Cellulomonas flavigena</i> (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134).	Phosphinothricin acetyltransferase.	173	9.5E-12	161	32.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
614	G2LVK3_9XANT	G2LVK3	<i>Xanthomonas axonopodis</i> pv. <i>citrumelo</i> F1.	Sortase and related acyltransferase.	173	9.5E-12	162	31.5
615	F0QB6_9XANT	F0QB6	<i>Xanthomonas perforans</i> 91-118.	Sortase-like acyltransferase.	173	9.5E-12	162	31.5
616	G2SCJ7_ENTAL	G2SCJ7	<i>Enterobacter asburiae</i> (strain LF7a).	GCN5-related N-acetyltransferase.	184	9.9E-12	172	30.8
617	C8NDZ5_9LACT	C8NDZ5	<i>Granulicatella adiacens</i> ATCC 49175.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	186	1E-11	175	26.9
618	F2ESH1_PANAA	F2ESH1	<i>Pantoea ananatis</i> (strain AJ13355).	Phosphinothricin N-acetyltransferase Pat.	188	1E-11	161	31.7
619	B2TC27_BURPP	B2TC27	<i>Burkholderia phytofirmans</i> (strain DSM 17436 / PsJN).	GCN5-related N-acetyltransferase.	197	1.1E-11	163	33.7
620	G2J2S8_PSEUL	G2J2S8	<i>Pseudogulbenkiania</i> sp. (strain NH8B).	GNAT family acetyltransferase.	170	1.1E-11	169	33.7
621	F0CD82_9XANT	F0CD82	<i>Xanthomonas gardneri</i> ATCC 19865.	Sortase-like acyltransferase.	173	1.1E-11	162	31.5
622	Q2P816_XANOM	Q2P816	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain MAFF 311018).	Phosphinothricin acetyltransferase.	173	1.1E-11	162	32.1
623	B2SL64_XANOP	B2SL64	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain PXO99A).	N-acetyltransferase.	173	1.1E-11	162	32.1
624	Q4UVE2_XANC8	Q4UVE2	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain 8004).	Phosphinothricin N-acetyltransferase.	175	1.1E-11	171	32.2
625	Q8P8P0_XANCP	Q8P8P0	<i>Xanthomonas campestris</i> pv. <i>campestris</i> .	Phosphinothricin N-acetyltransferase.	175	1.1E-11	171	32.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
626	B2IBY0_BEII9	B2IBY0	<i>Beijerinckia indica</i> subsp. <i>indica</i> (strain ATCC 9039 / DSM 1715 / NCIB 8712).	GCN5-related N-acetyltransferase.	180	1.2E-11	160	33.1
627	G7UL37_PANAN	G7UL37	<i>Pantoea ananatis</i> PA13.	Phosphinothricin N-acetyltransferase Pat.	223	1.2E-11	161	31.7
628	C3MAI1_RHISN	C3MAI1	<i>Rhizobium</i> sp. (strain NGR234).	Putative GCN5-related N-acetyltransferase.	185	1.2E-11	177	28.8
629	G0VMY5_MEGEL	G0VMY5	<i>Megasphaera elsdenii</i> DSM 20460.	Putative uncharacterized protein.	186	1.2E-11	183	28.4
630	A3MD70_BURM7	A3MD70	<i>Burkholderia mallei</i> (strain NCTC 10247).	Phosphinothricin N-acetyltransferase.	188	1.2E-11	163	32.5
631	A5TGV6_BURMA	A5TGV6	<i>Burkholderia mallei</i> 2002721280.	Phosphinothricin N-acetyltransferase.	188	1.2E-11	163	32.5
632	G2TF93_RHORU	G2TF93	<i>Rhodospirillum rubrum</i> F11.	GCN5-related N-acetyltransferase.	195	1.2E-11	183	33.9
633	Q2RRN8_RHORT	Q2RRN8	<i>Rhodospirillum rubrum</i> (strain ATCC 11170 / NCIB 8255).	GCN5-related N-acetyltransferase.	195	1.2E-11	183	33.9
634	E8LEU0_9FIRM	E8LEU0	<i>Phascolarctobacterium</i> sp. YIT 12067.	Putative phosphinothricin N-acetyltransferase.	203	1.3E-11	154	30.5
635	B9Z7S9_9NEIS	B9Z7S9	<i>Lutiella nitroferum</i> 2002.	GCN5-related N-acetyltransferase.	170	1.3E-11	171	33.9
636	Q62BK6_BURMA	Q62BK6	<i>Burkholderia mallei</i> (<i>Pseudomonas mallei</i>).	Phosphinothricin N-acetyltransferase.	210	1.3E-11	163	32.5
637	C4APS3_BURMA	C4APS3	<i>Burkholderia mallei</i> GB8 horse 4.	Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein). EC=2.3.1.-.	210	1.3E-11	163	32.5
638	C5NBQ2_BURMA	C5NBQ2	<i>Burkholderia mallei</i> PRL-20.	Phosphinothricin N-acetyltransferase.	210	1.3E-11	163	32.5
639	F0HP84_9ACTN	F0HP84	<i>Eggerthella</i> sp. HGA1.	Putative phosphinothricin N-acetyltransferase.	213	1.3E-11	179	31.3
640	F2LJS4_BURGS	F2LJS4	<i>Burkholderia gladioli</i> (strain BSR3).	GCN5-related N-acetyltransferase.	174	1.3E-11	177	35.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
641	F0BDJ9_9XANT	F0BDJ9	<i>Xanthomonas vesicatoria</i> ATCC 35937.	Sortase-like acyltransferase.	175	1.3E-11	171	31.6
642	E2MH09_PSEUB	E2MH09	<i>Pseudomonas syringae</i> pv. <i>tomato</i> T1.	Phosphinothricin N-acetyltransferase.	179	1.4E-11	168	32.7
643	F0L834_AGRSH	F0L834	<i>Agrobacterium</i> sp. (strain H13-3) (<i>Rhizobium lupini</i> (strain H13-3)).	GCN5-related N-acetyltransferase. EC=2.3.1.-.	180	1.4E-11	167	29.3
644	B0SZI2_CAUSK	B0SZI2	<i>Caulobacter</i> sp. (strain K31).	GCN5-related N-acetyltransferase.	185	1.4E-11	174	32.2
645	D5U775_BRAM5	D5U775	<i>Brachyspira murdochii</i> (strain ATCC 51284 / DSM 12563 / 56-150) (<i>Serpulina murdochii</i>).	GCN5-related N-acetyltransferase.	190	1.4E-11	161	28.0
646	G6G1C7_9FIRM	G6G1C7	<i>Desulfosporosinus meridiei</i> DSM 13257.	GCN5-related N-acetyltransferase.	191	1.4E-11	180	29.4
647	A1TNC9_ACIAC	A1TNC9	<i>Acidovorax citrulli</i> (strain AAC00-1) (<i>Acidovorax avenae</i> subsp. <i>citrulli</i>).	GCN5-related N-acetyltransferase.	197	1.5E-11	168	31.5
648	Q1MAM1_RHIL3	Q1MAM1	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> (strain 3841).	Putative acetyltransferase.	200	1.5E-11	171	28.1
649	F4GQU8_PUSST	F4GQU8	<i>Pusillimonas</i> sp. (strain T7-7).	N-acetyltransferase.	201	1.5E-11	176	31.2
650	A2RXF1_BURM9	A2RXF1	<i>Burkholderia mallei</i> (strain NCTC 10229).	Phosphinothricin N-acetyltransferase.	247	1.5E-11	163	32.5
651	A9JY69_BURMA	A9JY69	<i>Burkholderia mallei</i> ATCC 10399.	Phosphinothricin N-acetyltransferase.	247	1.5E-11	163	32.5
652	A5XKJ5_BURMA	A5XKJ5	<i>Burkholderia mallei</i> JHU.	Phosphinothricin N-acetyltransferase.	247	1.5E-11	163	32.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
653	A1UV91_BURMS	A1UV91	<i>Burkholderia mallei</i> (strain SAVP1).	Phosphinothricin N-acetyltransferase.	247	1.5E-11	163	32.5
654	A4BD82_9GAMM	A4BD82	<i>Reinekea blandensis</i> MED297.	Putative phosphinothricin N-acetyltransferase.	167	1.5E-11	160	32.5
655	E3NTS4_CAERE	E3NTS4	<i>Caenorhabditis remanei</i> (<i>Caenorhabditis vulgaris</i>).	Putative uncharacterized protein.	379	1.5E-11	179	31.3
656	F0E400_9PSED	F0E400	<i>Pseudomonas</i> sp. TJI-51.	GCN5-related N-acetyltransferase.	171	1.5E-11	169	32.0
657	G7GP05_9ACTO	G7GP05	<i>Gordonia amarae</i> NBRC 15530.	Putative acetyltransferase.	184	1.6E-11	167	32.3
658	D4N0V9_9FIRM	D4N0V9	<i>butyrate-producing bacterium</i> SSC/2.	Sortase and related acyltransferases. EC=2.3.1.-.	185	1.6E-11	169	32.0
659	Q2K3A0_RHIEC	Q2K3A0	<i>Rhizobium etli</i> (strain CFN 42 / ATCC 51251).	Putative phosphinothricin N-acetyltransferase (Antibiotic resistance) protein.	185	1.6E-11	171	28.1
660	F5VEP9_9LACO	F5VEP9	<i>Lactobacillus salivarius</i> NIAS840.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	198	1.7E-11	183	28.4
661	F7QVS4_9LACO	F7QVS4	<i>Lactobacillus salivarius</i> GJ-24.	Phosphinothricin N-acetyltransferase.	198	1.7E-11	183	28.4
662	B1Z955_METPB	B1Z955	<i>Methylobacterium populi</i> (strain ATCC BAA-705 / NCIMB 13946 / BJ001).	GCN5-related N-acetyltransferase.	204	1.8E-11	173	31.8
663	C5NUM4_9BACL	C5NUM4	<i>Gemella haemolysans</i> ATCC 10379.	Phosphinothricin N-acetyltransferase.	167	1.8E-11	160	26.9
664	E0M089_9ENTR	E0M089	<i>Pantoea</i> sp. aB.	Phosphinothricin acetyltransferase.	174	1.8E-11	173	28.9
665	Q6D8L6_ERWCT	Q6D8L6	<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> (<i>Pectobacterium atrosepticum</i>).	Putative acetyltransferase.	175	1.9E-11	161	31.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
666	F8BU02_OLICO	F8BU02	<i>Oligotropha carboxidovorans</i> (strain ATCC 49405 / DSM 1227 / OM5).	Phosphinothricin N-acetyltransferase Pat. EC=2.3.1.183.	176	1.9E-11	153	33.3
667	F8BJ96_OLICM	F8BJ96	<i>Oligotropha carboxidovorans</i> (strain OM4).	Phosphinothricin N-acetyltransferase Pat. EC=2.3.1.183.	176	1.9E-11	153	33.3
668	Q2KZT5_BORA1	Q2KZT5	<i>Bordetella avium</i> (strain 197N).	Acetyltransferase. EC=2.3.1.-. Flags: Fragment.	178	1.9E-11	171	32.7
669	C0RGE9_BRUMB	C0RGE9	<i>Brucella melitensis</i> biotype 2 (strain ATCC 23457).	Phosphinothricin N-acetyltransferase.	179	1.9E-11	162	32.1
670	F2HUM4_BRUMM	F2HUM4	<i>Brucella melitensis</i> (strain M28).	Phosphinothricin N-acetyltransferase.	179	1.9E-11	162	32.1
671	F2GPV9_BRUM5	F2GPV9	<i>Brucella melitensis</i> (strain M5-90).	Phosphinothricin N-acetyltransferase.	179	1.9E-11	162	32.1
672	G4PEN0_BRUML	G4PEN0	<i>Brucella melitensis</i> NI.	Phosphinothricin N-acetyltransferase.	179	1.9E-11	162	32.1
673	D0GHW1_BRUML	D0GHW1	<i>Brucella melitensis</i> bv. 2 str. 63/9.	Phosphinothricin acetyltransferase.	179	1.9E-11	162	32.1
674	B6JCY8_OLICO	B6JCY8	<i>Oligotropha carboxidovorans</i> (strain ATCC 49405 / DSM 1227 / OM5).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	185	1.9E-11	153	33.3
675	B2IHQ9_BEI19	B2IHQ9	<i>Beijerinckia indica</i> subsp. <i>indica</i> (strain ATCC 9039 / DSM 1715 / NCIB 8712).	GCN5-related N-acetyltransferase.	186	2E-11	179	30.7
676	E3I3U9_RHOVT	E3I3U9	<i>Rhodococcus vanniellii</i> (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299).	Phosphinothricin acetyltransferase.	190	2E-11	175	33.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
677	C7CE53_METED	C7CE53	<i>Methylobacterium extorquens</i> (strain DSM 5838 / DM4) (<i>Methylobacterium dichloromethanicum</i> (strain DM4)).	Phosphinothricin N-acetyltransferase.	204	2.1E-11	178	30.9
678	C5AVM7_METEA	C5AVM7	<i>Methylobacterium extorquens</i> (strain ATCC 14718 / DSM 1338 / AM1).	Phosphinothricin N-acetyltransferase.	204	2.1E-11	178	30.9
679	D0M1J7_VIBSE	D0M1J7	<i>Vibrio</i> sp. (strain Ex25).	Toxin resistance protein.	169	2.1E-11	166	31.3
680	G2LUP1_9XANT	G2LUP1	<i>Xanthomonas axonopodis</i> pv. <i>citrumelo</i> F1.	Phosphinothricin N-acetyltransferase.	179	2.2E-11	176	30.7
681	A4WCG8_ENT38	A4WCG8	<i>Enterobacter</i> sp. (strain 638).	GCN5-related N-acetyltransferase.	184	2.3E-11	176	31.2
682	B3PQZ9_RHIE6	B3PQZ9	<i>Rhizobium etli</i> (strain CIAT 652).	Putative phosphinothricin N-acetyltransferase (Antibiotic resistance) protein. EC=2.3.1.-.	185	2.3E-11	161	28.6
683	D8FQT1_LACDE	D8FQT1	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> PB2003/044-T3-4.	Acetyltransferase, GNAT family.	190	2.3E-11	184	31.5
684	Q1WU91_LACS1	Q1WU91	<i>Lactobacillus salivarius</i> (strain UCC118).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	198	2.4E-11	183	28.4
685	C2EEX5_9LACO	C2EEX5	<i>Lactobacillus salivarius</i> ATCC 11741.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	198	2.4E-11	183	28.4
686	E1JK26_9LACO	E1JK26	<i>Lactobacillus salivarius</i> ACS-116-V-Col5a.	Acetyltransferase, GNAT family.	198	2.4E-11	183	28.4
687	A5FG65_FLAJ1	A5FG65	<i>Flavobacterium johnsoniae</i> (strain ATCC 17061 / DSM 2064 / UW101) (<i>Cytophaga johnsonae</i>).	GCN5-related N-acetyltransferase.	165	2.5E-11	161	30.4

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
688	E2NI37_9BACE	E2NI37	<i>Bacteroides cellulosilyticus</i> DSM 14838.	Putative uncharacterized protein.	170	2.5E-11	170	30.6
689	E0MMT7_9RHOB	E0MMT7	<i>Ahrensia</i> sp. R2A130.	Toxin-antitoxin system, toxin component, gnat family.	171	2.5E-11	161	32.9
690	G7TJI0_9XANT	G7TJI0	<i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> BLS256.	N-acetyltransferase.	173	2.6E-11	162	31.5
691	Q3BSN0_XANC5	Q3BSN0	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> (strain 85-10).	Putative phosphinothricin N-acetyltransferase.	179	2.6E-11	176	30.7
692	F1CYM6_9BACT	F1CYM6	bacterium enrichment culture clone P69-9E.	GCN5-related N-acetyltransferase.	184	2.7E-11	172	30.2
693	A7VT25_9CLOT	A7VT25	<i>Clostridium leptum</i> DSM 753.	Putative uncharacterized protein.	189	2.8E-11	164	28.7
694	D8IKN9_LACSC	D8IKN9	<i>Lactobacillus salivarius</i> (strain CECT 5713).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	195	2.8E-11	183	28.4
695	F3S176_VIBPA	F3S176	<i>Vibrio parahaemolyticus</i> 10329.	Toxin resistance protein.	169	3E-11	166	31.3
696	B5SK57_RALSL	B5SK57	<i>Ralstonia solanacearum</i> IPO1609.	Antibiotic resistance (Acetyltransferase) protein. EC=2.3.1.-.	182	3.2E-11	165	33.3
697	A3RQX7_RALSL	A3RQX7	<i>Ralstonia solanacearum</i> UW551.	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	182	3.2E-11	165	33.3
698	G2ISE1_9SPHN	G2ISE1	<i>Sphingobium</i> sp. SYK-6.	Putative acetyltransferase. EC=2.3.1.-.	186	3.2E-11	178	31.5
699	F3ZXV0_MAHA5	F3ZXV0	<i>Mahella australiensis</i> (strain DSM 15567 / CIP 107919 / 50-1 BON).	Phosphinothricin acetyltransferase.	170	3.5E-11	162	29.0
700	G4RBP9_9RHIZ	G4RBP9	<i>Pelagibacterium halotolerans</i> B2.	GCN5-related N-acetyltransferase.	172	3.6E-11	172	31.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
701	B4U4D0_STREM	B4U4D0	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> (strain MGCS10565).	Phosphinothricin N-acetyltransferase.	225	3.7E-11	177	32.8
702	F0K2L3_LACD2	F0K2L3	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> (strain 2038).	Phosphinothricin acetyltransferase.	190	3.9E-11	184	31.5
703	F3S1A1_VIBPA	F3S1A1	<i>Vibrio parahaemolyticus</i> 10329.	Toxin resistance protein.	157	3.9E-11	152	33.6
704	Q2YW81_STAAB	Q2YW81	<i>Staphylococcus aureus</i> (strain bovine RF122 / ET3-1).	Probable phosphinothricin N-acetyltransferase. EC=2.3.1.-.	163	4E-11	163	30.7
705	O68850_VIBCH	O68850	<i>Vibrio cholerae</i> .	Putative uncharacterized protein.	169	4.1E-11	152	32.9
706	D0H4L7_VIBCH	D0H4L7	<i>Vibrio cholerae</i> RC27.	Toxin resistance protein.	169	4.1E-11	152	32.9
707	A5EZ11_VIBC3	A5EZ11	<i>Vibrio cholerae</i> serotype O1 (strain ATCC 39541 / Ogawa 395 / O395).	GCN5-related N-acetyltransferase. Toxin resistance protein.	169	4.1E-11	152	32.9
708	A6VSK0_MARMS	A6VSK0	<i>Marinomonas</i> sp. (strain MWYL1).	GCN5-related N-acetyltransferase.	170	4.2E-11	163	30.7
709	D8MSE4_ERWBE	D8MSE4	<i>Erwinia billingiae</i> (strain Eb661).	Phosphinothricin N-acetyltransferase.	174	4.2E-11	160	30.6
710	F0BTT8_9XANT	F0BTT8	<i>Xanthomonas perforans</i> 91-118.	Sortase-like acyltransferase.	179	4.3E-11	176	30.1
711	D4GI08_PANAM	D4GI08	<i>Pantoea ananatis</i> (strain LMG 20103).	Pat.	223	4.4E-11	161	31.1
712	B5RX66_RALSL	B5RX66	<i>Ralstonia solanacearum</i> (<i>Pseudomonas solanacearum</i>).	Antibiotic resistance (Acetyltransferase) protein. EC=2.3.1.-.	182	4.4E-11	163	32.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
713	D2TRF5_CITRI	D2TRF5	<i>Citrobacter rodentium</i> (strain ICC168) (<i>Citrobacter freundii</i> biotype 4280).	Putative acetyltransferase.	184	4.4E-11	172	30.8
714	Q6ADC6_LEIXX	Q6ADC6	<i>Leifsonia xyli</i> subsp. <i>xyli</i> (strain CTCB07).	Phosphinothricin acetyltransferase protein.	192	4.6E-11	163	31.9
715	C6LEY9_9FIRM	C6LEY9	<i>Marvinbryantia formatexigens</i> DSM 14469.	Phosphinothricin N-acetyltransferase.	199	4.7E-11	181	30.9
716	C4W785_STAWA	C4W785	<i>Staphylococcus warneri</i> L37603.	Phosphinothricin acetyltransferase.	167	4.8E-11	162	28.4
717	A6VSJ6_MARMS	A6VSJ6	<i>Marinomonas</i> sp. (strain MWYL1).	GCN5-related N-acetyltransferase.	167	4.8E-11	162	30.9
718	D4KEP4_9FIRM	D4KEP4	<i>Megamonas hypermegale</i> ART12/1.	Sortase and related acyltransferases. EC=2.3.1.-.	168	4.9E-11	157	25.5
719	F2ZNT7_9PSED	F2ZNT7	<i>Pseudomonas syringae</i> pv. <i>oryzae</i> str. 1_6.	Phosphinothricin N-acetyltransferase.	209	4.9E-11	178	31.5
720	Q8PK72_XANAC	Q8PK72	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> (Citrus canker).	Phosphinothricin N-acetyltransferase.	179	5.1E-11	172	32.0
721	G8AFS7_AZOBR	G8AFS7	<i>Azospirillum brasilense</i> Sp245.	Phosphinothricin acetyltransferase (PPT N-acetyltransferase). EC=2.3.1.-.	187	5.3E-11	185	29.7
722	E4KPT3_9LACT	E4KPT3	<i>Eremococcus coleocola</i> ACS-139-V-Col8.	Acetyltransferase, GNAT family.	195	5.5E-11	182	29.1
723	G5JUC3_9STRE	G5JUC3	<i>Streptococcus macacae</i> NCTC 11558.	Acetyltransferase, GNAT family.	161	5.5E-11	159	27.7
724	F7QY71_9LACO	F7QY71	<i>Lactobacillus ruminis</i> SPM0211.	Putative Phosphinothricin acetyltransferase.	202	5.6E-11	183	27.9
725	F9AAH0_VIBCH	F9AAH0	<i>Vibrio cholerae</i> HE-09.	Acetyltransferase family protein.	169	5.8E-11	152	32.9
726	E6WKX1_PANSA	E6WKX1	<i>Pantoea</i> sp. (strain At-9b).	Phosphinothricin acetyltransferase.	171	5.8E-11	161	29.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
727	E6UZQ2_VARPE	E6UZQ2	<i>Variovorax paradoxus</i> (strain EPS).	Phosphinothricin acetyltransferase.	173	5.9E-11	161	33.5
728	A8IE06_AZOC5	A8IE06	<i>Azorhizobium caulinodans</i> (strain ATCC 43989 / DSM 5975 / ORS 571).	Acetyltransferase.	181	6.1E-11	178	31.5
729	D6DRI5_ENTCL	D6DRI5	<i>Enterobacter cloacae</i> .	Sortase and related acyltransferases. EC=2.3.1.-.	184	6.2E-11	177	30.5
730	D2NAB1_STAA5	D2NAB1	<i>Staphylococcus aureus</i> (strain MRSA ST398 / isolate S0385).	Hypothetical acetyltransferase YncA. EC=2.3.1.-.	163	6.6E-11	161	31.1
731	D9RDV4_STAAJ	D9RDV4	<i>Staphylococcus aureus</i> (strain JKD6159).	Acetyltransferase, GNAT family.	163	6.6E-11	161	30.4
732	D7HHL0_VIBCH	D7HHL0	<i>Vibrio cholerae</i> RC385.	Toxin resistance protein.	169	6.8E-11	152	34.2
733	Q1VCE5_VIBAL	Q1VCE5	<i>Vibrio alginolyticus</i> 12G01.	Toxin resistance protein.	169	6.8E-11	166	30.7
734	C5CSM5_VARPS	C5CSM5	<i>Variovorax paradoxus</i> (strain S110).	Phosphinothricin acetyltransferase. EC=2.3.1.183.	174	7E-11	159	32.7
735	B8H2P5_CAUCN	B8H2P5	<i>Caulobacter crescentus</i> (strain NA1000 / CB15N).	Phosphinothricin N-acetyltransferase. EC=2.3.1.-.	183	7.3E-11	174	32.2
736	F9PKA4_9ACTO	F9PKA4	<i>Actinomyces</i> sp. oral taxon 175 str. F0384.	FR47-like protein.	427	7.5E-11	169	33.7
737	Q1GA17_LACDA	Q1GA17	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> (strain ATCC 11842 / DSM 20081).	Acyltransferase. EC=2.3.1.-.	190	7.5E-11	184	31.0
738	G6F601_LACDE	G6F601	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> CNCM I-1519.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	190	7.5E-11	184	31.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
739	D2ZEL7_ENTR	D2ZEL7	<i>Enterobacter cancerogenus</i> ATCC 35316.	Toxin-antitoxin system, toxin component, GNAT family.	191	7.5E-11	172	30.2
740	A9W1E1_METEP	A9W1E1	<i>Methylobacterium extorquens</i> (strain PA1).	GCN5-related N-acetyltransferase.	191	7.5E-11	171	31.0
741	F3QUI7_9BACT	F3QUI7	<i>Paraprevotella xylaniphila</i> YIT 11841.	Putative phosphinothricin N-acetyltransferase.	162	7.8E-11	156	33.3
742	B1CA93_9FIRM	B1CA93	<i>Anaerofustis stercorihominis</i> DSM 17244.	Putative uncharacterized protein.	199	7.8E-11	178	25.3
743	F9KAX0_STAAU	F9KAX0	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 21235.	Toxin-antitoxin system, toxin component, GNAT family.	163	7.8E-11	161	30.4
744	F3A3E5_9BACL	F3A3E5	<i>Gemella haemolysans</i> M341.	Putative uncharacterized protein.	167	8E-11	160	26.9
745	C2JCJ8_VIBCH	C2JCJ8	<i>Vibrio cholerae</i> BX 330286.	Toxin resistance protein.	169	8E-11	152	32.9
746	A3GK98_VIBCH	A3GK98	<i>Vibrio cholerae</i> NCTC 8457.	Toxin resistance protein.	169	8E-11	152	32.9
747	C6S031_VIBCH	C6S031	<i>Vibrio cholerae</i> CIRS101.	Phosphinothricin N-acetyltransferase.	169	8E-11	152	32.9
748	F8ZPM0_VIBCH	F8ZPM0	<i>Vibrio cholerae</i> HC-70A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
749	G7CAG6_VIBCH	G7CAG6	<i>Vibrio cholerae</i> HC-61A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
750	G7BDU6_VIBCH	G7BDU6	<i>Vibrio cholerae</i> HC-43A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
751	F8ZJZ0_VIBCH	F8ZJZ0	<i>Vibrio cholerae</i> HC-49A2.	Acetyltransferase family protein.	169	8E-11	152	32.9
752	G6ZWG9_VIBCH	G6ZWG9	<i>Vibrio cholerae</i> HC-22A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
753	F9A9X9_VIBCH	F9A9X9	<i>Vibrio cholerae</i> HCUF01.	Acetyltransferase family protein.	169	8E-11	152	32.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
754	G7B1P5_VIBCH	G7B1P5	<i>Vibrio cholerae</i> HC-32A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
755	D0HKQ4_VIBCH	D0HKQ4	<i>Vibrio cholerae</i> INDRE 91/1.	Phosphinothricin N-acetyltransferase.	169	8E-11	152	32.9
756	G6ZJD9_VIBCH	G6ZJD9	<i>Vibrio cholerae</i> HC-19A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
757	F9BF91_VIBCH	F9BF91	<i>Vibrio cholerae</i> HFU-02.	Acetyltransferase family protein.	169	8E-11	152	32.9
758	F8Z388_VIBCH	F8Z388	<i>Vibrio cholerae</i> HC-48A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
759	G7BQD1_VIBCH	G7BQD1	<i>Vibrio cholerae</i> HC-48B2.	Acetyltransferase family protein.	169	8E-11	152	32.9
760	A1F1Z9_VIBCH	A1F1Z9	<i>Vibrio cholerae</i> 2740-80.	Toxin resistance protein.	169	8E-11	152	32.9
761	G7AI37_VIBCH	G7AI37	<i>Vibrio cholerae</i> HC-28A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
762	A3GVS8_VIBCH	A3GVS8	<i>Vibrio cholerae</i> B33.	Toxin resistance protein.	169	8E-11	152	32.9
763	G6Z0C9_VIBCH	G6Z0C9	<i>Vibrio cholerae</i> HC-06A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
764	C3NXL6_VIBCJ	C3NXL6	<i>Vibrio cholerae</i> serotype O1 (strain MJ-1236).	Toxin resistance protein.	169	8E-11	152	32.9
765	G7BBC6_VIBCH	G7BBC6	<i>Vibrio cholerae</i> HC-33A2.	Acetyltransferase family protein.	169	8E-11	152	32.9
766	C2IDI3_VIBCH	C2IDI3	<i>Vibrio cholerae</i> RC9.	Toxin resistance protein.	169	8E-11	152	32.9
767	F9CBB9_VIBCH	F9CBB9	<i>Vibrio cholerae</i> HC-38A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
768	G7TWM3_VIBCH	G7TWM3	<i>Vibrio cholerae</i> O1 str. 2010EL-1786.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	169	8E-11	152	32.9
769	G7A7G1_VIBCH	G7A7G1	<i>Vibrio cholerae</i> HC-23A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
770	G6ZL38_VIBCH	G6ZL38	<i>Vibrio cholerae</i> HC-21A1.	Acetyltransferase family protein.	169	8E-11	152	32.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
771	F8YSP6_VIBCH	F8YSP6	<i>Vibrio cholerae</i> HC-40A1.	Acetyltransferase family protein.	169	8E-11	152	32.9
772	F3UXN0_STRSA	F3UXN0	<i>Streptococcus sanguinis</i> SK49.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	173	8.2E-11	135	34.1
773	F0B7M9_9XANT	F0B7M9	<i>Xanthomonas vesicatoria</i> ATCC 35937.	Sortase-like acyltransferase.	173	8.2E-11	158	30.4
774	D5CDR1_ENTCC	D5CDR1	<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> (strain ATCC 13047 / DSM 30054 / NBRC 13535 / NCDC 279-56).	Putative acetyltransferase.	176	8.3E-11	174	29.3
775	C5CRT8_VARPS	C5CRT8	<i>Variovorax paradoxus</i> (strain S110).	Phosphinothricin acetyltransferase. EC=2.3.1.183.	177	8.3E-11	160	33.8
776	G7TI97_9XANT	G7TI97	<i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> BLS256.	Phosphinothricin N-acetyltransferase.	179	8.4E-11	181	34.3
777	F0HTC8_LACDL	F0HTC8	<i>Lactobacillus delbrueckii</i> subsp. <i>lactis</i> DSM 20072.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	190	8.8E-11	184	31.0
778	G2EW37_9LACO	G2EW37	<i>Lactobacillus ruminis</i> ATCC 25644.	Sortase-like acyltransferase.	199	9.2E-11	183	27.9
779	E7FML5_9LACO	E7FML5	<i>Lactobacillus ruminis</i> ATCC 25644.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	202	9.3E-11	183	27.9
780	Q2KAU6_RHIEC	Q2KAU6	<i>Rhizobium etli</i> (strain CFN 42 / ATCC 51251).	Probable phosphinothricin acetyltransferase (Antibiotic resistance) protein.	171	9.6E-11	157	32.5
781	A9MQZ0_SALAR	A9MQZ0	<i>Salmonella arizonae</i> (strain ATCC BAA-731 / CDC346-86 / RSK2980).	Putative uncharacterized protein.	172	9.6E-11	172	33.7
782	G0CA47_XANCA	G0CA47	<i>Xanthomonas campestris</i> pv. <i>raphani</i> 756C.	Phosphinothricin acetyltransferase.	173	9.7E-11	162	31.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
783	F5Y3P7_RAMTT	F5Y3P7	<i>Ramlibacter tataouinensis</i> (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310).	Phosphinothricin N-acetyltransferase (Phosphinothricin-resistance protein)-like protein.	173	9.7E-11	160	32.5
784	Q9A9P1_CAUCR	Q9A9P1	<i>Caulobacter crescentus</i> (<i>Caulobacter vibrioides</i>).	Phosphinothricin N-acetyltransferase.	180	1E-10	172	32.0
785	E6LPM9_9FIRM	E6LPM9	<i>Eubacterium saburreum</i> DSM 3986.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	190	1E-10	164	27.4
786	E4SZU5_LACDN	E4SZU5	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> (strain ND02).	Sortase related acyltransferase.	194	1.1E-10	184	31.0
787	F3A6G7_9BACL	F3A6G7	<i>Gemella sanguinis</i> M325.	Putative uncharacterized protein.	162	1.1E-10	160	25.6
788	E4WEJ3_RHOE1	E4WEJ3	<i>Rhodococcus equi</i> (strain 103S) (<i>Corynebacterium equi</i>).	GNAT acetyltransferase.	162	1.1E-10	159	30.8
789	D3KZ23_PSECI	D3KZ23	<i>Pseudomonas cichorii</i> .	Phosphinothricin N-acetyltransferase.	199	1.1E-10	172	30.2
790	A1ZZP1_9BACT	A1ZZP1	<i>Microcilla marina</i> ATCC 23134.	Acetyltransferase, gnat family.	163	1.1E-10	162	29.6
791	F7S8U1_9PROT	F7S8U1	<i>Acidiphilium</i> sp. <i>PM</i> .	GCN5-related N-acetyltransferase. EC=2.3.1.183.	167	1.1E-10	161	32.3
792	A5FZR8_ACICJ	A5FZR8	<i>Acidiphilium cryptum</i> (strain JF-5).	GCN5-related N-acetyltransferase.	167	1.1E-10	161	32.3
793	F0J0C9_ACIMA	F0J0C9	<i>Acidiphilium multivorum</i> (strain DSM 11245 / JCM 8867 / AIU301).	Putative acetyltransferase.	167	1.1E-10	161	32.3
794	C0Q4P1_SALPC	C0Q4P1	<i>Salmonella paratyphi</i> C (strain RKS4594).	Putative acetyltransferase.	171	1.1E-10	168	33.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
795	F8JMX8_STREN	F8JMX8	<i>Streptomyces cattleya</i> (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057).	Phosphinothricin N-acetyltransferase. EC=2.3.1.183.	176	1.2E-10	159	30.8
796	Q4ZRN5_PSEU2	Q4ZRN5	<i>Pseudomonas syringae</i> pv. <i>syringae</i> (strain B728a).	GCN5-related N-acetyltransferase.	179	1.2E-10	160	31.9
797	F3EIJ7_PSESL	F3EIJ7	<i>Pseudomonas syringae</i> pv. <i>lachrymans</i> str. M301315.	Phosphinothricin N-acetyltransferase.	179	1.2E-10	159	32.7
798	D6JQ21_ACIG3	D6JQ21	<i>Acinetobacter</i> sp. SH024.	Putative uncharacterized protein.	181	1.2E-10	178	28.1
799	Q04A94_LACDB	Q04A94	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> (strain ATCC BAA-365).	Sortase related acyltransferase.	190	1.2E-10	184	31.0
800	B8ETE1_METSB	B8ETE1	<i>Methylocella silvestris</i> (strain BL2 / DSM 15510 / NCIMB 13906).	GCN5-related N-acetyltransferase.	195	1.3E-10	159	34.0
801	A4E9V0_9ACTN	A4E9V0	<i>Collinsella aerofaciens</i> ATCC 25986.	Putative uncharacterized protein.	196	1.3E-10	187	28.3
802	G2SNI2_LACRR	G2SNI2	<i>Lactobacillus ruminis</i> (strain ATCC 27782 / RF3).	Sortase-like acyltransferase.	202	1.3E-10	183	27.9
803	D1AJ73_SEBTE	D1AJ73	<i>Sebaldella termitidis</i> (strain ATCC 33386 / NCTC 11300).	Phosphinothricin acetyltransferase.	165	1.3E-10	156	28.8
804	G4D3G7_9FIRM	G4D3G7	<i>Peptoniphilus indolicus</i> ATCC 29427.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	172	1.3E-10	166	27.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
805	F0Q949_ACIAP	F0Q949	<i>Acidovorax avenae</i> (strain ATCC 19860 / DSM 7227 / JCM 20985 / NCPPB 1011).	Phosphinothricin acetyltransferase.	173	1.3E-10	159	31.4
806	E4T556_PALPW	E4T556	<i>Paludibacter propionigenes</i> (strain DSM 17365 / JCM 13257 / WB4).	GCN5-related N-acetyltransferase.	175	1.4E-10	170	29.4
807	F3K0Y5_PSESZ	F3K0Y5	<i>Pseudomonas syringae</i> pv. <i>tabaci</i> ATCC 11528.	Phosphinothricin N-acetyltransferase.	179	1.4E-10	159	32.7
808	C4WGG6_9RHIZ	C4WGG6	<i>Ochrobactrum intermedium</i> LMG 3301.	Phosphinothricin N-acetyltransferase.	196	1.5E-10	182	31.3
809	F3SSI9_STAWA	F3SSI9	<i>Staphylococcus warneri</i> VCU121.	Toxin-antitoxin system, toxin component, GNAT family.	167	1.5E-10	162	28.4
810	F2AAX6_RHIET	F2AAX6	<i>Rhizobium etli</i> CNPAF512.	Putative phosphinothricin acetyltransferase (Antibiotic resistance) protein.	171	1.6E-10	170	32.4
811	Q4UQ24_XANC8	Q4UQ24	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain 8004).	Phosphinothricin acetyltransferase.	173	1.6E-10	164	31.7
812	Q8P4G9_XANCP	Q8P4G9	<i>Xanthomonas campestris</i> pv. <i>campestris</i> .	Phosphinothricin acetyltransferase.	173	1.6E-10	164	31.7
813	B0RWP8_XANCB	B0RWP8	<i>Xanthomonas campestris</i> pv. <i>campestris</i> (strain B100).	N-acetyltransferase. EC=2.3.1.-.	173	1.6E-10	164	31.7
814	B0CFD4_ACAM1	B0CFD4	<i>Acaryochloris marina</i> (strain MBIC 11017).	Acetyltransferase, putative.	175	1.6E-10	177	29.4
815	F3H6A7_PSESX	F3H6A7	<i>Pseudomonas syringae</i> Cit 7.	GCN5-related N-acetyltransferase.	179	1.6E-10	161	31.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
816	A9G3R6_SORC5	A9G3R6	<i>Sorangium cellulosum</i> (strain So ce56) (<i>Polyangium cellulosum</i> (strain So ce56)).	Putative acetyltransferase. EC=2.3.1.8.	333	1.6E-10	170	34.7
817	G0E3N0_ENTAK	G0E3N0	<i>Enterobacter aerogenes</i> (strain ATCC 13048 / DSM 30053 / JCM 1235 / KCTC 2190 / NBRC 13534 / NCIMB 10102 / NCTC 10006) (<i>Aerobacter aerogenes</i>).	Phosphinothricin acetyltransferase.	184	1.7E-10	172	30.2
818	D7AAN1_STAND	D7AAN1	<i>Starkeya novella</i> (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113).	Phosphinothricin acetyltransferase.	194	1.7E-10	182	30.2
819	B6VYN5_9BACE	B6VYN5	<i>Bacteroides dorei</i> DSM 17855.	Putative uncharacterized protein.	161	1.8E-10	161	29.8
820	C3Q436_9BACE	C3Q436	<i>Bacteroides</i> sp. 9_1_42FAA.	Putative uncharacterized protein.	161	1.8E-10	161	29.8
821	C3RC83_9BACE	C3RC83	<i>Bacteroides dorei</i> 5_1_36/D4.	Putative uncharacterized protein.	161	1.8E-10	161	29.8
822	D3KZ27_PSECI	D3KZ27	<i>Pseudomonas cichorii</i> .	Phosphinothricin N-acetyltransferase.	199	1.8E-10	173	31.2
823	C0Z502_BREBN	C0Z502	<i>Brevibacillus brevis</i> (strain 47 / JCM 6285 / NBRC 100599).	Putative phosphinothricin acetyltransferase.	163	1.8E-10	158	28.5
824	B7L282_METC4	B7L282	<i>Methylobacterium chloromethanicum</i> (strain CM4 / NCIMB 13688).	GCN5-related N-acetyltransferase.	204	1.8E-10	178	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
825	D3AZ83_POLPA	D3AZ83	<i>Polysphondylium pallidum</i> (Cellular slime mold).	Putative uncharacterized protein.	208	1.8E-10	163	28.8
826	Q2P3S8_XANOM	Q2P3S8	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain MAFF 311018).	Phosphinothricin N-acetyltransferase.	179	1.9E-10	176	30.7
827	Q5H0U2_XANOR	Q5H0U2	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> .	Phosphinothricin N-acetyltransferase.	179	1.9E-10	176	30.7
828	B2SLI3_XANOP	B2SLI3	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> (strain PXO99A).	Phosphinothricin N-acetyltransferase.	179	1.9E-10	176	30.7
829	B1SDG8_9STRE	B1SDG8	<i>Streptococcus infantarius</i> subsp. <i>infantarius</i> ATCC BAA-102.	Putative uncharacterized protein.	234	2E-10	188	27.7
830	F4LMC1_TREBD	F4LMC1	<i>Treponema brennaborensis</i> (strain DSM 12168 / CIP 105900 / DD5/3).	GCN5-related N-acetyltransferase.	195	2.1E-10	179	29.1
831	F7L9M9_BACOV	F7L9M9	<i>Bacteroides ovatus</i> 3_8_47FAA.	Putative uncharacterized protein.	162	2.1E-10	165	29.7
832	D3KZ24_PSECI	D3KZ24	<i>Pseudomonas cichorii</i> .	Phosphinothricin N-acetyltransferase.	199	2.1E-10	173	31.8
833	E7GQZ4_CLOSY	E7GQZ4	<i>Clostridium symbiosum</i> WAL-14163.	GNAT family Toxin-antitoxin system.	163	2.1E-10	160	30.0
834	E9SRQ1_CLOSY	E9SRQ1	<i>Clostridium symbiosum</i> WAL-14673.	Putative uncharacterized protein.	163	2.1E-10	160	30.0
835	B9DV26_STRU0	B9DV26	<i>Streptococcus uberis</i> (strain ATCC BAA-854 / 0140J).	Acetyltransferase (GNAT) family protein.	202	2.1E-10	164	29.3
836	B4CWF6_9BACT	B4CWF6	<i>Chthoniobacter flavus</i> Ellin428.	GCN5-related N-acetyltransferase.	168	2.2E-10	163	30.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
837	E8FY94_SALMO	E8FY94	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>IA_2010008283</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
838	F2FFW6_SALDU	F2FFW6	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Dublin</i> str. <i>SD3246</i> .	Putative acyltransferase.	171	2.2E-10	168	33.3
839	E7YID7_SALMO	E7YID7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>19N</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
840	E8E5E5_SALMO	E8E5E5	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>2009083312</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
841	E8BRF0_SALMO	E8BRF0	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>609460</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
842	E8CMD3_SALMO	E8CMD3	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>MB101509-0077</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
843	E7XAV3_SALMO	E7XAV3	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>531954</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
844	B5P042_SALET	B5P042	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Heidelberg</i> str. <i>SL486</i> .	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
845	E8CHS3_SALMO	E8CHS3	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>556152</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
846	B4T5X9_SALNS	B4T5X9	<i>Salmonella newport</i> (strain <i>SL254</i>).	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
847	B5BJB7_SALPK	B5BJB7	<i>Salmonella paratyphi A</i> (strain AKU_12601).	Putative acetyltransferase.	171	2.2E-10	168	33.3
848	G5SBS0_SALET	G5SBS0	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Wandsworth str. A4-580.	Acyl-CoA N-acyltransferaseeee.	171	2.2E-10	168	33.3
849	E7XUZ3_SALMO	E7XUZ3	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Montevideo str. OH_2009072675.	Putative acetyltransferase.	171	2.2E-10	168	33.3
850	G5NCW6_SALET	G5NCW6	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Inverness str. R8-3668.	Acyl-CoA N-acyltransferaseeee.	171	2.2E-10	168	33.3
851	E7ZZ87_SALMO	E7ZZ87	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Montevideo str. 366867.	Putative acetyltransferase.	171	2.2E-10	168	33.3
852	G5RVA4_SALET	G5RVA4	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Urbana str. R8-2977.	Acyl-CoA N-acyltransferaseeee.	171	2.2E-10	168	33.3
853	E7YVX3_SALMO	E7YVX3	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Montevideo str. 81038-01.	Putative acetyltransferase.	171	2.2E-10	168	33.3
854	B3YD53_SALET	B3YD53	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Kentucky str. CVM29188.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
855	E1WBS1_SALTS	E1WBS1	<i>Salmonella typhimurium</i> (strain SL1344).	Putative acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
856	B5F5T9_SALA4	B5F5T9	<i>Salmonella agona</i> (strain SL483).	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
857	E8APE7_SALMO	E8APE7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 446600.	Putative acetyltransferase.	171	2.2E-10	168	33.3
858	B4TW39_SALSV	B4TW39	<i>Salmonella schwarzengrund</i> (strain CVM19633).	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
859	B5QBG3_SALVI	B5QBG3	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Virchow</i> str. SL491.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
860	E8FDB4_SALMO	E8FDB4	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. IA_2010008282.	Putative acetyltransferase.	171	2.2E-10	168	33.3
861	E7ZQW7_SALMO	E7ZQW7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 414877.	Putative acetyltransferase.	171	2.2E-10	168	33.3
862	G7T1S9_SALGL	G7T1S9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Gallinarum</i> str. RKS5078.	Putative acetyltransferase.	171	2.2E-10	168	33.3
863	B4TIL3_SALHS	B4TIL3	<i>Salmonella heidelberg</i> (strain SL476).	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
864	E7ZC53_SALMO	E7ZC53	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. MD_MDA09249507.	Putative acetyltransferase.	171	2.2E-10	168	33.3
865	B5QTL2_SALEP	B5QTL2	<i>Salmonella enteritidis</i> PT4 (strain P125109).	Putative acetyltransferase. EC=2.3.1.-. Flags: Precursor.	171	2.2E-10	168	33.3
866	E7VAM8_SALMO	E7VAM8	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 315996572.	Putative acetyltransferase.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
867	E7XMZ7_SALMO	E7XMZ7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. NC_MB110209-0054.	Putative acetyltransferase.	171	2.2E-10	168	33.3
868	B5CAS0_SALET	B5CAS0	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Schwarzengrund</i> str. SL480.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
869	E7W9P7_SALMO	E7W9P7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 495297-4.	Putative acetyltransferase.	171	2.2E-10	168	33.3
870	B5NB81_SALET	B5NB81	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Javiana</i> str. GA_MM04042433.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
871	G5M3H1_SALET	G5M3H1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Gaminara</i> str. A4-567.	Acyl-CoA N-acyltransferaseeee.	171	2.2E-10	168	33.3
872	B5RA91_SALG2	B5RA91	<i>Salmonella gallinarum</i> (strain 287/91 / NCTC 13346).	Putative acetyltransferase. EC=2.3.1.-. Flags: Precursor.	171	2.2E-10	168	33.3
873	E8B8G3_SALMO	E8B8G3	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 556150-1.	Putative acetyltransferase.	171	2.2E-10	168	33.3
874	G5R005_SALSE	G5R005	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Senftenberg</i> str. A4-543.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3
875	E8F8I8_SALMO	E8F8I8	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. IA_2009159199.	Putative acetyltransferase.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
876	E8GTT1_SALMO	E8GTT1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>IA_2010008287</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
877	E7YD13_SALMO	E7YD13	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>CASC_09SCPH15965</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
878	B5NLE8_SALET	B5NLE8	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Kentucky</i> str. <i>CDC 191</i> .	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
879	E8DPA1_SALMO	E8DPA1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>MB111609-0052</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
880	B5MJB7_SALET	B5MJB7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Saintpaul</i> str. <i>SARA29</i> .	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
881	B5PPU9_SALHA	B5PPU9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Hadar</i> str. <i>RI_05P066</i> .	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
882	G5P929_SALET	G5P929	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Minnesota</i> str. <i>A4-603</i> .	Acyl-CoA N-acyltransferaseeee.	171	2.2E-10	168	33.3
883	E7UYP9_SALTY	E7UYP9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i> str. <i>TN061786</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
884	E8AY42_SALMO	E8AY42	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>609458-1</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
885	C9XHL9_SALTD	C9XHL9	<i>Salmonella typhimurium</i> (strain D23580).	Putative acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
886	G5QIW2_SALRU	G5QIW2	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Rubislaw</i> str. A4-653.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3
887	B3ZZV1_SALNE	B3ZZV1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Newport</i> str. SL317.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
888	B5N1N9_SALET	B5N1N9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar 4,[5],12:i:- str. CVM23701.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
889	Q5PHW1_SALPA	Q5PHW1	<i>Salmonella paratyphi</i> A.	Putative acetyltransferase.	171	2.2E-10	168	33.3
890	E7WGQ0_SALMO	E7WGQ0	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 515920-1.	Putative acetyltransferase.	171	2.2E-10	168	33.3
891	G5LNT9_SALET	G5LNT9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Alachua</i> str. R6-377.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3
892	E8GGU4_SALMO	E8GGU4	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. IA_2010008285.	Putative acetyltransferase.	171	2.2E-10	168	33.3
893	F2FXM9_SALGL	F2FXM9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Gallinarum</i> str. SG9.	Putative acyltransferase.	171	2.2E-10	168	33.3
894	G5NU65_SALET	G5NU65	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Johannesburg</i> str. S5-703.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
895	G4C4U6_SALIN	G4C4U6	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Infantis</i> str. SARB27.	Toxin-antitoxin system, toxin component, GNAT family.	171	2.2E-10	168	33.3
896	E8EI58_SALMO	E8EI58	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 2009085258.	Putative acetyltransferase.	171	2.2E-10	168	33.3
897	E8AEI6_SALMO	E8AEI6	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 413180.	Putative acetyltransferase.	171	2.2E-10	168	33.3
898	E8G8S5_SALMO	E8G8S5	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. IA_2010008284.	Putative acetyltransferase.	171	2.2E-10	168	33.3
899	E8D8X6_SALMO	E8D8X6	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. MB102109-0047.	Putative acetyltransferase.	171	2.2E-10	168	33.3
900	D0ZXS8_SALT1	D0ZXS8	<i>Salmonella typhimurium</i> (strain 14028s / SGSC 2262).	Putative acyltransferase.	171	2.2E-10	168	33.3
901	E7WUZ5_SALMO	E7WUZ5	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 515920-2.	Putative acetyltransferase.	171	2.2E-10	168	33.3
902	E7W1X7_SALMO	E7W1X7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 495297-3.	Putative acetyltransferase.	171	2.2E-10	168	33.3
903	E8XJ38_SALT4	E8XJ38	<i>Salmonella typhimurium</i> (strain 4/74).	Putative acyltransferase.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
904	E8ESP0_SALMO	E8ESP0	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. 315731156.	Putative acetyltransferase.	171	2.2E-10	168	33.3
905	B5FHH2_SALDC	B5FHH2	<i>Salmonella dublin</i> (strain CT_02021853).	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
906	B5C0Z9_SALET	B5C0Z9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Saintpaul</i> str. SARA23.	Phosphinothricin acetyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3
907	G5MSR9_SALET	G5MSR9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Hvittingfoss</i> str. A4-620.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3
908	G5MIB1_SALET	G5MIB1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Give</i> str. S5-487.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3
909	G5Q2M9_SALMO	G5Q2M9	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. S5-403.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3
910	G5PN11_SALET	G5PN11	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Mississippi</i> str. A4-633.	Acyl-CoA N-acyltransferaseeeee.	171	2.2E-10	168	33.3
911	E8DA84_SALMO	E8DA84	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. MB110209-0055.	Putative acetyltransferase.	171	2.2E-10	168	33.3
912	G5L924_SALET	G5L924	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Adelaide</i> str. A4-669.	Acyl-CoA N-acyltransferaseeee.	171	2.2E-10	168	33.3
913	Q8ZPD3_SALTY	Q8ZPD3	<i>Salmonella typhimurium</i> .	Putative acyltransferase. EC=2.3.1.-.	171	2.2E-10	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
914	G5RFI6_SALET	G5RFI6	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Uganda</i> str. <i>R8-3404</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
915	E8C6H1_SALMO	E8C6H1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>507440-20</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
916	F5ZQR0_SALTU	F5ZQR0	<i>Salmonella typhimurium</i> (strain <i>ATCC 68169 / UK-1</i>).	Putative acyltransferase.	171	2.2E-10	168	33.3
917	E7VMI7_SALMO	E7VMI7	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Montevideo</i> str. <i>495297-1</i> .	Putative acetyltransferase.	171	2.2E-10	168	33.3
918	F3J547_PSEAP	F3J547	<i>Pseudomonas syringae</i> pv. <i>aptata</i> str. <i>DSM 50252</i> .	GCN5-related N-acetyltransferase.	179	2.3E-10	160	31.9
919	F3G8J0_PSESJ	F3G8J0	<i>Pseudomonas syringae</i> pv. <i>pisi</i> str. <i>1704B</i> .	GCN5-related N-acetyltransferase.	179	2.3E-10	160	31.9
920	F9VXP7_9ACTO	F9VXP7	<i>Gordonia alkanivorans</i> <i>NBRC 16433</i> .	Putative acetyltransferase.	182	2.3E-10	171	29.8
921	Q39I61_BURS3	Q39I61	<i>Burkholderia</i> sp. (strain 383) (<i>Burkholderia cepacia</i> (strain <i>ATCC 17760 / NCIB 9086 / R18194</i>)).	GCN5-related N-acetyltransferase.	182	2.3E-10	178	32.0
922	B6FSI6_9CLOT	B6FSI6	<i>Clostridium nexile</i> <i>DSM 1787</i> .	Putative uncharacterized protein.	196	2.5E-10	166	30.7
923	D1K794_9BACE	D1K794	<i>Bacteroides</i> sp. <i>3_1_33FAA</i> .	Putative uncharacterized protein.	161	2.5E-10	161	29.2
924	D3KZ26_PSECI	D3KZ26	<i>Pseudomonas cichorii</i> .	Phosphinothricin N-acetyltransferase.	199	2.5E-10	173	31.2
925	C4FV52_9FIRM	C4FV52	<i>Catonella morbi</i> <i>ATCC 51271</i> .	Putative uncharacterized protein.	166	2.5E-10	161	26.7

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
926	B2UG85_RALPJ	B2UG85	<i>Ralstonia pickettii</i> (strain 12J).	GCN5-related N-acetyltransferase.	171	2.6E-10	170	34.1
927	Q57P68_SALCH	Q57P68	<i>Salmonella choleraesuis</i> .	Putative acyltransferase.	171	2.6E-10	168	33.3
928	D4MI16_9FIRM	D4MI16	<i>Eubacterium siraeum</i> V10Sc8a.	Sortase and related acyltransferases. EC=2.3.1.-.	172	2.6E-10	164	29.9
929	F3JM56_PSESX	F3JM56	<i>Pseudomonas syringae</i> pv. <i>aceris</i> str. M302273PT.	GCN5-related N-acetyltransferase.	179	2.7E-10	160	31.2
930	Q48H90_PSE14	Q48H90	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> (strain 1448A / Race 6).	Phosphinothricin N-acetyltransferase.	179	2.7E-10	159	32.7
931	E7PQP6_PSESG	E7PQP6	<i>Pseudomonas syringae</i> pv. <i>glycinea</i> str. race 4.	Phosphinothricin N-acetyltransferase.	179	2.7E-10	159	32.7
932	D8NLL0_RALSL	D8NLL0	<i>Ralstonia solanacearum</i> (<i>Pseudomonas solanacearum</i>).	Putative antibiotic resistance protein (Acetyltransferase). EC=2.3.1.-.	182	2.7E-10	165	32.1
933	F2UZ87_ACTVI	F2UZ87	<i>Actinomyces viscosus</i> C505.	Acetyltransferase, GNAT family.	182	2.7E-10	167	31.1
934	F6G6V7_RALS8	F6G6V7	<i>Ralstonia solanacearum</i> (strain Po82).	Phosphinothricin n-acetyltransferase (Ppt n-acetyltransferase) (Phosphinothricin-resistance protein).	182	2.7E-10	165	31.5
935	C0MH67_STRS7	C0MH67	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> (strain H70).	Acetyltransferase (GNAT) family protein.	193	2.9E-10	177	32.2
936	F1TK23_COREQ	F1TK23	<i>Rhodococcus equi</i> ATCC 33707.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	162	2.9E-10	159	30.2
937	Q8NUS8_STAAW	Q8NUS8	<i>Staphylococcus aureus</i> (strain MW2).	MW2449 protein.	163	2.9E-10	161	29.8
938	E1E2K8_STAAU	E1E2K8	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> TCH70.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	163	2.9E-10	161	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
939	D6UFD4_STAAU	D6UFD4	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC 51811.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	163	2.9E-10	161	29.8
940	G0LQ14_STAAU	G0LQ14	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> LGA251.	Acetyltransferase (GNAT) family protein.	163	2.9E-10	161	29.8
941	Q6G6E6_STAAS	Q6G6E6	<i>Staphylococcus aureus</i> (strain MSSA476).	Acetyltransferase (GNAT) family protein.	163	2.9E-10	161	29.8
942	Q92Q01_RHIME	Q92Q01	<i>Rhizobium meliloti</i> (strain 1021) (<i>Ensifer meliloti</i>) (<i>Sinorhizobium meliloti</i>).	N-acetyltransferase. EC=2.3.1.-.	169	3E-10	171	31.0
943	F6DZT1_SINMK	F6DZT1	<i>Sinorhizobium meliloti</i> (strain AK83).	Phosphinothricin acetyltransferase.	169	3E-10	171	31.0
944	F6BNH1_SINMB	F6BNH1	<i>Sinorhizobium meliloti</i> (strain BL225C).	Phosphinothricin acetyltransferase.	169	3E-10	171	31.0
945	Q9KMG9_VIBCH	Q9KMG9	<i>Vibrio cholerae</i> .	Toxin resistance protein.	169	3E-10	152	32.2
946	F7X0S9_SINMM	F7X0S9	<i>Sinorhizobium meliloti</i> (strain SM11).	N-acetyltransferase. EC=2.3.1.-.	169	3E-10	171	31.0
947	E8NMD8_SALET	E8NMD8	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Choleraesuis</i> str. SCSA50.	Putative acyltransferase.	171	3.1E-10	168	33.3
948	C5CXJ0_VARPS	C5CXJ0	<i>Variovorax paradoxus</i> (strain S110).	GCN5-related N-acetyltransferase.	173	3.1E-10	166	32.5
949	D2UG15_XANAP	D2UG15	<i>Xanthomonas albilineans</i> (strain GPE PC73 / CFBP 7063).	Putative n-acetyltransferase protein.	173	3.1E-10	160	31.9
950	C9Y9Q4_9BURK	C9Y9Q4	<i>Curvibacter putative symbiont of Hydra magnipapillata</i> .	Phosphinothricin N-acetyltransferase. EC=2.3.1.183.	174	3.1E-10	173	28.3
951	E6V4J7_VARPE	E6V4J7	<i>Variovorax paradoxus</i> (strain EPS).	Phosphinothricin acetyltransferase.	174	3.1E-10	169	30.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
952	Q46QV7_CUPPJ	Q46QV7	<i>Cupriavidus pinatubonensis</i> (strain JMP134 / LMG 1197) (<i>Alcaligenes eutrophus</i>) (<i>Ralstonia eutropha</i>).	GCN5-related N-acetyltransferase.	175	3.1E-10	173	34.1
953	F5Y1P3_RAMTT	F5Y1P3	<i>Ramlibacter tataouinensis</i> (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310).	Candidate antibiotic resistance protein (Acetyltransferase).	177	3.2E-10	159	31.4
954	D7I1A3_PSESS	D7I1A3	<i>Pseudomonas savastanoi</i> pv. <i>savastanoi</i> NCPPB 3335.	GCN5-related N-acetyltransferase.	179	3.2E-10	159	32.1
955	F3EWN0_9PSED	F3EWN0	<i>Pseudomonas syringae</i> pv. <i>mori</i> str. 301020.	Phosphinothricin N-acetyltransferase.	179	3.2E-10	159	32.1
956	F3DB99_9PSED	F3DB99	<i>Pseudomonas syringae</i> pv. <i>aesculi</i> str. 0893_23.	Phosphinothricin N-acetyltransferase.	179	3.2E-10	159	32.1
957	B3QDV6_RHOPT	B3QDV6	<i>Rhodopseudomonas palustris</i> (strain TIE-1).	GCN5-related N-acetyltransferase.	180	3.2E-10	176	30.7
958	Q07LT3_RHOP5	Q07LT3	<i>Rhodopseudomonas palustris</i> (strain BisA53).	GCN5-related N-acetyltransferase.	180	3.2E-10	174	32.2
959	C8LAN0_STAAU	C8LAN0	<i>Staphylococcus aureus</i> A5948.	Acetyltransferase.	163	3.5E-10	161	29.8
960	E7MYV4_STAAU	E7MYV4	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MRSA131.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
961	A8Z3C4_STAAT	A8Z3C4	<i>Staphylococcus aureus</i> (strain USA300 / TCH1516).	Acetyltransferase. EC=2.3.1.-.	163	3.5E-10	161	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
962	F0DCM6_STAAU	F0DCM6	<i>Staphylococcus aureus</i> O46.	Phosphinothricin N-acetyltransferase.	163	3.5E-10	161	29.8
963	F3T427_STAAU	F3T427	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 21189.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
964	C8A9A5_STAAU	C8A9A5	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 68-397.	Acetyltransferase.	163	3.5E-10	161	29.8
965	F5W3D0_STAAU	F5W3D0	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 21305.	FR47-like protein.	163	3.5E-10	161	29.8
966	E0P4Z2_STAAU	E0P4Z2	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ATCC BAA-39.	Phosphinothricin acetyltransferase. EC=2.3.1.183.	163	3.5E-10	161	29.8
967	Q5HD24_STAAC	Q5HD24	<i>Staphylococcus aureus</i> (strain COL).	Acetyltransferase, GNAT family.	163	3.5E-10	161	29.8
968	D6M128_STAAU	D6M128	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> EMRSA16.	Acetyltransferase.	163	3.5E-10	161	29.8
969	D9RJF5_STAAK	D9RJF5	<i>Staphylococcus aureus</i> (strain JKD6008).	Acetyltransferase, GNAT family.	163	3.5E-10	161	29.8
970	D2GM12_STAAU	D2GM12	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> C160.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
971	G7ZSR2_STAAU	G7ZSR2	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MSHR1132.	Acetyltransferase, GNAT family protein.	163	3.5E-10	161	29.8
972	Q6GDR9_STAAR	Q6GDR9	<i>Staphylococcus aureus</i> (strain MRSA252).	Acetyltransferase (GNAT) family protein.	163	3.5E-10	161	29.8
973	D2G4B0_STAAU	D2G4B0	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> WBG10049.	Acetyltransferase family protein.	163	3.5E-10	161	29.8
974	D4U7C5_STAAU	D4U7C5	<i>Staphylococcus aureus</i> A9754.	Acetyltransferase.	163	3.5E-10	161	29.8
975	E5QWG5_STAAH	E5QWG5	<i>Staphylococcus aureus</i> (strain TCH60).	Phosphinothricin acetyltransferase. EC=2.3.1.183.	163	3.5E-10	161	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
976	D2GKD9_STAAU	D2GKD9	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> Btn1260.	Acetyltransferase GNAT family protein.	163	3.5E-10	161	29.8
977	F9JQY5_STAAU	F9JQY5	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 21195.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
978	D6H4Q7_STAAU	D6H4Q7	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> M1015.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
979	D2GCS4_STAAU	D2GCS4	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> WW2703/97.	Acetyltransferase family protein.	163	3.5E-10	161	29.8
980	F3TL72_STAAU	F3TL72	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 21193.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
981	Q2FDX6_STAA3	Q2FDX6	<i>Staphylococcus aureus</i> (strain USA300).	Acetyltransferase, GNAT family. EC=2.3.1.-.	163	3.5E-10	161	29.8
982	C8A0A7_STAAU	C8A0A7	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> 65-1322.	Acetyltransferase family protein.	163	3.5E-10	161	29.8
983	D6J3H2_STAAU	D6J3H2	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> M809.	Acetyltransferase.	163	3.5E-10	161	29.8
984	C5N078_STAA3	C5N078	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> USA300_TCH959.	Possible Phosphinothricin acetyltransferase. EC=2.3.1.183.	163	3.5E-10	161	29.8
985	D2UV94_STAAU	D2UV94	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> A017934/97.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
986	D2FYM4_STAAU	D2FYM4	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> M899.	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
987	E5TC52_STAAU	E5TC52	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> CGS00.	Acetyltransferase (GNAT) family protein.	163	3.5E-10	161	29.8
988	G5FCM2_9CLOT	G5FCM2	<i>Clostridium</i> sp. 7_3_54FAA.	Putative uncharacterized protein.	163	3.5E-10	160	29.4
989	C8AF70_STAAU	C8AF70	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> E1410.	Acetyltransferase.	163	3.5E-10	161	29.8

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
990	D6HCL8_STAAU	D6HCL8	<i>Staphylococcus aureus subsp. aureus 58-424.</i>	Acetyltransferase (GNAT) family protein.	163	3.5E-10	161	29.8
991	D6SC45_STAAU	D6SC45	<i>Staphylococcus aureus subsp. aureus MN8.</i>	Phosphinothricin acetyltransferase. EC=2.3.1.183.	163	3.5E-10	161	29.8
992	C8ANI9_STAAU	C8ANI9	<i>Staphylococcus aureus subsp. aureus M876.</i>	Acetyltransferase.	163	3.5E-10	161	29.8
993	F9KNU1_STAAU	F9KNU1	<i>Staphylococcus aureus subsp. aureus 21266.</i>	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
994	C7ZSM2_STAAU	C7ZSM2	<i>Staphylococcus aureus subsp. aureus 55/2053.</i>	Acetyltransferase family protein.	163	3.5E-10	161	29.8
995	A6QK17_STAAE	A6QK17	<i>Staphylococcus aureus (strain Newman).</i>	Acetyltransferase, GNAT family protein.	163	3.5E-10	161	29.8
996	C8KMT0_STAAU	C8KMT0	<i>Staphylococcus aureus 930918-3.</i>	Putative uncharacterized protein.	163	3.5E-10	161	29.8
997	F4FLD9_STAAU	F4FLD9	<i>Staphylococcus aureus subsp. aureus T0131.</i>	Acetyltransferase, GNAT family protein.	163	3.5E-10	161	29.8
998	D2FA91_STAAU	D2FA91	<i>Staphylococcus aureus subsp. aureus C101.</i>	Acetyltransferase.	163	3.5E-10	161	29.8
999	E7MCT8_STAAU	E7MCT8	<i>Staphylococcus aureus subsp. aureus MRSA177.</i>	Toxin-antitoxin system, toxin component, GNAT family.	163	3.5E-10	161	29.8
1000	D2FGM6_STAAU	D2FGM6	<i>Staphylococcus aureus subsp. aureus C427.</i>	Acetyltransferase.	163	3.5E-10	161	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

6.3. Table 3 - PDB database

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
1	3DR6_B	3DR6_B	<i>Salmonella typhimurium</i>	Structure of ynca, a putative acetyltransferase from <i>Salmonella typhimurium</i>	174	1.1E-10	168	33.3
2	3DR6_A	3DR6_A	<i>Salmonella typhimurium</i>	Structure of ynca, a putative acetyltransferase from <i>Salmonella typhimurium</i>	174	1.1E-10	168	33.3
3	3DR8_A	3DR8_A	<i>Salmonella typhimurium</i>	Structure of ynca, a putative acetyltransferase from <i>Salmonella typhimurium</i> with its cofactor acetyl-coa	174	1.1E-10	168	33.3
4	3DR6_C	3DR6_C	<i>Salmonella typhimurium</i>	Structure of ynca, a putative acetyltransferase from <i>Salmonella typhimurium</i>	174	1.1E-10	168	33.3
5	3DR8_B	3DR8_B	<i>Salmonella typhimurium</i>	Structure of ynca, a putative acetyltransferase from <i>Salmonella typhimurium</i> with its cofactor acetyl-coa	174	1.1E-10	168	33.3
6	2J8M_A	2J8M_A	<i>Pseudomonas aeruginosa</i>	Structure of P. aeruginosa acetyltransferase pa4866	172	1.1E-9	172	30.8
7	2J8R_A	2J8R_A	<i>Pseudomonas aeruginosa</i>	Structure of P. aeruginosa acetyltransferase pa4866 solved in complex with l-methionine sulfoximine	172	1.1E-9	172	30.8
8	2J8N_A	2J8N_A	<i>Pseudomonas aeruginosa</i>	Structure of P. aeruginosa acetyltransferase pa4866 solved at room temperature	172	1.1E-9	172	30.8
9	2J8M_B	2J8M_B	<i>Pseudomonas aeruginosa</i>	Structure of P. aeruginosa acetyltransferase pa4866	172	1.1E-9	172	30.8
10	2J8N_B	2J8N_B	<i>Pseudomonas aeruginosa</i>	Structure of P. aeruginosa acetyltransferase pa4866 solved at room temperature	172	1.1E-9	172	30.8
11	2J8R_B	2J8R_B	<i>Pseudomonas aeruginosa</i>	Structure of P. aeruginosa acetyltransferase pa4866 solved in complex with l-methionine sulfoximine	172	1.1E-9	172	30.8
12	1YVO_A	1YVO_A	<i>Pseudomonas aeruginosa</i>	Hypothetical acetyltransferase from p.aeruginosa pa01	172	3.8E-9	172	30.8
13	1YVO_B	1YVO_B	<i>Pseudomonas aeruginosa</i>	Hypothetical acetyltransferase from p.aeruginosa pa01	172	3.8E-9	172	30.8
14	2BL1_A	2BL1_A	<i>Pseudomonas aeruginosa</i>	Crystal structure of a putative phosphinothricin acetyltransferase (pa4866) from pseudomonas aeruginosa pac1	172	3.8E-9	172	30.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
15	2JLM_C	2JLM_C	<i>Acinetobacter baylyi</i>	Structure of a putative acetyltransferase (aciad1637) from <i>Acinetobacter baylyi</i> adp1	182	4.7E-9	160	28.1
16	2JLM_E	2JLM_E	<i>Acinetobacter baylyi</i>	Structure of a putative acetyltransferase (aciad1637) from <i>Acinetobacter baylyi</i> adp1	182	4.7E-9	160	28.1
17	2JLM_D	2JLM_D	<i>Acinetobacter baylyi</i>	Structure of a putative acetyltransferase (aciad1637) from <i>Acinetobacter baylyi</i> adp1	182	4.7E-9	160	28.1
18	2JLM_A	2JLM_A	<i>Acinetobacter baylyi</i>	Structure of a putative acetyltransferase (aciad1637) from <i>Acinetobacter baylyi</i> adp1	182	4.7E-9	160	28.1
19	2JLM_B	2JLM_B	<i>Acinetobacter baylyi</i>	Structure of a putative acetyltransferase (aciad1637) from <i>Acinetobacter baylyi</i> adp1	182	4.7E-9	160	28.1
20	2JLM_F	2JLM_F	<i>Acinetobacter baylyi</i>	Structure of a putative acetyltransferase (aciad1637) from <i>Acinetobacter baylyi</i> adp1	182	4.7E-9	160	28.1
21	1YR0_D	1YR0_D	<i>Agrobacterium tumefaciens str.</i>	Crystal structure of phosphinothricin acetyltransferase from <i>Agrobacterium tumefaciens</i>	175	8.5E-8	158	27.8
22	1YR0_C	1YR0_C	<i>Agrobacterium tumefaciens str.</i>	Crystal structure of phosphinothricin acetyltransferase from <i>Agrobacterium tumefaciens</i>	175	8.5E-8	158	27.8
23	1YR0_B	1YR0_B	<i>Agrobacterium tumefaciens str.</i>	Crystal structure of phosphinothricin acetyltransferase from <i>Agrobacterium tumefaciens</i>	175	8.5E-8	158	27.8
24	1YR0_A	1YR0_A	<i>Agrobacterium tumefaciens str.</i>	Crystal structure of phosphinothricin acetyltransferase from <i>Agrobacterium tumefaciens</i>	175	8.5E-8	158	27.8
25	1VHS_B	1VHS_B	<i>Bacillus subtilis</i>	Crystal structure of a putative phosphinothricin n-acetyltransferase	175	0.00014	161	26.1
26	1VHS_A	1VHS_A	<i>Bacillus subtilis</i>	Crystal structure of a putative phosphinothricin n-acetyltransferase	175	0.00014	161	26.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

6.4. Table 4 - DAD database

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
1	CAA46314.1	X65195-21	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes phosphinothricin acetyl transferase protein.	183	4.5E-77	183	94.5
2	AAA72709.1	M22827-2	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes phosphinothricin-N-acetyltransferase protein.	183	4.5E-77	183	94.5
3	AAU00088.1	AY632421-19	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes phosphinothricin N-acetyltransferase protein.	183	4.5E-77	183	94.5
4	EFL30511.1	GG657757-1029	<i>Streptomyces viridochromogenes DSM 40736</i>	Streptomyces viridochromogenes DSM 40736 phosphinothricin- N-acetyltransferase protein.	183	4.5E-77	183	94.5
5	AAA72709.1	M22827-2	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes phosphinothricin-N-acetyltransferase protein.	183	4.5E-77	183	94.5
6	AAU00088.1	AY632421-19	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes phosphinothricin N-acetyltransferase protein.	183	4.5E-77	183	94.5
7	CAA46314.1	X65195-21	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes phosphinothricin acetyl transferase protein.	183	4.5E-77	183	94.5
8	CAA29262.1	X05822-1	<i>Streptomyces hygroscopicus</i>	Streptomyces hygroscopicus protein (Streptomyces hygroscopicus bar gene conferring resistance to herbicide bialaphos.).	183	8.8E-65	183	80.3
9	CAA29262.1	X05822-1	<i>Streptomyces hygroscopicus</i>	Streptomyces hygroscopicus protein (Streptomyces hygroscopicus bar gene conferring resistance to herbicide bialaphos.).	183	8.8E-65	183	80.3
10	CAA35093.1	X17220-1	<i>Streptomyces hygroscopicus</i>	Streptomyces hygroscopicus protein (Streptomyces hygroscopicus bar gene for phosphinothricin acetyl).	183	8.8E-65	183	80.3
11	CAA35093.1	X17220-1	<i>Streptomyces hygroscopicus</i>	Streptomyces hygroscopicus protein (Streptomyces hygroscopicus bar gene for phosphinothricin acetyl).	183	8.8E-65	183	80.3
12	ABP52567.1	CP000667-82	<i>Salinispora tropica CNB-440</i>	Salinispora tropica CNB-440 GCN5-related N-acetyltransferase protein.	192	2E-35	178	51.1
13	ABP52567.1	CP000667-82	<i>Salinispora tropica CNB-440</i>	Salinispora tropica CNB-440 GCN5-related N-acetyltransferase protein.	192	2E-35	178	51.1

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
14	AAV36550.1	CP000075-1499	<i>Pseudomonas syringae pv</i>	Pseudomonas syringae pv. syringae B728a GCN5-related N-acetyltransferase protein.	184	2.3E-24	174	38.5
15	AAV36550.1	CP000075-1499	<i>Pseudomonas syringae pv</i>	Pseudomonas syringae pv. syringae B728a GCN5-related N-acetyltransferase protein.	184	2.3E-24	174	38.5
16	BAC90467.1	BA000045-2526	<i>Gloeobacter violaceus PCC 7421</i>	Gloeobacter violaceus PCC 7421 phosphinothricin N-acetyltransferase protein.	212	1.3E-23	170	41.8
17	BAC90467.1	BA000045-2526	<i>Gloeobacter violaceus PCC 7421</i>	Gloeobacter violaceus PCC 7421 phosphinothricin N-acetyltransferase protein.	212	1.3E-23	170	41.8
18	CAI49626.1	CR936257-1528	<i>Natronomonas pharaonis DSM 2160</i>	Natronomonas pharaonis DSM 2160 probable N-acetyltransferase protein.	206	1.5E-23	177	40.7
19	CAI49626.1	CR936257-1528	<i>Natronomonas pharaonis DSM 2160</i>	Natronomonas pharaonis DSM 2160 probable N-acetyltransferase protein.	206	1.5E-23	177	40.7
20	ACY16899.1	CP001804-4257	<i>Haliangium ochraceum DSM 14365</i>	Haliangium ochraceum DSM 14365 Phosphinothricin acetyltransferase protein.	190	1.7E-23	179	39.1
21	ADJ64600.1	CP002039-3071	<i>Herbaspirillum seropedicae SmR1</i>	Herbaspirillum seropedicae SmR1 phosphinothricin N-acetyltransferase (sortase) protein.	167	5.7E-23	156	41.0
22	ADJ64600.1	CP002039-3071	<i>Herbaspirillum seropedicae SmR1</i>	Herbaspirillum seropedicae SmR1 phosphinothricin N-acetyltransferase (sortase) protein.	167	5.7E-23	156	41.0
23	ABQ66891.1	CP000699-518	<i>Sphingomonas wittichii RW1</i>	Sphingomonas wittichii RW1 GCN5-related N-acetyltransferase protein.	182	6.2E-23	177	39.5
24	ABQ66891.1	CP000699-518	<i>Sphingomonas wittichii RW1</i>	Sphingomonas wittichii RW1 GCN5-related N-acetyltransferase protein.	182	6.2E-23	177	39.5
25	ADD05387.1	CP001932-1787	<i>Natrialba magadii ATCC 43099</i>	Natrialba magadii ATCC 43099 Phosphinothricin acetyltransferase protein.	198	9.2E-23	176	39.8
26	EBG61073.1	EP175263-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	177	2.3E-22	174	38.5
27	ACV11309.1	CP001687-1119	<i>Halorhabdus utahensis DSM 12940</i>	Halorhabdus utahensis DSM 12940 GCN5-related N-acetyltransferase protein.	200	2.5E-22	173	38.7
28	AEA23167.1	CP002593-882	<i>Pseudonocardia dioxanivorans CB1190</i>	Pseudonocardia dioxanivorans CB1190 Phosphinothricin acetyltransferase se protein.	193	2.5E-21	175	40.0
29	AEA23167.1	CP002593-882	<i>Pseudonocardia dioxanivorans CB1190</i>	Pseudonocardia dioxanivorans CB1190 Phosphinothricin acetyltransferase se protein.	193	2.5E-21	175	40.0
30	ABX06254.1	CP000875-3602	<i>Herpetosiphon aurantiacus DSM 785</i>	Herpetosiphon aurantiacus DSM 785 GCN5-related N-acetyltransferase protein.	198	2.5E-21	176	39.8

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
31	ABX06254.1	CP000875-3602	<i>Herpetosiphon aurantiacus</i> DSM 785	Herpetosiphon aurantiacus DSM 785 GCN5-related N-acetyltransferase protein.	198	2.5E-21	176	39.8
32	ADP80465.1	CP002299-2377	<i>Frankia</i> sp	Frankia sp. Eul1c Phosphinothricin acetyltransferase protein.	180	8.8E-21	175	38.3
33	ADP80465.1	CP002299-2377	<i>Frankia</i> sp	Frankia sp. Eul1c Phosphinothricin acetyltransferase protein.	180	8.8E-21	175	38.3
34	EDH66676.1	EP587742-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	171	1.2E-20	171	36.8
35	AEJ20413.1	CP002868-2241	<i>Spirochaeta caldaria</i> DSM 7334	Spirochaeta caldaria DSM 7334 Phosphinothricin acetyltransferase protein.	162	1.3E-20	156	40.4
36	AEJ20413.1	CP002868-2241	<i>Spirochaeta caldaria</i> DSM 7334	Spirochaeta caldaria DSM 7334 Phosphinothricin acetyltransferase protein.	162	1.3E-20	156	40.4
37	ABC80319.1	CP000251-541	<i>Anaeromyxobacter dehalogenans</i> 2CP-C	Anaeromyxobacter dehalogenans 2CP-C GCN5-related N-acetyltransferase protein.	197	2.2E-20	172	40.1
38	ABC80319.1	CP000251-541	<i>Anaeromyxobacter dehalogenans</i> 2CP-C	Anaeromyxobacter dehalogenans 2CP-C GCN5-related N-acetyltransferase protein.	197	2.2E-20	172	40.1
39	ADE04346.1	CP001956-2864	<i>Haloferax volcanii</i> DS2	Haloferax volcanii DS2 Phosphinothricin N-acetyltransferase protein.	199	3.6E-20	174	36.8
40	EDB06108.1	EP875358-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	159	4.9E-20	156	39.7
41	EFL05370.1	GG657746-1041	<i>Streptomyces</i> sp	Streptomyces sp. AA4 phosphinothricin N-acetyltransferase protein.	179	5.4E-20	170	36.5
42	AEF21235.1	CP002727-1248	<i>Pseudomonas fulva</i> 12-X	Pseudomonas fulva 12-X Phosphinothricin acetyltransferase protein.	187	5.6E-20	175	36.6
43	AEF21235.1	CP002727-1248	<i>Pseudomonas fulva</i> 12-X	Pseudomonas fulva 12-X Phosphinothricin acetyltransferase protein.	187	5.6E-20	175	36.6
44	ADB35192.1	CP001736-6061	<i>Kribbella flavida</i> DSM 17836	Kribbella flavida DSM 17836 Phosphinothricin acetyltransferase protein.	178	6.4E-20	171	37.4
45	ACG71814.1	CP001131-571	<i>Anaeromyxobacter</i> sp	Anaeromyxobacter sp. K GCN5-related N-acetyltransferase protein.	197	6.9E-20	172	39.5
46	AEK63353.1	CP002745-3514	<i>Collimonas fungivorans</i> Ter331	Collimonas fungivorans Ter331 Phosphinothricin N-acetyltransferase protein.	174	7.4E-20	157	39.5
47	AEK63353.1	CP002745-3514	<i>Collimonas fungivorans</i> Ter331	Collimonas fungivorans Ter331 Phosphinothricin N-acetyltransferase protein.	174	7.4E-20	157	39.5

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
48	ABS05399.1	CP000750-2786	<i>Kineococcus radiotolerans</i> SRS30216	Kineococcus radiotolerans SRS30216 GCN5-related N-acetyltransferase protein.	176	8.8E-20	170	38.2
49	ABS05399.1	CP000750-2786	<i>Kineococcus radiotolerans</i> SRS30216	Kineococcus radiotolerans SRS30216 GCN5-related N-acetyltransferase protein.	176	8.8E-20	170	38.2
50	ADB74907.1	CP001867-2095	<i>Geodermatophilus obscurus</i> DSM 43160	Geodermatophilus obscurus DSM 43160 Phosphinothricin acetyltransferase protein.	198	3.1E-19	171	39.2
51	ABG64725.1	CP000390-3320	<i>Chelativorans</i> sp	Chelativorans sp. BNC1 GCN5-related N-acetyltransferase protein.	186	3.5E-19	174	37.4
52	ABG64725.1	CP000390-3320	<i>Chelativorans</i> sp	Chelativorans sp. BNC1 GCN5-related N-acetyltransferase protein.	186	3.5E-19	174	37.4
53	ACL63929.1	CP001359-568	<i>Anaeromyxobacter dehalogenans</i> 2CP-1	Anaeromyxobacter dehalogenans 2CP-1 GCN5-related N-acetyltransferase protein.	197	6E-19	173	38.7
54	ECQ05335.1	EM127305-3	<i>marine metagenome</i>	marine metagenome hypothetical protein.	160	7E-19	156	37.2
55	ADB49183.1	CP001854-747	<i>Conexibacter woesei</i> DSM 14684	Conexibacter woesei DSM 14684 GCN5-related N-acetyltransferase protein.	176	7.5E-19	173	39.3
56	ADG76341.1	CP001964-3421	<i>Cellulomonas flavigena</i> DSM 20109	Cellulomonas flavigena DSM 20109 Phosphinothricin acetyltransferase protein.	193	8.1E-19	184	35.9
57	AEH35939.1	CP002839-615	<i>Halopiger xanaduensis</i> SH-6	Halopiger xanaduensis SH-6 Phosphinothricin acetyltransferase protein.	202	8.5E-19	169	37.3
58	AEH35939.1	CP002839-615	<i>Halopiger xanaduensis</i> SH-6	Halopiger xanaduensis SH-6 Phosphinothricin acetyltransferase protein.	202	8.5E-19	169	37.3
59	ABL99549.1	CP000507-1337	<i>Shewanella amazonensis</i> SB2B	Shewanella amazonensis SB2B phosphinothricin N-acetyltransferase, putative protein.	171	8.7E-19	161	37.9
60	ABL99549.1	CP000507-1337	<i>Shewanella amazonensis</i> SB2B	Shewanella amazonensis SB2B phosphinothricin N-acetyltransferase, putative protein.	171	8.7E-19	161	37.9
61	ABS62889.1	CP000774-1266	<i>Parvibaculum lavamentivorans</i> DS-1	Parvibaculum lavamentivorans DS-1 GCN5-related N-acetyltransferase protein.	197	9.8E-19	174	35.6
62	ABS62889.1	CP000774-1266	<i>Parvibaculum lavamentivorans</i> DS-1	Parvibaculum lavamentivorans DS-1 GCN5-related N-acetyltransferase protein.	197	9.8E-19	174	35.6

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
63	ACV48465.1	CP001688-2314	<i>Halomicrobium mukohataei</i> DSM 12286	Halomicrobium mukohataei DSM 12286 GCN5-related N-acetyltransferase protein.	196	3.7E-18	174	34.5
64	ADB59146.1	CP001860-245	<i>Haloterrigena turkmenica</i> DSM 5511	Haloterrigena turkmenica DSM 5511 GCN5-related N-acetyltransferase protein.	203	4.5E-18	172	36.6
65	AAS02406.1	AE016958-89	<i>Mycobacterium avium</i> subsp	Mycobacterium avium subsp. paratuberculosis K-10 hypothetical protein.	192	5E-18	175	36.0
66	AAS02406.1	AE016958-89	<i>Mycobacterium avium</i> subsp	Mycobacterium avium subsp. paratuberculosis K-10 hypothetical protein.	192	5E-18	175	36.0
67	CAZ56031.1	FM252032-1181	<i>Streptococcus suis</i> BM407	Streptococcus suis BM407 putative acetyltransferase protein.	169	5.3E-18	161	35.4
68	ADE31149.1	CP000837-684	<i>Streptococcus suis</i> GZ1	Streptococcus suis GZ1 GCN5-related N-acetyltransferase protein.	169	5.3E-18	161	35.4
69	ADV69875.1	CP002465-761	<i>Streptococcus suis</i> JS14	Streptococcus suis JS14 sortase and related acyltransferase protein.	169	5.3E-18	161	35.4
70	CAZ51402.1	FM252031-625	<i>Streptococcus suis</i> SC84	Streptococcus suis SC84 putative acetyltransferase protein.	169	5.3E-18	161	35.4
71	ABP91861.1	CP000408-701	<i>Streptococcus suis</i> 98HAH33	Streptococcus suis 98HAH33 Sortase and related acyltransferase protein.	169	5.3E-18	161	35.4
72	ABP89667.1	CP000407-693	<i>Streptococcus suis</i> 05ZYH33	Streptococcus suis 05ZYH33 Sortase and related acyltransferase protein.	169	5.3E-18	161	35.4
73	ABP91861.1	CP000408-701	<i>Streptococcus suis</i> 98HAH33	Streptococcus suis 98HAH33 Sortase and related acyltransferase protein.	169	5.3E-18	161	35.4
74	CAZ56031.1	FM252032-1181	<i>Streptococcus suis</i> BM407	Streptococcus suis BM407 putative acetyltransferase protein.	169	5.3E-18	161	35.4
75	ADV69875.1	CP002465-761	<i>Streptococcus suis</i> JS14	Streptococcus suis JS14 sortase and related acyltransferase protein.	169	5.3E-18	161	35.4
76	CAR45419.1	AM946016-628	<i>Streptococcus suis</i> P1/7	Streptococcus suis P1/7 putative acetyltransferase protein.	169	5.3E-18	161	35.4
77	ABP89667.1	CP000407-693	<i>Streptococcus suis</i> 05ZYH33	Streptococcus suis 05ZYH33 Sortase and related acyltransferase protein.	169	5.3E-18	161	35.4
78	ADE31149.1	CP000837-684	<i>Streptococcus suis</i> GZ1	Streptococcus suis GZ1 GCN5-related N-acetyltransferase protein.	169	5.3E-18	161	35.4

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
79	CAZ51402.1	FM252031-625	<i>Streptococcus suis</i> SC84	Streptococcus suis SC84 putative acetyltransferase protein.	169	5.3E-18	161	35.4
80	CAR45419.1	AM946016-628	<i>Streptococcus suis</i> P1/7	Streptococcus suis P1/7 putative acetyltransferase protein.	169	5.3E-18	161	35.4
81	ABJ66459.1	CP000419-1064	<i>Streptococcus thermophilus</i> LMD-9	Streptococcus thermophilus LMD-9 Sortase or related acyltransferase protein.	170	5.3E-18	171	35.1
82	ABJ66459.1	CP000419-1064	<i>Streptococcus thermophilus</i> LMD-9	Streptococcus thermophilus LMD-9 Sortase or related acyltransferase protein.	170	5.3E-18	171	35.1
83	ABK66397.1	CP000479-91	<i>Mycobacterium avium</i> 104	Mycobacterium avium 104 phosphinothricin N-acetyltransferase protein.	188	5.8E-18	172	36.6
84	ABK66397.1	CP000479-91	<i>Mycobacterium avium</i> 104	Mycobacterium avium 104 phosphinothricin N-acetyltransferase protein.	188	5.8E-18	172	36.6
85	AEF42949.1	CP002786-4489	<i>Amycolicococcus subflavus</i> DQS3-9A1	Amycolicococcus subflavus DQS3-9A1 Phosphinothricin N-acetyltransferase protein.	172	6.4E-18	171	34.5
86	AEF42949.1	CP002786-4489	<i>Amycolicococcus subflavus</i> DQS3-9A1	Amycolicococcus subflavus DQS3-9A1 Phosphinothricin N-acetyltransferase protein.	172	6.4E-18	171	34.5
87	CAM63117.1	CU458896-3014	<i>Mycobacterium abscessus</i>	Mycobacterium abscessus Hypothetical phosphinothricin N-acetyltransferase protein.	177	7.7E-18	158	36.1
88	CAM63117.1	CU458896-3014	<i>Mycobacterium abscessus</i>	Mycobacterium abscessus Hypothetical phosphinothricin N-acetyltransferase protein.	177	7.7E-18	158	36.1
89	ADJ16359.1	CP002062-2967	<i>Halalkalicoccus jeotgali</i> B3	Halalkalicoccus jeotgali B3 phosphinothricin N-acetyltransferase protein.	196	8.4E-18	171	36.3
90	ADJ16359.1	CP002062-2967	<i>Halalkalicoccus jeotgali</i> B3	Halalkalicoccus jeotgali B3 phosphinothricin N-acetyltransferase protein.	196	8.4E-18	171	36.3
91	ABR90070.1	CP000269-2445	<i>Janthinobacterium</i> sp	Janthinobacterium sp. Marseille phosphinothricin N-acetyltransferase protein.	173	8.9E-18	156	37.8
92	ABR90070.1	CP000269-2445	<i>Janthinobacterium</i> sp	Janthinobacterium sp. Marseille phosphinothricin N-acetyltransferase protein.	173	8.9E-18	156	37.8
93	ADI12131.1	CP002047-9010	<i>Streptomyces bingchenggensis</i> BCW-1	Streptomyces bingchenggensis BCW-1 Phosphinothricin acetyltransferase protein.	185	1.1E-17	184	36.4
94	ADI12131.1	CP002047-9010	<i>Streptomyces bingchenggensis</i> BCW-1	Streptomyces bingchenggensis BCW-1 Phosphinothricin acetyltransferase protein.	185	1.1E-17	184	36.4

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
95	ADH67464.1	CP002040-2011	<i>Nocardiopsis dassonvillei</i> subsp.	<i>Nocardiopsis dassonvillei</i> subsp. <i>dassonvillei</i> DSM 43111 Phosphinothricin acetyltransferase protein.	175	1.3E-17	163	33.7
96	ADH67464.1	CP002040-2011	<i>Nocardiopsis dassonvillei</i> subsp.	<i>Nocardiopsis dassonvillei</i> subsp. <i>dassonvillei</i> DSM 43111 Phosphinothricin acetyltransferase protein.	175	1.3E-17	163	33.7
97	AAV81627.1	AE017340-783	<i>Idiomarina loihiensis</i> L2TR	<i>Idiomarina loihiensis</i> L2TR Phosphinothricin N-acetyltransferase, putative protein.	166	1.4E-17	157	36.3
98	AAV81627.1	AE017340-783	<i>Idiomarina loihiensis</i> L2TR	<i>Idiomarina loihiensis</i> L2TR Phosphinothricin N-acetyltransferase, putative protein.	166	1.4E-17	157	36.3
99	ACR11359.1	CP001614-3037	<i>Teredinibacter turnerae</i> T7901	<i>Teredinibacter turnerae</i> T7901 phosphinothricin N-acetyltransferase protein.	204	1.7E-17	168	33.3
100	ADQ63288.1	CP002340-1213	<i>Streptococcus thermophilus</i> ND03	<i>Streptococcus thermophilus</i> ND03 Sortase acyltransferase-like protein.	170	3.3E-17	171	34.5
101	CCC20205.1	FR875178-1388	<i>Streptococcus thermophilus</i> JIM 8232	<i>Streptococcus thermophilus</i> JIM 8232 GCN5-related N-acetyltransferase protein.	170	3.3E-17	171	34.5
102	ADQ63288.1	CP002340-1213	<i>Streptococcus thermophilus</i> ND03	<i>Streptococcus thermophilus</i> ND03 Sortase acyltransferase-like protein.	170	3.3E-17	171	34.5
103	CCC20205.1	FR875178-1388	<i>Streptococcus thermophilus</i> JIM 8232	<i>Streptococcus thermophilus</i> JIM 8232 GCN5-related N-acetyltransferase protein.	170	3.3E-17	171	34.5
104	ADZ90538.1	CP002583-1232	<i>Marinomonas mediterranea</i> MMB-1	<i>Marinomonas mediterranea</i> MMB-1 Phosphinothricin acetyltransferase protein.	163	3.8E-17	157	34.4
105	ADZ90538.1	CP002583-1232	<i>Marinomonas mediterranea</i> MMB-1	<i>Marinomonas mediterranea</i> MMB-1 Phosphinothricin acetyltransferase protein.	163	3.8E-17	157	34.4
106	AEJ53202.1	CP002888-774	<i>Streptococcus salivarius</i> 57	<i>Streptococcus salivarius</i> 57.I phosphinothricin acetyltransferase protein.	177	4E-17	170	33.5
107	AEJ53202.1	CP002888-774	<i>Streptococcus salivarius</i> 57	<i>Streptococcus salivarius</i> 57.I phosphinothricin acetyltransferase protein.	177	4E-17	170	33.5
108	ACS64906.1	CP001645-182	<i>Ralstonia pickettii</i> 12D	<i>Ralstonia pickettii</i> 12D GCN5-related N-acetyltransferase protein.	182	4.1E-17	170	36.5
109	ACD29808.1	CP001069-932	<i>Ralstonia pickettii</i> 12J	<i>Ralstonia pickettii</i> 12J GCN5-related N-acetyltransferase protein.	182	4.1E-17	170	36.5
110	AAV62843.1	CP000024-1224	<i>Streptococcus thermophilus</i> CNRZ1066	<i>Streptococcus thermophilus</i> CNRZ1066 phosphinothricin acetyltransferase, putative protein.	193	4.3E-17	177	33.9

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
111	AAV62843.1	CP000024-1224	<i>Streptococcus thermophilus</i> CNRZ1066	Streptococcus thermophilus CNRZ1066 phosphinothricin acetyltransferase, putative protein.	193	4.3E-17	177	33.9
112	ACD58849.1	CP000967-2182	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae PXO99A phosphinothricin N-acetyltransferase protein.	170	4.6E-17	164	35.4
113	CCB95608.1	FR873482-1211	<i>Streptococcus salivarius</i> JIM8777	Streptococcus salivarius JIM8777 phosphinothricin acetyltransferase, putative, GNAT family acetyltransferase protein.	170	5.4E-17	162	34.6
114	CCB95608.1	FR873482-1211	<i>Streptococcus salivarius</i> JIM8777	Streptococcus salivarius JIM8777 phosphinothricin acetyltransferase, putative, GNAT family acetyltransferase protein.	170	5.4E-17	162	34.6
115	EBU35068.1	EN340829-1	marine metagenome	marine metagenome hypothetical protein.	207	5.4E-17	174	36.2
116	CAM78141.1	CU459003-4180	<i>Magnetospirillum gryphiswaldense</i>	Magnetospirillum gryphiswaldense phosphinothricin acetyltransferase protein.	176	6.6E-17	165	37.6
117	AAV60931.1	CP000023-1201	<i>Streptococcus thermophilus</i> LMG 18311	Streptococcus thermophilus LMG 18311 phosphinothricin acetyltransferase, putative protein.	193	8.4E-17	177	33.3
118	AAV60931.1	CP000023-1201	<i>Streptococcus thermophilus</i> LMG 18311	Streptococcus thermophilus LMG 18311 phosphinothricin acetyltransferase, putative protein.	193	8.4E-17	177	33.3
119	CCB93097.1	FR873481-732	<i>Streptococcus salivarius</i> CCHSS3	Streptococcus salivarius CCHSS3 phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	170	8.9E-17	162	34.6
120	CCB93097.1	FR873481-732	<i>Streptococcus salivarius</i> CCHSS3	Streptococcus salivarius CCHSS3 phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	170	8.9E-17	162	34.6
121	AEB81304.1	CP002633-816	<i>Streptococcus suis</i> ST3	Streptococcus suis ST3 GCN5-related N-acetyltransferase protein.	169	1.2E-16	161	33.5
122	AEB81304.1	CP002633-816	<i>Streptococcus suis</i> ST3	Streptococcus suis ST3 GCN5-related N-acetyltransferase protein.	169	1.2E-16	161	33.5
123	EEV28740.1	GG670385-625	<i>Enterococcus casseliflavus</i> EC30	Enterococcus casseliflavus EC30 conserved hypothetical protein.	177	1.3E-16	160	36.9

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
124	EEV35075.1	GG692815-636	<i>Enterococcus casseliflavus</i> EC10	Enterococcus casseliflavus EC10 conserved hypothetical protein.	177	1.3E-16	160	36.9
125	ACI50980.1	CP001189-1178	<i>Gluconacetobacter diazotrophicus</i> PAI 5	Gluconacetobacter diazotrophicus PAI 5 GCN5-related N-acetyltransferase protein.	184	1.3E-16	182	36.8
126	ADV10129.1	CP002447-954	<i>Mesorhizobium ciceri</i> biovar <i>biserrulae</i> WSM1271	Mesorhizobium ciceri biovar biserrulae WSM1271 Phosphinothricin acetyltransferase protein.	190	1.4E-16	174	35.6
127	ADV10129.1	CP002447-954	<i>Mesorhizobium ciceri</i> biovar <i>biserrulae</i> WSM1271	Mesorhizobium ciceri biovar biserrulae WSM1271 Phosphinothricin acetyltransferase protein.	190	1.4E-16	174	35.6
128	ACB27434.1	CP001001-5407	<i>Methylobacterium radiotolerans</i> JCM 2831	Methylobacterium radiotolerans JCM 2831 GCN5-related N-acetyltransferase protein.	176	1.5E-16	172	37.8
129	EEV38370.1	GG670300-639	<i>Enterococcus casseliflavus</i> EC20	Enterococcus casseliflavus EC20 conserved hypothetical protein.	177	1.5E-16	160	36.9
130	CAP54763.1	AM889285-820	<i>Gluconacetobacter diazotrophicus</i> PAI 5	Gluconacetobacter diazotrophicus PAI 5 putative phosphinothricin N-acetyltransferase protein.	222	1.6E-16	182	36.8
131	CAP54763.1	AM889285-820	<i>Gluconacetobacter diazotrophicus</i> PAI 5	Gluconacetobacter diazotrophicus PAI 5 putative phosphinothricin N-acetyltransferase protein.	222	1.6E-16	182	36.8
132	AEH85485.1	CP002279-987	<i>Mesorhizobium opportunistum</i> WSM2075	Mesorhizobium opportunistum WSM2075 Phosphinothricin acetyltransferase protein.	191	1.6E-16	174	35.6
133	AEH85485.1	CP002279-987	<i>Mesorhizobium opportunistum</i> WSM2075	Mesorhizobium opportunistum WSM2075 Phosphinothricin acetyltransferase protein.	191	1.6E-16	174	35.6
134	ADN77475.1	CP002209-3261	<i>Ferrimonas balearica</i> DSM 9799	Ferrimonas balearica DSM 9799 Phosphinothricin acetyltransferase protein.	165	2.3E-16	159	36.5
135	ADN77475.1	CP002209-3261	<i>Ferrimonas balearica</i> DSM 9799	Ferrimonas balearica DSM 9799 Phosphinothricin acetyltransferase protein.	165	2.3E-16	159	36.5
136	ADJ46484.1	CP002000-4658	<i>Amycolatopsis mediterranei</i> U32	Amycolatopsis mediterranei U32 acetyltransferase protein.	171	2.4E-16	159	35.8
137	AEK43283.1	CP002896-4788	<i>Amycolatopsis mediterranei</i> S699	Amycolatopsis mediterranei S699 acetyltransferase protein.	171	2.4E-16	159	35.8

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
138	ADJ46484.1	CP002000-4658	<i>Amycolatopsis mediterranei</i> U32	Amycolatopsis mediterranei U32 acetyltransferase protein.	171	2.4E-16	159	35.8
139	AEK43283.1	CP002896-4788	<i>Amycolatopsis mediterranei</i> S699	Amycolatopsis mediterranei S699 acetyltransferase protein.	171	2.4E-16	159	35.8
140	CAJ62083.1	CT573213-3360	<i>Frankia alni</i> ACN14a	Frankia alni ACN14a putative N-acetyltransferase protein.	184	2.6E-16	177	36.2
141	CAJ62083.1	CT573213-3360	<i>Frankia alni</i> ACN14a	Frankia alni ACN14a putative N-acetyltransferase protein.	184	2.6E-16	177	36.2
142	ACM38029.1	CP000633-3069	<i>Agrobacterium vitis</i> S4	Agrobacterium vitis S4 acetyltransferase protein.	209	5.6E-16	162	34.6
143	ACM38029.1	CP000633-3069	<i>Agrobacterium vitis</i> S4	Agrobacterium vitis S4 acetyltransferase protein.	209	5.6E-16	162	34.6
144	CBJ34703.1	FP885891-338	<i>Ralstonia solanacearum</i> PSI07	Ralstonia solanacearum PSI07 Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	183	5.9E-16	164	36.6
145	CBJ34703.1	FP885891-338	<i>Ralstonia solanacearum</i> PSI07	Ralstonia solanacearum PSI07 Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	183	5.9E-16	164	36.6
146	ABE45344.1	CP000316-3377	<i>Polaromonas</i> sp	Polaromonas sp. JS666 GCN5-related N-acetyltransferase protein.	226	5.9E-16	159	37.7
147	ABE45344.1	CP000316-3377	<i>Polaromonas</i> sp	Polaromonas sp. JS666 GCN5-related N-acetyltransferase protein.	226	5.9E-16	159	37.7
148	EEY79747.1	GG704941-4	<i>Streptococcus</i> sp	Streptococcus sp. 2_1_36FAA acyltransferase protein.	189	6E-16	167	34.7
149	ADB39309.1	CP001769-3235	<i>Spirosoma linguale</i> DSM 74	Spirosoma linguale DSM 74 GCN5-related N-acetyltransferase protein.	185	7E-16	171	34.5
150	CAL96308.1	AM406670-3689	<i>Azoarcus</i> sp	Azoarcus sp. BH72 putative N-acetyltransferase protein.	188	7.1E-16	178	37.6
151	CAL96308.1	AM406670-3689	<i>Azoarcus</i> sp	Azoarcus sp. BH72 putative N-acetyltransferase protein.	188	7.1E-16	178	37.6
152	EBL84409.1	EN880832-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	164	8.8E-16	158	32.3
153	ACI12185.1	CP000965-51	<i>Klebsiella pneumoniae</i> 342	Klebsiella pneumoniae 342 putative phosphinothricin N-acetyltransferase protein.	178	9.4E-16	155	35.5

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
154	ADF64788.1	CP001919-100	<i>Enterobacter cloacae</i> subsp	Enterobacter cloacae subsp. cloacae ATCC 13047 putative phosphinothricin N-acetyltransferase protein.	178	9.4E-16	155	35.5
155	ABX70689.1	CP000886-5245	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 hypothetical protein.	171	1.1E-15	163	30.1
156	EFX55272.1	GL698449-867	<i>Streptococcus</i> sp	Streptococcus sp. C150 phosphinothricin N-acetyltransferase protein.	172	1.1E-15	162	32.7
157	EGB93900.1	GL870809-132	<i>Clostridium</i> sp	Clostridium sp. D5 phosphinothricin N-acetyltransferase protein.	190	1.2E-15	182	30.8
158	ACZ87922.1	CP001814-4860	<i>Streptosporangium roseum</i> DSM 43021	Streptosporangium roseum DSM 43021 Phosphinothricin acetyltransferase protein.	170	1.3E-15	167	37.1
159	ACA20330.1	CP000943-5742	<i>Methylobacterium</i> sp	Methylobacterium sp. 4-46 GCN5-related N-acetyltransferase protein.	180	1.3E-15	170	38.2
160	AEF54328.1	CP002771-1259	<i>Marinomonas posidonica</i> IVIA-Po-181	Marinomonas posidonica IVIA-Po-181 Phosphinothricin acetyltransferase protein.	161	1.4E-15	157	35.0
161	AEF54328.1	CP002771-1259	<i>Marinomonas posidonica</i> IVIA-Po-181	Marinomonas posidonica IVIA-Po-181 Phosphinothricin acetyltransferase protein.	161	1.4E-15	157	35.0
162	BAF86956.1	AP009384-958	<i>Azorhizobium caulinodans</i> ORS 571	Azorhizobium caulinodans ORS 571 GCN5-related N-acetyltransferase protein.	174	1.5E-15	162	37.0
163	BAF86956.1	AP009384-958	<i>Azorhizobium caulinodans</i> ORS 571	Azorhizobium caulinodans ORS 571 GCN5-related N-acetyltransferase protein.	174	1.5E-15	162	37.0
164	AAN67541.1	AE015451-1907	<i>Pseudomonas putida</i> KT2440	Pseudomonas putida KT2440 phosphinothricin N-acetyltransferase, putative protein.	186	1.6E-15	178	33.1
165	AAN67541.1	AE015451-1907	<i>Pseudomonas putida</i> KT2440	Pseudomonas putida KT2440 phosphinothricin N-acetyltransferase, putative protein.	186	1.6E-15	178	33.1
166	CAM74335.1	CU459003-374	<i>Magnetospirillum gryphiswaldense</i>	Magnetospirillum gryphiswaldense GCN5-related N-acetyltransferase protein.	195	2.7E-15	181	36.5
167	EFL40856.1	GG657758-3660	<i>Streptomyces griseoflavus</i> Tu4000	Streptomyces griseoflavus Tu4000 phosphinothricin N-acetyltransferase protein.	172	2.9E-15	173	31.8
168	EEV32026.1	GG670286-628	<i>Enterococcus gallinarum</i> EG2	Enterococcus gallinarum EG2 phosphinothricin N-acetyltransferase protein.	178	3E-15	178	32.0
169	ADU22362.1	CP002403-1798	<i>Ruminococcus albus</i> 7	Ruminococcus albus 7 Phosphinothricin acetyltransferase protein.	191	3.2E-15	186	31.2

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
170	ADU22362.1	CP002403-1798	<i>Ruminococcus albus</i> 7	Ruminococcus albus 7 Phosphinothricin acetyltransferase protein.	191	3.2E-15	186	31.2
171	AEF85027.1	CP001843-1130	<i>Treponema primitia</i> ZAS-2	Treponema primitia ZAS-2 phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	169	3.4E-15	156	32.7
172	ABN44603.1	CP000387-1133	<i>Streptococcus sanguinis</i> SK36	Streptococcus sanguinis SK36 Phosphinothricin acetyltransferase, putative protein.	215	3.5E-15	167	32.9
173	ABN44603.1	CP000387-1133	<i>Streptococcus sanguinis</i> SK36	Streptococcus sanguinis SK36 Phosphinothricin acetyltransferase, putative protein.	215	3.5E-15	167	32.9
174	ABV10255.1	CP000725-1174	<i>Streptococcus gordonii</i> str	Streptococcus gordonii str. Challis substr. CH1 acyltransferase protein.	178	3.5E-15	173	32.4
175	ABV10255.1	CP000725-1174	<i>Streptococcus gordonii</i> str	Streptococcus gordonii str. Challis substr. CH1 acyltransferase protein.	178	3.5E-15	173	32.4
176	CCA87652.1	FR854090-163	<i>Ralstonia syzygii</i> R24	Ralstonia syzygii R24 phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	183	3.6E-15	162	36.4
177	CCA81665.1	FR854071-220	<i>blood disease bacterium</i> R229	blood disease bacterium R229 phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (phosphinothricin-resistance protein) protein.	183	3.6E-15	164	36.0
178	CCA87652.1	FR854090-163	<i>Ralstonia syzygii</i> R24	Ralstonia syzygii R24 phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	183	3.6E-15	162	36.4
179	CCA81665.1	FR854071-220	<i>blood disease bacterium</i> R229	blood disease bacterium R229 phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (phosphinothricin-resistance protein) protein.	183	3.6E-15	164	36.0
180	AEH55562.1	CP002843-531	<i>Streptococcus parasanguinis</i> ATCC 15912	Streptococcus parasanguinis ATCC 15912 phosphinothricin acetyltransferase protein.	174	4.1E-15	160	30.6
181	AEH55562.1	CP002843-531	<i>Streptococcus parasanguinis</i> ATCC 15912	Streptococcus parasanguinis ATCC 15912 phosphinothricin acetyltransferase protein.	174	4.1E-15	160	30.6
182	EFE77338.1	DS999644-4704	<i>Streptomyces roseosporus</i> NRRL 15998	Streptomyces roseosporus NRRL 15998 conserved hypothetical protein.	212	4.1E-15	169	35.5

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
183	EFL83667.1	GL383995-744	<i>Burkholderiales bacterium 1_1_47</i>	Burkholderiales bacterium 1_1_47 phosphinothricin N-acetyltransferase protein.	176	4.1E-15	165	33.3
184	ABJ04266.1	CP000463-305	<i>Rhodopseudomonas palustris BisA53</i>	Rhodopseudomonas palustris BisA53 GCN5-related N-acetyltransferase protein.	179	4.2E-15	176	35.2
185	ABJ04266.1	CP000463-305	<i>Rhodopseudomonas palustris BisA53</i>	Rhodopseudomonas palustris BisA53 GCN5-related N-acetyltransferase protein.	179	4.2E-15	176	35.2
186	ABE37766.1	CP000283-526	<i>Rhodopseudomonas palustris BisB5</i>	Rhodopseudomonas palustris BisB5 GCN5-related N-acetyltransferase protein.	181	4.2E-15	159	37.7
187	ABE37766.1	CP000283-526	<i>Rhodopseudomonas palustris BisB5</i>	Rhodopseudomonas palustris BisB5 GCN5-related N-acetyltransferase protein.	181	4.2E-15	159	37.7
188	CAD17548.1	AL646053-397	<i>Ralstonia solanacearum GMI1000</i>	Ralstonia solanacearum GMI1000 probable phosphinothricin acetyltransferase protein.	183	4.3E-15	162	36.4
189	CAD17548.1	AL646053-397	<i>Ralstonia solanacearum GMI1000</i>	Ralstonia solanacearum GMI1000 probable phosphinothricin acetyltransferase protein.	183	4.3E-15	162	36.4
190	AAZ28061.1	CP000083-2504	<i>Colwellia psychrerythraea 34H</i>	Colwellia psychrerythraea 34H phosphinothricin N-acetyltransferase protein.	169	4.7E-15	160	33.1
191	AAZ28061.1	CP000083-2504	<i>Colwellia psychrerythraea 34H</i>	Colwellia psychrerythraea 34H phosphinothricin N-acetyltransferase protein.	169	4.7E-15	160	33.1
192	EEQ58471.1	DS990260-2180	<i>Clostridiales bacterium 1_7_47FAA</i>	Clostridiales bacterium 1_7_47FAA phosphinothricin N-acetyltransferase protein.	189	5.2E-15	178	32.6
193	ACL61976.1	CP001349-6924	<i>Methylobacterium nodulans ORS 2060</i>	Methylobacterium nodulans ORS 2060 GCN5-related N-acetyltransferase protein.	182	5.9E-15	171	36.3
194	ABV40460.1	CP000826-1350	<i>Serratia proteamaculans 568</i>	Serratia proteamaculans 568 GCN5-related N-acetyltransferase protein.	181	7E-15	163	34.4
195	ABV40460.1	CP000826-1350	<i>Serratia proteamaculans 568</i>	Serratia proteamaculans 568 GCN5-related N-acetyltransferase protein.	181	7E-15	163	34.4
196	ADY25834.1	CP002536-655	<i>Deinococcus proteolyticus MRP</i>	Deinococcus proteolyticus MRP Phosphinothricin acetyltransferase protein.	178	8.1E-15	173	35.3
197	ADY25834.1	CP002536-655	<i>Deinococcus proteolyticus MRP</i>	Deinococcus proteolyticus MRP Phosphinothricin acetyltransferase protein.	178	8.1E-15	173	35.3
198	ABR80302.1	CP000648-65	<i>Klebsiella pneumoniae subsp</i>	Klebsiella pneumoniae subsp. pneumoniae MGH 78578 putative acetyltransferase protein.	178	9.5E-15	173	34.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
199	ABR80302.1	CP000648-65	<i>Klebsiella pneumoniae subsp</i>	Klebsiella pneumoniae subsp. pneumoniae MGH 78578 putative acetyltransferase protein.	178	9.5E-15	173	34.1
200	EBP01491.1	EN721155-3	<i>marine metagenome</i>	marine metagenome hypothetical protein.	177	1.1E-14	178	33.1
201	CAL98527.1	AM406671-1918	<i>Lactococcus lactis subsp</i>	Lactococcus lactis subsp. cremoris MG1363 phosphinothricin N-acetyltransferase protein.	186	1.2E-14	157	32.5
202	ADJ60933.1	CP002094-1913	<i>Lactococcus lactis subsp</i>	Lactococcus lactis subsp. cremoris NZ9000 phosphinothricin N-acetyltransferase protein.	186	1.2E-14	157	32.5
203	CBK99483.1	FP929045-1756	<i>Faecalibacterium prausnitzii L2-6</i>	Faecalibacterium prausnitzii L2-6 Sortase and related acyltransferases protein.	186	1.2E-14	179	32.4
204	CBK99483.1	FP929045-1756	<i>Faecalibacterium prausnitzii L2-6</i>	Faecalibacterium prausnitzii L2-6 Sortase and related acyltransferases protein.	186	1.2E-14	179	32.4
205	ADJ60933.1	CP002094-1913	<i>Lactococcus lactis subsp</i>	Lactococcus lactis subsp. cremoris NZ9000 phosphinothricin N-acetyltransferase protein.	186	1.2E-14	157	32.5
206	CAL98527.1	AM406671-1918	<i>Lactococcus lactis subsp</i>	Lactococcus lactis subsp. cremoris MG1363 phosphinothricin N-acetyltransferase protein.	186	1.2E-14	157	32.5
207	BAI76415.1	AP010951-70	<i>Azospirillum sp</i>	Azospirillum sp. B510 acetyltransferase protein.	189	1.2E-14	161	36.6
208	BAI76415.1	AP010951-70	<i>Azospirillum sp</i>	Azospirillum sp. B510 acetyltransferase protein.	189	1.2E-14	161	36.6
209	BAB51021.1	BA000012-3340	<i>Mesorhizobium loti MAFF303099</i>	Mesorhizobium loti MAFF303099 phosphinothricin acetyltransferase protein.	194	1.2E-14	172	35.5
210	BAB51021.1	BA000012-3340	<i>Mesorhizobium loti MAFF303099</i>	Mesorhizobium loti MAFF303099 phosphinothricin acetyltransferase protein.	194	1.2E-14	172	35.5
211	EGJ48326.1	GL890784-1258	<i>Ruminococcaceae bacterium D16</i>	Ruminococcaceae bacterium D16 phosphinothricin N-acetyltransferase protein.	187	1.4E-14	175	31.4
212	EDX82050.1	DS989898-1952	<i>Brevundimonas sp</i>	Brevundimonas sp. BAL3 acetyltransferase, GNAT family protein.	189	1.4E-14	177	35.0
213	CBA32211.1	FN543093-2804	<i>Cronobacter turicensis z3032</i>	Cronobacter turicensis z3032 Phosphinothricin N-acetyltransferase protein.	181	1.6E-14	170	33.5
214	CBA32211.1	FN543093-2804	<i>Cronobacter turicensis z3032</i>	Cronobacter turicensis z3032 Phosphinothricin N-acetyltransferase protein.	181	1.6E-14	170	33.5
215	ADY57012.1	CP002547-2631	<i>Syntrophobotulus glycolicus DSM 8271</i>	Syntrophobotulus glycolicus DSM 8271 Phosphinothricin acetyltransferase protein.	190	1.7E-14	156	32.1

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
216	ADY57012.1	CP002547-2631	<i>Syntrophobotulus glycolicus</i> DSM 8271	Syntrophobotulus glycolicus DSM 8271 Phosphinothricin acetyltransferase protein.	190	1.7E-14	156	32.1
217	ADB48097.1	CP001859-1687	<i>Acidaminococcus fermentans</i> DSM 20731	Acidaminococcus fermentans DSM 20731 GCN5-related N-acetyltransferase protein.	191	1.7E-14	182	29.7
218	ACZ75861.1	CP001836-963	<i>Dickeya dadantii</i> Ech586	Dickeya dadantii Ech586 Phosphinothricin acetyltransferase protein.	176	1.8E-14	163	33.7
219	EEH94351.1	GG657367-321	<i>Citrobacter</i> sp	Citrobacter sp. 30_2 yceA protein.	178	1.9E-14	163	30.7
220	CAP44871.1	AM902716-4540	<i>Bordetella petrii</i>	Bordetella petrii acetyltransferase protein.	183	1.9E-14	177	35.0
221	CAP44871.1	AM902716-4540	<i>Bordetella petrii</i>	Bordetella petrii acetyltransferase protein.	183	1.9E-14	177	35.0
222	ABD04999.1	CP000250-287	<i>Rhodopseudomonas palustris</i> HaA2	Rhodopseudomonas palustris HaA2 GCN5-related N-acetyltransferase protein.	205	2.1E-14	159	37.1
223	ABD04999.1	CP000250-287	<i>Rhodopseudomonas palustris</i> HaA2	Rhodopseudomonas palustris HaA2 GCN5-related N-acetyltransferase protein.	205	2.1E-14	159	37.1
224	ACU37922.1	CP001630-3948	<i>Actinosynnema mirum</i> DSM 43827	Actinosynnema mirum DSM 43827 GCN5-related N-acetyltransferase protein.	169	2.1E-14	166	35.5
225	ADA65524.1	CP001834-1952	<i>Lactococcus lactis</i> subsp	Lactococcus lactis subsp. lactis KF147 Acetyltransferase, GNAT family protein.	187	2.3E-14	176	29.0
226	ABJ73431.1	CP000425-1794	<i>Lactococcus lactis</i> subsp	Lactococcus lactis subsp. cremoris SK11 Sortase related acyltransferase protein.	186	2.7E-14	157	32.5
227	ABJ73431.1	CP000425-1794	<i>Lactococcus lactis</i> subsp	Lactococcus lactis subsp. cremoris SK11 Sortase related acyltransferase protein.	186	2.7E-14	157	32.5
228	EEH97746.1	EQ999773-1372	<i>Clostridium</i> sp	Clostridium sp. 7_2_43FAA phosphinothricin acetyltransferase protein.	197	3.3E-14	177	28.8
229	ABJ62429.1	CP000414-1257	<i>Leuconostoc mesenteroides</i> subsp	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 Sortase related acyltransferase protein.	177	3.6E-14	177	28.8
230	ABJ62429.1	CP000414-1257	<i>Leuconostoc mesenteroides</i> subsp	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293 Sortase related acyltransferase protein.	177	3.6E-14	177	28.8
231	EDI20406.1	EP565697-1	marine metagenome	marine metagenome hypothetical protein.	328	3.7E-14	169	33.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
232	ADM97326.1	CP002038-1109	<i>Dickeya dadantii</i> 3937	<i>Dickeya dadantii</i> 3937 Phosphinothricin N-acetyltransferase protein.	187	3.7E-14	161	34.8
233	ADM97326.1	CP002038-1109	<i>Dickeya dadantii</i> 3937	<i>Dickeya dadantii</i> 3937 Phosphinothricin N-acetyltransferase protein.	187	3.7E-14	161	34.8
234	EFL87430.1	GL384287-1201	<i>Desulfovibrio</i> sp	<i>Desulfovibrio</i> sp. 3_1_syn3 phosphinothricin N-acetyltransferase protein.	189	3.8E-14	178	33.7
235	EFF92798.1	GG753626-3116	<i>Streptomyces</i> sp	<i>Streptomyces</i> sp. e14 GNAT family toxin-antitoxin system, toxin component protein.	168	4E-14	159	36.5
236	CAL74344.1	CU234118-371	<i>Bradyrhizobium</i> sp	<i>Bradyrhizobium</i> sp. ORS278 phosphinothricin acetyltransferase (PPT N-acetyltransferase) protein.	175	4.2E-14	160	34.4
237	CAL74344.1	CU234118-371	<i>Bradyrhizobium</i> sp	<i>Bradyrhizobium</i> sp. ORS278 phosphinothricin acetyltransferase (PPT N-acetyltransferase) protein.	175	4.2E-14	160	34.4
238	ADZ64335.1	CP002365-1667	<i>Lactococcus lactis</i> subsp	<i>Lactococcus lactis</i> subsp. lactis CV56 phosphinothricin acetyltransferase protein.	187	4.4E-14	176	28.4
239	AAK05875.1	AE005176-1777	<i>Lactococcus lactis</i> subsp	<i>Lactococcus lactis</i> subsp. lactis II1403 acyltransferase protein.	187	4.4E-14	176	28.4
240	ADZ64335.1	CP002365-1667	<i>Lactococcus lactis</i> subsp	<i>Lactococcus lactis</i> subsp. lactis CV56 phosphinothricin acetyltransferase protein.	187	4.4E-14	176	28.4
241	AAK05875.1	AE005176-1777	<i>Lactococcus lactis</i> subsp	<i>Lactococcus lactis</i> subsp. lactis II1403 acyltransferase protein.	187	4.4E-14	176	28.4
242	BAE50982.1	AP007255-2178	<i>Magnetospirillum magneticum</i> AMB-1	<i>Magnetospirillum magneticum</i> AMB-1 Phosphinothricin N-acetyltransferase protein.	197	4.6E-14	187	35.8
243	BAE50982.1	AP007255-2178	<i>Magnetospirillum magneticum</i> AMB-1	<i>Magnetospirillum magneticum</i> AMB-1 Phosphinothricin N-acetyltransferase protein.	197	4.6E-14	187	35.8
244	ABX40674.1	CP000885-283	<i>Clostridium phytofermentans</i> ISDg	<i>Clostridium phytofermentans</i> ISDg GCN5-related N-acetyltransferase protein.	184	5.1E-14	176	30.1
245	BAH87990.1	AP010655-964	<i>Streptococcus mutans</i> NN2025	<i>Streptococcus mutans</i> NN2025 putative acetyltransferase protein.	163	5.5E-14	159	28.9
246	BAH87990.1	AP010655-964	<i>Streptococcus mutans</i> NN2025	<i>Streptococcus mutans</i> NN2025 putative acetyltransferase protein.	163	5.5E-14	159	28.9
247	EFL32774.1	GG657757-3292	<i>Streptomyces viridochromogenes</i> DSM 40736	<i>Streptomyces viridochromogenes</i> DSM 40736 phosphinothricin N-acetyltransferase protein.	172	5.7E-14	171	32.2

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
248	AEF49412.1	CP002774-1295	<i>Serratia sp</i>	Serratia sp. AS12 Phosphinothricin acetyltransferase protein.	178	5.9E-14	173	32.9
249	AEG27119.1	CP002775-1294	<i>Serratia sp</i>	Serratia sp. AS13 Phosphinothricin acetyltransferase protein.	178	5.9E-14	173	32.9
250	AEG27119.1	CP002775-1294	<i>Serratia sp</i>	Serratia sp. AS13 Phosphinothricin acetyltransferase protein.	178	5.9E-14	173	32.9
251	AEF44460.1	CP002773-1295	<i>Serratia sp</i>	Serratia sp. AS9 Phosphinothricin acetyltransferase protein.	178	5.9E-14	173	32.9
252	AEF49412.1	CP002774-1295	<i>Serratia sp</i>	Serratia sp. AS12 Phosphinothricin acetyltransferase protein.	178	5.9E-14	173	32.9
253	AEF44460.1	CP002773-1295	<i>Serratia sp</i>	Serratia sp. AS9 Phosphinothricin acetyltransferase protein.	178	5.9E-14	173	32.9
254	ACG79132.1	CP000747-2718	<i>Phenylobacterium zucineum</i> HLK1	Phenylobacterium zucineum HLK1 phosphinothricin N-acetyltransferase protein.	179	5.9E-14	172	36.0
255	ACG79132.1	CP000747-2718	<i>Phenylobacterium zucineum</i> HLK1	Phenylobacterium zucineum HLK1 phosphinothricin N-acetyltransferase protein.	179	5.9E-14	172	36.0
256	ADP19236.1	CP002287-5874	<i>Achromobacter xylosoxidans</i> A8	Achromobacter xylosoxidans A8 acetyltransferase, GNAT family protein 28 protein.	181	6E-14	182	33.0
257	ADP19236.1	CP002287-5874	<i>Achromobacter xylosoxidans</i> A8	Achromobacter xylosoxidans A8 acetyltransferase, GNAT family protein 28 protein.	181	6E-14	182	33.0
258	ADE38698.1	CP001751-455	<i>Candidatus Puniceispirillum marinum</i> IMCC1322	Candidatus Puniceispirillum marinum IMCC1322 GCN5-related N-acetyltransferase protein.	182	6E-14	163	35.6
259	ECV11620.1	EQ085150-1762	<i>marine metagenome</i>	marine metagenome hypothetical protein.	283	6.3E-14	172	33.1
260	ADO83767.1	CP002282-88	<i>Ilyobacter polytropus</i> DSM 2926	Ilyobacter polytropus DSM 2926 Phosphinothricin acetyltransferase protein.	161	6.4E-14	156	28.8
261	ADO83767.1	CP002282-88	<i>Ilyobacter polytropus</i> DSM 2926	Ilyobacter polytropus DSM 2926 Phosphinothricin acetyltransferase protein.	161	6.4E-14	156	28.8
262	CAJ88465.1	AM238664-758	<i>Streptomyces ambofaciens</i> ATCC 23877	Streptomyces ambofaciens ATCC 23877 putative acetyltransferase protein.	200	6.5E-14	165	34.5

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
263	CAJ88465.1	AM238664-758	<i>Streptomyces ambofaciens</i> ATCC 23877	Streptomyces ambofaciens ATCC 23877 putative acetyltransferase protein.	200	6.5E-14	165	34.5
264	EGF89917.1	GL883080-498	<i>Asticcacaulis biprosthicum</i> C19	Asticcacaulis biprosthicum C19 acetyltransferase GNAT family protein.	178	7E-14	170	32.9
265	EAY70698.1	CH482381-679	<i>Burkholderia dolosa</i> AUO158	Burkholderia dolosa AUO158 hypothetical protein.	191	7.4E-14	179	33.0
266	CAZ87971.1	FP475956-1205	<i>Thiomonas</i> sp	Thiomonas sp. 3As Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	175	8.1E-14	170	34.7
267	CAZ87971.1	FP475956-1205	<i>Thiomonas</i> sp	Thiomonas sp. 3As Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) protein.	175	8.1E-14	170	34.7
268	EEY84235.1	GG705149-179	<i>Bacteroides</i> sp	Bacteroides sp. 2_1_33B conserved hypothetical protein.	165	9.1E-14	165	33.3
269	AAP09761.1	AE016877-2651	<i>Bacillus cereus</i> ATCC 14579	Bacillus cereus ATCC 14579 Phosphinothricin N-acetyltransferase protein.	170	9.3E-14	169	33.1
270	ADH07325.1	CP001903-2507	<i>Bacillus thuringiensis</i> BMB171	Bacillus thuringiensis BMB171 phosphinothricin N-acetyltransferase protein.	170	9.3E-14	169	32.0
271	AAP09761.1	AE016877-2651	<i>Bacillus cereus</i> ATCC 14579	Bacillus cereus ATCC 14579 Phosphinothricin N-acetyltransferase protein.	170	9.3E-14	169	33.1
272	ABI89612.1	CP000441-838	<i>Burkholderia ambifaria</i> AMMD	Burkholderia ambifaria AMMD GCN5-related N-acetyltransferase protein.	207	9.3E-14	179	33.0
273	ABI89612.1	CP000441-838	<i>Burkholderia ambifaria</i> AMMD	Burkholderia ambifaria AMMD GCN5-related N-acetyltransferase protein.	207	9.3E-14	179	33.0
274	ACJ00874.1	CP000613-3441	<i>Rhodospirillum centenum</i> SW	Rhodospirillum centenum SW phosphinothricin N-acetyltransferase protein.	180	9.8E-14	155	38.7
275	ACJ00874.1	CP000613-3441	<i>Rhodospirillum centenum</i> SW	Rhodospirillum centenum SW phosphinothricin N-acetyltransferase protein.	180	9.8E-14	155	38.7
276	ABR42252.1	CP000140-457	<i>Parabacteroides distasonis</i> ATCC 8503	Parabacteroides distasonis ATCC 8503 phosphinothricin N-acetyltransferase, putative protein.	167	1.1E-13	165	33.3
277	ABR42252.1	CP000140-457	<i>Parabacteroides distasonis</i> ATCC 8503	Parabacteroides distasonis ATCC 8503 phosphinothricin N-acetyltransferase, putative protein.	167	1.1E-13	165	33.3

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
278	ACU37263.1	CP001630-3289	<i>Actinosynnema mirum</i> DSM 43827	Actinosynnema mirum DSM 43827 GCN5-related N-acetyltransferase protein.	168	1.1E-13	160	32.5
279	AEA16471.1	CP001907-2778	<i>Bacillus thuringiensis</i> serovar <i>chinensis</i> CT-43	Bacillus thuringiensis serovar chinensis CT-43 phosphinothricin N-acetyltransferase protein.	170	1.1E-13	169	32.5
280	EFD68697.1	GG657756-4337	<i>Streptomyces lividans</i> TK24	Streptomyces lividans TK24 phosphorinothrycin n-acetyltransferase protein.	171	1.1E-13	170	33.5
281	AAA26705.1	M62753-1	<i>Streptomyces coelicolor</i>	Streptomyces coelicolor phosphorinothrycin n-acetyltransferase protein.	171	1.1E-13	170	33.5
282	CAB90987.1	AL939115-150	<i>Streptomyces coelicolor</i>	Streptomyces coelicolor phosphinothricin acetyltransferase protein.	171	1.1E-13	170	33.5
283	AAA26705.1	M62753-1	<i>Streptomyces coelicolor</i>	Streptomyces coelicolor phosphorinothrycin n-acetyltransferase protein.	171	1.1E-13	170	33.5
284	CAB90987.1	AL939115-150	<i>Streptomyces coelicolor</i>	Streptomyces coelicolor phosphinothricin acetyltransferase protein.	171	1.1E-13	170	33.5
285	EBC67853.1	EP400582-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	212	1.1E-13	157	34.4
286	ACS86706.1	CP001654-2887	<i>Dickeya dadantii</i> Ech703	Dickeya dadantii Ech703 Phosphinothricin acetyltransferase protein.	178	1.1E-13	175	32.6
287	ECO11400.1	EM242952-4	<i>marine metagenome</i>	marine metagenome hypothetical protein.	137	1.3E-13	134	35.8
288	ACK94161.1	CP001186-2690	<i>Bacillus cereus</i> G9842	Bacillus cereus G9842 acetyltransferase, GNAT family protein.	170	1.3E-13	169	32.5
289	ACF51345.1	CP001111-1640	<i>Stenotrophomonas maltophilia</i> R551-3	Stenotrophomonas maltophilia R551-3 GCN5-related N-acetyltransferase protein.	176	1.3E-13	171	33.9
290	EBA65397.1	EP534879-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	181	1.4E-13	173	34.7
291	EFI07237.1	GG774765-107	<i>Bacteroides</i> sp	Bacteroides sp. 3_1_19 phosphinothricin N-acetyltransferase protein.	167	1.5E-13	165	33.3
292	ACK58907.1	CP001176-2662	<i>Bacillus cereus</i> B4264	Bacillus cereus B4264 acetyltransferase, GNAT family protein.	170	1.5E-13	169	32.5
293	ABY43813.1	CP000903-2544	<i>Bacillus weihenstephanensis</i> KBAB4	Bacillus weihenstephanensis KBAB4 GCN5-related N-acetyltransferase protein.	170	1.5E-13	169	33.1

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
294	ACP16794.1	CP001215-1699	<i>Bacillus anthracis str</i>	Bacillus anthracis str. CDC 684 acetyltransferase, GNAT family protein.	170	1.5E-13	169	32.0
295	BAC71407.1	BA000030-3702	<i>Streptomyces avermitilis MA-4680</i>	Streptomyces avermitilis MA-4680 putative phosphinothricin N-acetyltransferase protein.	172	1.5E-13	174	33.3
296	BAC71407.1	BA000030-3702	<i>Streptomyces avermitilis MA-4680</i>	Streptomyces avermitilis MA-4680 putative phosphinothricin N-acetyltransferase protein.	172	1.5E-13	174	33.3
297	EED40350.1	DS999412-2925	<i>Stenotrophomonas sp</i>	Stenotrophomonas sp. SKA14 phosphinothricin N-acetyltransferase protein.	176	1.6E-13	171	33.9
298	ADU42080.1	CP002418-435	<i>Rhodopseudomonas palustris DX-1</i>	Rhodopseudomonas palustris DX-1 Phosphinothricin acetyltransferase protein.	176	1.6E-13	161	35.4
299	ADU42080.1	CP002418-435	<i>Rhodopseudomonas palustris DX-1</i>	Rhodopseudomonas palustris DX-1 Phosphinothricin acetyltransferase protein.	176	1.6E-13	161	35.4
300	ADG39646.1	CP001758-103	<i>Leuconostoc kimchii IMSNU 11154</i>	Leuconostoc kimchii IMSNU 11154 hypothetical protein.	180	1.6E-13	178	31.5
301	AEJ30492.1	CP002898-428	<i>Leuconostoc sp</i>	Leuconostoc sp. C2 hypothetical protein.	180	1.6E-13	178	31.5
302	AEJ30492.1	CP002898-428	<i>Leuconostoc sp</i>	Leuconostoc sp. C2 hypothetical protein.	180	1.6E-13	178	31.5
303	BAG46332.1	AP009386-1284	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 acetyltransferase protein.	186	1.7E-13	172	32.6
304	ABX17706.1	CP000869-865	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 GCN5-related N-acetyltransferase protein.	186	1.7E-13	172	32.6
305	ABX17706.1	CP000869-865	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 GCN5-related N-acetyltransferase protein.	186	1.7E-13	172	32.6
306	BAG46332.1	AP009386-1284	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 acetyltransferase protein.	186	1.7E-13	172	32.6
307	AEA63630.1	CP002600-1147	<i>Burkholderia gladioli BSR3</i>	Burkholderia gladioli BSR3 GCN5-related N-acetyltransferase protein.	192	1.7E-13	182	34.1
308	AEA63630.1	CP002600-1147	<i>Burkholderia gladioli BSR3</i>	Burkholderia gladioli BSR3 GCN5-related N-acetyltransferase protein.	192	1.7E-13	182	34.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
309	BAH16771.1	AP009484-64	<i>Macrococcus caseolyticus JCSC5402</i>	Macrococcus caseolyticus JCSC5402 acetyltransferase family protein.	162	1.7E-13	159	32.7
310	BAH16771.1	AP009484-64	<i>Macrococcus caseolyticus JCSC5402</i>	Macrococcus caseolyticus JCSC5402 acetyltransferase family protein.	162	1.7E-13	159	32.7
311	ACM13075.1	CP000227-2546	<i>Bacillus cereus Q1</i>	Bacillus cereus Q1 possible phosphinothricin N-acetyltransferase protein.	170	1.8E-13	169	32.0
312	ADY22036.1	CP002508-2782	<i>Bacillus thuringiensis serovar finitimus YBT-020</i>	Bacillus thuringiensis serovar finitimus YBT-020 acetyltransferase, GNAT family protein.	170	1.8E-13	169	32.0
313	ABK85807.1	CP000485-2385	<i>Bacillus thuringiensis str</i>	Bacillus thuringiensis str. Al Hakam phosphinothricin N-acetyltransferase, acetyltransferase, GNAT family protein.	170	1.8E-13	169	32.0
314	ABK85807.1	CP000485-2385	<i>Bacillus thuringiensis str</i>	Bacillus thuringiensis str. Al Hakam phosphinothricin N-acetyltransferase, acetyltransferase, GNAT family protein.	170	1.8E-13	169	32.0
315	ACK90482.1	CP001283-2727	<i>Bacillus cereus AH820</i>	Bacillus cereus AH820 acetyltransferase, GNAT family protein.	170	1.8E-13	169	32.0
316	ACO26316.1	CP001407-2717	<i>Bacillus cereus 03BB102</i>	Bacillus cereus 03BB102 acetyltransferase, GNAT family protein.	170	1.8E-13	169	32.0
317	ACM13075.1	CP000227-2546	<i>Bacillus cereus Q1</i>	Bacillus cereus Q1 possible phosphinothricin N-acetyltransferase protein.	170	1.8E-13	169	32.0
318	ACJ78537.1	CP001177-2675	<i>Bacillus cereus AH187</i>	Bacillus cereus AH187 acetyltransferase, GNAT family protein.	170	1.8E-13	169	32.0
319	ADY22036.1	CP002508-2782	<i>Bacillus thuringiensis serovar finitimus YBT-020</i>	Bacillus thuringiensis serovar finitimus YBT-020 acetyltransferase, GNAT family protein.	170	1.8E-13	169	32.0
320	CAQ45545.1	AM743169-1927	<i>Stenotrophomonas maltophilia K279a</i>	Stenotrophomonas maltophilia K279a putative acetyltransferase protein.	176	1.9E-13	171	33.9
321	CAQ45545.1	AM743169-1927	<i>Stenotrophomonas maltophilia K279a</i>	Stenotrophomonas maltophilia K279a putative acetyltransferase protein.	176	1.9E-13	171	33.9
322	EBT84493.1	EN381717-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	129	2E-13	112	42.0
323	EDE32090.1	EP715068-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	193	2E-13	177	32.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
324	EBM45966.1	EN849757-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	193	2E-13	177	32.8
325	ADK16103.1	CP001666-2989	<i>Clostridium ljungdahlii</i> DSM 13528	<i>Clostridium ljungdahlii</i> DSM 13528 predicted acetyltransferase protein.	194	2E-13	185	29.2
326	ADK05404.1	CP001746-2590	<i>Bacillus cereus</i> biovar anthracis str	<i>Bacillus cereus</i> biovar anthracis str. CI possible phosphinothricin N-acetyltransferase protein.	170	2.1E-13	169	31.4
327	ECC86939.1	EM789126-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	174	2.2E-13	173	32.4
328	EDI30400.1	EP561309-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	328	2.3E-13	159	31.4
329	EBX51802.1	EN049721-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	274	2.3E-13	166	30.7
330	EBF21608.1	EP260604-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	193	2.4E-13	170	31.2
331	ECD28229.1	EM771612-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	241	2.4E-13	164	35.4
332	ACO70893.1	FJ872373-6	<i>uncultured Verrucomicrobia bacterium</i>	uncultured Verrucomicrobia bacterium putative acetyltransferase protein.	164	2.4E-13	152	34.2
333	EDE01240.1	EP726950-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	254	2.5E-13	177	33.9
334	CAE25643.1	BX572593-200	<i>Rhodopseudomonas palustris</i> CGA009	<i>Rhodopseudomonas palustris</i> CGA009 putative phosphinothricin acetyltransferase protein.	176	2.6E-13	159	34.0
335	ACT07944.1	CP001655-3050	<i>Dickeya zeae</i> Ech1591	<i>Dickeya zeae</i> Ech1591 Phosphinothricin acetyltransferase protein.	176	2.6E-13	161	34.2
336	ACE98756.1	CP001096-194	<i>Rhodopseudomonas palustris</i> TIE-1	<i>Rhodopseudomonas palustris</i> TIE-1 GCN5-related N-acetyltransferase protein.	176	2.6E-13	159	34.0
337	CAE25643.1	BX572593-200	<i>Rhodopseudomonas palustris</i> CGA009	<i>Rhodopseudomonas palustris</i> CGA009 putative phosphinothricin acetyltransferase protein.	176	2.6E-13	159	34.0
338	AEM21853.1	CP002874-1217	<i>Brachyspira intermedia</i> PWS/A	<i>Brachyspira intermedia</i> PWS/A Sortase related acyltransferase protein.	190	2.8E-13	178	27.5
339	AEM21853.1	CP002874-1217	<i>Brachyspira intermedia</i> PWS/A	<i>Brachyspira intermedia</i> PWS/A Sortase related acyltransferase protein.	190	2.8E-13	178	27.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
340	CBK80336.1	FP929038-1346	<i>Coprococcus catus GD/7</i>	Coprococcus catus GD/7 Sortase and related acyltransferases protein.	197	2.9E-13	165	33.3
341	CBK80336.1	FP929038-1346	<i>Coprococcus catus GD/7</i>	Coprococcus catus GD/7 Sortase and related acyltransferases protein.	197	2.9E-13	165	33.3
342	CAE36004.1	BX640424-94	<i>Bordetella parapertussis</i>	Bordetella parapertussis putative acetyltransferase protein.	182	3.1E-13	182	35.7
343	CAE30920.1	BX640438-88	<i>Bordetella bronchiseptica</i>	Bordetella bronchiseptica putative acetyltransferase protein.	182	3.1E-13	182	35.7
344	AEE65705.1	CP002695-181	<i>Bordetella pertussis CS</i>	Bordetella pertussis CS putative acetyltransferase protein.	182	3.1E-13	182	35.7
345	AEE65705.1	CP002695-181	<i>Bordetella pertussis CS</i>	Bordetella pertussis CS putative acetyltransferase protein.	182	3.1E-13	182	35.7
346	CAE36004.1	BX640424-94	<i>Bordetella parapertussis</i>	Bordetella parapertussis putative acetyltransferase protein.	182	3.1E-13	182	35.7
347	CAE40593.1	BX640411-213	<i>Bordetella pertussis</i>	Bordetella pertussis putative acetyltransferase protein.	182	3.1E-13	182	35.7
348	CAE40593.1	BX640411-213	<i>Bordetella pertussis</i>	Bordetella pertussis putative acetyltransferase protein.	182	3.1E-13	182	35.7
349	CAE30920.1	BX640438-88	<i>Bordetella bronchiseptica</i>	Bordetella bronchiseptica putative acetyltransferase protein.	182	3.1E-13	182	35.7
350	ECW45180.1	EQ047138-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	193	3.3E-13	170	31.2
351	ECW48207.1	EQ046232-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	193	3.3E-13	170	31.2
352	EBA72462.1	EP531349-3	<i>marine metagenome</i>	marine metagenome hypothetical protein.	193	3.3E-13	170	31.2
353	ADX77212.1	CP002478-1859	<i>Staphylococcus pseudintermedius ED99</i>	Staphylococcus pseudintermedius ED99 phosphinothricin N-acetyltransferase, putative protein.	165	3.4E-13	163	31.9
354	ADV05010.1	CP002439-481	<i>Staphylococcus pseudintermedius HKU10-03</i>	Staphylococcus pseudintermedius HKU10-03 Phosphinothricin N-acetyltransferase protein.	165	3.4E-13	163	31.9
355	EEU51105.1	GG698740-333	<i>Parabacteroides sp</i>	Parabacteroides sp. D13 conserved hypothetical protein.	165	3.4E-13	165	32.7

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
356	ADX77212.1	CP002478-1859	<i>Staphylococcus pseudintermedius</i> ED99	Staphylococcus pseudintermedius ED99 phosphinothricin N-acetyltransferase, putative protein.	165	3.4E-13	163	31.9
357	ADV05010.1	CP002439-481	<i>Staphylococcus pseudintermedius</i> HKU10-03	Staphylococcus pseudintermedius HKU10-03 Phosphinothricin N-acetyltransferase protein.	165	3.4E-13	163	31.9
358	EBD89973.1	EP325971-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	305	3.5E-13	159	35.8
359	BAK14871.1	AP012157-448	<i>Solibacillus silvestris</i> StLB046	Solibacillus silvestris StLB046 sortase protein.	170	3.5E-13	167	32.3
360	BAK14871.1	AP012157-448	<i>Solibacillus silvestris</i> StLB046	Solibacillus silvestris StLB046 sortase protein.	170	3.5E-13	167	32.3
361	AAS41749.1	AE017194-2813	<i>Bacillus cereus</i> ATCC 10987	Bacillus cereus ATCC 10987 acetyltransferase, GNAT family protein.	170	3.5E-13	169	31.4
362	AAS41749.1	AE017194-2813	<i>Bacillus cereus</i> ATCC 10987	Bacillus cereus ATCC 10987 acetyltransferase, GNAT family protein.	170	3.5E-13	169	31.4
363	BAB91588.1	AP005147-22	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium sortase and related acyltransferases protein.	178	3.6E-13	163	28.2
364	BAB91588.1	AP005147-22	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium sortase and related acyltransferases protein.	178	3.6E-13	163	28.2
365	ABB11268.1	CP000152-1151	<i>Burkholderia</i> sp	Burkholderia sp. 383 GCN5-related N-acetyltransferase protein.	186	3.8E-13	172	32.0
366	ABB11268.1	CP000152-1151	<i>Burkholderia</i> sp	Burkholderia sp. 383 GCN5-related N-acetyltransferase protein.	186	3.8E-13	172	32.0
367	AEI78829.1	CP002877-3459	<i>Cupriavidus necator</i> N-1	Cupriavidus necator N-1 phosphinothricin N-acetyltransferase Pat protein.	193	3.9E-13	167	32.3
368	AEI78829.1	CP002877-3459	<i>Cupriavidus necator</i> N-1	Cupriavidus necator N-1 phosphinothricin N-acetyltransferase Pat protein.	193	3.9E-13	167	32.3
369	EBH77498.1	EP114613-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	109	4E-13	98	41.8
370	ACV38218.1	CP001685-281	<i>Leptotrichia buccalis</i> C-1013-b	Leptotrichia buccalis C-1013-b GCN5-related N-acetyltransferase protein.	197	4E-13	174	27.6
371	ABU76373.1	CP000783-1064	<i>Cronobacter sakazakii</i> ATCC BAA-894	Cronobacter sakazakii ATCC BAA-894 hypothetical protein.	199	4E-13	170	32.9

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
372	ABU76373.1	CP000783-1064	<i>Cronobacter sakazakii</i> ATCC BAA-894	Cronobacter sakazakii ATCC BAA-894 hypothetical protein.	199	4E-13	170	32.9
373	ABI76675.1	CP000158-1655	<i>Hyphomonas neptunium</i> ATCC 15444	Hyphomonas neptunium ATCC 15444 acetyltransferase, GNAT family protein.	190	4.5E-13	159	35.2
374	ABI76675.1	CP000158-1655	<i>Hyphomonas neptunium</i> ATCC 15444	Hyphomonas neptunium ATCC 15444 acetyltransferase, GNAT family protein.	190	4.5E-13	159	35.2
375	ADX58989.1	CP002520-1974	<i>Burkholderia</i> sp	Burkholderia sp. CCGE1001 Phosphinothricin acetyltransferase protein.	195	4.6E-13	181	33.7
376	ADX58989.1	CP002520-1974	<i>Burkholderia</i> sp	Burkholderia sp. CCGE1001 Phosphinothricin acetyltransferase protein.	195	4.6E-13	181	33.7
377	AEH80586.1	CP001830-3298	<i>Sinorhizobium meliloti</i> SM11	Sinorhizobium meliloti SM11 acetyltransferase protein.	183	5.2E-13	172	29.1
378	EFE46705.1	GG749079-243	<i>Erysipelotrichaceae bacterium 5_2_54FAA</i>	Erysipelotrichaceae bacterium 5_2_54FAA phosphinothricin N-acetyltransferase protein.	195	5.5E-13	171	32.7
379	AAT60066.1	AE017355-2533	<i>Bacillus thuringiensis</i> serovar <i>konkukian</i> str	Bacillus thuringiensis serovar konkukian str. 97-27 possible phosphinothricin N-acetyltransferase protein.	170	5.8E-13	169	30.8
380	AAU17722.1	CP000001-2505	<i>Bacillus cereus</i> E33L	Bacillus cereus E33L phosphinothricin N-acetyltransferase protein.	170	5.8E-13	169	31.4
381	AAU17722.1	CP000001-2505	<i>Bacillus cereus</i> E33L	Bacillus cereus E33L phosphinothricin N-acetyltransferase protein.	170	5.8E-13	169	31.4
382	AAT60066.1	AE017355-2533	<i>Bacillus thuringiensis</i> serovar <i>konkukian</i> str	Bacillus thuringiensis serovar konkukian str. 97-27 possible phosphinothricin N-acetyltransferase protein.	170	5.8E-13	169	30.8
383	ECX10580.1	EQ023875-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	208	5.8E-13	159	36.5
384	AEM51014.1	CP002986-1678	<i>Burkholderia</i> sp	Burkholderia sp. JV3 Phosphinothricin acetyltransferase protein.	176	5.9E-13	171	33.3
385	AEM51014.1	CP002986-1678	<i>Burkholderia</i> sp	Burkholderia sp. JV3 Phosphinothricin acetyltransferase protein.	176	5.9E-13	171	33.3
386	CBL02997.1	FP929046-2514	<i>Faecalibacterium prausnitzii</i> SL3/3	Faecalibacterium prausnitzii SL3/3 Sortase and related acyltransferases protein.	184	6.2E-13	164	31.1
387	CBL02997.1	FP929046-2514	<i>Faecalibacterium prausnitzii</i> SL3/3	Faecalibacterium prausnitzii SL3/3 Sortase and related acyltransferases protein.	184	6.2E-13	164	31.1

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
388	EEO30298.1	GG658170-1326	<i>Oxalobacter formigenes</i> OXCC13	Oxalobacter formigenes OXCC13 conserved hypothetical protein.	188	6.3E-13	175	32.0
389	CBL41830.1	FP929062-1909	<i>butyrate-producing bacterium</i> SS3/4	butyrate-producing bacterium SS3/4 Sortase and related acyltransferases protein.	189	6.3E-13	183	28.4
390	CBL41830.1	FP929062-1909	<i>butyrate-producing bacterium</i> SS3/4	butyrate-producing bacterium SS3/4 Sortase and related acyltransferases protein.	189	6.3E-13	183	28.4
391	ACN83076.1	CP001357-573	<i>Brachyspira hyodysenteriae</i> WA1	Brachyspira hyodysenteriae WA1 Sortase related acyltransferase protein.	190	6.3E-13	178	28.1
392	CAJ94644.1	AM260479-3492	<i>Ralstonia eutropha</i> H16	Ralstonia eutropha H16 Phosphinothricin N-acetyltransferase protein.	193	6.4E-13	177	31.1
393	CAJ94644.1	AM260479-3492	<i>Ralstonia eutropha</i> H16	Ralstonia eutropha H16 Phosphinothricin N-acetyltransferase protein.	193	6.4E-13	177	31.1
394	ACQ70466.1	CP001615-1531	<i>Exiguobacterium</i> sp	Exiguobacterium sp. AT1b GCN5-related N-acetyltransferase protein.	170	6.8E-13	168	33.3
395	ADG30418.1	CP002021-1002	<i>Thiomonas intermedia</i> K12	Thiomonas intermedia K12 Phosphinothricin acetyltransferase protein.	175	7E-13	170	33.5
396	ADG30418.1	CP002021-1002	<i>Thiomonas intermedia</i> K12	Thiomonas intermedia K12 Phosphinothricin acetyltransferase protein.	175	7E-13	170	33.5
397	ABM36774.1	CP000529-1447	<i>Polaromonas naphthalenivorans</i> CJ2	Polaromonas naphthalenivorans CJ2 GCN5-related N-acetyltransferase protein.	178	7.1E-13	173	33.5
398	ABM36774.1	CP000529-1447	<i>Polaromonas naphthalenivorans</i> CJ2	Polaromonas naphthalenivorans CJ2 GCN5-related N-acetyltransferase protein.	178	7.1E-13	173	33.5
399	CAC47802.1	AL591688-3242	<i>Sinorhizobium meliloti</i> 1021	Sinorhizobium meliloti 1021 Acetyltransferase protein.	185	7.3E-13	173	28.9
400	AEG05892.1	CP002740-2940	<i>Sinorhizobium meliloti</i> BL225C	Sinorhizobium meliloti BL225C Phosphinothricin acetyltransferase protein.	185	7.3E-13	173	28.9
401	AEG54927.1	CP002781-3152	<i>Sinorhizobium meliloti</i> AK83	Sinorhizobium meliloti AK83 Phosphinothricin acetyltransferase protein.	185	7.3E-13	173	28.9
402	CAC47802.1	AL591688-3242	<i>Sinorhizobium meliloti</i> 1021	Sinorhizobium meliloti 1021 Acetyltransferase protein.	185	7.3E-13	173	28.9
403	AEG54927.1	CP002781-3152	<i>Sinorhizobium meliloti</i> AK83	Sinorhizobium meliloti AK83 Phosphinothricin acetyltransferase protein.	185	7.3E-13	173	28.9
404	AEG05892.1	CP002740-2940	<i>Sinorhizobium meliloti</i> BL225C	Sinorhizobium meliloti BL225C Phosphinothricin acetyltransferase protein.	185	7.3E-13	173	28.9

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
405	ACI56997.1	CP001191-3694	<i>Rhizobium leguminosarum</i> bv	Rhizobium leguminosarum bv. trifolii WSM2304 GCN5-related N-acetyltransferase protein.	185	7.3E-13	171	29.8
406	EEO31280.1	EQ999878-232	<i>Coprobacillus</i> sp	Coprobacillus sp. D7 phosphinothricin N-acetyltransferase protein.	186	7.3E-13	178	29.8
407	EBQ55196.1	EN635745-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	189	7.4E-13	163	35.0
408	ACZ08778.1	CP001739-1890	<i>Sebaldella termitidis</i> ATCC 33386	Sebaldella termitidis ATCC 33386 Phosphinothricin acetyltransferase protein.	165	7.8E-13	160	33.1
409	ABF10309.1	CP000352-3620	<i>Cupriavidus metallidurans</i> CH34	Cupriavidus metallidurans CH34 Phosphinothricin N-acetyltransferase protein.	206	8E-13	167	31.7
410	EEE77719.1	EQ138464-1	<i>Populus trichocarpa</i>	Populus trichocarpa predicted protein.	206	8E-13	167	31.7
411	ABF10309.1	CP000352-3620	<i>Cupriavidus metallidurans</i> CH34	Cupriavidus metallidurans CH34 Phosphinothricin N-acetyltransferase protein.	206	8E-13	167	31.7
412	EGF94392.1	GL883086-510	<i>Brevundimonas diminuta</i> ATCC 11568	Brevundimonas diminuta ATCC 11568 phosphinothricin N-acetyltransferase protein.	180	8.4E-13	169	36.1
413	ACB66973.1	CP001026-1396	<i>Burkholderia ambifaria</i> MC40-6	Burkholderia ambifaria MC40-6 GCN5-related N-acetyltransferase protein.	187	8.7E-13	175	32.0
414	EBX52786.1	EN048776-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	161	9E-13	159	30.8
415	ACD05748.1	CP001071-1901	<i>Akkermansia muciniphila</i> ATCC BAA-835	Akkermansia muciniphila ATCC BAA-835 GCN5-related N-acetyltransferase protein.	199	9.2E-13	176	33.5
416	EFK61418.1	GG774998-69	<i>Bacteroides</i> sp	Bacteroides sp. 20_3 phosphinothricin N-acetyltransferase protein.	164	9.2E-13	161	32.9
417	ABD85776.1	CP000301-197	<i>Rhodopseudomonas palustris</i> BisB18	Rhodopseudomonas palustris BisB18 GCN5-related N-acetyltransferase protein.	174	9.7E-13	161	32.9
418	ABD85776.1	CP000301-197	<i>Rhodopseudomonas palustris</i> BisB18	Rhodopseudomonas palustris BisB18 GCN5-related N-acetyltransferase protein.	174	9.7E-13	161	32.9
419	ADG97869.1	CP001958-1376	<i>Segniliparus rotundus</i> DSM 44985	Segniliparus rotundus DSM 44985 GCN5-related N-acetyltransferase protein.	174	9.7E-13	159	33.3
420	BAC45728.1	BA000040-463	<i>Bradyrhizobium japonicum</i> USDA 110	Bradyrhizobium japonicum USDA 110 acetyltransferase protein.	176	9.8E-13	170	33.5

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
421	BAC45728.1	BA000040-463	<i>Bradyrhizobium japonicum</i> USDA 110	Bradyrhizobium japonicum USDA 110 acetyltransferase protein.	176	9.8E-13	170	33.5
422	ACM28110.1	CP000628-3317	<i>Agrobacterium radiobacter</i> K84	Agrobacterium radiobacter K84 phosphinothricin N-acetyltransferase (antibiotic resistance) protein.	185	1E-12	169	29.6
423	ACM28110.1	CP000628-3317	<i>Agrobacterium radiobacter</i> K84	Agrobacterium radiobacter K84 phosphinothricin N-acetyltransferase (antibiotic resistance) protein.	185	1E-12	169	29.6
424	AAN58770.1	AE014133-977	<i>Streptococcus mutans</i> UA159	Streptococcus mutans UA159 putative acetyltransferase protein.	163	1.1E-12	159	27.7
425	AAN58770.1	AE014133-977	<i>Streptococcus mutans</i> UA159	Streptococcus mutans UA159 putative acetyltransferase protein.	163	1.1E-12	159	27.7
426	EFL20358.1	GG657754-70	<i>Streptomyces hygroscopicus</i> ATCC 53653	Streptomyces hygroscopicus ATCC 53653 GNAT family toxin-antitoxin system, toxin component protein.	172	1.1E-12	164	36.6
427	EBO46592.1	EN751828-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	225	1.2E-12	176	33.0
428	EEW93212.1	GG703805-94	<i>Granulicatella elegans</i> ATCC 700633	Granulicatella elegans ATCC 700633 phosphinothricin N-acetyltransferase protein.	192	1.2E-12	162	27.8
429	ACB26369.1	CP001001-4342	<i>Methylobacterium radiotolerans</i> JCM 2831	Methylobacterium radiotolerans JCM 2831 GCN5-related N-acetyltransferase protein.	192	1.2E-12	184	33.7
430	AAN00690.1	AE009948-1781	<i>Streptococcus agalactiae</i> 2603V/R	Streptococcus agalactiae 2603V/R phosphinothricin N-acetyltransferase protein.	163	1.3E-12	157	29.3
431	AAN00690.1	AE009948-1781	<i>Streptococcus agalactiae</i> 2603V/R	Streptococcus agalactiae 2603V/R phosphinothricin N-acetyltransferase protein.	163	1.3E-12	157	29.3
432	CAD47527.1	AL766854-11	<i>Streptococcus agalactiae</i> NEM316	Streptococcus agalactiae NEM316 Unknown protein.	163	1.3E-12	157	29.3
433	CAD47527.1	AL766854-11	<i>Streptococcus agalactiae</i> NEM316	Streptococcus agalactiae NEM316 Unknown protein.	163	1.3E-12	157	29.3
434	BAJ73445.1	AP012052-481	<i>Microbacterium testaceum</i> StLB037	Microbacterium testaceum StLB037 sortase protein.	203	1.3E-12	171	32.7
435	BAJ73445.1	AP012052-481	<i>Microbacterium testaceum</i> StLB037	Microbacterium testaceum StLB037 sortase protein.	203	1.3E-12	171	32.7
436	ABQ32672.1	CP000494-367	<i>Bradyrhizobium</i> sp	Bradyrhizobium sp. BTAi1 phosphinothricin acetyltransferase (PPT N-acetyltransferase) protein.	176	1.4E-12	160	33.1

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
437	ABQ32672.1	CP000494-367	<i>Bradyrhizobium</i> sp	Bradyrhizobium sp. BTAi1 phosphinothricin acetyltransferase (PPT N-acetyltransferase) protein.	176	1.4E-12	160	33.1
438	BAI98938.1	AP010804-575	<i>Sphingobium japonicum</i> UT26S	Sphingobium japonicum UT26S putative acetyltransferase protein.	181	1.4E-12	159	34.6
439	BAI98938.1	AP010804-575	<i>Sphingobium japonicum</i> UT26S	Sphingobium japonicum UT26S putative acetyltransferase protein.	181	1.4E-12	159	34.6
440	ABM59645.1	CP000542-3852	<i>Verminephrobacter eiseniae</i> EF01-2	Verminephrobacter eiseniae EF01-2 GCN5-related N-acetyltransferase protein.	181	1.4E-12	159	34.0
441	ABM59645.1	CP000542-3852	<i>Verminephrobacter eiseniae</i> EF01-2	Verminephrobacter eiseniae EF01-2 GCN5-related N-acetyltransferase protein.	181	1.4E-12	159	34.0
442	ADO47829.1	CP002272-1550	<i>Enterobacter cloacae</i> SCF1	Enterobacter cloacae SCF1 Phosphinothricin acetyltransferase protein.	184	1.4E-12	172	32.0
443	ADN61622.1	CP002218-2150	<i>Burkholderia</i> sp	Burkholderia sp. CCGE1003 Phosphinothricin acetyltransferase protein.	184	1.4E-12	166	33.1
444	ADN61622.1	CP002218-2150	<i>Burkholderia</i> sp	Burkholderia sp. CCGE1003 Phosphinothricin acetyltransferase protein.	184	1.4E-12	166	33.1
445	ADO47829.1	CP002272-1550	<i>Enterobacter cloacae</i> SCF1	Enterobacter cloacae SCF1 Phosphinothricin acetyltransferase protein.	184	1.4E-12	172	32.0
446	ADW05103.1	CP002475-3618	<i>Streptomyces flavogriseus</i> ATCC 33331	Streptomyces flavogriseus ATCC 33331 Phosphinothricin acetyltransferase protein.	192	1.5E-12	187	32.6
447	ADW05103.1	CP002475-3618	<i>Streptomyces flavogriseus</i> ATCC 33331	Streptomyces flavogriseus ATCC 33331 Phosphinothricin acetyltransferase protein.	192	1.5E-12	187	32.6
448	ACK49206.1	CP001280-221	<i>Methylocella silvestris</i> BL2	Methylocella silvestris BL2 GCN5-related N-acetyltransferase protein.	193	1.5E-12	169	30.8
449	ADJ45989.1	CP002000-4163	<i>Amycolatopsis mediterranei</i> U32	Amycolatopsis mediterranei U32 acetyltransferase protein.	162	1.5E-12	160	33.1
450	ADI12551.1	CP002047-9430	<i>Streptomyces bingchenggensis</i> BCW-1	Streptomyces bingchenggensis BCW-1 GCN5-related N-acetyltransferase protein.	162	1.5E-12	154	35.1
451	ADJ45989.1	CP002000-4163	<i>Amycolatopsis mediterranei</i> U32	Amycolatopsis mediterranei U32 acetyltransferase protein.	162	1.5E-12	160	33.1

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
452	ADI12551.1	CP002047-9430	<i>Streptomyces bingchenggensis</i> BCW-1	Streptomyces bingchenggensis BCW-1 GCN5-related N-acetyltransferase protein.	162	1.5E-12	154	35.1
453	AEK42773.1	CP002896-4278	<i>Amycolatopsis mediterranei</i> S699	Amycolatopsis mediterranei S699 acetyltransferase protein.	162	1.5E-12	160	33.1
454	AEK42773.1	CP002896-4278	<i>Amycolatopsis mediterranei</i> S699	Amycolatopsis mediterranei S699 acetyltransferase protein.	162	1.5E-12	160	33.1
455	ECT60761.1	EM704871-4	marine metagenome	marine metagenome hypothetical protein.	153	1.7E-12	150	37.3
456	AEG59860.1	CP002780-1553	<i>Desulfotomaculum ruminis</i> DSM 2154	Desulfotomaculum ruminis DSM 2154 GCN5-related N-acetyltransferase protein.	191	1.7E-12	185	31.4
457	AEG59860.1	CP002780-1553	<i>Desulfotomaculum ruminis</i> DSM 2154	Desulfotomaculum ruminis DSM 2154 GCN5-related N-acetyltransferase protein.	191	1.7E-12	185	31.4
458	ABR33160.1	CP000721-970	<i>Clostridium beijerinckii</i> NCIMB 8052	Clostridium beijerinckii NCIMB 8052 GCN5-related N-acetyltransferase protein.	170	1.8E-12	168	31.5
459	ABR33160.1	CP000721-970	<i>Clostridium beijerinckii</i> NCIMB 8052	Clostridium beijerinckii NCIMB 8052 GCN5-related N-acetyltransferase protein.	170	1.8E-12	168	31.5
460	ABS65271.1	CP000781-12	<i>Xanthobacter autotrophicus</i> Py2	Xanthobacter autotrophicus Py2 GCN5-related N-acetyltransferase protein.	180	1.9E-12	159	36.5
461	ABS65271.1	CP000781-12	<i>Xanthobacter autotrophicus</i> Py2	Xanthobacter autotrophicus Py2 GCN5-related N-acetyltransferase protein.	180	1.9E-12	159	36.5
462	ADU35719.1	CP002417-1496	<i>Variovorax paradoxus</i> EPS	Variovorax paradoxus EPS Phosphinothricin acetyltransferase protein.	182	1.9E-12	161	34.8
463	ADL01778.1	CP002102-2462	<i>Brevundimonas subvibrioides</i> ATCC 15264	Brevundimonas subvibrioides ATCC 15264 Phosphinothricin acetyltransferase protein.	182	1.9E-12	173	31.2
464	ADU35719.1	CP002417-1496	<i>Variovorax paradoxus</i> EPS	Variovorax paradoxus EPS Phosphinothricin acetyltransferase protein.	182	1.9E-12	161	34.8
465	ADL01778.1	CP002102-2462	<i>Brevundimonas subvibrioides</i> ATCC 15264	Brevundimonas subvibrioides ATCC 15264 Phosphinothricin acetyltransferase protein.	182	1.9E-12	173	31.2
466	AAK78834.1	AE001437-847	<i>Clostridium acetobutylicum</i> ATCC 824	Clostridium acetobutylicum ATCC 824 Phosphinothricin acetyltransferase protein.	196	2.1E-12	175	26.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
467	ADZ19909.1	CP002118-866	<i>Clostridium acetobutylicum</i> EA 2018	Clostridium acetobutylicum EA 2018 Phosphinothricin acetyltransferase protein.	196	2.1E-12	175	26.3
468	AEI33525.1	CP002660-866	<i>Clostridium acetobutylicum</i> DSM 1731	Clostridium acetobutylicum DSM 1731 phosphinothricin acetyltransferase protein.	196	2.1E-12	175	26.3
469	ADZ19909.1	CP002118-866	<i>Clostridium acetobutylicum</i> EA 2018	Clostridium acetobutylicum EA 2018 Phosphinothricin acetyltransferase protein.	196	2.1E-12	175	26.3
470	AAK78834.1	AE001437-847	<i>Clostridium acetobutylicum</i> ATCC 824	Clostridium acetobutylicum ATCC 824 Phosphinothricin acetyltransferase protein.	196	2.1E-12	175	26.3
471	AEI33525.1	CP002660-866	<i>Clostridium acetobutylicum</i> DSM 1731	Clostridium acetobutylicum DSM 1731 phosphinothricin acetyltransferase protein.	196	2.1E-12	175	26.3
472	AEG44753.1	CP002810-1935	<i>Isoptericola variabilis</i> 225	Isoptericola variabilis 225 GCN5-related N-acetyltransferase protein.	206	2.2E-12	189	34.4
473	AEG44753.1	CP002810-1935	<i>Isoptericola variabilis</i> 225	Isoptericola variabilis 225 GCN5-related N-acetyltransferase protein.	206	2.2E-12	189	34.4
474	CBG72325.1	FN554889-5096	<i>Streptomyces scabiei</i> 87	Streptomyces scabiei 87.22 putative N-acetyltransferase protein.	172	2.2E-12	174	31.6
475	CBG72325.1	FN554889-5096	<i>Streptomyces scabiei</i> 87	Streptomyces scabiei 87.22 putative N-acetyltransferase protein.	172	2.2E-12	174	31.6
476	EDE25953.1	EP717397-2	marine metagenome	marine metagenome hypothetical protein.	177	2.2E-12	170	35.3
477	ABS12832.1	CP000758-100	<i>Ochrobactrum anthropi</i> ATCC 49188	Ochrobactrum anthropi ATCC 49188 GCN5-related N-acetyltransferase protein.	193	2.4E-12	177	31.6
478	ABS12832.1	CP000758-100	<i>Ochrobactrum anthropi</i> ATCC 49188	Ochrobactrum anthropi ATCC 49188 GCN5-related N-acetyltransferase protein.	193	2.4E-12	177	31.6
479	CBL25177.1	FP929055-355	<i>Ruminococcus torques</i> L2-14	Ruminococcus torques L2-14 Sortase and related acyltransferases protein.	196	2.4E-12	178	29.2
480	CBL25177.1	FP929055-355	<i>Ruminococcus torques</i> L2-14	Ruminococcus torques L2-14 Sortase and related acyltransferases protein.	196	2.4E-12	178	29.2

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
481	CBL24674.1	FP929054-3007	<i>Ruminococcus obeum</i> A2-162	Ruminococcus obeum A2-162 Sortase and related acyltransferases protein.	202	2.5E-12	171	30.4
482	CBL24674.1	FP929054-3007	<i>Ruminococcus obeum</i> A2-162	Ruminococcus obeum A2-162 Sortase and related acyltransferases protein.	202	2.5E-12	171	30.4
483	ACV23140.1	CP001684-2063	<i>Slackia heliotrinireducens</i> DSM 20476	Slackia heliotrinireducens DSM 20476 sortase-like acyltransferase protein.	210	2.6E-12	183	31.7
484	AAO56799.1	AE016853-3249	<i>Pseudomonas syringae</i> pv	Pseudomonas syringae pv. tomato str. DC3000 phosphinothricin N-acetyltransferase protein.	179	2.7E-12	168	33.3
485	AAO56799.1	AE016853-3249	<i>Pseudomonas syringae</i> pv	Pseudomonas syringae pv. tomato str. DC3000 phosphinothricin N-acetyltransferase protein.	179	2.7E-12	168	33.3
486	AAK86681.2	AE007869-857	<i>Agrobacterium tumefaciens</i> str	Agrobacterium tumefaciens str. C58 acetyltransferase protein.	180	2.7E-12	170	32.9
487	AAK86681.2	AE007869-857	<i>Agrobacterium tumefaciens</i> str	Agrobacterium tumefaciens str. C58 acetyltransferase protein.	180	2.7E-12	170	32.9
488	ABO58146.1	CP000615-1844	<i>Burkholderia vietnamiensis</i> G4	Burkholderia vietnamiensis G4 GCN5-related N-acetyltransferase protein.	186	2.8E-12	179	31.3
489	ABO58146.1	CP000615-1844	<i>Burkholderia vietnamiensis</i> G4	Burkholderia vietnamiensis G4 GCN5-related N-acetyltransferase protein.	186	2.8E-12	179	31.3
490	BAC48441.1	BA000040-3176	<i>Bradyrhizobium japonicum</i> USDA 110	Bradyrhizobium japonicum USDA 110 acetyltransferase protein.	194	2.9E-12	179	31.3
491	BAC48441.1	BA000040-3176	<i>Bradyrhizobium japonicum</i> USDA 110	Bradyrhizobium japonicum USDA 110 acetyltransferase protein.	194	2.9E-12	179	31.3
492	ABP67601.1	CP000679-1936	<i>Caldicellulosiruptor saccharolyticus</i> DSM 8903	Caldicellulosiruptor saccharolyticus DSM 8903 GCN5-related N-acetyltransferase protein.	162	2.9E-12	157	29.3
493	ABP67601.1	CP000679-1936	<i>Caldicellulosiruptor saccharolyticus</i> DSM 8903	Caldicellulosiruptor saccharolyticus DSM 8903 GCN5-related N-acetyltransferase protein.	162	2.9E-12	157	29.3
494	AAZ62631.1	CP000090-3249	<i>Ralstonia eutropha</i> JMP134	Ralstonia eutropha JMP134 GCN5-related N-acetyltransferase protein.	210	3.1E-12	172	32.6
495	AAZ62631.1	CP000090-3249	<i>Ralstonia eutropha</i> JMP134	Ralstonia eutropha JMP134 GCN5-related N-acetyltransferase protein.	210	3.1E-12	172	32.6

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
496	AAQ58050.1	AE016825-372	<i>Chromobacterium violaceum</i> ATCC 12472	Chromobacterium violaceum ATCC 12472 probable resistance protein.	174	3.1E-12	174	32.2
497	AAQ58050.1	AE016825-372	<i>Chromobacterium violaceum</i> ATCC 12472	Chromobacterium violaceum ATCC 12472 probable resistance protein.	174	3.1E-12	174	32.2
498	ADG17728.1	CP002014-498	<i>Burkholderia</i> sp	Burkholderia sp. CCGE1002 Phosphinothricin acetyltransferase protein.	193	3.4E-12	181	30.9
499	ADG17728.1	CP002014-498	<i>Burkholderia</i> sp	Burkholderia sp. CCGE1002 Phosphinothricin acetyltransferase protein.	193	3.4E-12	181	30.9
500	ABA45966.1	CP000114-1717	<i>Streptococcus agalactiae</i> A909	Streptococcus agalactiae A909 phosphinothricin N-acetyltransferase, putative protein.	163	3.4E-12	157	28.7
501	ABA45966.1	CP000114-1717	<i>Streptococcus agalactiae</i> A909	Streptococcus agalactiae A909 phosphinothricin N-acetyltransferase, putative protein.	163	3.4E-12	157	28.7
502	ABE34181.1	CP000271-1213	<i>Burkholderia xenovorans</i> LB400	Burkholderia xenovorans LB400 putative phosphinothricin N-acetyltransferase protein.	200	3.5E-12	178	33.7
503	ABE34181.1	CP000271-1213	<i>Burkholderia xenovorans</i> LB400	Burkholderia xenovorans LB400 putative phosphinothricin N-acetyltransferase protein.	200	3.5E-12	178	33.7
504	EDU10965.1	CH899718-386	<i>Burkholderia pseudomallei</i> 1655	Burkholderia pseudomallei 1655 phosphinothricin N-acetyltransferase protein.	247	3.5E-12	163	33.1
505	ACV56324.1	CP001726-2329	<i>Eggerthella lenta</i> DSM 2243	Eggerthella lenta DSM 2243 GCN5-related N-acetyltransferase protein.	213	3.7E-12	179	32.4
506	EEZ15653.1	EQ999573-395	<i>Brucella melitensis</i> bv	Brucella melitensis bv. 1 str. Rev.1 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
507	EEZ30278.1	EQ999546-397	<i>Brucella pinnipedialis</i> M292/94/1	Brucella pinnipedialis M292/94/1 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
508	ABQ61144.1	CP000708-81	<i>Brucella ovis</i> ATCC 25840	Brucella ovis ATCC 25840 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
509	AAL53039.1	AE008917-1857	<i>Brucella melitensis</i> bv	Brucella melitensis bv. 1 str. 16M phosphinothricin n-acetyltransferase protein.	179	3.7E-12	162	32.7
510	ACU47112.1	CP001578-90	<i>Brucella microti</i> CCM 4915	Brucella microti CCM 4915 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
511	ABX61192.1	CP000872-85	<i>Brucella canis</i> ATCC 23365	Brucella canis ATCC 23365 Phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
512	AAL53039.1	AE008917-1857	<i>Brucella melitensis</i> bv	Brucella melitensis bv. 1 str. 16M phosphinothricin n-acetyltransferase protein.	179	3.7E-12	162	32.7
513	AEM17457.1	CP002997-87	<i>Brucella suis</i> 1330	Brucella suis 1330 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
514	ABQ61144.1	CP000708-81	<i>Brucella ovis</i> ATCC 25840	Brucella ovis ATCC 25840 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
515	AAN29045.1	AE014291-87	<i>Brucella suis</i> 1330	Brucella suis 1330 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
516	AAN29045.1	AE014291-87	<i>Brucella suis</i> 1330	Brucella suis 1330 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
517	EEY27185.1	GG663486-399	<i>Brucella</i> sp	Brucella sp. F5/99 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
518	EEY33657.1	DS999748-404	<i>Brucella suis</i> bv	Brucella suis bv. 3 str. 686 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
519	AEK53413.1	CP002078-87	<i>Brucella pinnipedialis</i> B2/94	Brucella pinnipedialis B2/94 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
520	EEY29095.1	DS999724-403	<i>Brucella suis</i> bv	Brucella suis bv. 5 str. 513 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
521	EEX89749.1	DS999687-398	<i>Brucella ceti</i> M13/05/1	Brucella ceti M13/05/1 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
522	EEY03684.1	EQ999582-395	<i>Brucella neotomae</i> 5K33	Brucella neotomae 5K33 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
523	EEY07216.1	DS999752-150	<i>Brucella pinnipedialis</i> M163/99/10	Brucella pinnipedialis M163/99/10 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
524	AEK53413.1	CP002078-87	<i>Brucella pinnipedialis</i> B2/94	Brucella pinnipedialis B2/94 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
525	EEZ10937.1	EQ999591-408	<i>Brucella melitensis</i> bv	Brucella melitensis bv. 3 str. Ether phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
526	EEX97247.1	DS999670-490	<i>Brucella ceti</i> M644/93/1	Brucella ceti M644/93/1 phosphinothricin acetyltransferase protein.	179	3.7E-12	162	32.7
527	AEM17457.1	CP002997-87	<i>Brucella suis</i> 1330	Brucella suis 1330 phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
528	EFG37082.1	GG770510-391	<i>Brucella</i> sp	Brucella sp. NVSL 07-0026 acetyltransferase protein.	179	3.7E-12	162	32.7

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
529	EEW91865.1	GG703793-1385	<i>Brucella suis</i> bv	Brucella suis bv. 4 str. 40 phosphinotricin acetyltransferase protein.	179	3.7E-12	162	32.7
530	ABY37197.1	CP000911-86	<i>Brucella suis</i> ATCC 23445	Brucella suis ATCC 23445 Phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
531	EEW88274.1	GG703778-383	<i>Brucella melitensis</i> bv	Brucella melitensis bv. 1 str. 16M phosphinotricin acetyltransferase protein.	179	3.7E-12	162	32.7
532	ABX61192.1	CP000872-85	<i>Brucella canis</i> ATCC 23365	Brucella canis ATCC 23365 Phosphinothricin N-acetyltransferase protein.	179	3.7E-12	162	32.7
533	EEX99467.1	DS999848-397	<i>Brucella pinnipedialis</i> B2/94	Brucella pinnipedialis B2/94 phosphinotricin acetyltransferase protein.	179	3.7E-12	162	32.7
534	ADU14683.1	CP002396-649	<i>Asticcacaulis excentricus</i> CB 48	Asticcacaulis excentricus CB 48 Phosphinothricin acetyltransferase protein.	180	3.7E-12	170	35.3
535	ADU14683.1	CP002396-649	<i>Asticcacaulis excentricus</i> CB 48	Asticcacaulis excentricus CB 48 Phosphinothricin acetyltransferase protein.	180	3.7E-12	170	35.3
536	AEB14137.1	CP002631-1167	<i>Treponema succinifaciens</i> DSM 2489	Treponema succinifaciens DSM 2489 Phosphinothricin acetyltransferase protein.	184	3.8E-12	177	28.2
537	AEB14137.1	CP002631-1167	<i>Treponema succinifaciens</i> DSM 2489	Treponema succinifaciens DSM 2489 Phosphinothricin acetyltransferase protein.	184	3.8E-12	177	28.2
538	EEC19730.1	DS966174-1	<i>Ixodes scapularis</i>	Ixodes scapularis phosphinothricin N-acetyltransferase, putative protein.	164	4.1E-12	161	34.8
539	ACS58299.1	CP001622-3987	<i>Rhizobium leguminosarum</i> bv	Rhizobium leguminosarum bv. trifolii WSM1325 GCN5-related N-acetyltransferase protein.	200	4.1E-12	171	28.7
540	CCA91761.1	FR856862-784	<i>Novosphingobium</i> sp	Novosphingobium sp. PP1Y phosphinothricin acetyltransferase protein.	181	4.4E-12	166	34.9
541	CCA91761.1	FR856862-784	<i>Novosphingobium</i> sp	Novosphingobium sp. PP1Y phosphinothricin acetyltransferase protein.	181	4.4E-12	166	34.9
542	ADF62978.1	CP001918-3410	<i>Enterobacter cloacae</i> subsp	Enterobacter cloacae subsp. cloacae ATCC 13047 GCN5-related N-acetyltransferase protein.	184	4.5E-12	172	32.0
543	CAR55667.1	AM747721-1814	<i>Burkholderia cenocepacia</i> J2315	Burkholderia cenocepacia J2315 putative acetyltransferase protein.	186	4.5E-12	172	30.2
544	CAR55667.1	AM747721-1814	<i>Burkholderia cenocepacia</i> J2315	Burkholderia cenocepacia J2315 putative acetyltransferase protein.	186	4.5E-12	172	30.2

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
545	EEB79741.1	DS999223-22	<i>marine gamma proteobacterium HTCC2148</i>	marine gamma proteobacterium HTCC2148 acetyltransferase, GNAT family protein.	154	4.6E-12	147	34.0
546	ADG76526.1	CP001964-3606	<i>Cellulomonas flavigena DSM 20109</i>	Cellulomonas flavigena DSM 20109 Phosphinothricin acetyltransferase protein.	168	4.9E-12	161	31.1
547	ADG76526.1	CP001964-3606	<i>Cellulomonas flavigena DSM 20109</i>	Cellulomonas flavigena DSM 20109 Phosphinothricin acetyltransferase protein.	168	4.9E-12	161	31.1
548	CAJ25646.1	AM039952-3915	<i>Xanthomonas euvesicatoria</i>	Xanthomonas euvesicatoria N-acetyltransferase protein.	173	5E-12	162	32.1
549	CAJ25646.1	AM039952-3915	<i>Xanthomonas euvesicatoria</i>	Xanthomonas euvesicatoria N-acetyltransferase protein.	173	5E-12	162	32.1
550	AAM38633.1	AE008923-3741	<i>Xanthomonas axonopodis pv</i>	Xanthomonas axonopodis pv. citri str. 306 phosphinothricin acetyltransferase protein.	173	5E-12	162	32.1
551	AAM38633.1	AE008923-3741	<i>Xanthomonas axonopodis pv</i>	Xanthomonas axonopodis pv. citri str. 306 phosphinothricin acetyltransferase protein.	173	5E-12	162	32.1
552	AEJ25860.1	CP002904-1627	<i>Streptococcus equi subsp</i>	Streptococcus equi subsp. zooepidemicus ATCC 35246 Phosphinothricin N-acetyltransferase protein.	212	5.1E-12	177	33.3
553	AEJ25860.1	CP002904-1627	<i>Streptococcus equi subsp</i>	Streptococcus equi subsp. zooepidemicus ATCC 35246 Phosphinothricin N-acetyltransferase protein.	212	5.1E-12	177	33.3
554	CBK74492.1	FP929036-1479	<i>Butyrivibrio fibrisolvens 16/4</i>	Butyrivibrio fibrisolvens 16/4 Sortase and related acyltransferases protein.	175	5.1E-12	161	29.8
555	CBK74492.1	FP929036-1479	<i>Butyrivibrio fibrisolvens 16/4</i>	Butyrivibrio fibrisolvens 16/4 Sortase and related acyltransferases protein.	175	5.1E-12	161	29.8
556	CAO97291.1	CU468135-2245	<i>Erwinia tasmaniensis</i>	Erwinia tasmaniensis Putative N-acetyltransferase protein.	179	5.2E-12	160	31.9
557	CAO97291.1	CU468135-2245	<i>Erwinia tasmaniensis</i>	Erwinia tasmaniensis Putative N-acetyltransferase protein.	179	5.2E-12	160	31.9
558	ADO09381.1	CP002206-1158	<i>Pantoea vagans C9-1</i>	Pantoea vagans C9-1 putative acetyltransferase protein.	222	5.3E-12	172	28.5
559	ADO09381.1	CP002206-1158	<i>Pantoea vagans C9-1</i>	Pantoea vagans C9-1 putative acetyltransferase protein.	222	5.3E-12	172	28.5
560	ABE61138.1	CP000319-236	<i>Nitrobacter hamburgensis X14</i>	Nitrobacter hamburgensis X14 GCN5-related N-acetyltransferase protein.	183	5.3E-12	161	33.5

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
561	ABE61138.1	CP000319-236	<i>Nitrobacter hamburgensis</i> X14	Nitrobacter hamburgensis X14 GCN5-related N-acetyltransferase protein.	183	5.3E-12	161	33.5
562	ACU94607.1	CP001682-870	<i>Cryptobacterium curtum</i> DSM 15641	Cryptobacterium curtum DSM 15641 sortase-like acyltransferase protein.	185	5.3E-12	175	30.9
563	ABF78591.1	CP000379-710	<i>Burkholderia cenocepacia</i> AU 1054	Burkholderia cenocepacia AU 1054 GCN5-related N-acetyltransferase protein.	186	5.4E-12	172	30.2
564	ABK11403.1	CP000459-1490	<i>Burkholderia cenocepacia</i> HI2424	Burkholderia cenocepacia HI2424 GCN5-related N-acetyltransferase protein.	186	5.4E-12	172	30.2
565	ABK11403.1	CP000459-1490	<i>Burkholderia cenocepacia</i> HI2424	Burkholderia cenocepacia HI2424 GCN5-related N-acetyltransferase protein.	186	5.4E-12	172	30.2
566	ABF78591.1	CP000379-710	<i>Burkholderia cenocepacia</i> AU 1054	Burkholderia cenocepacia AU 1054 GCN5-related N-acetyltransferase protein.	186	5.4E-12	172	30.2
567	ACA94756.1	CP000959-2415	<i>Burkholderia cenocepacia</i> MC0-3	Burkholderia cenocepacia MC0-3 GCN5-related N-acetyltransferase protein.	186	5.4E-12	172	30.2
568	CAQ70960.1	CU633749-2969	<i>Cupriavidus taiwanensis</i>	Cupriavidus taiwanensis Phosphinothricin N-acetyltransferase protein.	197	5.6E-12	167	31.1
569	CAQ70960.1	CU633749-2969	<i>Cupriavidus taiwanensis</i>	Cupriavidus taiwanensis Phosphinothricin N-acetyltransferase protein.	197	5.6E-12	167	31.1
570	BAE17515.1	AP008934-370	<i>Staphylococcus saprophyticus</i> subsp.	Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305 putative acetyltransferase protein.	163	5.6E-12	162	30.2
571	BAE17515.1	AP008934-370	<i>Staphylococcus saprophyticus</i> subsp.	Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305 putative acetyltransferase protein.	163	5.6E-12	162	30.2
572	ABE43625.1	CP000316-1658	<i>Polaromonas</i> sp.	Polaromonas sp. JS666 GCN5-related N-acetyltransferase protein.	178	6.1E-12	176	34.1
573	ABE43625.1	CP000316-1658	<i>Polaromonas</i> sp.	Polaromonas sp. JS666 GCN5-related N-acetyltransferase protein.	178	6.1E-12	176	34.1
574	ADG11792.1	CP002008-3258	<i>Caulobacter segnis</i> ATCC 21756	Caulobacter segnis ATCC 21756 Phosphinothricin acetyltransferase protein.	185	6.3E-12	174	32.8
575	ADG11792.1	CP002008-3258	<i>Caulobacter segnis</i> ATCC 21756	Caulobacter segnis ATCC 21756 Phosphinothricin acetyltransferase protein.	185	6.3E-12	174	32.8
576	EAY64636.1	CH482378-48	<i>Burkholderia cenocepacia</i> PC184	Burkholderia cenocepacia PC184 GCN5-related N-acetyltransferase protein.	186	6.3E-12	172	30.2
577	ABS65892.1	CP000781-633	<i>Xanthobacter autotrophicus</i> Py2	Xanthobacter autotrophicus Py2 GCN5-related N-acetyltransferase protein.	186	6.3E-12	183	30.6

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
578	ABS65892.1	CP000781-633	<i>Xanthobacter autotrophicus</i> Py2	Xanthobacter autotrophicus Py2 GCN5-related N-acetyltransferase protein.	186	6.3E-12	183	30.6
579	ABM94064.1	CP000555-1102	<i>Methylibium petroleiphilum</i> PM1	Methylibium petroleiphilum PM1 putative phosphinothricin acetyltransferase protein.	190	6.4E-12	176	32.4
580	ABM94064.1	CP000555-1102	<i>Methylibium petroleiphilum</i> PM1	Methylibium petroleiphilum PM1 putative phosphinothricin acetyltransferase protein.	190	6.4E-12	176	32.4
581	AAW73849.1	AE013598-579	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae KACC10331 phosphinothricin acetyltransferase protein.	201	6.7E-12	171	32.2
582	AAW73849.1	AE013598-579	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae KACC10331 phosphinothricin acetyltransferase protein.	201	6.7E-12	171	32.2
583	BAI73745.1	AP010947-214	<i>Azospirillum</i> sp	Azospirillum sp. B510 acetyltransferase protein.	177	7.1E-12	155	32.9
584	BAI73745.1	AP010947-214	<i>Azospirillum</i> sp	Azospirillum sp. B510 acetyltransferase protein.	177	7.1E-12	155	32.9
585	EEZ32121.1	DS999649-394	<i>Brucella</i> sp	Brucella sp. 83/13 phosphinothricin acetyltransferase protein.	179	7.2E-12	162	32.1
586	ABR61903.1	CP000738-3043	<i>Sinorhizobium medicae</i> WSM419	Sinorhizobium medicae WSM419 GCN5-related N-acetyltransferase protein.	185	7.4E-12	177	29.9
587	ABR61903.1	CP000738-3043	<i>Sinorhizobium medicae</i> WSM419	Sinorhizobium medicae WSM419 GCN5-related N-acetyltransferase protein.	185	7.4E-12	177	29.9
588	ACB32955.1	CP001013-679	<i>Leptothrix cholodnii</i> SP-6	Leptothrix cholodnii SP-6 GCN5-related N-acetyltransferase protein.	186	7.5E-12	171	33.9
589	EET04097.1	CM000833-418	<i>Burkholderia pseudomallei</i> 1710a	Burkholderia pseudomallei 1710a phosphinothricin N-acetyltransferase protein.	188	7.5E-12	163	32.5
590	CAH38393.1	BX571966-950	<i>Burkholderia pseudomallei</i> K96243	Burkholderia pseudomallei K96243 putative phosphinothricin N-acetyltransferase protein.	188	7.5E-12	163	32.5
591	CAH38393.1	BX571966-950	<i>Burkholderia pseudomallei</i> K96243	Burkholderia pseudomallei K96243 putative phosphinothricin N-acetyltransferase protein.	188	7.5E-12	163	32.5
592	ADK30062.1	CP002025-53	<i>Brachyspira pilosicoli</i> 95/1000	Brachyspira pilosicoli 95/1000 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase protein.	189	7.6E-12	175	28.6
593	ADK30062.1	CP002025-53	<i>Brachyspira pilosicoli</i> 95/1000	Brachyspira pilosicoli 95/1000 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase protein.	189	7.6E-12	175	28.6
594	ECE32840.1	EM724634-2	marine metagenome	marine metagenome hypothetical protein.	162	7.8E-12	158	30.4

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
595	EDY53486.1	CM000951-3571	<i>Streptomyces sviveus</i> ATCC 29083	Streptomyces sviveus ATCC 29083 phosphinothricin N-acetyltransferase protein.	169	8.1E-12	169	30.8
596	ECV06255.1	EQ085183-16	<i>marine metagenome</i>	marine metagenome hypothetical protein.	208	8.2E-12	171	32.7
597	AEL07343.1	CP002789-2413	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. raphani 756C phosphinothricin N-acetyltransferase protein.	175	8.4E-12	171	32.2
598	AEL07343.1	CP002789-2413	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. raphani 756C phosphinothricin N-acetyltransferase protein.	175	8.4E-12	171	32.2
599	ACM26997.1	CP000628-2201	<i>Agrobacterium radiobacter K84</i>	Agrobacterium radiobacter K84 phosphinothricin acetyltransferase (antibiotic resistance) protein.	183	8.7E-12	169	34.9
600	ACM26997.1	CP000628-2201	<i>Agrobacterium radiobacter K84</i>	Agrobacterium radiobacter K84 phosphinothricin acetyltransferase (antibiotic resistance) protein.	183	8.7E-12	169	34.9
601	ADY37320.1	CP002530-2704	<i>Bacteroides salanitronis DSM 18170</i>	Bacteroides salanitronis DSM 18170 Phosphinothricin acetyltransferase protein.	160	9.1E-12	161	32.9
602	ADY37320.1	CP002530-2704	<i>Bacteroides salanitronis DSM 18170</i>	Bacteroides salanitronis DSM 18170 Phosphinothricin acetyltransferase protein.	160	9.1E-12	161	32.9
603	EDO93371.1	CH899749-366	<i>Burkholderia pseudomallei Pasteur 52237</i>	Burkholderia pseudomallei Pasteur 52237 phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
604	ABN94562.1	CP000573-1263	<i>Burkholderia pseudomallei 1106a</i>	Burkholderia pseudomallei 1106a phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
605	EES20766.1	CM000775-915	<i>Burkholderia pseudomallei 1106b</i>	Burkholderia pseudomallei 1106b phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
606	EDO87006.1	CH899736-354	<i>Burkholderia pseudomallei 406e</i>	Burkholderia pseudomallei 406e phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
607	ABN88367.1	CP000571-1299	<i>Burkholderia pseudomallei 668</i>	Burkholderia pseudomallei 668 phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
608	ABA53754.1	CP000125-2521	<i>Burkholderia pseudomallei 1710b</i>	Burkholderia pseudomallei 1710b phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
609	EDS82575.1	CH899760-354	<i>Burkholderia pseudomallei S13</i>	Burkholderia pseudomallei S13 phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
610	ABA53754.1	CP000125-2521	<i>Burkholderia pseudomallei</i> 1710b	Burkholderia pseudomallei 1710b phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
611	ABN88367.1	CP000571-1299	<i>Burkholderia pseudomallei</i> 668	Burkholderia pseudomallei 668 phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
612	ABN94562.1	CP000573-1263	<i>Burkholderia pseudomallei</i> 1106a	Burkholderia pseudomallei 1106a phosphinothricin N-acetyltransferase protein.	247	9.5E-12	163	32.5
613	CAP51333.1	AM920689-2005	<i>Xanthomonas campestris</i> pv	Xanthomonas campestris pv. campestris Putative phosphinothricin N-acetyltransferase protein.	175	9.9E-12	172	32.6
614	CAP51333.1	AM920689-2005	<i>Xanthomonas campestris</i> pv	Xanthomonas campestris pv. campestris Putative phosphinothricin N-acetyltransferase protein.	175	9.9E-12	172	32.6
615	EEX86557.1	EQ999621-401	<i>Brucella ceti</i> B1/94	Brucella ceti B1/94 phosphinothricin acetyltransferase protein.	179	1E-11	162	32.1
616	EEZ07738.1	EQ999608-401	<i>Brucella ceti</i> M490/95/1	Brucella ceti M490/95/1 phosphinothricin acetyltransferase protein.	179	1E-11	162	32.1
617	ABC35766.1	CP000085-1461	<i>Burkholderia thailandensis</i> E264	Burkholderia thailandensis E264 phosphinothricin N-acetyltransferase protein.	188	1E-11	173	32.9
618	ABC35766.1	CP000085-1461	<i>Burkholderia thailandensis</i> E264	Burkholderia thailandensis E264 phosphinothricin N-acetyltransferase protein.	188	1E-11	173	32.9
619	EES75633.1	GG696056-14	<i>Ruminococcus</i> sp	Ruminococcus sp. 5_1_39BFAA conserved hypothetical protein.	194	1.1E-11	164	28.7
620	EBY65917.1	EM981354-2	marine metagenome	marine metagenome hypothetical protein.	140	1.1E-11	142	35.2
621	EDX20992.1	DS570385-131	<i>Streptomyces</i> sp	Streptomyces sp. Mg1 conserved hypothetical protein.	172	1.1E-11	168	34.5
622	ADG73303.1	CP001964-383	<i>Cellulomonas flavigena</i> DSM 20109	Cellulomonas flavigena DSM 20109 Phosphinothricin acetyltransferase protein.	173	1.2E-11	161	32.9
623	BAK13605.1	AP012032-3525	<i>Pantoea ananatis</i> AJ13355	Pantoea ananatis AJ13355 phosphinothricin N-acetyltransferase Pat protein.	188	1.2E-11	161	31.7
624	BAK13605.1	AP012032-3525	<i>Pantoea ananatis</i> AJ13355	Pantoea ananatis AJ13355 phosphinothricin N-acetyltransferase Pat protein.	188	1.2E-11	161	31.7
625	ACD19247.1	CP001053-872	<i>Burkholderia phytofirmans</i> PsJN	Burkholderia phytofirmans PsJN GCN5-related N-acetyltransferase protein.	197	1.3E-11	163	33.7
626	ACD57341.1	CP000967-674	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae PXO99A N-acetyltransferase protein.	173	1.4E-11	162	32.1

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
627	BAE67311.1	AP008229-556	<i>Xanthomonas oryzae pv</i>	Xanthomonas oryzae pv. oryzae MAFF 311018 phosphinothricin acetyltransferase protein.	173	1.4E-11	162	32.1
628	BAE67311.1	AP008229-556	<i>Xanthomonas oryzae pv</i>	Xanthomonas oryzae pv. oryzae MAFF 311018 phosphinothricin acetyltransferase protein.	173	1.4E-11	162	32.1
629	AAM41480.1	AE008922-2161	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. ATCC 33913 phosphinothricin N-acetyltransferase protein.	175	1.4E-11	171	32.2
630	AAY48981.1	CP000050-1887	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. 8004 phosphinothricin N-acetyltransferase protein.	175	1.4E-11	171	32.2
631	AAY48981.1	CP000050-1887	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. 8004 phosphinothricin N-acetyltransferase protein.	175	1.4E-11	171	32.2
632	AAM41480.1	AE008922-2161	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. ATCC 33913 phosphinothricin N-acetyltransferase protein.	175	1.4E-11	171	32.2
633	ACB95238.1	CP001016-1579	<i>Beijerinckia indica subsp</i>	Beijerinckia indica subsp. indica ATCC 9039 GCN5-related N-acetyltransferase protein.	180	1.4E-11	160	33.1
634	ACP26974.1	CP001389-3170	<i>Sinorhizobium fredii NGR234</i>	Sinorhizobium fredii NGR234 putative GCN5-related N-acetyltransferase protein.	185	1.4E-11	177	28.8
635	CCC72813.1	HE576794-589	<i>Megasphaera elsdenii DSM 20460</i>	Megasphaera elsdenii DSM 20460 putative uncharacterized protein.	186	1.4E-11	183	28.4
636	CCC72813.1	HE576794-589	<i>Megasphaera elsdenii DSM 20460</i>	Megasphaera elsdenii DSM 20460 putative uncharacterized protein.	186	1.4E-11	183	28.4
637	ABO02876.1	CP000547-912	<i>Burkholderia mallei NCTC 10247</i>	Burkholderia mallei NCTC 10247 phosphinothricin N-acetyltransferase protein.	188	1.5E-11	163	32.5
638	EDK84125.1	CH899692-455	<i>Burkholderia mallei 2002721280</i>	Burkholderia mallei 2002721280 phosphinothricin N-acetyltransferase protein.	188	1.5E-11	163	32.5
639	ABO02876.1	CP000547-912	<i>Burkholderia mallei NCTC 10247</i>	Burkholderia mallei NCTC 10247 phosphinothricin N-acetyltransferase protein.	188	1.5E-11	163	32.5
640	ABC23207.1	CP000230-2402	<i>Rhodospirillum rubrum ATCC 11170</i>	Rhodospirillum rubrum ATCC 11170 GCN5-related N-acetyltransferase protein.	195	1.5E-11	183	33.9
641	ABC23207.1	CP000230-2402	<i>Rhodospirillum rubrum ATCC 11170</i>	Rhodospirillum rubrum ATCC 11170 GCN5-related N-acetyltransferase protein.	195	1.5E-11	183	33.9
642	AAU46447.1	CP000011-1244	<i>Burkholderia mallei ATCC 23344</i>	Burkholderia mallei ATCC 23344 phosphinothricin N-acetyltransferase protein.	210	1.6E-11	163	32.5
643	AAU46447.1	CP000011-1244	<i>Burkholderia mallei ATCC 23344</i>	Burkholderia mallei ATCC 23344 phosphinothricin N-acetyltransferase protein.	210	1.6E-11	163	32.5

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
644	AEA63118.1	CP002600-635	<i>Burkholderia gladioli</i> BSR3	Burkholderia gladioli BSR3 GCN5-related N-acetyltransferase protein.	174	1.6E-11	177	35.0
645	AEA63118.1	CP002600-635	<i>Burkholderia gladioli</i> BSR3	Burkholderia gladioli BSR3 GCN5-related N-acetyltransferase protein.	174	1.6E-11	177	35.0
646	ADY63795.1	CP002248-798	<i>Agrobacterium</i> sp	Agrobacterium sp. H13-3 GCN5-related N-acetyltransferase protein.	180	1.7E-11	167	29.3
647	ADY63795.1	CP002248-798	<i>Agrobacterium</i> sp	Agrobacterium sp. H13-3 GCN5-related N-acetyltransferase protein.	180	1.7E-11	167	29.3
648	ABZ70472.1	CP000927-1334	<i>Caulobacter</i> sp	Caulobacter sp. K31 GCN5-related N-acetyltransferase protein.	185	1.7E-11	174	32.2
649	ADG72799.1	CP001959-2688	<i>Brachyspira murdochii</i> DSM 12563	Brachyspira murdochii DSM 12563 GCN5-related N-acetyltransferase protein.	190	1.7E-11	161	28.0
650	ABM32467.1	CP000512-1849	<i>Acidovorax citrulli</i> AAC00-1	Acidovorax citrulli AAC00-1 GCN5-related N-acetyltransferase protein.	197	1.8E-11	168	31.5
651	ABM32467.1	CP000512-1849	<i>Acidovorax citrulli</i> AAC00-1	Acidovorax citrulli AAC00-1 GCN5-related N-acetyltransferase protein.	197	1.8E-11	168	31.5
652	CAK10017.1	AM236080-4530	<i>Rhizobium leguminosarum</i> bv	Rhizobium leguminosarum bv. viciae 3841 putative acetyltransferase protein.	200	1.8E-11	171	28.1
653	CAK10017.1	AM236080-4530	<i>Rhizobium leguminosarum</i> bv	Rhizobium leguminosarum bv. viciae 3841 putative acetyltransferase protein.	200	1.8E-11	171	28.1
654	AEC20648.1	CP002663-2108	<i>Pusillimonas</i> sp	Pusillimonas sp. T7-7 N-acetyltransferase protein.	201	1.8E-11	176	31.2
655	AEC20648.1	CP002663-2108	<i>Pusillimonas</i> sp	Pusillimonas sp. T7-7 N-acetyltransferase protein.	201	1.8E-11	176	31.2
656	ABM47945.1	CP000525-272	<i>Burkholderia mallei</i> SAVP1	Burkholderia mallei SAVP1 phosphinothricin N-acetyltransferase protein.	247	1.8E-11	163	32.5
657	ABM47945.1	CP000525-272	<i>Burkholderia mallei</i> SAVP1	Burkholderia mallei SAVP1 phosphinothricin N-acetyltransferase protein.	247	1.8E-11	163	32.5
658	EDK61383.1	DS264106-352	<i>Burkholderia mallei</i> JHU	Burkholderia mallei JHU phosphinothricin N-acetyltransferase protein.	247	1.8E-11	163	32.5
659	ABM99800.1	CP000545-496	<i>Burkholderia mallei</i> NCTC 10229	Burkholderia mallei NCTC 10229 phosphinothricin N-acetyltransferase protein.	247	1.8E-11	163	32.5
660	ABM99800.1	CP000545-496	<i>Burkholderia mallei</i> NCTC 10229	Burkholderia mallei NCTC 10229 phosphinothricin N-acetyltransferase protein.	247	1.8E-11	163	32.5

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
661	EDP85632.1	CH899679-121	<i>Burkholderia mallei</i> ATCC 10399	Burkholderia mallei ATCC 10399 phosphinothricin N-acetyltransferase protein.	247	1.8E-11	163	32.5
662	EFO92792.1	DS270287-2	<i>Caenorhabditis remanei</i>	Caenorhabditis remanei hypothetical protein.	379	1.9E-11	179	31.3
663	ABC92686.1	CP000133-3884	<i>Rhizobium etli</i> CFN 42	Rhizobium etli CFN 42 putative phosphinothricin N-acetyltransferase (antibiotic resistance) protein.	185	2E-11	171	28.1
664	CBL38504.1	FP929061-1371	<i>butyrate-producing bacterium</i> SSC/2	butyrate-producing bacterium SSC/2 Sortase and related acyltransferases protein.	185	2E-11	169	32.0
665	CBL38504.1	FP929061-1371	<i>butyrate-producing bacterium</i> SSC/2	butyrate-producing bacterium SSC/2 Sortase and related acyltransferases protein.	185	2E-11	169	32.0
666	ABC92686.1	CP000133-3884	<i>Rhizobium etli</i> CFN 42	Rhizobium etli CFN 42 putative phosphinothricin N-acetyltransferase (antibiotic resistance) protein.	185	2E-11	171	28.1
667	ACB79111.1	CP001029-915	<i>Methylobacterium populi</i> BJ001	Methylobacterium populi BJ001 GCN5-related N-acetyltransferase protein.	204	2.2E-11	173	31.8
668	CAG73868.1	BX950851-944	<i>Pectobacterium atrosepticum</i> SCRI1043	Pectobacterium atrosepticum SCRI1043 putative acetyltransferase protein.	175	2.3E-11	161	31.7
669	CAG73868.1	BX950851-944	<i>Pectobacterium atrosepticum</i> SCRI1043	Pectobacterium atrosepticum SCRI1043 putative acetyltransferase protein.	175	2.3E-11	161	31.7
670	AEI08044.1	CP002826-3310	<i>Oligotropha carboxidovorans</i> OM5	Oligotropha carboxidovorans OM5 phosphinothricin N-acetyltransferase Pat protein.	176	2.3E-11	153	33.3
671	AEI08044.1	CP002826-3310	<i>Oligotropha carboxidovorans</i> OM5	Oligotropha carboxidovorans OM5 phosphinothricin N-acetyltransferase Pat protein.	176	2.3E-11	153	33.3
672	AEI04414.1	CP002821-3256	<i>Oligotropha carboxidovorans</i> OM4	Oligotropha carboxidovorans OM4 phosphinothricin N-acetyltransferase Pat protein.	176	2.3E-11	153	33.3
673	AEI04414.1	CP002821-3256	<i>Oligotropha carboxidovorans</i> OM4	Oligotropha carboxidovorans OM4 phosphinothricin N-acetyltransferase Pat protein.	176	2.3E-11	153	33.3
674	CAJ47923.1	AM167904-318	<i>Bordetella avium</i> 197N	Bordetella avium 197N acetyltransferase protein.	178	2.3E-11	171	32.7
675	CAJ47923.1	AM167904-318	<i>Bordetella avium</i> 197N	Bordetella avium 197N acetyltransferase protein.	178	2.3E-11	171	32.7
676	ADZ65167.1	CP002459-91	<i>Brucella melitensis</i> M28	Brucella melitensis M28 phosphinothricin N-acetyltransferase protein.	179	2.3E-11	162	32.1

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
677	ACN99906.1	CP001488-82	<i>Brucella melitensis</i> ATCC 23457	Brucella melitensis ATCC 23457 Phosphinothricin N-acetyltransferase protein.	179	2.3E-11	162	32.1
678	ADZ65167.1	CP002459-91	<i>Brucella melitensis</i> M28	Brucella melitensis M28 phosphinothricin N-acetyltransferase protein.	179	2.3E-11	162	32.1
679	ADZ86031.1	CP001851-87	<i>Brucella melitensis</i> M5-90	Brucella melitensis M5-90 phosphinothricin N-acetyltransferase protein.	179	2.3E-11	162	32.1
680	ACI91718.1	CP001196-566	<i>Oligotropha carboxidovorans</i> OM5	Oligotropha carboxidovorans OM5 phosphinothricin N-acetyltransferase protein.	185	2.4E-11	153	33.3
681	ACB94578.1	CP001016-919	<i>Beijerinckia indica</i> subsp	Beijerinckia indica subsp. indica ATCC 9039 GCN5-related N-acetyltransferase protein.	186	2.4E-11	179	30.7
682	ADP71512.1	CP002292-2221	<i>Rhodomicrobium vannielii</i> ATCC 17100	Rhodomicrobium vannielii ATCC 17100 Phosphinothricin acetyltransferase protein.	190	2.4E-11	175	33.7
683	ADP71512.1	CP002292-2221	<i>Rhodomicrobium vannielii</i> ATCC 17100	Rhodomicrobium vannielii ATCC 17100 Phosphinothricin acetyltransferase protein.	190	2.4E-11	175	33.7
684	CAX22757.1	FP103042-1077	<i>Methylobacterium extorquens</i> DM4	Methylobacterium extorquens DM4 phosphinothricin N-acetyltransferase protein.	204	2.6E-11	178	30.9
685	ACS38695.1	CP001510-722	<i>Methylobacterium extorquens</i> AM1	Methylobacterium extorquens AM1 phosphinothricin N-acetyltransferase protein.	204	2.6E-11	178	30.9
686	CAX22757.1	FP103042-1077	<i>Methylobacterium extorquens</i> DM4	Methylobacterium extorquens DM4 phosphinothricin N-acetyltransferase protein.	204	2.6E-11	178	30.9
687	ACY51383.1	CP001805-1611	<i>Vibrio</i> sp	Vibrio sp. Ex25 toxin resistance protein.	169	2.6E-11	166	31.3
688	EBV22199.1	EN235121-1	marine metagenome	marine metagenome hypothetical protein.	211	2.6E-11	169	30.8
689	ABP61398.1	CP000653-2708	<i>Enterobacter</i> sp	Enterobacter sp. 638 GCN5-related N-acetyltransferase protein.	184	2.8E-11	176	31.2
690	ABP61398.1	CP000653-2708	<i>Enterobacter</i> sp	Enterobacter sp. 638 GCN5-related N-acetyltransferase protein.	184	2.8E-11	176	31.2
691	ACE93153.1	CP001074-4165	<i>Rhizobium etli</i> CIAT 652	Rhizobium etli CIAT 652 putative phosphinothricin N-acetyltransferase (antibiotic resistance) protein.	185	2.8E-11	161	28.6
692	ABD99444.1	CP000233-621	<i>Lactobacillus salivarius</i> UCC118	Lactobacillus salivarius UCC118 Phosphinothricin N-acetyltransferase protein.	198	3E-11	183	28.4
693	ABD99444.1	CP000233-621	<i>Lactobacillus salivarius</i> UCC118	Lactobacillus salivarius UCC118 Phosphinothricin N-acetyltransferase protein.	198	3E-11	183	28.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
694	ABQ05801.1	CP000685-2763	<i>Flavobacterium johnsoniae UW101</i>	Flavobacterium johnsoniae UW101 GCN5-related N-acetyltransferase protein.	165	3E-11	161	30.4
695	ABQ05801.1	CP000685-2763	<i>Flavobacterium johnsoniae UW101</i>	Flavobacterium johnsoniae UW101 GCN5-related N-acetyltransferase protein.	165	3E-11	161	30.4
696	CAJ24179.1	AM039952-2502	<i>Xanthomonas euvesicatoria</i>	Xanthomonas euvesicatoria putative phosphinothricin N-acetyltransferase protein.	179	3.2E-11	176	30.7
697	CAJ24179.1	AM039952-2502	<i>Xanthomonas euvesicatoria</i>	Xanthomonas euvesicatoria putative phosphinothricin N-acetyltransferase protein.	179	3.2E-11	176	30.7
698	EBH64249.1	EP121223-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	183	3.3E-11	176	31.8
699	ADY39465.1	HQ601968-2	<i>bacterium enrichment culture clone P69-9E</i>	bacterium enrichment culture clone P69-9E GCN5-related N-acetyltransferase protein.	184	3.3E-11	172	30.2
700	ADJ78841.1	CP002034-486	<i>Lactobacillus salivarius CECT 5713</i>	Lactobacillus salivarius CECT 5713 Phosphinothricin N-acetyltransferase protein.	195	3.4E-11	183	28.4
701	ADJ78841.1	CP002034-486	<i>Lactobacillus salivarius CECT 5713</i>	Lactobacillus salivarius CECT 5713 Phosphinothricin N-acetyltransferase protein.	195	3.4E-11	183	28.4
702	EBX41328.1	EN059271-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	115	3.6E-11	108	41.7
703	CAQ63002.1	CU914168-2873	<i>Ralstonia solanacearum IPO1609</i>	Ralstonia solanacearum IPO1609 antibiotic resistance (acetyltransferase) protein.	182	3.8E-11	165	33.3
704	CAQ63002.1	CU914168-2873	<i>Ralstonia solanacearum IPO1609</i>	Ralstonia solanacearum IPO1609 antibiotic resistance (acetyltransferase) protein.	182	3.8E-11	165	33.3
705	AEE96620.1	CP002360-1396	<i>Mahella australiensis 50-1 BON</i>	Mahella australiensis 50-1 BON Phosphinothricin acetyltransferase protein.	170	4.3E-11	162	29.0
706	AEE96620.1	CP002360-1396	<i>Mahella australiensis 50-1 BON</i>	Mahella australiensis 50-1 BON Phosphinothricin acetyltransferase protein.	170	4.3E-11	162	29.0
707	ECW58806.1	EQ042439-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	183	4.5E-11	176	31.8
708	ACG62847.1	CP001129-1460	<i>Streptococcus equi subsp</i>	Streptococcus equi subsp. zooepidemicus MGCS10565 Phosphinothricin N-acetyltransferase protein.	225	4.6E-11	177	32.8
709	ADY85178.1	CP000156-993	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus 2038 Phosphinothricin acetyltransferase protein.	190	4.7E-11	184	31.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
710	ADY85178.1	CP000156-993	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus 2038 Phosphinothricin acetyltransferase protein.	190	4.7E-11	184	31.5
711	CAI82091.1	AJ938182-2402	<i>Staphylococcus aureus RF122</i>	Staphylococcus aureus RF122 probable phosphinothricin N-acetyltransferase protein.	163	4.9E-11	163	30.7
712	CAI82091.1	AJ938182-2402	<i>Staphylococcus aureus RF122</i>	Staphylococcus aureus RF122 probable phosphinothricin N-acetyltransferase protein.	163	4.9E-11	163	30.7
713	ABQ18834.1	CP000626-930	<i>Vibrio cholerae O395</i>	Vibrio cholerae O395 toxin resistance protein.	169	5E-11	152	32.9
714	AAC38427.1	AF055586-8	<i>Vibrio cholerae</i>	Vibrio cholerae unknown protein.	169	5E-11	152	32.9
715	ACP11177.1	CP001236-330	<i>Vibrio cholerae O395</i>	Vibrio cholerae O395 GCN5-related N-acetyltransferase protein.	169	5E-11	152	32.9
716	AAC38427.1	AF055586-8	<i>Vibrio cholerae</i>	Vibrio cholerae unknown protein.	169	5E-11	152	32.9
717	ABQ18834.1	CP000626-930	<i>Vibrio cholerae O395</i>	Vibrio cholerae O395 toxin resistance protein.	169	5E-11	152	32.9
718	ABR69429.1	CP000749-486	<i>Marinomonas sp</i>	Marinomonas sp. MWYL1 GCN5-related N-acetyltransferase protein.	170	5E-11	163	30.7
719	ABR69429.1	CP000749-486	<i>Marinomonas sp</i>	Marinomonas sp. MWYL1 GCN5-related N-acetyltransferase protein.	170	5E-11	163	30.7
720	CAX59751.1	FP236843-2220	<i>Erwinia billingiae</i>	Erwinia billingiae Phosphinothricin N-acetyltransferase protein.	174	5.1E-11	160	30.6
721	CAX59751.1	FP236843-2220	<i>Erwinia billingiae</i>	Erwinia billingiae Phosphinothricin N-acetyltransferase protein.	174	5.1E-11	160	30.6
722	CAQ17746.1	CU694391-247	<i>Ralstonia solanacearum</i>	Ralstonia solanacearum antibiotic resistance (acetyltransferase) protein.	182	5.3E-11	163	32.5
723	CAQ17746.1	CU694391-247	<i>Ralstonia solanacearum</i>	Ralstonia solanacearum antibiotic resistance (acetyltransferase) protein.	182	5.3E-11	163	32.5
724	ADD75538.1	CP001875-371	<i>Pantoea ananatis LMG 20103</i>	Pantoea ananatis LMG 20103 Pat protein.	223	5.4E-11	161	31.1
725	CBG89001.1	FN543502-2223	<i>Citrobacter rodentium ICC168</i>	Citrobacter rodentium ICC168 putative acetyltransferase protein.	184	5.4E-11	172	30.8
726	CBG89001.1	FN543502-2223	<i>Citrobacter rodentium ICC168</i>	Citrobacter rodentium ICC168 putative acetyltransferase protein.	184	5.4E-11	172	30.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
727	AAT89618.1	AE016822-1510	<i>Leifsonia xyli subsp</i>	Leifsonia xyli subsp. xyli str. CTCB07 phosphinothricin acetyltransferase protein.	192	5.6E-11	163	31.9
728	AAT89618.1	AE016822-1510	<i>Leifsonia xyli subsp</i>	Leifsonia xyli subsp. xyli str. CTCB07 phosphinothricin acetyltransferase protein.	192	5.6E-11	163	31.9
729	ABR69425.1	CP000749-482	<i>Marinomonas sp</i>	Marinomonas sp. MWYL1 GCN5-related N-acetyltransferase protein.	167	5.9E-11	162	30.9
730	ABR69425.1	CP000749-482	<i>Marinomonas sp</i>	Marinomonas sp. MWYL1 GCN5-related N-acetyltransferase protein.	167	5.9E-11	162	30.9
731	CBL06841.1	FP929048-1585	<i>Megamonas hypermegale ART12/1</i>	Megamonas hypermegale ART12/1 Sortase and related acyltransferases protein.	168	5.9E-11	157	25.5
732	CBL06841.1	FP929048-1585	<i>Megamonas hypermegale ART12/1</i>	Megamonas hypermegale ART12/1 Sortase and related acyltransferases protein.	168	5.9E-11	157	25.5
733	AAM37157.1	AE008923-2265	<i>Xanthomonas axonopodis pv</i>	Xanthomonas axonopodis pv. citri str. 306 phosphinothricin N-acetyltransferase protein.	179	6.2E-11	172	32.0
734	AAM37157.1	AE008923-2265	<i>Xanthomonas axonopodis pv</i>	Xanthomonas axonopodis pv. citri str. 306 phosphinothricin N-acetyltransferase protein.	179	6.2E-11	172	32.0
735	ADU71733.1	CP002434-444	<i>Pantoea sp</i>	Pantoea sp. At-9b Phosphinothricin acetyltransferase protein.	171	7E-11	161	29.2
736	ADU71733.1	CP002434-444	<i>Pantoea sp</i>	Pantoea sp. At-9b Phosphinothricin acetyltransferase protein.	171	7E-11	161	29.2
737	ADU37860.1	CP002417-3637	<i>Variovorax paradoxus EPS</i>	Variovorax paradoxus EPS Phosphinothricin acetyltransferase protein.	173	7.1E-11	161	33.5
738	ADU37860.1	CP002417-3637	<i>Variovorax paradoxus EPS</i>	Variovorax paradoxus EPS Phosphinothricin acetyltransferase protein.	173	7.1E-11	161	33.5
739	BAF89018.1	AP009384-3020	<i>Azorhizobium caulinodans ORS 571</i>	Azorhizobium caulinodans ORS 571 acetyltransferase protein.	181	7.4E-11	178	31.5
740	BAF89018.1	AP009384-3020	<i>Azorhizobium caulinodans ORS 571</i>	Azorhizobium caulinodans ORS 571 acetyltransferase protein.	181	7.4E-11	178	31.5
741	CBK87248.1	FP929040-3145	<i>Enterobacter cloacae subsp</i>	Enterobacter cloacae subsp. cloacae NCTC 9394 Sortase and related acyltransferases protein.	184	7.5E-11	177	30.5
742	CBK87248.1	FP929040-3145	<i>Enterobacter cloacae subsp</i>	Enterobacter cloacae subsp. cloacae NCTC 9394 Sortase and related acyltransferases protein.	184	7.5E-11	177	30.5
743	CAQ50959.1	AM990992-2519	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus ST398 hypothetical acetyltransferase YncA protein.	163	8E-11	161	31.1

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
744	ADL24342.1	CP002114-2376	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus JKD6159 acetyltransferase, GNAT family protein.	163	8E-11	161	30.4
745	CAQ50959.1	AM990992-2519	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus ST398 hypothetical acetyltransferase YncA protein.	163	8E-11	161	31.1
746	ADL24342.1	CP002114-2376	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus JKD6159 acetyltransferase, GNAT family protein.	163	8E-11	161	30.4
747	EFH72488.1	GG774565-45	<i>Vibrio cholerae RC385</i>	Vibrio cholerae RC385 toxin resistance protein.	169	8.2E-11	152	34.2
748	ACS18123.1	CP001635-1460	<i>Variovorax paradoxus S110</i>	Variovorax paradoxus S110 Phosphinothricin acetyltransferase protein.	174	8.4E-11	159	32.7
749	ACL94449.1	CP001340-982	<i>Caulobacter crescentus NA1000</i>	Caulobacter crescentus NA1000 phosphinothricin N-acetyltransferase protein.	183	8.8E-11	174	32.2
750	CAI97967.1	CR954253-1121	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842 Acyltransferase protein.	190	9.1E-11	184	31.0
751	CAI97967.1	CR954253-1121	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842 Acyltransferase protein.	190	9.1E-11	184	31.0
752	ABY29397.1	CP000908-968	<i>Methylobacterium extorquens PA1</i>	Methylobacterium extorquens PA1 GCN5-related N-acetyltransferase protein.	191	9.1E-11	171	31.0
753	ACQ62862.1	CP001486-892	<i>Vibrio cholerae MJ-1236</i>	Vibrio cholerae MJ-1236 toxin resistance protein.	169	9.7E-11	152	32.9
754	ADF60024.1	CP001918-456	<i>Enterobacter cloacae subsp</i>	Enterobacter cloacae subsp. cloacae ATCC 13047 putative acetyltransferase protein.	176	1E-10	174	29.3
755	ACS18020.1	CP001635-1357	<i>Variovorax paradoxus S110</i>	Variovorax paradoxus S110 Phosphinothricin acetyltransferase protein.	177	1E-10	160	33.8
756	ABC90040.1	CP000133-1217	<i>Rhizobium etli CFN 42</i>	Rhizobium etli CFN 42 probable phosphinothricin acetyltransferase (antibiotic resistance) protein.	171	1.2E-10	157	32.5
757	ABC90040.1	CP000133-1217	<i>Rhizobium etli CFN 42</i>	Rhizobium etli CFN 42 probable phosphinothricin acetyltransferase (antibiotic resistance) protein.	171	1.2E-10	157	32.5
758	ABX21285.1	CP000880-1331	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. arizonae serovar 62:z4,z23: -- hypothetical protein.	172	1.2E-10	172	33.7
759	ABX21285.1	CP000880-1331	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. arizonae serovar 62:z4,z23: -- hypothetical protein.	172	1.2E-10	172	33.7
760	AEL05487.1	CP002789-557	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. raphani 756C phosphinothricin acetyltransferase protein.	173	1.2E-10	162	31.5

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
761	AEL05487.1	CP002789-557	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. raphani 756C phosphinothricin acetyltransferase protein.	173	1.2E-10	162	31.5
762	AEG93704.1	CP000245-2645	<i>Ramlibacter tataouinensis TTB310</i>	Ramlibacter tataouinensis TTB310 phosphinothricin N-acetyltransferase e (Phosphinothricin-resistance protein)-like protein.	173	1.2E-10	160	32.5
763	AEG93704.1	CP000245-2645	<i>Ramlibacter tataouinensis TTB310</i>	Ramlibacter tataouinensis TTB310 phosphinothricin N-acetyltransferase e (Phosphinothricin-resistance protein)-like protein.	173	1.2E-10	160	32.5
764	ECF30789.1	EM642573-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	178	1.2E-10	167	30.5
765	AAK22919.1	AE005673-931	<i>Caulobacter crescentus CB15</i>	Caulobacter crescentus CB15 phosphinothricin N-acetyltransferase protein.	180	1.2E-10	172	32.0
766	AAK22919.1	AE005673-931	<i>Caulobacter crescentus CB15</i>	Caulobacter crescentus CB15 phosphinothricin N-acetyltransferase protein.	180	1.2E-10	172	32.0
767	ADQ61082.1	CP002341-1025	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus ND02 Sortase related acyltransferase protein.	194	1.3E-10	184	31.0
768	ADQ61082.1	CP002341-1025	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus ND02 Sortase related acyltransferase protein.	194	1.3E-10	184	31.0
769	CBH47347.1	FN563149-1186	<i>Rhodococcus equi 103S</i>	Rhodococcus equi 103S GNAT acetyltransferase protein.	162	1.3E-10	159	30.8
770	CBH47347.1	FN563149-1186	<i>Rhodococcus equi 103S</i>	Rhodococcus equi 103S GNAT acetyltransferase protein.	162	1.3E-10	159	30.8
771	BAI77989.1	AB548432-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	1.3E-10	172	30.2
772	BAI77989.1	AB548432-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	1.3E-10	172	30.2
773	BAJ81489.1	AP012035-2142	<i>Acidiphilium multivorum AIU301</i>	Acidiphilium multivorum AIU301 putative acetyltransferase protein.	167	1.3E-10	161	32.3
774	ABQ31100.1	CP000697-1871	<i>Acidiphilium cryptum JF-5</i>	Acidiphilium cryptum JF-5 GCN5-related N-acetyltransferase protein.	167	1.3E-10	161	32.3
775	BAJ81489.1	AP012035-2142	<i>Acidiphilium multivorum AIU301</i>	Acidiphilium multivorum AIU301 putative acetyltransferase protein.	167	1.3E-10	161	32.3
776	ABQ31100.1	CP000697-1871	<i>Acidiphilium cryptum JF-5</i>	Acidiphilium cryptum JF-5 GCN5-related N-acetyltransferase protein.	167	1.3E-10	161	32.3

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
777	ACN46274.1	CP000857-2079	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Paratyphi C strain putative acetyltransferase protein.	171	1.4E-10	168	33.9
778	ACN46274.1	CP000857-2079	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Paratyphi C strain putative acetyltransferase protein.	171	1.4E-10	168	33.9
779	CCB72329.1	FQ859184-1303	<i>Streptomyces cattleya NRRL 8057</i>	Streptomyces cattleya NRRL 8057 Phosphinothricin N-acetyltransferase protein.	176	1.4E-10	159	30.8
780	CCB72329.1	FQ859184-1303	<i>Streptomyces cattleya NRRL 8057</i>	Streptomyces cattleya NRRL 8057 Phosphinothricin N-acetyltransferase protein.	176	1.4E-10	159	30.8
781	AAAY38187.1	CP000075-3154	<i>Pseudomonas syringae pv</i>	Pseudomonas syringae pv. syringae B728a GCN5-related N-acetyltransferase protein.	179	1.4E-10	160	31.9
782	AAAY38187.1	CP000075-3154	<i>Pseudomonas syringae pv</i>	Pseudomonas syringae pv. syringae B728a GCN5-related N-acetyltransferase protein.	179	1.4E-10	160	31.9
783	EFF87236.1	GG753600-425	<i>Acinetobacter sp</i>	Acinetobacter sp. SH024 conserved hypothetical protein.	181	1.4E-10	178	28.1
784	ABJ58628.1	CP000412-932	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365 Sortase related acyltransferase protein.	190	1.5E-10	184	31.0
785	ABJ58628.1	CP000412-932	<i>Lactobacillus delbrueckii subsp</i>	Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365 Sortase related acyltransferase protein.	190	1.5E-10	184	31.0
786	ACK51783.1	CP001280-2798	<i>Methylocella silvestris BL2</i>	Methylocella silvestris BL2 GCN5-related N-acetyltransferase protein.	195	1.5E-10	159	34.0
787	ACZ08761.1	CP001739-1873	<i>Sebaldella termitidis ATCC 33386</i>	Sebaldella termitidis ATCC 33386 Phosphinothricin acetyltransferase protein.	165	1.6E-10	156	28.8
788	ADX47179.1	CP002521-3251	<i>Acidovorax avenae subsp</i>	Acidovorax avenae subsp. avenae ATCC 19860 Phosphinothricin acetyltransferase protein.	173	1.6E-10	159	31.4
789	ADX47179.1	CP002521-3251	<i>Acidovorax avenae subsp</i>	Acidovorax avenae subsp. avenae ATCC 19860 Phosphinothricin acetyltransferase protein.	173	1.6E-10	159	31.4
790	ADQ79850.1	CP002345-1688	<i>Paludibacter propionigenes WB4</i>	Paludibacter propionigenes WB4 GCN5-related N-acetyltransferase protein.	175	1.6E-10	170	29.4
791	ADQ79850.1	CP002345-1688	<i>Paludibacter propionigenes WB4</i>	Paludibacter propionigenes WB4 GCN5-related N-acetyltransferase protein.	175	1.6E-10	170	29.4
792	ECA67527.1	EM889901-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	198	1.8E-10	161	35.4
793	AAAY50849.1	CP000050-3755	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. 8004 phosphinothricin acetyltransferase protein.	173	1.9E-10	164	31.7

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
794	AAM42996.1	AE008922-3689	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. ATCC 33913 phosphinothricin acetyltransferase protein.	173	1.9E-10	164	31.7
795	CAP53287.1	AM920689-3959	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris N-acetyltransferase protein.	173	1.9E-10	164	31.7
796	CAP53287.1	AM920689-3959	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris N-acetyltransferase protein.	173	1.9E-10	164	31.7
797	AAM42996.1	AE008922-3689	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. ATCC 33913 phosphinothricin acetyltransferase protein.	173	1.9E-10	164	31.7
798	AAV50849.1	CP000050-3755	<i>Xanthomonas campestris pv</i>	Xanthomonas campestris pv. campestris str. 8004 phosphinothricin acetyltransferase protein.	173	1.9E-10	164	31.7
799	ABW25821.1	CP000828-730	<i>Acaryochloris marina MBIC11017</i>	Acaryochloris marina MBIC11017 acetyltransferase, putative protein.	175	1.9E-10	177	29.4
800	ABW25821.1	CP000828-730	<i>Acaryochloris marina MBIC11017</i>	Acaryochloris marina MBIC11017 acetyltransferase, putative protein.	175	1.9E-10	177	29.4
801	AEG99660.1	CP002824-4721	<i>Enterobacter aerogenes KCTC 2190</i>	Enterobacter aerogenes KCTC 2190 phosphinothricin acetyltransferase protein.	184	2E-10	172	30.2
802	AEG99660.1	CP002824-4721	<i>Enterobacter aerogenes KCTC 2190</i>	Enterobacter aerogenes KCTC 2190 phosphinothricin acetyltransferase protein.	184	2E-10	172	30.2
803	CAN95790.1	AM746676-5634	<i>Sorangium cellulosum So ce 56</i>	Sorangium cellulosum So ce 56 putative acetyltransferase protein.	333	2E-10	170	34.7
804	CAN95790.1	AM746676-5634	<i>Sorangium cellulosum So ce 56</i>	Sorangium cellulosum So ce 56 putative acetyltransferase protein.	333	2E-10	170	34.7
805	EBH86441.1	EP110235-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	156	2.1E-10	148	31.1
806	ADH90898.1	CP002026-3561	<i>Starkeya novella DSM 506</i>	Starkeya novella DSM 506 Phosphinothricin acetyltransferase protein.	194	2.1E-10	182	30.2
807	ADH90898.1	CP002026-3561	<i>Starkeya novella DSM 506</i>	Starkeya novella DSM 506 Phosphinothricin acetyltransferase protein.	194	2.1E-10	182	30.2
808	EEO46642.1	EQ999648-3	<i>Bacteroides dorei 5_1_36/D4</i>	Bacteroides dorei 5_1_36/D4 conserved hypothetical protein.	161	2.1E-10	161	29.8
809	EEO62335.1	EQ973132-191	<i>Bacteroides sp</i>	Bacteroides sp. 9_1_42FAA conserved hypothetical protein.	161	2.1E-10	161	29.8
810	BAH41879.1	AP008955-902	<i>Brevibacillus brevis NBRC 100599</i>	Brevibacillus brevis NBRC 100599 putative phosphinothricin acetyltransferase protein.	163	2.2E-10	158	28.5

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
811	BAH41879.1	AP008955-902	<i>Brevibacillus brevis</i> NBRC 100599	Brevibacillus brevis NBRC 100599 putative phosphinothricin acetyltransferase protein.	163	2.2E-10	158	28.5
812	BAI77993.1	AB548436-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	2.2E-10	173	31.2
813	BAI77993.1	AB548436-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	2.2E-10	173	31.2
814	ACK81872.1	CP001298-902	<i>Methylobacterium chloromethanicum</i> CM4	Methylobacterium chloromethanicum CM4 GCN5-related N-acetyltransferase protein.	204	2.2E-10	178	29.8
815	EBH37119.1	EP134459-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	176	2.3E-10	169	29.6
816	AAW75429.1	AE013598-2137	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae KACC10331 phosphinothricin N-acetyltransferase protein.	179	2.3E-10	176	30.7
817	ACD59045.1	CP000967-2378	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae PXO99A phosphinothricin N-acetyltransferase protein.	179	2.3E-10	176	30.7
818	AAW75429.1	AE013598-2137	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae KACC10331 phosphinothricin N-acetyltransferase protein.	179	2.3E-10	176	30.7
819	BAE68799.1	AP008229-2044	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae MAFF 311018 phosphinothricin N-acetyltransferase protein.	179	2.3E-10	176	30.7
820	BAE68799.1	AP008229-2044	<i>Xanthomonas oryzae</i> pv	Xanthomonas oryzae pv. oryzae MAFF 311018 phosphinothricin N-acetyltransferase protein.	179	2.3E-10	176	30.7
821	AEE17787.1	CP002696-2327	<i>Treponema brennaborensis</i> DSM 12168	Treponema brennaborensis DSM 12168 GCN5-related N-acetyltransferase protein.	195	2.5E-10	179	29.1
822	AEE17787.1	CP002696-2327	<i>Treponema brennaborensis</i> DSM 12168	Treponema brennaborensis DSM 12168 GCN5-related N-acetyltransferase protein.	195	2.5E-10	179	29.1
823	BAI77990.1	AB548433-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	2.6E-10	173	31.8
824	BAI77990.1	AB548433-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	2.6E-10	173	31.8
825	CAR42959.1	AM946015-1337	<i>Streptococcus uberis</i> 0140J	Streptococcus uberis 0140J acetyltransferase (GNAT) family protein.	202	2.6E-10	164	29.3

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
826	CAR42959.1	AM946015-1337	<i>Streptococcus uberis</i> 0140J	Streptococcus uberis 0140J acetyltransferase (GNAT) family protein.	202	2.6E-10	164	29.3
827	ADX17290.1	CP002487-1544	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 putative acyltransferase protein.	171	2.7E-10	168	33.3
828	EGE29647.1	CM001151-1605	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Dublin str. SD3246 putative acyltransferase protein.	171	2.7E-10	168	33.3
829	CAR59350.1	FM200053-1243	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Paratyphi A str. putative acetyltransferase protein.	171	2.7E-10	168	33.3
830	CBW17615.1	FQ312003-1514	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344 putative acetyltransferase protein.	171	2.7E-10	168	33.3
831	CAR59350.1	FM200053-1243	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Paratyphi A str. putative acetyltransferase protein.	171	2.7E-10	168	33.3
832	BAJ36552.1	AP011957-1608	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium str. putative acetyltransferase protein.	171	2.7E-10	168	33.3
833	CAR37400.1	AM933173-1490	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91 putative acetyltransferase protein.	171	2.7E-10	168	33.3
834	AAL20508.1	AE006468-1544	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2 putative acyltransferase protein.	171	2.7E-10	168	33.3
835	AAV77227.1	CP000026-1188	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC putative acetyltransferase protein.	171	2.7E-10	168	33.3
836	CBW17615.1	FQ312003-1514	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344 putative acetyltransferase protein.	171	2.7E-10	168	33.3
837	CAR33044.1	AM933172-1453	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Enteritidis str. putative acetyltransferase protein.	171	2.7E-10	168	33.3
838	ACF69055.1	CP001120-1663	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476 phosphinothricin acetyltransferase protein.	171	2.7E-10	168	33.3
839	ACH50175.1	CP001138-1466	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Agona str. SL483 phosphinothricin acetyltransferase protein.	171	2.7E-10	168	33.3
840	CBG24597.1	FN424405-1579	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 putative acetyltransferase protein.	171	2.7E-10	168	33.3
841	EGE34138.1	CM001153-1430	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Gallinarum str. SG9 putative acyltransferase protein.	171	2.7E-10	168	33.3
842	BAJ36552.1	AP011957-1608	<i>Salmonella enterica</i> subsp	Salmonella enterica subsp. enterica serovar Typhimurium str. putative acetyltransferase protein.	171	2.7E-10	168	33.3

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
843	AEF07460.1	CP002614-1526	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 putative acyltransferase protein.	171	2.7E-10	168	33.3
844	ACH76859.1	CP001144-1601	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853 phosphinothricin acetyltransferase protein.	171	2.7E-10	168	33.3
845	CAR37400.1	AM933173-1490	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91 putative acetyltransferase protein.	171	2.7E-10	168	33.3
846	AEF07460.1	CP002614-1526	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1 putative acyltransferase protein.	171	2.7E-10	168	33.3
847	CAR33044.1	AM933172-1453	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Enteritidis str. putative acetyltransferase protein.	171	2.7E-10	168	33.3
848	ADX17290.1	CP002487-1544	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74 putative acyltransferase protein.	171	2.7E-10	168	33.3
849	ACF89322.1	CP001127-1606	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Schwarzengrund str. phosphinothricin acetyltransferase protein.	171	2.7E-10	168	33.3
850	AAL20508.1	AE006468-1544	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2 putative acyltransferase protein.	171	2.7E-10	168	33.3
851	CBG24597.1	FN424405-1579	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 putative acetyltransferase protein.	171	2.7E-10	168	33.3
852	AAV77227.1	CP000026-1188	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC putative acetyltransferase protein.	171	2.7E-10	168	33.3
853	ACF63334.1	CP001113-1609	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Newport str. SL254 phosphinothricin acetyltransferase protein.	171	2.7E-10	168	33.3
854	ACY88396.1	CP001363-1883	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S putative acyltransferase protein.	171	2.7E-10	168	33.3
855	ABB07855.1	CP000151-1072	<i>Burkholderia sp</i>	Burkholderia sp. 383 GCN5-related N-acetyltransferase protein.	182	2.8E-10	178	32.0
856	ABB07855.1	CP000151-1072	<i>Burkholderia sp</i>	Burkholderia sp. 383 GCN5-related N-acetyltransferase protein.	182	2.8E-10	178	32.0
857	EEZ20450.1	GG705232-217	<i>Bacteroides sp</i>	Bacteroides sp. 3_1_33FAA conserved hypothetical protein.	161	3E-10	161	29.2
858	BAI77992.1	AB548435-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	3E-10	173	31.2
859	BAI77992.1	AB548435-1	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	3E-10	173	31.2

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
860	AAX65493.1	AE017220-1587	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Choleraesuis str. putative acyltransferase protein.	171	3.1E-10	168	33.3
861	ACD28612.1	CP001068-3445	<i>Ralstonia pickettii</i> 12J	Ralstonia pickettii 12J GCN5-related N-acetyltransferase protein.	171	3.1E-10	170	34.1
862	AAX65493.1	AE017220-1587	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Choleraesuis str. putative acyltransferase protein.	171	3.1E-10	168	33.3
863	CBL33399.1	FP929059-161	<i>Eubacterium siraeum V10Sc8a</i>	Eubacterium siraeum V10Sc8a Sortase and related acyltransferases protein.	172	3.1E-10	164	29.9
864	CBL33399.1	FP929059-161	<i>Eubacterium siraeum V10Sc8a</i>	Eubacterium siraeum V10Sc8a Sortase and related acyltransferases protein.	172	3.1E-10	164	29.9
865	EDA90267.1	EP880780-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	178	3.2E-10	174	32.2
866	AAZ34956.1	CP000058-2931	<i>Pseudomonas syringae pv</i>	Pseudomonas syringae pv. phaseolicola 1448A phosphinothricin N-acetyltransferase protein.	179	3.3E-10	159	32.7
867	AAZ34956.1	CP000058-2931	<i>Pseudomonas syringae pv</i>	Pseudomonas syringae pv. phaseolicola 1448A phosphinothricin N-acetyltransferase protein.	179	3.3E-10	159	32.7
868	CBJ41614.1	FP885897-294	<i>Ralstonia solanacearum</i>	Ralstonia solanacearum putative antibiotic resistance protein (Acetyltransferase) protein.	182	3.3E-10	165	32.1
869	AEG67652.1	CP002819-348	<i>Ralstonia solanacearum Po82</i>	Ralstonia solanacearum Po82 phosphinothricin n-acetyltransferase (ppt n-acetyltransferase) (phosphinothricin-resistance protein) protein.	182	3.3E-10	165	31.5
870	EGE37491.1	GL877176-234	<i>Actinomyces viscosus C505</i>	Actinomyces viscosus C505 acetyltransferase, GNAT family protein.	182	3.3E-10	167	31.1
871	AEG67652.1	CP002819-348	<i>Ralstonia solanacearum Po82</i>	Ralstonia solanacearum Po82 phosphinothricin n-acetyltransferase (ppt n-acetyltransferase) (phosphinothricin-resistance protein) protein.	182	3.3E-10	165	31.5
872	CBJ41614.1	FP885897-294	<i>Ralstonia solanacearum</i>	Ralstonia solanacearum putative antibiotic resistance protein (Acetyltransferase) protein.	182	3.3E-10	165	32.1
873	CAW98359.1	FM204884-450	<i>Streptococcus equi subsp</i>	Streptococcus equi subsp. zooepidemicus acetyltransferase (GNAT) family protein.	193	3.5E-10	177	32.2
874	CAW98359.1	FM204884-450	<i>Streptococcus equi subsp</i>	Streptococcus equi subsp. zooepidemicus acetyltransferase (GNAT) family protein.	193	3.5E-10	177	32.2
875	CAG44230.1	BX571857-2434	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus MSSA476 acetyltransferase (GNAT) family protein.	163	3.5E-10	161	29.8

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
876	BAB96314.1	BA000033-2449	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus MW2 MW2449 protein.	163	3.5E-10	161	29.8
877	CCC89068.1	FR821779-2299	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus LGA251 acetyltransferase (GNAT) family protein.	163	3.5E-10	161	29.8
878	CCC89068.1	FR821779-2299	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus LGA251 acetyltransferase (GNAT) family protein.	163	3.5E-10	161	29.8
879	CAG44230.1	BX571857-2434	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus MSSA476 acetyltransferase (GNAT) family protein.	163	3.5E-10	161	29.8
880	BAB96314.1	BA000033-2449	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus MW2 MW2449 protein.	163	3.5E-10	161	29.8
881	CAC46141.1	AL591688-1567	<i>Sinorhizobium meliloti 1021</i>	Sinorhizobium meliloti 1021 N-acetyltransferase protein.	169	3.7E-10	171	31.0
882	CAC46141.1	AL591688-1567	<i>Sinorhizobium meliloti 1021</i>	Sinorhizobium meliloti 1021 N-acetyltransferase protein.	169	3.7E-10	171	31.0
883	AEH79266.1	CP001830-1978	<i>Sinorhizobium meliloti SM11</i>	Sinorhizobium meliloti SM11 N-acetyltransferase protein.	169	3.7E-10	171	31.0
884	AEG04155.1	CP002740-1203	<i>Sinorhizobium meliloti BL225C</i>	Sinorhizobium meliloti BL225C Phosphinothricin acetyltransferase protein.	169	3.7E-10	171	31.0
885	AEG53202.1	CP002781-1427	<i>Sinorhizobium meliloti AK83</i>	Sinorhizobium meliloti AK83 Phosphinothricin acetyltransferase protein.	169	3.7E-10	171	31.0
886	AEG04155.1	CP002740-1203	<i>Sinorhizobium meliloti BL225C</i>	Sinorhizobium meliloti BL225C Phosphinothricin acetyltransferase protein.	169	3.7E-10	171	31.0
887	AAF96293.1	AE003853-379	<i>Vibrio cholerae O1 biovar El Tor str</i>	Vibrio cholerae O1 biovar El Tor str. N16961 toxin resistance protein.	169	3.7E-10	152	32.2
888	AAF96293.1	AE003853-379	<i>Vibrio cholerae O1 biovar El Tor str</i>	Vibrio cholerae O1 biovar El Tor str. N16961 toxin resistance protein.	169	3.7E-10	152	32.2
889	AEG53202.1	CP002781-1427	<i>Sinorhizobium meliloti AK83</i>	Sinorhizobium meliloti AK83 Phosphinothricin acetyltransferase protein.	169	3.7E-10	171	31.0
890	EFZ06201.1	CM001062-1611	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Choleraesuis str. putative acyltransferase protein.	171	3.7E-10	168	33.3
891	CBA17326.1	FP565176-2788	<i>Xanthomonas albilineans</i>	Xanthomonas albilineans putative n-acetyltransferase protein.	173	3.7E-10	160	31.9
892	CBA17326.1	FP565176-2788	<i>Xanthomonas albilineans</i>	Xanthomonas albilineans putative n-acetyltransferase protein.	173	3.7E-10	160	31.9

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Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
893	ACS18846.1	CP001635-2183	<i>Variovorax paradoxus</i> S110	Variovorax paradoxus S110 GCN5-related N-acetyltransferase protein.	173	3.7E-10	166	32.5
894	ADU35838.1	CP002417-1615	<i>Variovorax paradoxus</i> EPS	Variovorax paradoxus EPS Phosphinothricin acetyltransferase protein.	174	3.7E-10	169	30.2
895	ADU35838.1	CP002417-1615	<i>Variovorax paradoxus</i> EPS	Variovorax paradoxus EPS Phosphinothricin acetyltransferase protein.	174	3.7E-10	169	30.2
896	CBA28717.1	FN543104-855	<i>Curvibacter putative symbiont of Hydra magnipapillata</i>	Curvibacter putative symbiont of Hydra magnipapillata Phosphinothricin N-acetyltransferase protein.	174	3.7E-10	173	28.3
897	CBA28717.1	FN543104-855	<i>Curvibacter putative symbiont of Hydra magnipapillata</i>	Curvibacter putative symbiont of Hydra magnipapillata Phosphinothricin N-acetyltransferase protein.	174	3.7E-10	173	28.3
898	AAZ64477.1	CP000091-1656	<i>Ralstonia eutropha</i> JMP134	Ralstonia eutropha JMP134 GCN5-related N-acetyltransferase protein.	175	3.8E-10	173	34.1
899	AAZ64477.1	CP000091-1656	<i>Ralstonia eutropha</i> JMP134	Ralstonia eutropha JMP134 GCN5-related N-acetyltransferase protein.	175	3.8E-10	173	34.1
900	AEG92294.1	CP000245-1235	<i>Ramlibacter tataouinensis</i> TTB310	Ramlibacter tataouinensis TTB310 candidate antibiotic resistance protein (acetyltransferase) protein.	177	3.8E-10	159	31.4
901	AEG92294.1	CP000245-1235	<i>Ramlibacter tataouinensis</i> TTB310	Ramlibacter tataouinensis TTB310 candidate antibiotic resistance protein (acetyltransferase) protein.	177	3.8E-10	159	31.4
902	EFH99095.1	GG774651-58	<i>Pseudomonas savastanoi</i> pv	Pseudomonas savastanoi pv. savastanoi NCPPB 3335 GCN5- related N-acetyltransferase protein.	179	3.8E-10	159	32.1
903	ABJ07101.1	CP000463-3140	<i>Rhodopseudomonas palustris</i> BisA53	Rhodopseudomonas palustris BisA53 GCN5-related N-acetyltransferase protein.	180	3.9E-10	174	32.2
904	ACF00857.1	CP001096-2294	<i>Rhodopseudomonas palustris</i> TIE-1	Rhodopseudomonas palustris TIE-1 GCN5-related N-acetyltransferase protein.	180	3.9E-10	176	30.7
905	ABJ07101.1	CP000463-3140	<i>Rhodopseudomonas palustris</i> BisA53	Rhodopseudomonas palustris BisA53 GCN5-related N-acetyltransferase protein.	180	3.9E-10	174	32.2
906	ABD31837.1	CP000253-2686	<i>Staphylococcus aureus</i> subsp	Staphylococcus aureus subsp. aureus NCTC 8325 conserved hypothetical protein.	163	4.2E-10	161	29.8
907	ADL66566.1	CP002120-2478	<i>Staphylococcus aureus</i> subsp	Staphylococcus aureus subsp. aureus str. JKD6008 acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8
908	AAW37317.1	CP000046-2475	<i>Staphylococcus aureus</i> subsp	Staphylococcus aureus subsp. aureus COL acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
909	EEV12981.1	GG700598-349	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus E1410 acetyltransferase protein.	163	4.2E-10	161	29.8
910	AEB89621.1	CP002643-2485	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus T0131 Acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8
911	CBI50514.1	FN433596-2635	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus TW20 acetyltransferase (GNAT) family protein.	163	4.2E-10	161	29.8
912	ABD22256.1	CP000255-2380	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus USA300_FPR3757 acetyltransferase , GNAT family protein.	163	4.2E-10	161	29.8
913	BAF68699.1	AP009351-2437	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus str. Newman acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8
914	BAF68699.1	AP009351-2437	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus str. Newman acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8
915	AAW37317.1	CP000046-2475	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus COL acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8
916	EEV05126.1	GG700533-350	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus 55/2053 acetyltransferase family protein.	163	4.2E-10	161	29.8
917	EFC01855.1	GG730274-366	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus C160 toxin-antitoxin system, toxin component, GNAT family protein.	163	4.2E-10	161	29.8
918	CBI50514.1	FN433596-2635	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus TW20 acetyltransferase (GNAT) family protein.	163	4.2E-10	161	29.8
919	AEB89621.1	CP002643-2485	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus T0131 Acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8
920	EFB45904.1	GG730158-360	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus C427 acetyltransferase protein.	163	4.2E-10	161	29.8
921	EFE26969.1	GG749056-353	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus 58-424 acetyltransferase (GNAT) family protein.	163	4.2E-10	161	29.8
922	ABX30504.1	CP000730-2458	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus USA300_TCH1516 acetyltransferase protein.	163	4.2E-10	161	29.8
923	EEV07769.1	GG700560-355	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus 65-1322 acetyltransferase family protein.	163	4.2E-10	161	29.8
924	EFB59283.1	GG730269-350	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus Btn1260 acetyltransferase GNAT family protein.	163	4.2E-10	161	29.8
925	ABD22256.1	CP000255-2380	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus USA300_FPR3757 acetyltransferase , GNAT family protein.	163	4.2E-10	161	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
926	ADQ76124.1	CP002110-662	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus TCH60 phosphinothricin acetyltransferase protein.	163	4.2E-10	161	29.8
927	ABX30504.1	CP000730-2458	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus USA300_TCH1516 acetyltransferase protein.	163	4.2E-10	161	29.8
928	ADL66566.1	CP002120-2478	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus str. JKD6008 acetyltransferase, GNAT family protein.	163	4.2E-10	161	29.8
929	EFC27717.1	GG731513-299	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus A017934/97 toxin-antitoxin system, toxin component, GNAT family protein.	163	4.2E-10	161	29.8
930	EEV10390.1	GG700574-347	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus 68-397 acetyltransferase protein.	163	4.2E-10	161	29.8
931	EFB54099.1	GG730218-347	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus WBG10049 acetyltransferase family protein.	163	4.2E-10	161	29.8
932	EFG56510.1	GG770532-139	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus EMRSA16 acetyltransferase protein.	163	4.2E-10	161	29.8
933	ADQ76124.1	CP002110-662	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus TCH60 phosphinothricin acetyltransferase protein.	163	4.2E-10	161	29.8
934	EFB43249.1	GG730139-366	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus C101 acetyltransferase protein.	163	4.2E-10	161	29.8
935	EFD96090.1	GG749014-363	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus M1015 toxin-antitoxin system, toxin component, GNAT family protein.	163	4.2E-10	161	29.8
936	EFB56714.1	GG730254-227	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus WW2703/97 acetyltransferase family protein.	163	4.2E-10	161	29.8
937	EEV15642.1	GG700615-350	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus M876 acetyltransferase protein.	163	4.2E-10	161	29.8
938	ADI99011.1	CP001996-2472	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus ED133 probable phosphinothricin N-acetyltransferase protein.	163	4.2E-10	161	29.8
939	EFB51438.1	GG730206-365	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus M899 toxin-antitoxin system, toxin component, GNAT family protein.	163	4.2E-10	161	29.8
940	ABD31837.1	CP000253-2686	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus NCTC 8325 conserved hypothetical protein.	163	4.2E-10	161	29.8
941	CAG41588.1	BX571856-2560	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus MRSA252 acetyltransferase (GNAT) family protein.	163	4.2E-10	161	29.8
942	EFF08514.1	GG749321-170	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus M809 acetyltransferase protein.	163	4.2E-10	161	29.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
943	ADI99011.1	CP001996-2472	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus ED133 probable phosphinothricin N-acetyltransferase protein.	163	4.2E-10	161	29.8
944	CAG41588.1	BX571856-2560	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus MRSA252 acetyltransferase (GNAT) family protein.	163	4.2E-10	161	29.8
945	EBG16705.1	EP206371-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	164	4.2E-10	148	32.4
946	ECP53260.1	EM149402-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	166	4.2E-10	163	28.2
947	CAE27493.1	BX572599-189	<i>Rhodopseudomonas palustris CGA009</i>	Rhodopseudomonas palustris CGA009 putative phosphinothricin N-acetyltransferase protein.	203	4.3E-10	176	30.7
948	CAE27493.1	BX572599-189	<i>Rhodopseudomonas palustris CGA009</i>	Rhodopseudomonas palustris CGA009 putative phosphinothricin N-acetyltransferase protein.	203	4.3E-10	176	30.7
949	ACM35907.1	CP000633-941	<i>Agrobacterium vitis S4</i>	Agrobacterium vitis S4 Phosphinothricin acetyltransferase protein.	168	4.3E-10	155	32.3
950	ACM35907.1	CP000633-941	<i>Agrobacterium vitis S4</i>	Agrobacterium vitis S4 Phosphinothricin acetyltransferase protein.	168	4.3E-10	155	32.3
951	EBZ92525.1	EM924754-3	<i>marine metagenome</i>	marine metagenome hypothetical protein.	208	4.4E-10	169	33.1
952	ABQ80844.1	CP000712-4667	<i>Pseudomonas putida F1</i>	Pseudomonas putida F1 GCN5-related N-acetyltransferase protein.	171	4.4E-10	169	32.0
953	ABQ80844.1	CP000712-4667	<i>Pseudomonas putida F1</i>	Pseudomonas putida F1 GCN5-related N-acetyltransferase protein.	171	4.4E-10	169	32.0
954	ABZ00788.1	CP000926-4871	<i>Pseudomonas putida GB-1</i>	Pseudomonas putida GB-1 GCN5-related N-acetyltransferase protein.	171	4.4E-10	169	31.4
955	ADJ66028.1	CP002039-4500	<i>Herbaspirillum seropedicae SmR1</i>	Herbaspirillum seropedicae SmR1 sortase/acetyltransferase (antibiotic resistance) protein.	173	4.4E-10	161	32.3
956	ADJ66028.1	CP002039-4500	<i>Herbaspirillum seropedicae SmR1</i>	Herbaspirillum seropedicae SmR1 sortase/acetyltransferase (antibiotic resistance) protein.	173	4.4E-10	161	32.3
957	CBJ36480.1	FP885895-265	<i>Ralstonia solanacearum</i>	Ralstonia solanacearum putative antibiotic resistance protein (Acetyltransferase) protein.	182	4.6E-10	180	31.7
958	CBJ36480.1	FP885895-265	<i>Ralstonia solanacearum</i>	Ralstonia solanacearum putative antibiotic resistance protein (Acetyltransferase) protein.	182	4.6E-10	180	31.7
959	EDB14837.1	EP872136-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	227	4.7E-10	157	33.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
960	CAW94759.1	FM204883-1616	<i>Streptococcus equi subsp</i>	Streptococcus equi subsp. equi 4047 acetyltransferase (GNAT) family protein.	193	4.8E-10	178	33.1
961	CAW94759.1	FM204883-1616	<i>Streptococcus equi subsp</i>	Streptococcus equi subsp. equi 4047 acetyltransferase (GNAT) family protein.	193	4.8E-10	178	33.1
962	ABA47267.1	DQ168848-6	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	5E-10	173	31.8
963	ABA47267.1	DQ168848-6	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii phosphinothricin N-acetyltransferase protein.	199	5E-10	173	31.8
964	BAE03851.1	AP006716-542	<i>Staphylococcus haemolyticus JCSC1435</i>	Staphylococcus haemolyticus JCSC1435 protein (Staphylococcus haemolyticus JCSC1435 DNA, complete genome.).	164	5E-10	162	28.4
965	BAE03851.1	AP006716-542	<i>Staphylococcus haemolyticus JCSC1435</i>	Staphylococcus haemolyticus JCSC1435 protein (Staphylococcus haemolyticus JCSC1435 DNA, complete genome.).	164	5E-10	162	28.4
966	AAN70415.1	AE015451-4781	<i>Pseudomonas putida KT2440</i>	Pseudomonas putida KT2440 phosphinothricin N-acetyltransferase, putative protein.	171	5.1E-10	169	32.0
967	ACS64434.1	CP001644-3121	<i>Ralstonia pickettii 12D</i>	Ralstonia pickettii 12D GCN5-related N-acetyltransferase protein.	171	5.1E-10	170	33.5
968	AAN70415.1	AE015451-4781	<i>Pseudomonas putida KT2440</i>	Pseudomonas putida KT2440 phosphinothricin N-acetyltransferase, putative protein.	171	5.1E-10	169	32.0
969	CBK84854.1	FP929040-751	<i>Enterobacter cloacae subsp</i>	Enterobacter cloacae subsp. cloacae NCTC 9394 Sortase and related acyltransferases protein.	172	5.2E-10	168	32.1
970	CBK84854.1	FP929040-751	<i>Enterobacter cloacae subsp</i>	Enterobacter cloacae subsp. cloacae NCTC 9394 Sortase and related acyltransferases protein.	172	5.2E-10	168	32.1
971	ADK79284.1	CP002116-124	<i>Spirochaeta smaragdinae DSM 11293</i>	Spirochaeta smaragdinae DSM 11293 GCN5-related N-acetyltransferase protein.	173	5.2E-10	167	29.3
972	ADK79284.1	CP002116-124	<i>Spirochaeta smaragdinae DSM 11293</i>	Spirochaeta smaragdinae DSM 11293 GCN5-related N-acetyltransferase protein.	173	5.2E-10	167	29.3
973	ACM34139.1	CP001392-2650	<i>Acidovorax ebreus TPSY</i>	Acidovorax ebreus TPSY GCN5-related N-acetyltransferase protein.	173	5.2E-10	159	30.8
974	ECO63717.1	EM218395-3	<i>marine metagenome</i>	marine metagenome hypothetical protein.	118	5.2E-10	100	43.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
975	BAD56534.1	AP006618-1698	<i>Nocardia farcinica IFM 10152</i>	Nocardia farcinica IFM 10152 putative acetyltransferase protein.	177	5.3E-10	173	33.5
976	BAD56534.1	AP006618-1698	<i>Nocardia farcinica IFM 10152</i>	Nocardia farcinica IFM 10152 putative acetyltransferase protein.	177	5.3E-10	173	33.5
977	EFB48525.1	GG730183-160	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus D139 acetyltransferase protein.	163	5.8E-10	161	29.8
978	EFC08571.1	GG730336-345	<i>Staphylococcus aureus subsp</i>	Staphylococcus aureus subsp. aureus H19 acetyltransferase protein.	163	5.8E-10	161	29.8
979	EFL17601.1	GG657750-4853	<i>Streptomyces sp</i>	Streptomyces sp. C phosphorinothycin n-acetyltransferase protein.	165	5.9E-10	163	29.4
980	EBY14050.1	EN005855-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	166	5.9E-10	146	29.5
981	ABX67091.1	CP000886-1647	<i>Salmonella enterica subsp</i>	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7 hypothetical protein.	171	6.1E-10	168	32.7
982	EBX72301.1	EN033712-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	145	6.2E-10	142	31.0
983	EDF84288.1	EP657755-3	<i>marine metagenome</i>	marine metagenome hypothetical protein.	395	6.3E-10	169	33.1
984	ADP14519.1	CP002287-1157	<i>Achromobacter xylosoxidans A8</i>	Achromobacter xylosoxidans A8 acetyltransferase, GNAT family protein 4 protein.	185	6.5E-10	157	33.1
985	ADP14519.1	CP002287-1157	<i>Achromobacter xylosoxidans A8</i>	Achromobacter xylosoxidans A8 acetyltransferase, GNAT family protein 4 protein.	185	6.5E-10	157	33.1
986	ACM30389.1	CP000629-1801	<i>Agrobacterium radiobacter K84</i>	Agrobacterium radiobacter K84 phosphinothricin N-acetyltransferase (antibiotic resistance) protein.	198	6.9E-10	184	31.5
987	ACM30389.1	CP000629-1801	<i>Agrobacterium radiobacter K84</i>	Agrobacterium radiobacter K84 phosphinothricin N-acetyltransferase (antibiotic resistance) protein.	198	6.9E-10	184	31.5
988	EDH65934.1	EP588005-2	<i>marine metagenome</i>	marine metagenome hypothetical protein.	170	7.1E-10	152	30.9
989	ACA75118.1	CP000949-4612	<i>Pseudomonas putida W619</i>	Pseudomonas putida W619 GCN5-related N-acetyltransferase protein.	171	7.2E-10	169	31.4
990	ADR62194.1	CP002290-4483	<i>Pseudomonas putida BIRD-1</i>	Pseudomonas putida BIRD-1 GCN5-related N-acetyltransferase protein.	171	7.2E-10	169	32.0
991	ADR62194.1	CP002290-4483	<i>Pseudomonas putida BIRD-1</i>	Pseudomonas putida BIRD-1 GCN5-related N-acetyltransferase protein.	171	7.2E-10	169	32.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
992	EBC29920.1	EP426306-1	<i>marine metagenome</i>	marine metagenome hypothetical protein.	210	7.2E-10	171	33.3
993	CAP63987.1	CU633751-279	<i>Cupriavidus taiwanensis</i>	Cupriavidus taiwanensis putative acyltransferase with acyl-CoA N-acyltransferase domain protein.	179	7.4E-10	176	30.7
994	CAP63987.1	CU633751-279	<i>Cupriavidus taiwanensis</i>	Cupriavidus taiwanensis putative acyltransferase with acyl-CoA N-acyltransferase domain protein.	179	7.4E-10	176	30.7
995	ABX15844.1	CP000868-2149	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 GCN5-related N-acetyltransferase protein.	184	7.6E-10	181	30.4
996	CAE38765.1	BX640433-258	<i>Bordetella parapertussis</i>	Bordetella parapertussis conserved hypothetical protein.	184	7.6E-10	163	33.7
997	ABX15844.1	CP000868-2149	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 GCN5-related N-acetyltransferase protein.	184	7.6E-10	181	30.4
998	BAG43026.1	AP009385-1063	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 acetyltransferase protein.	184	7.6E-10	181	30.4
999	BAG43026.1	AP009385-1063	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 acetyltransferase protein.	184	7.6E-10	181	30.4
1000	CAE38765.1	BX640433-258	<i>Bordetella parapertussis</i>	Bordetella parapertussis conserved hypothetical protein.	184	7.6E-10	163	33.7

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6.5. Table 5 - GenPept database

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
1	581786	X65195	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes strain Tue494 phosphinothricin tripeptide biosynthetic gene cluster: ORFB1, ORFB2, ORF1, phsB gene, ORFM, phsC gene, pmi gene, adhP gene, ORF3, pgdP gene, ppm gene, ppd gene, ORFx, pgmP gene, cpps gene, cppm gene, aldP gene, pmet gene, pms gene, phsA gene, pat gene, dea gene, the1 gene, the2 gene, trs gene, prpA gene, ORFE1, ORFE2 and ORFE3 (partial).	183	1.6E-78	183	94.5
2	219718109	FJ410919	<i>Binary vector pWY109</i>	Binary vector pWY109, complete sequence.	183	1.6E-78	183	94.5
3	29370081	AX683002	<i>synthetic construct</i>	Sequence 5 from Patent WO03006660.	183	1.6E-78	183	94.5
4	45862349	AY562536	<i>Binary vector pORE_E3</i>	Binary Vector pORE_E3, complete sequence.	183	1.6E-78	183	94.5
5	76799969	DQ156557	<i>Zea mays</i>	Zea mays transgenic phosphinothricin acetyltransferase gene, partial cds; and beta lactamase and phosphinothricin acetyltransferase genes, complete cds.	183	1.6E-78	183	94.5
6	45862380	AY562543	<i>Binary vector pORE_O5</i>	Binary Vector pORE_O5, complete sequence.	183	1.6E-78	183	94.5
7	29419154	AX695990	<i>synthetic construct</i>	Sequence 2 from Patent WO03008596.	183	1.6E-78	183	94.5
8	1248926	A29201	<i>synthetic construct</i>	Synthetic DNA for phosphinothricin resistance gene (viral/herbicide resistance) from patent WO9111517.	183	1.6E-78	183	94.5
9	45862364	AY562539	<i>Binary vector pORE_O1</i>	Binary Vector pORE_O1, complete sequence.	183	1.6E-78	183	94.5
10	51317963	AY632421	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes PTT biosynthetic gene.	183	1.6E-78	183	94.5
11	4526588	A02470	<i>synthetic construct</i>	Synthetic gene for polypeptide having plant-protecting capability against Bialaphos.	183	1.6E-78	183	94.5
12	45862372	AY562541	<i>Binary vector pORE_O3</i>	Binary Vector pORE_O3, complete sequence.	183	1.6E-78	183	94.5
13	45862405	AY562548	<i>Binary vector pORE_R5</i>	Binary Vector pORE_R5, complete sequence.	183	1.6E-78	183	94.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
14	345280	A02774	<i>synthetic construct</i>	Artificial phosphinothricin resistance gene.	183	1.6E-78	183	94.5
15	580655	A02804	<i>Streptomyces viridochromogenes</i>	S.viridochromogenes phosphinothricin resistance gene.	183	1.6E-78	183	94.5
16	295179	M22827	<i>Streptomyces viridochromogenes</i>	Streptomyces viridochromogenes phosphinothricin N-acetyltransferase (<i>pat</i>) gene, complete cds.	183	1.6E-78	183	94.5
17	45862341	AY562534	<i>Binary vector pORE_E1</i>	Binary Vector pORE_E1, complete sequence.	183	1.6E-78	183	94.5
18	4526680	A17371	<i>synthetic construct</i>	Artificial sequence for N-acetyltransferase.	185	1.6E-78	183	94.5
19	21727002	A10510	<i>synthetic construct</i>	Artificial sequence for PTC resistance.	166	2.6E-70	166	94.0
20	81238200	DQ225746	<i>Gene trapping Ds/T-DNA vector pUR224NA</i>	Gene trapping Ds/T-DNA vector pUR224NA, complete sequence.	183	4.8E-66	183	80.3
21	284506891	AB543146	<i>Gateway binary vector pGWB645</i>	Gateway binary vector pGWB645 DNA, complete sequence.	183	4.8E-66	183	80.3
22	284506946	AB543158	<i>Gateway binary vector R4pGWB607</i>	Gateway binary vector R4pGWB607 DNA, complete sequence.	183	4.8E-66	183	80.3
23	284506954	AB543160	<i>Gateway binary vector R4pGWB613</i>	Gateway binary vector R4pGWB613 DNA, complete sequence.	183	4.8E-66	183	80.3
24	321268288	HQ175992	<i>Cloning vector pVC4-bar</i>	Cloning vector pVC4-bar, complete sequence.	183	4.8E-66	183	80.3
25	284506979	AB543166	<i>Gateway binary vector R4pGWB633</i>	Gateway binary vector R4pGWB633 DNA, complete sequence.	183	4.8E-66	183	80.3
26	284506958	AB543161	<i>Gateway binary vector R4pGWB616</i>	Gateway binary vector R4pGWB616 DNA, complete sequence.	183	4.8E-66	183	80.3
27	78057576	DQ231580	<i>Gateway vector pFSPGW</i>	Gateway vector pFSPGW, complete sequence.	183	4.8E-66	183	80.3
28	78057580	DQ231581	<i>Gateway vector pFGCGW</i>	Gateway vector pFGCGW, complete sequence.	183	4.8E-66	183	80.3
29	284506896	AB543147	<i>Gateway binary vector pGWB650</i>	Gateway binary vector pGWB650 DNA, complete sequence.	183	4.8E-66	183	80.3
30	284506747	AB543111	<i>Gateway binary vector pGWB602</i>	Gateway binary vector pGWB602 DNA, complete sequence.	183	4.8E-66	183	80.3
31	67677817	AY739897	<i>Cloning vector pRGK335</i>	Cloning vector pRGK335, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
32	47129	X17220	<i>Streptomyces hygroscopicus</i>	Streptomyces hygroscopicus bar gene for phosphinothricin acetyl transferase.	183	4.8E-66	183	80.3
33	284506966	AB543163	Gateway binary vector R4pGWB622	Gateway binary vector R4pGWB622 DNA, complete sequence.	183	4.8E-66	183	80.3
34	81238228	DQ225750	Gene trapping Ds/T-DNA vector pNU435	Gene trapping Ds/T-DNA vector pNU435, complete sequence.	183	4.8E-66	183	80.3
35	87042831	DQ370427	Binary vector pFYFPBT	Binary vector pFYFPBT, complete sequence.	183	4.8E-66	183	80.3
36	57634580	AY860533	Cloning vector p713-905	Cloning vector p713-905, complete sequence.	183	4.8E-66	183	80.3
37	57634585	AY860534	Cloning vector p713-947	Cloning vector p713-947, complete sequence.	183	4.8E-66	183	80.3
38	57634590	AY860535	Cloning vector p713-1511	Cloning vector p713-1511, complete sequence.	183	4.8E-66	183	80.3
39	284506901	AB543148	Gateway binary vector pGWB651	Gateway binary vector pGWB651 DNA, complete sequence.	183	4.8E-66	183	80.3
40	284506761	AB543114	Gateway binary vector pGWB605	Gateway binary vector pGWB605 DNA, complete sequence.	183	4.8E-66	183	80.3
41	149691279	DQ469636	Transformation vector pYW210	Transformation vector pYW210, complete sequence.	183	4.8E-66	183	80.3
42	149691332	DQ469637	Transformation vector pYW220	Transformation vector pYW220, complete sequence.	183	4.8E-66	183	80.3
43	149691337	DQ469638	Transformation vector pYW230	Transformation vector pYW230, complete sequence.	183	4.8E-66	183	80.3
44	149691356	DQ469639	Transformation vector pYW300	Transformation vector pYW300, complete sequence.	183	4.8E-66	183	80.3
45	149691381	DQ469640	Transformation vector pYW301	Transformation vector pYW301, complete sequence.	183	4.8E-66	183	80.3
46	149691245	DQ469634	Transformation vector pYW100b	Transformation vector pYW100b, complete sequence.	183	4.8E-66	183	80.3
47	149691264	DQ469635	Transformation vector pYW200	Transformation vector pYW200, complete sequence.	183	4.8E-66	183	80.3
48	306450687	HM439362	Plant binary vector pXS2pat-Strep	Plant binary vector pXS2pat-Strep, complete sequence.	183	4.8E-66	183	80.3
49	312618306	HM750245	Cloning vector pSIM1	Cloning vector pSIM1, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
50	312618312	HM750246	<i>Cloning vector pSIM3</i>	Cloning vector pSIM3, complete sequence.	183	4.8E-66	183	80.3
51	284506833	AB543132	<i>Gateway binary vector pGWB623</i>	Gateway binary vector pGWB623 DNA, complete sequence.	183	4.8E-66	183	80.3
52	7453573	AF218816	<i>Cloning vector pEGAD</i>	Cloning vector pEGAD, complete sequence.	183	4.8E-66	183	80.3
53	149691400	DQ469641	<i>Transformation vector pYW310</i>	Transformation vector pYW310, complete sequence.	183	4.8E-66	183	80.3
54	284506910	AB543150	<i>Gateway binary vector pGWB653</i>	Gateway binary vector pGWB653 DNA, complete sequence.	183	4.8E-66	183	80.3
55	87042809	DQ370421	<i>Gateway adapted binary vector pFYTAG</i>	Gateway adapted binary vector pFYTAG, complete sequence.	183	4.8E-66	183	80.3
56	226331143	FJ524331	<i>Cloning vector pNIGEL 11</i>	Cloning vector pNIGEL 11, complete sequence.	183	4.8E-66	183	80.3
57	226331146	FJ524332	<i>Cloning vector pNIGEL 13</i>	Cloning vector pNIGEL 13, complete sequence.	183	4.8E-66	183	80.3
58	81238207	DQ225747	<i>Gene trapping Ds/T-DNA vector pUR224NB</i>	Gene trapping Ds/T-DNA vector pUR224NB, complete sequence.	183	4.8E-66	183	80.3
59	81238214	DQ225748	<i>Gene trapping Ds/T-DNA vector pNU393A1</i>	Gene trapping Ds/T-DNA vector pNU393A1, complete sequence.	183	4.8E-66	183	80.3
60	81238221	DQ225749	<i>Gene trapping Ds/T-DNA vector pNU393B2</i>	Gene trapping Ds/T-DNA vector pNU393B2, complete sequence.	183	4.8E-66	183	80.3
61	284506875	AB543142	<i>Gateway binary vector pGWB641</i>	Gateway binary vector pGWB641 DNA, complete sequence.	183	4.8E-66	183	80.3
62	284506879	AB543143	<i>Gateway binary vector pGWB642</i>	Gateway binary vector pGWB642 DNA, complete sequence.	183	4.8E-66	183	80.3
63	284506950	AB543159	<i>Gateway binary vector R4pGWB610</i>	Gateway binary vector R4pGWB610 DNA, complete sequence.	183	4.8E-66	183	80.3
64	110555472	DQ666282	<i>Cloning vector pRGK 366</i>	Cloning vector pRGK 366, complete sequence.	183	4.8E-66	183	80.3
65	110555476	DQ666283	<i>Cloning vector pRGK 367</i>	Cloning vector pRGK 367, complete sequence.	183	4.8E-66	183	80.3
66	113073445	DQ869007	<i>Binary vector pMOA36</i>	Binary vector pMOA36, partial sequence.	183	4.8E-66	183	80.3
67	284506789	AB543121	<i>Gateway binary vector pGWB612</i>	Gateway binary vector pGWB612 DNA, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
68	62736932	AY995142	<i>Binary vector pPZP 35S hRluc-attR</i>	Binary vector pPZP 35S hRluc-attR, complete sequence.	183	4.8E-66	183	80.3
69	62736938	AY995143	<i>Binary vector pPZP 35S attR-hRluc</i>	Binary vector pPZP 35S attR-hRluc, complete sequence.	183	4.8E-66	183	80.3
70	111120118	AM295157	<i>Cloning vector pGWLuc</i>	Cloning vector pGWLuc.	183	4.8E-66	183	80.3
71	339515844	HQ699550	<i>Cloning vector pCASP1::BOR1sst:Citrine</i>	Cloning vector pCASP1::BOR1sst:Citrine, complete sequence.	183	4.8E-66	183	80.3
72	284506988	AB543168	<i>Gateway binary vector R4pGWB640</i>	Gateway binary vector R4pGWB640 DNA, complete sequence.	183	4.8E-66	183	80.3
73	284506924	AB543153	<i>Gateway binary vector pGWB659</i>	Gateway binary vector pGWB659 DNA, complete sequence.	183	4.8E-66	183	80.3
74	67679404	AY739898	<i>Cloning vector pRGK336</i>	Cloning vector pRGK336, complete sequence.	183	4.8E-66	183	80.3
75	334085756	JF909454	<i>Cloning vector pPLV01</i>	Cloning vector pPLV01, complete sequence.	183	4.8E-66	183	80.3
76	334085769	JF909458	<i>Cloning vector pPLV05</i>	Cloning vector pPLV05, complete sequence.	183	4.8E-66	183	80.3
77	284506743	AB543110	<i>Gateway binary vector pGWB601</i>	Gateway binary vector pGWB601 DNA, complete sequence.	183	4.8E-66	183	80.3
78	60285789	AY836546	<i>T-DNA vector pDs-Lox</i>	T-DNA vector pDs-Lox, complete sequence.	183	4.8E-66	183	80.3
79	284506751	AB543112	<i>Gateway binary vector pGWB602omega</i>	Gateway binary vector pGWB602omega DNA, complete sequence.	183	4.8E-66	183	80.3
80	284506756	AB543113	<i>Gateway binary vector pGWB604</i>	Gateway binary vector pGWB604 DNA, complete sequence.	183	4.8E-66	183	80.3
81	260101144	FJ858786	<i>Vector pwFRT-PCS12-bar</i>	Vector pwFRT-PCS12-bar, complete sequence.	183	4.8E-66	183	80.3
82	284506765	AB543115	<i>Gateway binary vector pGWB606</i>	Gateway binary vector pGWB606 DNA, complete sequence.	183	4.8E-66	183	80.3
83	284506769	AB543116	<i>Gateway binary vector pGWB607</i>	Gateway binary vector pGWB607 DNA, complete sequence.	183	4.8E-66	183	80.3
84	284506773	AB543117	<i>Gateway binary vector pGWB608</i>	Gateway binary vector pGWB608 DNA, complete sequence.	183	4.8E-66	183	80.3
85	284506777	AB543118	<i>Gateway binary vector pGWB609</i>	Gateway binary vector pGWB609 DNA, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
86	284506781	AB543119	<i>Gateway binary vector pGWB610</i>	Gateway binary vector pGWB610 DNA, complete sequence.	183	4.8E-66	183	80.3
87	284506785	AB543120	<i>Gateway binary vector pGWB611</i>	Gateway binary vector pGWB611 DNA, complete sequence.	183	4.8E-66	183	80.3
88	306450678	HM439359	<i>Plant binary vector pXNS1pat-Strep</i>	Plant binary vector pXNS1pat-Strep, complete sequence.	183	4.8E-66	183	80.3
89	284506793	AB543122	<i>Gateway binary vector pGWB613</i>	Gateway binary vector pGWB613 DNA, complete sequence.	183	4.8E-66	183	80.3
90	284506797	AB543123	<i>Gateway binary vector pGWB614</i>	Gateway binary vector pGWB614 DNA, complete sequence.	183	4.8E-66	183	80.3
91	284506801	AB543124	<i>Gateway binary vector pGWB615</i>	Gateway binary vector pGWB615 DNA, complete sequence.	183	4.8E-66	183	80.3
92	284506805	AB543125	<i>Gateway binary vector pGWB616</i>	Gateway binary vector pGWB616 DNA, complete sequence.	183	4.8E-66	183	80.3
93	284506809	AB543126	<i>Gateway binary vector pGWB617</i>	Gateway binary vector pGWB617 DNA, complete sequence.	183	4.8E-66	183	80.3
94	284506813	AB543127	<i>Gateway binary vector pGWB618</i>	Gateway binary vector pGWB618 DNA, complete sequence.	183	4.8E-66	183	80.3
95	306450684	HM439361	<i>Plant binary vector pXS1pat-Strep</i>	Plant binary vector pXS1pat-Strep, complete sequence.	183	4.8E-66	183	80.3
96	284506821	AB543129	<i>Gateway binary vector pGWB620</i>	Gateway binary vector pGWB620 DNA, complete sequence.	183	4.8E-66	183	80.3
97	284506825	AB543130	<i>Gateway binary vector pGWB621</i>	Gateway binary vector pGWB621 DNA, complete sequence.	183	4.8E-66	183	80.3
98	284506829	AB543131	<i>Gateway binary vector pGWB622</i>	Gateway binary vector pGWB622 DNA, complete sequence.	183	4.8E-66	183	80.3
99	45685339	AY568055	<i>Cloning vector pAGRIKOLA</i>	Cloning vector pAGRIKOLA, complete sequence.	183	4.8E-66	183	80.3
100	284506837	AB543133	<i>Gateway binary vector pGWB624</i>	Gateway binary vector pGWB624 DNA, complete sequence.	183	4.8E-66	183	80.3
101	284506905	AB543149	<i>Gateway binary vector pGWB652</i>	Gateway binary vector pGWB652 DNA, complete sequence.	183	4.8E-66	183	80.3
102	94481126	AB240452	<i>Cloning vector pBARST</i>	Cloning vector pBARST DNA, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
103	16903541	AF404854	<i>Binary vector pJawohl3-RNAi</i>	Binary vector pJawohl3-RNAi, complete sequence.	183	4.8E-66	183	80.3
104	284506853	AB543137	<i>Gateway binary vector pGWB628</i>	Gateway binary vector pGWB628 DNA, complete sequence.	183	4.8E-66	183	80.3
105	284506857	AB543138	<i>Gateway binary vector pGWB629</i>	Gateway binary vector pGWB629 DNA, complete sequence.	183	4.8E-66	183	80.3
106	226331150	FJ524333	<i>Cloning vector pNIGEL15</i>	Cloning vector pNIGEL15, complete sequence.	183	4.8E-66	183	80.3
107	226331154	FJ524334	<i>Cloning vector pNIGEL16</i>	Cloning vector pNIGEL16, complete sequence.	183	4.8E-66	183	80.3
108	163860172	EU327495	<i>Transformation vector pC23LB</i>	Transformation vector pC23LB, complete sequence.	183	4.8E-66	183	80.3
109	284506962	AB543162	<i>Gateway binary vector R4pGWB619</i>	Gateway binary vector R4pGWB619 DNA, complete sequence.	183	4.8E-66	183	80.3
110	306450681	HM439360	<i>Plant binary vector pXNS2pat-Strep</i>	Plant binary vector pXNS2pat-Strep, complete sequence.	183	4.8E-66	183	80.3
111	38231646	AY436765	<i>Binary vector pAMPAT-MCS</i>	Binary vector pAMPAT-MCS, complete sequence.	183	4.8E-66	183	80.3
112	284506887	AB543145	<i>Gateway binary vector pGWB644</i>	Gateway binary vector pGWB644 DNA, complete sequence.	183	4.8E-66	183	80.3
113	32265028	AY310901	<i>Binary vector pFGC5941</i>	Binary vector pFGC5941 phosphinothricin acetyl transferase (BAR) and aminoglycoside phosphotransferase (aadA) genes, complete cds.	183	4.8E-66	183	80.3
114	581681	X05822	<i>Streptomyces hygroscopicus</i>	Streptomyces hygroscopicus bar gene conferring resistance to herbicide bialaphos.	183	4.8E-66	183	80.3
115	4526659	A12456	<i>synthetic construct</i>	oligonucleotide encoding a protein with PPT acetyl transferase activity.	183	4.8E-66	183	80.3
116	42425657	AY528455	<i>synthetic construct</i>	Synthetic construct phosphinotricine acetyltransferase gene, complete cds.	183	4.8E-66	183	80.3
117	284506841	AB543134	<i>Gateway binary vector pGWB625</i>	Gateway binary vector pGWB625 DNA, complete sequence.	183	4.8E-66	183	80.3
118	226331124	FJ493465	<i>Cloning vector pNIGEL07</i>	Cloning vector pNIGEL07, complete sequence.	183	4.8E-66	183	80.3
119	284506915	AB543151	<i>Gateway binary vector pGWB654</i>	Gateway binary vector pGWB654 DNA, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
120	334085777	JF909460	<i>Cloning vector pPLV07</i>	Cloning vector pPLV07, complete sequence.	183	4.8E-66	183	80.3
121	45862533	AY572837	<i>Cloning vector pMCG161</i>	Cloning vector pMCG161, complete sequence.	183	4.8E-66	183	80.3
122	284506929	AB543154	<i>Gateway binary vector pGWB660</i>	Gateway binary vector pGWB660 DNA, complete sequence.	183	4.8E-66	183	80.3
123	284506933	AB543155	<i>Gateway binary vector pGWB661</i>	Gateway binary vector pGWB661 DNA, complete sequence.	183	4.8E-66	183	80.3
124	284506937	AB543156	<i>Gateway binary vector R4pGWB601</i>	Gateway binary vector R4pGWB601 DNA, complete sequence.	183	4.8E-66	183	80.3
125	284506942	AB543157	<i>Gateway binary vector R4pGWB604</i>	Gateway binary vector R4pGWB604 DNA, complete sequence.	183	4.8E-66	183	80.3
126	334085847	JF909478	<i>Cloning vector pPLV25</i>	Cloning vector pPLV25, complete sequence.	183	4.8E-66	183	80.3
127	146217633	EF535105	<i>Expression vector p7NBT</i>	Expression vector p7NBT, complete sequence.	183	4.8E-66	183	80.3
128	226439516	FJ826509	<i>Vector miniTn7-bar</i>	Vector miniTn7-bar, complete sequence.	183	4.8E-66	183	80.3
129	334085868	JF909485	<i>Cloning vector pPLV32</i>	Cloning vector pPLV32, complete sequence.	183	4.8E-66	183	80.3
130	4191251	Y18556	<i>Cloning vector pSLJ8313</i>	Cloning vector pSLJ8313, T-DNA region.	183	4.8E-66	183	80.3
131	2547092	AF013602	<i>synthetic construct</i>	Synthetic construct, Emericella nidulans TrpC promoter, complete sequence, Streptomyces spp. phosphinothricin acetyl transferase gene, complete cds.	183	4.8E-66	183	80.3
132	284506970	AB543164	<i>Gateway binary vector R4pGWB625</i>	Gateway binary vector R4pGWB625 DNA, complete sequence.	183	4.8E-66	183	80.3
133	284506974	AB543165	<i>Gateway binary vector R4pGWB628</i>	Gateway binary vector R4pGWB628 DNA, complete sequence.	183	4.8E-66	183	80.3
134	317447097	FR695418	<i>Binary vector pAMARENA</i>	Binary vector pAMARENA.	183	4.8E-66	183	80.3
135	284506984	AB543167	<i>Gateway binary vector R4pGWB635</i>	Gateway binary vector R4pGWB635 DNA, complete sequence.	183	4.8E-66	183	80.3
136	334085801	JF909466	<i>Cloning vector pPLV13</i>	Cloning vector pPLV13, complete sequence.	183	4.8E-66	183	80.3
137	284506992	AB543169	<i>Gateway binary vector R4pGWB643</i>	Gateway binary vector R4pGWB643 DNA, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
138	284506997	AB543170	<i>Gateway binary vector R4pGWB650</i>	Gateway binary vector R4pGWB650 DNA, complete sequence.	183	4.8E-66	183	80.3
139	284507002	AB543171	<i>Gateway binary vector R4pGWB653</i>	Gateway binary vector R4pGWB653 DNA, complete sequence.	183	4.8E-66	183	80.3
140	284507007	AB543172	<i>Gateway binary vector R4pGWB659</i>	Gateway binary vector R4pGWB659 DNA, complete sequence.	183	4.8E-66	183	80.3
141	42405463	AY457636	<i>Plant binary vector pXCS-HAStrep</i>	Plant binary vector pXCS-HAStrep, complete sequence.	183	4.8E-66	183	80.3
142	334085789	JF909463	<i>Cloning vector pPLV10</i>	Cloning vector pPLV10, complete sequence.	183	4.8E-66	183	80.3
143	284506867	AB543140	<i>Gateway binary vector pGWB635</i>	Gateway binary vector pGWB635 DNA, complete sequence.	183	4.8E-66	183	80.3
144	334085811	JF909469	<i>Cloning vector pPLV16</i>	Cloning vector pPLV16, complete sequence.	183	4.8E-66	183	80.3
145	334085823	JF909472	<i>Cloning vector pPLV19</i>	Cloning vector pPLV19, complete sequence.	183	4.8E-66	183	80.3
146	56553578	AY818376	<i>Phosphinothricin resistance plant expression vector pSAT6-bar</i>	Phosphinothricin resistance plant expression vector pSAT6-bar, complete sequence.	183	4.8E-66	183	80.3
147	300827483	HM014235	<i>Cloning vector pCHC01</i>	Cloning vector pCHC01, complete sequence.	183	4.8E-66	183	80.3
148	334085856	JF909481	<i>Cloning vector pPLV28</i>	Cloning vector pPLV28, complete sequence.	183	4.8E-66	183	80.3
149	29569311	AY093584	<i>Cloning Vector pBANF-bar</i>	Cloning Vector pBANF-bar, complete sequence.	183	4.8E-66	183	80.3
150	126361412	EF426459	<i>Binary gene-trap vector piGL</i>	Binary gene-trap vector piGL, complete sequence.	183	4.8E-66	183	80.3
151	284506871	AB543141	<i>Gateway binary vector pGWB640</i>	Gateway binary vector pGWB640 DNA, complete sequence.	183	4.8E-66	183	80.3
152	334085835	JF909475	<i>Cloning vector pPLV22</i>	Cloning vector pPLV22, complete sequence.	183	4.8E-66	183	80.3
153	284506817	AB543128	<i>Gateway binary vector pGWB619</i>	Gateway binary vector pGWB619 DNA, complete sequence.	183	4.8E-66	183	80.3
154	284506862	AB543139	<i>Gateway binary vector pGWB633</i>	Gateway binary vector pGWB633 DNA, complete sequence.	183	4.8E-66	183	80.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence lenght	E-value	Length of alignment	% Identity
155	63002555	DQ005454	<i>Cloning vector pRCS2-ocs-bar</i>	Cloning vector pRCS2-ocs-bar T-DNA region, complete sequence.	183	4.8E-66	183	80.3
156	284506919	AB543152	<i>Gateway binary vector pGWB655</i>	Gateway binary vector pGWB655 DNA, complete sequence.	183	4.8E-66	183	80.3
157	226331140	FJ524330	<i>Cloning vector pNIGEL09</i>	Cloning vector pNIGEL09, complete sequence.	183	4.8E-66	183	80.3
158	114325531	DQ989355	<i>Gene trapping Ds/T-DNA vector pDsG8</i>	Gene trapping Ds/T-DNA vector pDsG8, complete sequence.	183	4.8E-66	183	80.3
159	284506845	AB543135	<i>Gateway binary vector pGWB626</i>	Gateway binary vector pGWB626 DNA, complete sequence.	183	4.8E-66	183	80.3
160	67089188	DQ062658	<i>Cloning vector p713-1160</i>	Cloning vector p713-1160, complete sequence.	183	4.8E-66	183	80.3
161	284506883	AB543144	<i>Gateway binary vector pGWB643</i>	Gateway binary vector pGWB643 DNA, complete sequence.	183	4.8E-66	183	80.3
162	63002506	DQ005457	<i>Cloning vector pSAT1A-ocsAocsP-bar-ocsT</i>	Cloning vector pSAT1A-ocsAocsP-bar-ocsT, complete sequence.	183	4.8E-66	183	80.3
163	284506849	AB543136	<i>Gateway binary vector pGWB627</i>	Gateway binary vector pGWB627 DNA, complete sequence.	183	4.8E-66	183	80.3
164	67867074	DQ071887	<i>Cloning vector pRD29A-GUS</i>	Cloning vector pRD29A-GUS, complete sequence.	183	4.8E-66	183	80.3
165	334085859	JF909482	<i>Cloning vector pPLV29</i>	Cloning vector pPLV29, complete sequence.	183	4.8E-66	183	80.3
166	67867069	DQ071886	<i>Cloning vector pRD29A-GFP</i>	Cloning vector pRD29A-GFP, complete sequence.	183	4.8E-66	183	80.3
167	6537290	AF187951	<i>Activation-tagging vector pSKI015</i>	Activation-tagging vector pSKI015, complete sequence.	183	7.9E-66	183	79.8
168	106013230	DQ645630	<i>Activation-tagging vector pEnLox</i>	Activation-tagging vector pEnLox, complete sequence.	183	7.9E-66	183	79.8
169	307557071	HM047294	<i>Binary vector pBI121-ELEMENTS</i>	Binary vector pBI121-ELEMENTS, complete sequence.	183	9.3E-66	183	79.8
170	155733609	EU048867	<i>Cloning vector pGreenII 0229</i>	Cloning vector pGreenII 0229, T-DNA region.	183	9.3E-66	183	79.8
171	193227114	FM177584	<i>Cloning vector pG002</i>	Cloning vector pG002.	183	9.3E-66	183	79.8
172	193227120	FM177585	<i>Cloning vector pG004</i>	Cloning vector pG004.	183	9.3E-66	183	79.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
173	193227108	FM177583	<i>Cloning vector pG001</i>	Cloning vector pG001.	183	9.3E-66	183	79.8
174	155733613	EU048869	<i>Cloning vector pGreenII 0229 62-SK</i>	Cloning vector pGreenII 0229 62-SK, T-DNA region.	183	9.3E-66	183	79.8
175	239913995	FN398077	<i>Cloning vector pG003</i>	Cloning vector pG003.	183	9.3E-66	183	79.8
176	193227106	FM177582	<i>Cloning vector pDEX00</i>	Cloning vector pDEX00.	183	9.3E-66	183	79.8
177	9928281	AX004880	<i>synthetic construct</i>	Sequence 1 from Patent WO9910512.	183	1.1E-65	183	79.8
178	904322	A23334	<i>Escherichia coli</i>	PVE108 plasmid DNA.	183	1.1E-65	183	79.8
179	513159	A18053	<i>synthetic construct</i>	DNA for transforming monocotyledonous plants.	183	1.1E-65	183	79.8
180	29569725	AY234330	<i>Binary vector pLH7000</i>	Binary vector pLH7000, complete sequence.	183	1.1E-65	183	79.8
181	29569731	AY234331	<i>Binary vector pLH7500</i>	Binary vector pLH7500, complete sequence.	183	1.1E-65	183	79.8
182	6088115	A75886	<i>unidentified</i>	Sequence 1 from Patent WO9321335.	183	1.1E-65	183	79.8
183	40457466	AY346130	<i>Zea mays</i>	<i>Zea mays</i> transgenic clone pDE110 phosphinothricin acetyl transferase gene, complete cds.	183	1.1E-65	183	79.8
184	327466180	HQ233646	<i>Gossypium hirsutum</i>	<i>Gossypium hirsutum</i> transgenic clone LLcotton25 phosphinothricin N-acetyltransferase gene, complete cds.	183	1.1E-65	183	79.8
185	512577	A02465	<i>synthetic construct</i>	Synthetic gene for polypeptide having plant protecting capability against Bialaphos.	183	1.3E-65	183	79.8
186	14597397	AX168080	<i>synthetic construct</i>	Sequence 35 from Patent WO0144447.	181	1.5E-65	181	80.7
187	14597392	AX168079	<i>synthetic construct</i>	Sequence 34 from Patent WO0144447.	181	1.5E-65	181	80.7
188	13449972	AY028212	<i>synthetic construct</i>	Synthetic construct phosphinothricin acetyltransferase (bar) gene, complete cds.	184	1.6E-65	182	80.2
189	80261264	DQ211345	<i>synthetic construct</i>	Synthetic construct editing-dependent chimeric phosphinothricin acetyltransferase (Ebar) gene, complete cds.	187	1.6E-65	182	80.2
190	295149392	GU980700	<i>Tobacco plastid transformation vector pSS42</i>	Tobacco plastid transformation vector pSS42, complete sequence.	188	1.6E-65	182	80.2

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
191	295149389	GU980699	<i>Tobacco plastid transformation vector pSS33</i>	Tobacco plastid transformation vector pSS33, complete sequence.	188	1.6E-65	182	80.2
192	80261296	DQ211346	<i>synthetic construct</i>	Synthetic construct phosphinothricin acetyl transferase (b-bar-2) gene, complete cds.	197	1.6E-65	182	80.2
193	117209776	EF010978	<i>Silencing vector pFE12860S</i>	Silencing vector pFE12860S, complete sequence.	182	1.1E-62	183	78.1
194	117583118	DQ995484	<i>Overexpression vector pFE12860OE</i>	Overexpression vector pFE12860OE, complete sequence.	182	1.1E-62	183	78.1
195	117209782	EF010980	<i>Silencing vector p3UTR12850S</i>	Silencing vector p3UTR12850S, complete sequence.	182	1.1E-62	183	78.1
196	117583121	DQ995485	<i>Overexpression vector pLE12860OE</i>	Overexpression vector pLE12860OE, complete sequence.	182	1.1E-62	183	78.1
197	117583124	DQ995486	<i>Overexpression vector pFC12850OE</i>	Overexpression vector pFC12850OE, complete sequence.	182	1.1E-62	183	78.1
198	117583127	DQ995487	<i>Overexpression vector pFC12860OE</i>	Overexpression vector pFC12860OE, complete sequence.	182	1.1E-62	183	78.1
199	117209779	EF010979	<i>Silencing vector pSE12860S</i>	Silencing vector pSE12860S, complete sequence.	182	1.1E-62	183	78.1
200	76799967	DQ156557	<i>Zea mays</i>	Zea mays transgenic phosphinothricin acetyltransferase gene, partial cds; and beta lactamase and phosphinothricin acetyltransferase genes, complete cds.	109	2.4E-47	109	100.0
201	145301985	CP000667	<i>Salinispora tropica CNB-440</i>	Salinispora tropica CNB-440, complete genome.	192	2.9E-36	178	51.1
202	63255454	CP000075	<i>Pseudomonas syringae pv syringae B728a</i>	Pseudomonas syringae pv. syringae B728a, complete genome.	184	4.7E-25	174	38.5
203	35213094	BA000045	<i>Gloeobacter violaceus PCC 7421</i>	Gloeobacter violaceus PCC 7421 DNA, complete genome.	212	2.9E-24	170	41.8
204	76558040	CR936257	<i>Natronomonas pharaonis DSM 2160</i>	Natronomonas pharaonis DSM 2160 complete genome.	206	3.3E-24	177	40.7
205	262080930	CP001804	<i>Haliangium ochraceum DSM 14365</i>	Haliangium ochraceum DSM 14365, complete genome.	190	3.7E-24	179	39.1
206	300075201	CP002039	<i>Herbaspirillum seropedicae SmR1</i>	Herbaspirillum seropedicae SmR1, complete genome.	167	1.3E-23	156	41.0

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
207	148498637	CP000699	<i>Sphingomonas wittichii</i> RW1	Sphingomonas wittichii RW1, complete genome.	182	1.4E-23	177	39.5
208	289531036	CP001932	<i>Natrialba magadii</i> ATCC 43099	Natrialba magadii ATCC 43099, complete genome.	198	2E-23	176	39.8
209	256690972	CP001687	<i>Halorhabdus utahensis</i> DSM 12940	Halorhabdus utahensis DSM 12940, complete genome.	200	5.6E-23	173	38.7
210	326949470	CP002593	<i>Pseudonocardia dioxanivorans</i> CB1190	Pseudonocardia dioxanivorans CB1190, complete genome.	193	5.7E-22	175	40.0
211	159893174	CP000875	<i>Herpetosiphon aurantiacus</i> DSM 785	Herpetosiphon aurantiacus DSM 785, complete genome.	198	5.8E-22	176	39.8
212	311227610	CP002299	<i>Frankia</i> sp. Eul1c	Frankia sp. Eul1c, complete genome.	180	2.1E-21	175	38.3
213	338835235	CP002868	<i>Spirochaeta caldaria</i> DSM 7334	Spirochaeta caldaria DSM 7334, complete genome.	162	3.1E-21	156	40.4
214	85773482	CP000251	<i>Anaeromyxobacter dehalogenans</i> 2CP-C	Anaeromyxobacter dehalogenans 2CP-C, complete genome.	197	5.2E-21	172	40.1
215	291372119	CP001956	<i>Haloferax volcanii</i> DS2	Haloferax volcanii DS2, complete genome.	199	8.6E-21	174	36.8
216	333114721	CP002727	<i>Pseudomonas fulva</i> 12-X	Pseudomonas fulva 12-X, complete genome.	187	1.4E-20	175	36.6
217	283813353	CP001736	<i>Kribbella flavida</i> DSM 17836	Kribbella flavida DSM 17836, complete genome.	178	1.5E-20	171	37.4
218	196170841	CP001131	<i>Anaeromyxobacter</i> sp. K	Anaeromyxobacter sp. K, complete genome.	197	1.7E-20	172	39.5
219	340553978	CP002745	<i>Collimonas fungivorans</i> Ter331	Collimonas fungivorans Ter331, complete genome.	174	1.8E-20	157	39.5
220	151362396	CP000750	<i>Kineococcus radiotolerans</i> SRS30216	Kineococcus radiotolerans SRS30216, complete genome.	176	2.1E-20	170	38.2
221	284063969	CP001867	<i>Geodermatophilus obscurus</i> DSM 43160	Geodermatophilus obscurus DSM 43160, complete genome.	198	7.6E-20	171	39.2
222	110286666	CP000390	<i>Chelativorans</i> sp. BNC1	Chelativorans sp. BNC1, complete genome.	186	8.6E-20	174	37.4
223	219953545	CP001359	<i>Anaeromyxobacter dehalogenans</i> 2CP-1	Anaeromyxobacter dehalogenans 2CP-1, complete genome.	197	1.5E-19	173	38.7
224	283946439	CP001854	<i>Conexibacter woesei</i> DSM 14684	Conexibacter woesei DSM 14684, complete genome.	176	1.9E-19	173	39.3

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
225	296023105	CP001964	<i>Cellulomonas flavigena</i> DSM 20109	Cellulomonas flavigena DSM 20109, complete genome.	193	2E-19	184	35.9
226	335336700	CP002839	<i>Halopiger xanaduensis</i> SH-6	Halopiger xanaduensis SH-6, complete genome.	202	2.1E-19	169	37.3
227	119766979	CP000507	<i>Shewanella amazonensis</i> SB2B	Shewanella amazonensis SB2B, complete genome.	171	2.2E-19	161	37.9
228	154155672	CP000774	<i>Parvibaculum lavamentivorans</i> DS-1	Parvibaculum lavamentivorans DS-1, complete genome.	197	2.5E-19	174	35.6
229	257170706	CP001688	<i>Halomicrobium mukohataei</i> DSM 12286	Halomicrobium mukohataei DSM 12286, complete genome.	196	9.4E-19	174	34.5
230	284013195	CP001860	<i>Haloterrigena turkmenica</i> DSM 5511	Haloterrigena turkmenica DSM 5511, complete genome.	203	1.1E-18	172	36.6
231	41394535	AE016958	<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> K-10	Mycobacterium avium subsp. paratuberculosis str. k10, complete genome.	192	1.3E-18	175	36.0
232	319757933	CP002465	<i>Streptococcus suis</i> JS14	Streptococcus suis JS14, complete genome.	169	1.4E-18	161	35.4
233	251815796	FM252031	<i>Streptococcus suis</i> SC84	Streptococcus suis SC84 complete genome, strain SC84.	169	1.4E-18	161	35.4
234	292558148	CP000837	<i>Streptococcus suis</i> GZ1	Streptococcus suis GZ1, complete genome.	169	1.4E-18	161	35.4
235	145689161	CP000407	<i>Streptococcus suis</i> 05ZYH33	Streptococcus suis 05ZYH33, complete genome.	169	1.4E-18	161	35.4
236	145691356	CP000408	<i>Streptococcus suis</i> 98HAH33	Streptococcus suis 98HAH33, complete genome.	169	1.4E-18	161	35.4
237	251819654	AM946016	<i>Streptococcus suis</i> P1/7	Streptococcus suis P1/7 complete genome.	169	1.4E-18	161	35.4
238	251818227	FM252032	<i>Streptococcus suis</i> BM407	Streptococcus suis BM407 complet genome, strain BM407.	169	1.4E-18	161	35.4
239	116101313	CP000419	<i>Streptococcus thermophilus</i> LMD-9	Streptococcus thermophilus LMD-9, complete genome.	170	1.4E-18	171	35.1
240	118165500	CP000479	<i>Mycobacterium avium</i> 104	Mycobacterium avium 104, complete genome.	188	1.5E-18	172	36.6
241	333484389	CP002786	<i>Amycolicococcus subflavus</i> DQS3-9A1	Amycolicococcus subflavus DQS3-9A1, complete genome.	172	1.7E-18	171	34.5

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
242	169242089	CU458896	<i>Mycobacterium abscessus</i>	Mycobacterium abscessus chromosome, complete sequence.	177	2E-18	158	36.1
243	299126020	CP002062	<i>Halalkalicoccus jeotgali</i> B3	Halalkalicoccus jeotgali B3, complete genome.	196	2.2E-18	171	36.3
244	151281660	CP000269	<i>Janthinobacterium</i> sp Marseille	Janthinobacterium sp. Marseille, complete genome.	173	2.3E-18	156	37.8
245	297162419	CP002047	<i>Streptomyces bingchenggensis</i> BCW-1	Streptomyces bingchenggensis BCW-1, complete genome.	185	2.9E-18	184	36.4
246	296845444	CP002040	<i>Nocardiopsis dassonvillei</i> subsp <i>dassonvillei</i> DSM 43111	Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111, complete genome.	175	3.3E-18	163	33.7
247	56178905	AE017340	<i>Idiomarina loihiensis</i> L2TR	Idiomarina loihiensis L2TR, complete genome.	166	3.7E-18	157	36.3
248	237684095	CP001614	<i>Teredinibacter turnerae</i> T7901	Teredinibacter turnerae T7901, complete genome.	204	4.4E-18	168	33.3
249	339278457	FR875178	<i>Streptococcus thermophilus</i> JIM 8232	Streptococcus thermophilus JIM 8232 complete genome.	170	8.8E-18	171	34.5
250	312278631	CP002340	<i>Streptococcus thermophilus</i> ND03	Streptococcus thermophilus ND03, complete genome.	170	8.8E-18	171	34.5
251	326545318	CP002583	<i>Marinomonas mediterranea</i> MMB-1	Marinomonas mediterranea MMB-1, complete genome.	163	1E-17	157	34.4
252	339291855	CP002888	<i>Streptococcus salivarius</i> 57I	Streptococcus salivarius 57.I, complete genome.	177	1.1E-17	170	33.5
253	187728644	CP001069	<i>Ralstonia pickettii</i> 12J	Ralstonia pickettii 12J chromosome 2, complete sequence.	182	1.1E-17	170	36.5
254	240867246	CP001645	<i>Ralstonia pickettii</i> 12D	Ralstonia pickettii 12D chromosome 2, complete sequence.	182	1.1E-17	170	36.5
255	55739202	CP000024	<i>Streptococcus thermophilus</i> CNRZ1066	Streptococcus thermophilus CNRZ1066, complete genome.	193	1.1E-17	177	33.9
256	188520904	CP000967	<i>Xanthomonas oryzae</i> pv <i>oryzae</i> PXO99A	Xanthomonas oryzae pv. oryzae PXO99A, complete genome.	170	1.2E-17	164	35.4
257	338745242	FR873482	<i>Streptococcus salivarius</i> JIM8777	Streptococcus salivarius JIM8777 complete genome.	170	1.5E-17	162	34.6
258	144901277	CU459003	<i>Magnetospirillum gryphiswaldense</i> MSR-1	Magnetospirillum gryphiswaldense MSR-1, WORKING DRAFT SEQUENCE, 373 unordered pieces.	176	1.8E-17	165	37.6

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
259	55737289	CP000023	<i>Streptococcus thermophilus</i> LMG 18311	Streptococcus thermophilus LMG 18311, complete genome.	193	2.3E-17	177	33.3
260	338742592	FR873481	<i>Streptococcus salivarius</i> CCHSS3	Streptococcus salivarius CCHSS3 complete genome.	170	2.4E-17	162	34.6
261	329306888	CP002633	<i>Streptococcus suis</i> ST3	Streptococcus suis ST3, complete genome.	169	3.3E-17	161	33.5
262	209531043	CP001189	<i>Gluconacetobacter diazotrophicus</i> PAI 5	Gluconacetobacter diazotrophicus PAI 5, complete genome.	184	3.6E-17	182	36.8
263	317166591	CP002447	<i>Mesorhizobium ciceri</i> biovar biserrulae WSM1271	Mesorhizobium ciceri biovar biserrulae WSM1271, complete genome.	190	3.7E-17	174	35.6
264	170658379	CP001001	<i>Methylobacterium radiotolerans</i> JCM 2831	Methylobacterium radiotolerans JCM 2831, complete genome.	176	4.1E-17	172	37.8
265	161785217	AM889285	<i>Gluconacetobacter diazotrophicus</i> PAI 5	Gluconacetobacter diazotrophicus PAI 5 complete genome.	222	4.2E-17	182	36.8
266	336025834	CP002279	<i>Mesorhizobium opportunistum</i> WSM2075	Mesorhizobium opportunistum WSM2075, complete genome.	191	4.4E-17	174	35.6
267	307633173	CP002209	<i>Ferrimonas balearica</i> DSM 9799	Ferrimonas balearica DSM 9799, complete genome.	165	6.4E-17	159	36.5
268	340528078	CP002896	<i>Amycolatopsis mediterranei</i> S699	Amycolatopsis mediterranei S699, complete genome.	171	6.6E-17	159	35.8
269	299796109	CP002000	<i>Amycolatopsis mediterranei</i> U32	Amycolatopsis mediterranei U32, complete genome.	171	6.6E-17	159	35.8
270	111150386	CT573213	<i>Frankia alni</i> ACN14a	Frankia alni str. ACN14A chromosome, complete sequence.	184	7E-17	177	36.2
271	221737066	CP000633	<i>Agrobacterium vitis</i> S4	Agrobacterium vitis S4 chromosome 1, complete sequence.	209	1.5E-16	162	34.6
272	299075408	FP885891	<i>Ralstonia solanacearum</i> PSI07	Ralstonia solanacearum PSI07 megaplasmid mpPSI07, complete sequence.	183	1.6E-16	164	36.6
273	91698515	CP000316	<i>Polaromonas</i> sp JS666	Polaromonas sp. JS666, complete genome.	226	1.6E-16	159	37.7
274	283817471	CP001769	<i>Spirosoma linguale</i> DSM 74	Spirosoma linguale DSM 74, complete genome.	185	1.9E-16	171	34.5
275	119672394	AM406670	<i>Azoarcus</i> sp BH72	Azoarcus sp. BH72, complete genome.	188	2E-16	178	37.6

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
276	295060051	CP001919	<i>Enterobacter cloacae</i> subsp <i>cloacae</i> ATCC 13047	Enterobacter cloacae subsp. cloacae ATCC 13047 plasmid pECL_A, complete sequence.	178	2.6E-16	155	35.5
277	206570539	CP000965	<i>Klebsiella pneumoniae</i> 342	Klebsiella pneumoniae 342 plasmid pKP187, complete sequence.	178	2.6E-16	155	35.5
278	161366921	CP000886	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Paratyphi B str SPB7</i>	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome.	171	3E-16	163	30.1
279	270509644	CP001814	<i>Streptosporangium roseum</i> DSM 43021	Streptosporangium roseum DSM 43021, complete genome.	170	3.5E-16	167	37.1
280	168198383	CP000943	<i>Methylobacterium</i> sp 4-46	Methylobacterium sp. 4-46, complete genome.	180	3.7E-16	170	38.2
281	333477667	CP002771	<i>Marinomonas posidonica</i> IVIA-Po-181	Marinomonas posidonica IVIA-Po-181, complete genome.	161	4E-16	157	35.0
282	158329471	AP009384	<i>Azorhizobium caulinodans</i> ORS 571	Azorhizobium caulinodans ORS 571 DNA, complete genome.	174	4.3E-16	162	37.0
283	24983435	AE015451	<i>Pseudomonas putida</i> KT2440	Pseudomonas putida KT2440 complete genome.	186	4.5E-16	178	33.1
284	144897471	CU459003	<i>Magnetospirillum gryphiswaldense</i> MSR-1	Magnetospirillum gryphiswaldense MSR-1, WORKING DRAFT SEQUENCE, 373 unordered pieces.	195	7.7E-16	181	36.5
285	315448798	CP002403	<i>Ruminococcus albus</i> 7	Ruminococcus albus 7, complete genome.	191	9E-16	186	31.2
286	333739537	CP001843	<i>Treponema primitia</i> ZAS-2	Treponema primitia ZAS-2, complete genome.	169	9.6E-16	156	32.7
287	125497937	CP000387	<i>Streptococcus sanguinis</i> SK36	Streptococcus sanguinis SK36, complete genome.	215	9.9E-16	167	32.9
288	157075572	CP000725	<i>Streptococcus gordonii</i> str <i>Challis substr CH1</i>	Streptococcus gordonii str. Challis substr. CH1, complete genome.	178	1E-15	173	32.4
289	335369612	CP002843	<i>Streptococcus parasanguinis</i> ATCC 15912	Streptococcus parasanguinis ATCC 15912, complete genome.	174	1.2E-15	160	30.6
290	115516282	CP000463	<i>Rhodopseudomonas palustris</i> BisA53	Rhodopseudomonas palustris BisA53, complete genome.	179	1.2E-15	176	35.2
291	91681464	CP000283	<i>Rhodopseudomonas palustris</i> BisB5	Rhodopseudomonas palustris BisB5, complete genome.	181	1.2E-15	159	37.7

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
292	17430866	AL646053	<i>Ralstonia solanacearum</i> GMI1000	Ralstonia solanacearum GMI1000 megaplasmid complete sequence.	183	1.2E-15	162	36.4
293	71147588	CP000083	<i>Colwellia psychrerythraea</i> 34H	Colwellia psychrerythraea 34H, complete genome.	169	1.3E-15	160	33.1
294	219951584	CP001349	<i>Methylobacterium nodulans</i> ORS 2060	Methylobacterium nodulans ORS 2060, complete genome.	182	1.7E-15	171	36.3
295	157321363	CP000826	<i>Serratia proteamaculans</i> 568	Serratia proteamaculans 568, complete genome.	181	2E-15	163	34.4
296	324314719	CP002536	<i>Deinococcus proteolyticus</i> MRP	Deinococcus proteolyticus MRP, complete genome.	178	2.3E-15	173	35.3
297	150958273	CP000648	<i>Klebsiella pneumoniae</i> subsp <i>pneumoniae</i> MGH 78578	Klebsiella pneumoniae subsp. pneumoniae MGH 78578 plasmid pKPN3, complete sequence.	178	2.7E-15	173	34.1
298	295101938	FP929045	<i>Faecalibacterium prausnitzii</i> L2-6	Faecalibacterium prausnitzii L2/6 draft genome.	186	3.4E-15	179	32.4
299	124493545	AM406671	<i>Lactococcus lactis</i> subsp <i>cremoris</i> MG1363	Lactococcus lactis subsp. cremoris MG1363, complete genome.	186	3.4E-15	157	32.5
300	300071533	CP002094	<i>Lactococcus lactis</i> subsp <i>cremoris</i> NZ9000	Lactococcus lactis subsp. cremoris NZ9000, complete genome.	186	3.4E-15	157	32.5
301	288914931	AP010951	<i>Azospirillum</i> sp B510	Azospirillum sp. B510 plasmid pAB510e DNA, complete genome.	189	3.4E-15	161	36.6
302	14024417	BA000012	<i>Mesorhizobium loti</i> MAFF303099	Mesorhizobium loti MAFF303099 DNA, complete genome.	194	3.5E-15	172	35.5
303	260217772	FN543093	<i>Cronobacter turicensis</i> z3032	Cronobacter turicensis z3032 complete genome.	181	4.6E-15	170	33.5
304	324966233	CP002547	<i>Syntrophobotulus glycolicus</i> DSM 8271	Syntrophobotulus glycolicus DSM 8271, complete genome.	190	4.8E-15	156	32.1
305	283953294	CP001859	<i>Acidaminococcus fermentans</i> DSM 20731	Acidaminococcus fermentans DSM 20731, complete genome.	191	4.8E-15	182	29.7
306	270343096	CP001836	<i>Dickeya dadantii</i> Ech586	Dickeya dadantii Ech586, complete genome.	176	5.3E-15	163	33.7
307	163262568	AM902716	<i>Bordetella petrii</i>	Bordetella petrii strain DSM 12804, complete genome.	183	5.5E-15	177	35.0
308	86570442	CP000250	<i>Rhodopseudomonas palustris</i> HaA2	Rhodopseudomonas palustris HaA2, complete genome.	205	6E-15	159	37.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
309	255922411	CP001630	<i>Actinosynnema mirum</i> DSM 43827	Actinosynnema mirum DSM 43827, complete genome.	169	6.1E-15	166	35.5
310	281376033	CP001834	<i>Lactococcus lactis</i> subsp <i>lactis</i> KF147	Lactococcus lactis subsp. lactis KF147, complete genome.	187	6.6E-15	176	29.0
311	116108291	CP000425	<i>Lactococcus lactis</i> subsp <i>cremoris</i> SK11	Lactococcus lactis subsp. cremoris SK11, complete genome.	186	7.8E-15	157	32.5
312	116097278	CP000414	<i>Leuconostoc mesenteroides</i> subsp <i>mesenteroides</i> ATCC 8293	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293, complete genome.	177	1E-14	177	28.8
313	306527396	CP002038	<i>Dickeya dadantii</i> 3937	Dickeya dadantii 3937, complete genome.	187	1.1E-14	161	34.8
314	146190348	CU234118	<i>Bradyrhizobium</i> sp ORS278	Bradyrhizobium sp. ORS278, complete sequence.	175	1.2E-14	160	34.4
315	12724800	AE005176	<i>Lactococcus lactis</i> subsp <i>lactis</i> II1403	Lactococcus lactis subsp. lactis II1403, complete genome.	187	1.3E-14	176	28.4
316	326407264	CP002365	<i>Lactococcus lactis</i> subsp <i>lactis</i> CV56	Lactococcus lactis subsp. lactis CV56, complete genome.	187	1.3E-14	176	28.4
317	82946118	AP007255	<i>Magnetospirillum magneticum</i> AMB-1	Magnetospirillum magneticum AMB-1 DNA, complete genome.	197	1.4E-14	187	35.8
318	160427111	CP000885	<i>Clostridium phytofermentans</i> ISDg	Clostridium phytofermentans ISDg, complete genome.	184	1.5E-14	176	30.1
319	254997389	AP010655	<i>Streptococcus mutans</i> NN2025	Streptococcus mutans NN2025 DNA, complete genome.	163	1.6E-14	159	28.9
320	333960346	CP002775	<i>Serratia</i> sp AS13	Serratia sp. AS13, complete genome.	178	1.7E-14	173	32.9
321	333472750	CP002773	<i>Serratia</i> sp AS9	Serratia sp. AS9, complete genome.	178	1.7E-14	173	32.9
322	333490250	CP002774	<i>Serratia</i> sp AS12	Serratia sp. AS12, complete genome.	178	1.7E-14	173	32.9
323	196479604	CP000747	<i>Phenylobacterium zucineum</i> HLK1	Phenylobacterium zucineum HLK1, complete genome.	179	1.8E-14	172	36.0
324	310763787	CP002287	<i>Achromobacter xylosoxidans</i> A8	Achromobacter xylosoxidans A8, complete genome.	181	1.8E-14	182	33.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
325	292663597	CP001751	<i>Candidatus Puniceispirillum marinum</i> IMCC1322	Candidatus Puniceispirillum marinum IMCC1322, complete genome.	182	1.8E-14	163	35.6
326	309749106	CP002282	<i>Ilyobacter polytropus</i> DSM 2926	Ilyobacter polytropus DSM 2926 plasmid pILYOP01, complete sequence.	161	1.9E-14	156	28.8
327	117164913	AM238664	<i>Streptomyces ambofaciens</i> ATCC 23877	Streptomyces ambofaciens ATCC 23877 right chromosomal arm.	200	1.9E-14	165	34.5
328	294339612	FP475956	<i>Thiomonas</i> sp. 3As	Thiomonas sp. str. 3As chromosome, complete genome.	175	2.4E-14	170	34.7
329	115284096	CP000441	<i>Burkholderia ambifaria</i> AMMD	Burkholderia ambifaria AMMD chromosome 2, complete sequence.	207	2.8E-14	179	33.0
330	296324397	CP001903	<i>Bacillus thuringiensis</i> BMB171 (<i>Bacillus thuringiensis</i> serovar	Bacillus thuringiensis BMB171, complete genome.	170	2.8E-14	169	32.0
331	29896482	AE016877	<i>Bacillus cereus</i> ATCC 14579	Bacillus cereus ATCC 14579, complete genome.	170	2.8E-14	169	33.1
332	209960237	CP000613	<i>Rhodospirillum centenum</i> SW	Rhodospirillum centenum SW, complete genome.	180	2.9E-14	155	38.7
333	149935555	CP000140	<i>Parabacteroides distasonis</i> ATCC 8503	Parabacteroides distasonis ATCC 8503, complete genome.	167	3.2E-14	165	33.3
334	255921752	CP001630	<i>Actinosynnema mirum</i> DSM 43827	Actinosynnema mirum DSM 43827, complete genome.	168	3.3E-14	160	32.5
335	326940575	CP001907	<i>Bacillus thuringiensis</i> serovar <i>chinensis</i> CT-43	Bacillus thuringiensis serovar chinensis CT-43, complete genome.	170	3.3E-14	169	32.5
336	7799523	AL939115	<i>Streptomyces coelicolor</i> A3(2)	Streptomyces coelicolor A3(2) complete genome; segment 12/29.	171	3.3E-14	170	33.5
337	153179	M62753	<i>Streptomyces coelicolor</i>	S.coelicolor bar gene, complete cds.	171	3.3E-14	170	33.5
338	242132404	CP001654	<i>Dickeya dadantii</i> Ech703	Dickeya dadantii Ech703, complete genome.	178	3.4E-14	175	32.6
339	218541767	CP001186	<i>Bacillus cereus</i> G9842	Bacillus cereus G9842, complete genome.	170	3.9E-14	169	32.5
340	194348222	CP001111	<i>Stenotrophomonas maltophilia</i> R551-3	Stenotrophomonas maltophilia R551-3, complete genome.	176	4E-14	171	33.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
341	218158915	CP001176	<i>Bacillus cereus B4264</i>	Bacillus cereus B4264, complete genome.	170	4.6E-14	169	32.5
342	227007051	CP001215	<i>Bacillus anthracis str CDC 684</i>	Bacillus anthracis str. CDC 684, complete genome.	170	4.6E-14	169	32.0
343	163862754	CP000903	<i>Bacillus weihenstephanensis KBAB4</i>	Bacillus weihenstephanensis KBAB4, complete genome.	170	4.6E-14	169	33.1
344	29607349	BA000030	<i>Streptomyces avermitilis MA-4680</i>	Streptomyces avermitilis MA-4680 DNA, complete genome.	172	4.6E-14	174	33.3
345	315599545	CP002418	<i>Rhodopseudomonas palustris DX-1</i>	Rhodopseudomonas palustris DX-1, complete genome.	176	4.7E-14	161	35.4
346	295831765	CP001758	<i>Leuconostoc kimchii IMSNU 11154</i>	Leuconostoc kimchii IMSNU 11154, complete genome.	180	4.8E-14	178	31.5
347	338852282	CP002898	<i>Leuconostoc sp C2</i>	Leuconostoc sp. C2, complete genome.	180	4.8E-14	178	31.5
348	189337263	AP009386	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 genomic DNA, complete genome, chromosome 2.	186	5E-14	172	32.6
349	160344621	CP000869	<i>Burkholderia multivorans ATCC 17616</i>	Burkholderia multivorans ATCC 17616 chromosome 2, complete sequence.	186	5E-14	172	32.6
350	327372275	CP002600	<i>Burkholderia gladioli BSR3</i>	Burkholderia gladioli BSR3 chromosome 2, complete sequence.	192	5.1E-14	182	34.1
351	222119436	AP009484	<i>Macrococcus caseolyticus JCSC5402</i>	Macrococcus caseolyticus JCSC5402 DNA, complete genome.	162	5.2E-14	159	32.7
352	225786099	CP001407	<i>Bacillus cereus 03BB102</i>	Bacillus cereus 03BB102, complete genome.	170	5.4E-14	169	32.0
353	218538084	CP001283	<i>Bacillus cereus AH820</i>	Bacillus cereus AH820, complete genome.	170	5.4E-14	169	32.0
354	118417388	CP000485	<i>Bacillus thuringiensis str Al Hakam</i>	Bacillus thuringiensis str. Al Hakam, complete genome.	170	5.4E-14	169	32.0
355	221240365	CP000227	<i>Bacillus cereus Q1</i>	Bacillus cereus Q1, complete genome.	170	5.4E-14	169	32.0
356	217064287	CP001177	<i>Bacillus cereus AH187</i>	Bacillus cereus AH187, complete genome.	170	5.4E-14	169	32.0
357	324326776	CP002508	<i>Bacillus thuringiensis serovar finitimus YBT-020</i>	Bacillus thuringiensis serovar finitimus YBT-020, complete genome.	170	5.4E-14	169	32.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
358	190011924	AM743169	<i>Stenotrophomonas maltophilia</i> K279a	Stenotrophomonas maltophilia K279a complete genome, strain K279a.	176	5.6E-14	171	33.9
359	300436336	CP001666	<i>Clostridium ljungdahlii</i> DSM 13528	Clostridium ljungdahlii DSM 13528, complete genome.	194	6.1E-14	185	29.2
360	300376500	CP001746	<i>Bacillus cereus</i> biovar anthracis str CI	Bacillus cereus biovar anthracis str. CI, complete genome.	170	6.4E-14	169	31.4
361	226525294	FJ872373	uncultured <i>Verrucomicrobia</i> bacterium	Uncultured Verrucomicrobia bacterium clone 118 genomic sequence.	164	7.4E-14	152	34.2
362	39652901	BX572593	<i>Rhodopseudomonas palustris</i> CGA009	Rhodopseudomonas palustris CGA009 complete genome; segment 1/16.	176	7.8E-14	159	34.0
363	247539323	CP001655	<i>Dickeya zeae</i> Ech1591	Dickeya zeae Ech1591, complete genome.	176	7.8E-14	161	34.2
364	192282376	CP001096	<i>Rhodopseudomonas palustris</i> TIE-1	Rhodopseudomonas palustris TIE-1, complete genome.	176	7.8E-14	159	34.0
365	343386363	CP002874	<i>Brachyspira intermedia</i> PWS/A	Brachyspira intermedia PWS/A, complete genome.	190	8.3E-14	178	27.5
366	291522043	FP929038	<i>Coprococcus catus</i> GD/7	Coprococcus catus GD/7 draft genome.	197	8.6E-14	165	33.3
367	33571099	BX640411	<i>Bordetella pertussis</i> Tohama I	Bordetella pertussis strain Tohama I, complete genome; segment 1/12.	182	9.5E-14	182	35.7
368	33565206	BX640424	<i>Bordetella parapertussis</i>	Bordetella parapertussis strain 12822, complete genome; segment 2/14.	182	9.5E-14	182	35.7
369	33567007	BX640438	<i>Bordetella bronchiseptica</i> RB50	Bordetella bronchiseptica strain RB50, complete genome; segment 2/16.	182	9.5E-14	182	35.7
370	332380858	CP002695	<i>Bordetella pertussis</i> CS	Bordetella pertussis CS, complete genome.	182	9.5E-14	182	35.7
371	323465059	CP002478	<i>Staphylococcus pseudintermedius</i> ED99	Staphylococcus pseudintermedius ED99, complete genome.	165	1E-13	163	31.9
372	317161467	CP002439	<i>Staphylococcus pseudintermedius</i> HKU10-03	Staphylococcus pseudintermedius HKU10-03, complete genome.	165	1E-13	163	31.9
373	42737818	AE017194	<i>Bacillus cereus</i> ATCC 10987	Bacillus cereus ATCC 10987, complete genome.	170	1.1E-13	169	31.4

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
374	327438506	AP012157	<i>Solibacillus silvestris</i> StLB046	<i>Solibacillus silvestris</i> StLB046 DNA, complete genome.	170	1.1E-13	167	32.3
375	20521524	AP005147	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i> (Salmonella)	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Typhimurium</i> plasmid R64 DNA, complete sequence.	178	1.1E-13	163	28.2
376	77969889	CP000152	<i>Burkholderia</i> sp 383	<i>Burkholderia</i> sp. 383, complete sequence.	186	1.1E-13	172	32.0
377	338167774	CP002877	<i>Cupriavidus necator</i> N-1	<i>Cupriavidus necator</i> N-1 chromosome 1, complete sequence.	193	1.2E-13	167	32.3
378	257049034	CP001685	<i>Leptotrichia buccalis</i> C-1013-b	<i>Leptotrichia buccalis</i> DSM 1135, complete genome.	197	1.2E-13	174	27.6
379	156531547	CP000783	<i>Cronobacter sakazakii</i> ATCC BAA-894	<i>Cronobacter sakazakii</i> ATCC BAA-894, complete genome.	199	1.2E-13	170	32.9
380	114738550	CP000158	<i>Hyphomonas neptunium</i> ATCC 15444	<i>Hyphomonas neptunium</i> ATCC 15444, complete genome.	190	1.4E-13	159	35.2
381	323386899	CP002520	<i>Burkholderia</i> sp CCGE1001	<i>Burkholderia</i> sp. CCGE1001 chromosome 2, complete sequence.	195	1.4E-13	181	33.7
382	336034654	CP001830	<i>Sinorhizobium meliloti</i> SM11	<i>Sinorhizobium meliloti</i> SM11, complete genome.	183	1.6E-13	172	29.1
383	51976172	CP000001	<i>Bacillus cereus</i> E33L	<i>Bacillus cereus</i> E33L, complete genome.	170	1.8E-13	169	31.4
384	49329420	AE017355	<i>Bacillus thuringiensis</i> serovar <i>konkukian</i> str 97-27	<i>Bacillus thuringiensis</i> serovar <i>konkukian</i> str. 97-27, complete genome.	170	1.8E-13	169	30.8
385	295105453	FP929046	<i>Faecalibacterium prausnitzii</i> SL3/3	<i>Faecalibacterium prausnitzii</i> SL3/3 draft genome.	184	1.9E-13	164	31.1
386	291563014	FP929062	<i>butyrate-producing bacterium</i> SS3/4	Clostridiales sp. SS3/4 draft genome.	189	1.9E-13	183	28.4
387	225214342	CP001357	<i>Brachyspira hyodysenteriae</i> WA1	<i>Brachyspira hyodysenteriae</i> WA1, complete genome.	190	1.9E-13	178	28.1
388	113528299	AM260479	<i>Ralstonia eutropha</i> H16	<i>Ralstonia eutropha</i> H16 chromosome 1.	193	2E-13	177	31.1
389	229468694	CP001615	<i>Exiguobacterium</i> sp AT1b	<i>Exiguobacterium</i> sp. AT1b, complete genome.	170	2.1E-13	168	33.3
390	295795628	CP002021	<i>Thiomonas intermedia</i> K12	<i>Thiomonas intermedia</i> K12, complete genome.	175	2.1E-13	170	33.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
391	120593335	CP000529	<i>Polaromonas naphthalenivorans</i> CJ2	Polaromonas naphthalenivorans CJ2, complete genome.	178	2.2E-13	173	33.5
392	333813223	CP002740	<i>Sinorhizobium meliloti</i> BL225C	Sinorhizobium meliloti BL225C, complete genome.	185	2.2E-13	173	28.9
393	209537062	CP001191	<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304	Rhizobium leguminosarum bv. trifolii WSM2304, complete genome.	185	2.2E-13	171	29.8
394	334096916	CP002781	<i>Sinorhizobium meliloti</i> AK83	Sinorhizobium meliloti AK83 chromosome 1, complete sequence.	185	2.2E-13	173	28.9
395	15076249	AL591688	<i>Sinorhizobium meliloti</i> 1021	Sinorhizobium meliloti 1021 complete chromosome.	185	2.2E-13	173	28.9
396	268614410	CP001739	<i>Seibaldella termitidis</i> ATCC 33386	Seibaldella termitidis ATCC 33386, complete genome.	165	2.4E-13	160	33.1
397	93356220	CP000352	<i>Cupriavidus metallidurans</i> CH34	Cupriavidus metallidurans CH34, complete genome.	206	2.4E-13	167	31.7
398	171996055	CP001026	<i>Burkholderia ambifaria</i> MC40-6	Burkholderia ambifaria MC40-6 chromosome 2, complete sequence.	187	2.7E-13	175	32.0
399	187426469	CP001071	<i>Akkermansia muciniphila</i> ATCC BAA-835	Akkermansia muciniphila ATCC BAA-835, complete genome.	199	2.8E-13	176	33.5
400	90103739	CP000301	<i>Rhodopseudomonas palustris</i> BisB18	Rhodopseudomonas palustris BisB18, complete genome.	174	3E-13	161	32.9
401	296180963	CP001958	<i>Segniliparus rotundus</i> DSM 44985	Segniliparus rotundus DSM 44985, complete genome.	174	3E-13	159	33.3
402	27348711	BA000040	<i>Bradyrhizobium japonicum</i> USDA 110	Bradyrhizobium japonicum USDA 110 DNA, complete genome.	176	3E-13	170	33.5
403	221724954	CP000628	<i>Agrobacterium radiobacter</i> K84	Agrobacterium radiobacter K84 chromosome 1, complete sequence.	185	3.1E-13	169	29.6
404	24377449	AE014133	<i>Streptococcus mutans</i> UA159	Streptococcus mutans UA159, complete genome.	163	3.3E-13	159	27.7
405	170657314	CP001001	<i>Methylobacterium radiotolerans</i> JCM 2831	Methylobacterium radiotolerans JCM 2831, complete genome.	192	3.8E-13	184	33.7
406	22534866	AE009948	<i>Streptococcus agalactiae</i> 2603V/R	Streptococcus agalactiae 2603V/R, complete genome.	163	4E-13	157	29.3

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
407	24413449	AL766854	<i>Streptococcus agalactiae</i> NEM316	Streptococcus agalactiae NEM316 complete genome, segment 12.	163	4E-13	157	29.3
408	323273300	AP012052	<i>Microbacterium testaceum</i> StLB037	Microbacterium testaceum StLB037 DNA, complete genome.	203	4E-13	171	32.7
409	146404166	CP000494	<i>Bradyrhizobium</i> sp. BTAi1	Bradyrhizobium sp. BTAi1, complete genome.	176	4.2E-13	160	33.1
410	292677421	AP010804	<i>Sphingobium japonicum</i> UT26S	Sphingobium japonicum UT26S DNA, chromosome 2, complete genome.	181	4.3E-13	159	34.6
411	121555496	CP000542	<i>Verminephrobacter eiseniae</i> EF01-2	Verminephrobacter eiseniae EF01-2, complete genome.	181	4.3E-13	159	34.0
412	307588225	CP002218	<i>Burkholderia</i> sp. CCGE1003	Burkholderia sp. CCGE1003 chromosome 2, complete sequence.	184	4.4E-13	166	33.1
413	308748077	CP002272	<i>Enterobacter cloacae</i> SCF1	Enterobacter cloacae SCF1, complete genome.	184	4.4E-13	172	32.0
414	320010253	CP002475	<i>Streptomyces flavogriseus</i> ATCC 33331	Streptomyces flavogriseus ATCC 33331, complete genome.	192	4.5E-13	187	32.6
415	217501797	CP001280	<i>Methylocella silvestris</i> BL2	Methylocella silvestris BL2, complete genome.	193	4.5E-13	169	30.8
416	297162839	CP002047	<i>Streptomyces bingchenggensis</i> BCW-1	Streptomyces bingchenggensis BCW-1, complete genome.	162	4.6E-13	154	35.1
417	340527568	CP002896	<i>Amycolatopsis mediterranei</i> S699	Amycolatopsis mediterranei S699, complete genome.	162	4.6E-13	160	33.1
418	299795614	CP002000	<i>Amycolatopsis mediterranei</i> U32	Amycolatopsis mediterranei U32, complete genome.	162	4.6E-13	160	33.1
419	334091520	CP002780	<i>Desulfotomaculum ruminis</i> DSM 2154	Desulfotomaculum ruminis DSM 2154, complete genome.	191	5.3E-13	185	31.4
420	149902327	CP000721	<i>Clostridium beijerinckii</i> NCIMB 8052	Clostridium beijerinckii NCIMB 8052, complete genome.	170	5.7E-13	168	31.5
421	154158055	CP000781	<i>Xanthobacter autotrophicus</i> Py2	Xanthobacter autotrophicus Py2, complete genome.	180	6E-13	159	36.5
422	315594653	CP002417	<i>Variovorax paradoxus</i> EPS	Variovorax paradoxus EPS, complete genome.	182	6E-13	161	34.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
423	302194206	CP002102	<i>Brevundimonas subvibrioides</i> ATCC 15264	Brevundimonas subvibrioides ATCC 15264, complete genome.	182	6E-13	173	31.2
424	325508273	CP002118	<i>Clostridium acetobutylicum</i> EA 2018	Clostridium acetobutylicum EA 2018, complete genome.	196	6.4E-13	175	26.3
425	336292391	CP002660	<i>Clostridium acetobutylicum</i> DSM 1731	Clostridium acetobutylicum DSM 1731, complete genome.	196	6.4E-13	175	26.3
426	15023752	AE001437	<i>Clostridium acetobutylicum</i> ATCC 824	Clostridium acetobutylicum ATCC 824, complete genome.	196	6.4E-13	175	26.3
427	334107863	CP002810	<i>Isoptricola variabilis</i> 225	Isoptricola variabilis 225, complete genome.	206	6.7E-13	189	34.4
428	260649211	FN554889	<i>Streptomyces scabiei</i> 8722	Streptomyces scabiei 87.22 complete genome.	172	6.8E-13	174	31.6
429	151559334	CP000758	<i>Ochrobactrum anthropi</i> ATCC 49188	Ochrobactrum anthropi ATCC 49188 chromosome 1, complete sequence.	193	7.5E-13	177	31.6
430	291548915	FP929055	<i>Ruminococcus torques</i> L2-14	Ruminococcus torques L2-14 draft genome.	196	7.6E-13	178	29.2
431	295110721	FP929054	<i>Ruminococcus obeum</i> A2-162	Ruminococcus obeum A2-162 draft genome.	202	7.8E-13	171	30.4
432	256792470	CP001684	<i>Slackia heliotrinireducens</i> DSM 20476	Slackia heliotrinireducens DSM 20476, complete genome.	210	8E-13	183	31.7
433	28853732	AE016853	<i>Pseudomonas syringae</i> pv tomato str DC3000	Pseudomonas syringae pv. tomato str. DC3000, complete genome.	179	8.3E-13	168	33.3
434	159139818	AE007869	<i>Agrobacterium tumefaciens</i> str C58	Agrobacterium tumefaciens str. C58 circular chromosome, complete sequence.	180	8.4E-13	170	32.9
435	134137032	CP000615	<i>Burkholderia vietnamiensis</i> G4	Burkholderia vietnamiensis G4 chromosome 2, complete sequence.	186	8.6E-13	179	31.3
436	27351434	BA000040	<i>Bradyrhizobium japonicum</i> USDA 110	Bradyrhizobium japonicum USDA 110 DNA, complete genome.	194	8.9E-13	179	31.3
437	145410597	CP000679	<i>Caldicellulosiruptor saccharolyticus</i> DSM 8903	Caldicellulosiruptor saccharolyticus DSM 8903, complete genome.	162	9.1E-13	157	29.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
438	72120368	CP000090	<i>Ralstonia eutropha</i> JMP134	Ralstonia eutropha JMP134 chromosome 1, complete sequence.	210	9.5E-13	172	32.6
439	34101682	AE016825	<i>Chromobacterium violaceum</i> ATCC 12472	Chromobacterium violaceum ATCC 12472, complete genome.	174	9.6E-13	174	32.2
440	295438559	CP002014	<i>Burkholderia</i> sp CCGE1002	Burkholderia sp. CCGE1002 chromosome 2, complete sequence.	193	1E-12	181	30.9
441	91690983	CP000271	<i>Burkholderia xenovorans</i> LB400	Burkholderia xenovorans LB400 chromosome 2, complete sequence.	200	1.1E-12	178	33.7
442	76563382	CP000114	<i>Streptococcus agalactiae</i> A909	Streptococcus agalactiae A909, complete genome.	163	1.1E-12	157	28.7
443	257476004	CP001726	<i>Eggerthella lenta</i> DSM 2243	Eggerthella lenta DSM 2243, complete genome.	213	1.1E-12	179	32.4
444	148371165	CP000708	<i>Brucella ovis</i> ATCC 25840	Brucella ovis ATCC 25840 chromosome I, complete sequence.	179	1.2E-12	162	32.7
445	163673086	CP000911	<i>Brucella suis</i> ATCC 23445	Brucella suis ATCC 23445 chromosome I, complete sequence.	179	1.2E-12	162	32.7
446	161334887	CP000872	<i>Brucella canis</i> ATCC 23365	Brucella canis ATCC 23365 chromosome I, complete sequence.	179	1.2E-12	162	32.7
447	23346864	AE014291	<i>Brucella suis</i> 1330	Brucella suis 1330 chromosome I, complete sequence.	179	1.2E-12	162	32.7
448	255998713	CP001578	<i>Brucella microti</i> CCM 4915	Brucella microti CCM 4915 chromosome 1, complete sequence.	179	1.2E-12	162	32.7
449	17983898	AE008917	<i>Brucella melitensis</i> bv 1 str 16M	Brucella melitensis bv. 1 str. 16M chromosome I, complete sequence.	179	1.2E-12	162	32.7
450	340558175	CP002078	<i>Brucella pinnipedialis</i> B2/94	Brucella pinnipedialis B2/94 chromosome 1, complete sequence.	179	1.2E-12	162	32.7
451	343381965	CP002997	<i>Brucella suis</i> 1330	Brucella suis 1330 chromosome I, complete sequence.	179	1.2E-12	162	32.7
452	315418043	CP002396	<i>Asticcacaulis excentricus</i> CB 48	Asticcacaulis excentricus CB 48 chromosome 2, complete sequence.	180	1.2E-12	170	35.3
453	328448421	CP002631	<i>Treponema succinifaciens</i> DSM 2489	Treponema succinifaciens DSM 2489, complete genome.	184	1.2E-12	177	28.2
454	240860632	CP001622	<i>Rhizobium leguminosarum</i> bv trifolii WSM1325	Rhizobium leguminosarum bv. trifolii WSM1325, complete genome.	200	1.3E-12	171	28.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
455	333938403	FR856862	<i>Novosphingobium</i> sp PP1Y	Novosphingobium sp. PP1Y main chromosome, complete replicon.	181	1.4E-12	166	34.9
456	295058240	CP001918	<i>Enterobacter cloacae</i> subsp <i>cloacae</i> ATCC 13047	Enterobacter cloacae subsp. cloacae ATCC 13047, complete genome.	184	1.4E-12	172	32.0
457	198039697	AM747721	<i>Burkholderia cenocepacia</i> J2315	Burkholderia cenocepacia J2315 chromosome 2, complete genome.	186	1.4E-12	172	30.2
458	296023290	CP001964	<i>Cellulomonas flavigena</i> DSM 20109	Cellulomonas flavigena DSM 20109, complete genome.	168	1.6E-12	161	31.1
459	338847648	CP002904	<i>Streptococcus equi</i> subsp <i>zooepidemicus</i> ATCC 35246	Streptococcus equi subsp. zooepidemicus ATCC 35246, complete genome.	212	1.6E-12	177	33.3
460	21110185	AE008923	<i>Xanthomonas axonopodis</i> pv <i>citri</i> str 306	Xanthomonas axonopodis pv. citri str. 306, complete genome.	173	1.6E-12	162	32.1
461	78037901	AM039952	<i>Xanthomonas campestris</i> pv <i>vesicatoria</i> str 85-10 (<i>Xanthomonas</i>	Xanthomonas campestris pv. vesicatoria complete genome.	173	1.6E-12	162	32.1
462	291519271	FP929036	<i>Butyrivibrio fibrisolvens</i> 16/4	Butyrivibrio fibrisolvens 16/4 draft genome.	175	1.6E-12	161	29.8
463	188029414	CU468135	<i>Erwinia tasmaniensis</i> Et1/99	Erwinia tasmaniensis strain ET1/99 complete chromosome.	179	1.6E-12	160	31.9
464	308057209	CP002206	<i>Pantoea vagans</i> C9-1	Pantoea vagans C9-1, complete genome.	222	1.6E-12	172	28.5
465	91798763	CP000319	<i>Nitrobacter hamburgensis</i> X14	Nitrobacter hamburgensis X14, complete genome.	183	1.7E-12	161	33.5
466	256583473	CP001682	<i>Cryptobacterium curtum</i> DSM 15641	Cryptobacterium curtum DSM 15641, complete genome.	185	1.7E-12	175	30.9
467	169820174	CP000959	<i>Burkholderia cenocepacia</i> MC0-3	Burkholderia cenocepacia MC0-3 chromosome 2, complete sequence.	186	1.7E-12	172	30.2
468	105895427	CP000379	<i>Burkholderia cenocepacia</i> AU 1054	Burkholderia cenocepacia AU 1054 chromosome 2, complete sequence.	186	1.7E-12	172	30.2
469	116650763	CP000459	<i>Burkholderia cenocepacia</i> HI2424	Burkholderia cenocepacia HI2424 chromosome 2, complete sequence.	186	1.7E-12	172	30.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
470	193224949	CU633749	<i>Cupriavidus taiwanensis</i> LMG 19424	Cupriavidus taiwanensis str. LMG19424 chromosome 1, complete genome.	197	1.8E-12	167	31.1
471	72494194	AP008934	<i>Staphylococcus saprophyticus</i> subsp. <i>saprophyticus</i> ATCC 15305	Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305 DNA, complete genome.	163	1.8E-12	162	30.2
472	91696796	CP000316	<i>Polaromonas</i> sp. JS666	Polaromonas sp. JS666, complete genome.	178	1.9E-12	176	34.1
473	295432620	CP002008	<i>Caulobacter segnis</i> ATCC 21756	Caulobacter segnis ATCC 21756, complete genome.	185	2E-12	174	32.8
474	154158676	CP000781	<i>Xanthobacter autotrophicus</i> Py2	Xanthobacter autotrophicus Py2, complete genome.	186	2E-12	183	30.6
475	124259070	CP000555	<i>Methylibium petroleiphilum</i> PM1	Methylibium petroleiphilum PM1, complete genome.	190	2E-12	176	32.4
476	58424812	AE013598	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331	Xanthomonas oryzae pv. oryzae KACC10331, complete genome.	201	2.1E-12	171	32.2
477	288912257	AP010947	<i>Azospirillum</i> sp. B510	Azospirillum sp. B510 plasmid pAB510a DNA, complete genome.	177	2.3E-12	155	32.9
478	150029786	CP000738	<i>Sinorhizobium medicae</i> WSM419	Sinorhizobium medicae WSM419, complete genome.	185	2.3E-12	177	29.9
479	170774816	CP001013	<i>Leptothrix cholodnii</i> SP-6	Leptothrix cholodnii SP-6, complete genome.	186	2.4E-12	171	33.9
480	52212368	BX571966	<i>Burkholderia pseudomallei</i> K96243	Burkholderia pseudomallei strain K96243, chromosome 2, complete sequence.	188	2.4E-12	163	32.5
481	300687391	CP002025	<i>Brachyspira pilosicoli</i> 95/1000	Brachyspira pilosicoli 95/1000, complete genome.	189	2.4E-12	175	28.6
482	341937204	CP002789	<i>Xanthomonas campestris</i> pv. <i>raphani</i> 756C	Xanthomonas campestris pv. raphani 756C, complete genome.	175	2.7E-12	171	32.2
483	221723841	CP000628	<i>Agrobacterium radiobacter</i> K84	Agrobacterium radiobacter K84 chromosome 1, complete sequence.	183	2.8E-12	169	34.9
484	324319429	CP002530	<i>Bacteroides salanitronis</i> DSM 18170	Bacteroides salanitronis DSM 18170, complete genome.	160	2.9E-12	161	32.9
485	126224862	CP000571	<i>Burkholderia pseudomallei</i> 668	Burkholderia pseudomallei 668 chromosome II, complete sequence.	247	3E-12	163	32.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
486	126231149	CP000573	<i>Burkholderia pseudomallei</i> 1106a	Burkholderia pseudomallei 1106a chromosome II, complete sequence.	247	3E-12	163	32.5
487	76584280	CP000125	<i>Burkholderia pseudomallei</i> 1710b	Burkholderia pseudomallei 1710b chromosome II, complete sequence.	247	3E-12	163	32.5
488	167733135	AM920689	<i>Xanthomonas campestris</i> pv. <i>campestris</i>	Xanthomonas campestris pv. campestris complete genome, strain B100.	175	3.1E-12	172	32.6
489	83651702	CP000085	<i>Burkholderia thailandensis</i> E264	Burkholderia thailandensis E264 chromosome II, complete sequence.	188	3.3E-12	173	32.9
490	296020067	CP001964	<i>Cellulomonas flavigena</i> DSM 20109	Cellulomonas flavigena DSM 20109, complete genome.	173	3.7E-12	161	32.9
491	327396183	AP012032	<i>Pantoea ananatis</i> AJ13355	Pantoea ananatis AJ13355 DNA, complete genome.	188	3.9E-12	161	31.7
492	187718024	CP001053	<i>Burkholderia phytofirmans</i> PsJN	Burkholderia phytofirmans PsJN chromosome 2, complete sequence.	197	4.1E-12	163	33.7
493	84366153	AP008229	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> MAFF 311018	Xanthomonas oryzae pv. oryzae MAFF 311018 DNA, complete genome.	173	4.4E-12	162	32.1
494	188519396	CP000967	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A	Xanthomonas oryzae pv. oryzae PXO99A, complete genome.	173	4.4E-12	162	32.1
495	21113333	AE008922	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913	Xanthomonas campestris pv. campestris str. ATCC 33913, complete genome.	175	4.4E-12	171	32.2
496	66573571	CP000050	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. 8004	Xanthomonas campestris pv. campestris str. 8004, complete genome.	175	4.4E-12	171	32.2
497	182634464	CP001016	<i>Beijerinckia indica</i> subsp. <i>indica</i> ATCC 9039	Beijerinckia indica subsp. indica ATCC 9039, complete genome.	180	4.5E-12	160	33.1
498	227342756	CP001389	<i>Sinorhizobium fredii</i> NGR234	Sinorhizobium fredii NGR234, complete genome.	185	4.6E-12	177	28.8
499	341821889	HE576794	<i>Megasphaera elsdenii</i> DSM 20460	Megasphaera elsdenii strain DSM 20460 draft genome.	186	4.6E-12	183	28.4
500	126239764	CP000547	<i>Burkholderia mallei</i> NCTC 10247	Burkholderia mallei NCTC 10247 chromosome II, complete sequence.	188	4.7E-12	163	32.5
501	83576656	CP000230	<i>Rhodospirillum rubrum</i> ATCC 11170	Rhodospirillum rubrum ATCC 11170, complete genome.	195	4.8E-12	183	33.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
502	52422877	CP000011	<i>Burkholderia mallei</i> ATCC 23344	<i>Burkholderia mallei</i> ATCC 23344 chromosome 2, complete sequence.	210	5.1E-12	163	32.5
503	327371763	CP002600	<i>Burkholderia gladioli</i> BSR3	<i>Burkholderia gladioli</i> BSR3 chromosome 2, complete sequence.	174	5.2E-12	177	35.0
504	325060104	CP002248	<i>Agrobacterium</i> sp. H13-3	<i>Agrobacterium</i> sp. H13-3 circular chromosome, complete sequence.	180	5.3E-12	167	29.3
505	167347737	CP000927	<i>Caulobacter</i> sp. K31	<i>Caulobacter</i> sp. K31, complete genome.	185	5.4E-12	174	32.2
506	296019562	CP001959	<i>Brachyspira murdochii</i> DSM 12563	<i>Brachyspira murdochii</i> DSM 12563, complete genome.	190	5.6E-12	161	28.0
507	120589027	CP000512	<i>Acidovorax citrulli</i> AAC00-1	<i>Acidovorax citrulli</i> AAC00-1, complete genome.	197	5.7E-12	168	31.5
508	115258908	AM236080	<i>Rhizobium leguminosarum</i> bv. viciae 3841	<i>Rhizobium leguminosarum</i> bv. viciae chromosome complete genome, strain 3841.	200	5.8E-12	171	28.1
509	124290531	CP000545	<i>Burkholderia mallei</i> NCTC 10229	<i>Burkholderia mallei</i> NCTC 10229 chromosome II, complete sequence.	247	5.8E-12	163	32.5
510	121224414	CP000525	<i>Burkholderia mallei</i> SAVP1	<i>Burkholderia mallei</i> SAVP1 chromosome II, complete sequence.	247	5.8E-12	163	32.5
511	330429314	CP002663	<i>Pusillimonas</i> sp. T7-7	<i>Pusillimonas</i> sp. T7-7, complete genome.	201	5.8E-12	176	31.2
512	86283623	CP000133	<i>Rhizobium etli</i> CFN 42	<i>Rhizobium etli</i> CFN 42, complete genome.	185	6.4E-12	171	28.1
513	291559704	FP929061	<i>butyrate-producing bacterium</i> SSC/2	Clostridiales sp. SSC/2 draft genome.	185	6.4E-12	169	32.0
514	179343699	CP001029	<i>Methylobacterium populi</i> BJ001	<i>Methylobacterium populi</i> BJ001, complete genome.	204	7E-12	173	31.8
515	49610424	BX950851	<i>Pectobacterium atrosepticum</i> SCRI1043	<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043, complete genome.	175	7.3E-12	161	31.7
516	336096588	CP002821	<i>Oligotropha carboxidovorans</i> OM4	<i>Oligotropha carboxidovorans</i> OM4, complete genome.	176	7.3E-12	153	33.3
517	336100221	CP002826	<i>Oligotropha carboxidovorans</i> OM5	<i>Oligotropha carboxidovorans</i> OM5, complete genome.	176	7.3E-12	153	33.3
518	115421418	AM167904	<i>Bordetella avium</i> 197N	<i>Bordetella avium</i> 197N complete genome.	178	7.4E-12	171	32.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
519	326537816	CP001851	<i>Brucella melitensis</i> M5-90	Brucella melitensis M5-90 chromosome I, complete sequence.	179	7.4E-12	162	32.1
520	225639993	CP001488	<i>Brucella melitensis</i> ATCC 23457	Brucella melitensis ATCC 23457 chromosome I, complete sequence.	179	7.4E-12	162	32.1
521	326408102	CP002459	<i>Brucella melitensis</i> M28	Brucella melitensis M28 chromosome 1, complete sequence.	179	7.4E-12	162	32.1
522	209871922	CP001196	<i>Oligotropha carboxidovorans</i> OM5	Oligotropha carboxidovorans OM5 strain OM5, complete genome.	185	7.6E-12	153	33.3
523	182633804	CP001016	<i>Beijerinckia indica</i> subsp. indica ATCC 9039	Beijerinckia indica subsp. indica ATCC 9039, complete genome.	186	7.6E-12	179	30.7
524	311220144	CP002292	<i>Rhodomicrobium vannielii</i> ATCC 17100	Rhodomicrobium vannielii ATCC 17100, complete genome.	190	7.8E-12	175	33.7
525	254266958	FP103042	<i>Methylobacterium extorquens</i> DM4	Methylobacterium extorquens DM4 str. DM4 chromosome, complete genome.	204	8.2E-12	178	30.9
526	240007469	CP001510	<i>Methylobacterium extorquens</i> AM1	Methylobacterium extorquens AM1, complete genome.	204	8.2E-12	178	30.9
527	262337588	CP001805	<i>Vibrio</i> sp Ex25	Vibrio sp. Ex25 chromosome 1, complete sequence.	169	8.4E-12	166	31.3
528	145319251	CP000653	<i>Enterobacter</i> sp 638	Enterobacter sp. 638, complete genome.	184	9E-12	176	31.2
529	190699068	CP001074	<i>Rhizobium etli</i> CIAT 652	Rhizobium etli CIAT 652, complete genome.	185	9E-12	161	28.6
530	90820805	CP000233	<i>Lactobacillus salivarius</i> UCC118	Lactobacillus salivarius UCC118, complete genome.	198	9.5E-12	183	28.4
531	146154947	CP000685	<i>Flavobacterium johnsoniae</i> UW101	Flavobacterium johnsoniae UW101, complete genome.	165	9.7E-12	161	30.4
532	78036488	AM039952	<i>Xanthomonas campestris</i> pv. vesicatoria str 85-10 (<i>Xanthomonas</i>)	Xanthomonas campestris pv. vesicatoria complete genome.	179	1E-11	176	30.7
533	324497315	HQ601968	<i>bacterium enrichment culture clone P69-9E</i>	Bacterium enrichment culture clone P69-9E D-alanyl-D-alanine endopeptidase gene, partial cds; GCN5-related N-acetyltransferase, D-lactate dehydrogenase, and putative periplasmic beta-glucosidase precursor, genes, complete cds; and glycine/betaine/choline ABC transporter substrate-binding component gene, partial cds.	184	1.1E-11	172	30.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
534	300214425	CP002034	<i>Lactobacillus salivarius</i> CECT 5713	Lactobacillus salivarius CECT 5713, complete genome.	195	1.1E-11	183	28.4
535	206596075	CU914168	<i>Ralstonia solanacearum</i> IPO1609	Ralstonia solanacearum strain IPO1609 Genome Draft.	182	1.2E-11	165	33.3
536	332699679	CP002360	<i>Mahella australiensis</i> 50-1 BON	Mahella australiensis 50-1 BON, complete genome.	170	1.4E-11	162	29.0
537	195975321	CP001129	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> MGCS10565	Streptococcus equi subsp. zooepidemicus MGCS10565, complete genome.	225	1.5E-11	177	32.8
538	325125848	CP000156	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> 2038	Lactobacillus delbrueckii subsp. bulgaricus 2038, complete genome.	190	1.5E-11	184	31.5
539	82657643	AJ938182	<i>Staphylococcus aureus</i> RF122	Staphylococcus aureus RF122 complete genome.	163	1.6E-11	163	30.7
540	146314294	CP000626	<i>Vibrio cholerae</i> O395	Vibrio cholerae O395 chromosome 1, complete genome.	169	1.6E-11	152	32.9
541	3095168	AF055586	<i>Vibrio cholerae</i>	Vibrio cholerae initiation factor IF3 (infC), ribosomal protein L35 (rpmI), ribosomal protein L20 (rplT), and site-specific recombinase IntIa (intIa) genes, complete cds; and unknown genes.	169	1.6E-11	152	32.9
542	227014968	CP001236	<i>Vibrio cholerae</i> O395	Vibrio cholerae O395 chromosome II, complete sequence.	169	1.6E-11	152	32.9
543	150835453	CP000749	<i>Marinomonas</i> sp. MWYL1	Marinomonas sp. MWYL1, complete genome.	170	1.6E-11	163	30.7
544	299062631	FP236843	<i>Erwinia billingiae</i> Eb661	Erwinia billingiae strain Eb661 complete chromosome.	174	1.7E-11	160	30.6
545	291150954	CP001875	<i>Pantoea ananatis</i> LMG 20103	Pantoea ananatis LMG 20103, complete genome.	223	1.7E-11	161	31.1
546	206587162	CU694391	<i>Ralstonia solanacearum</i> MolK2	Ralstonia solanacearum strain MolK2 Genome Draft.	182	1.7E-11	163	32.5
547	282949389	FN543502	<i>Citrobacter rodentium</i> ICC168	Citrobacter rodentium ICC168, complete genome.	184	1.8E-11	172	30.8
548	50951917	AE016822	<i>Leifsonia xyli</i> subsp. <i>xyli</i> str. CTCB07	Leifsonia xyli subsp. xyli str. CTCB07, complete genome.	192	1.8E-11	163	31.9
549	150835449	CP000749	<i>Marinomonas</i> sp. MWYL1	Marinomonas sp. MWYL1, complete genome.	167	1.9E-11	162	30.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
550	291533728	FP929048	<i>Megamonas hypermegale</i> ART12/1	Megamonas hypermegale ART12/1 draft genome.	168	1.9E-11	157	25.5
551	21108549	AE008923	<i>Xanthomonas axonopodis</i> pv. citri str 306	Xanthomonas axonopodis pv. citri str. 306, complete genome.	179	2E-11	172	32.0
552	316952259	CP002434	<i>Pantoea</i> sp. At-9b	Pantoea sp. At-9b plasmid pPAT9B01, complete sequence.	171	2.3E-11	161	29.2
553	315596794	CP002417	<i>Variovorax paradoxus</i> EPS	Variovorax paradoxus EPS, complete genome.	173	2.3E-11	161	33.5
554	158331533	AP009384	<i>Azorhizobium caulinodans</i> ORS 571	Azorhizobium caulinodans ORS 571 DNA, complete genome.	181	2.4E-11	178	31.5
555	295098158	FP929040	<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> NCTC 9394	Enterobacter cloacae subsp. cloacae NCTC 9394 draft genome.	184	2.5E-11	177	30.5
556	302334149	CP002114	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> JKD6159	Staphylococcus aureus subsp. aureus JKD6159, complete genome.	163	2.6E-11	161	30.4
557	283471748	AM990992	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ST398	Staphylococcus aureus subsp. aureus ST398 complete genome, isolate SO385.	163	2.6E-11	161	31.1
558	239801056	CP001635	<i>Variovorax paradoxus</i> S110	Variovorax paradoxus S110 chromosome 1, complete sequence.	174	2.8E-11	159	32.7
559	220963093	CP001340	<i>Caulobacter crescentus</i> NA1000	Caulobacter crescentus NA1000, complete genome.	183	2.9E-11	174	32.2
560	103423174	CR954253	<i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> ATCC 11842	Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842 complete genome.	190	3E-11	184	31.0
561	163662030	CP000908	<i>Methylobacterium extorquens</i> PA1	Methylobacterium extorquens PA1, complete genome.	191	3E-11	171	31.0
562	229372440	CP001486	<i>Vibrio cholerae</i> MJ-1236	Vibrio cholerae MJ-1236 chromosome 2, complete sequence.	169	3.2E-11	152	32.9
563	295055286	CP001918	<i>Enterobacter cloacae</i> subsp. <i>cloacae</i> ATCC 13047	Enterobacter cloacae subsp. cloacae ATCC 13047, complete genome.	176	3.3E-11	174	29.3
564	239800953	CP001635	<i>Variovorax paradoxus</i> S110	Variovorax paradoxus S110 chromosome 1, complete sequence.	177	3.3E-11	160	33.8

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
565	86280977	CP000133	<i>Rhizobium etli</i> CFN 42	Rhizobium etli CFN 42, complete genome.	171	3.8E-11	157	32.5
566	160864662	CP000880	<i>Salmonella enterica</i> subsp <i>arizonae</i> serovar 62:z4,z23:--	Salmonella enterica subsp. arizonae serovar 62:z4,z23:-- , complete genome.	172	3.8E-11	172	33.7
567	341935348	CP002789	<i>Xanthomonas campestris</i> pv <i>raphani</i> 756C	Xanthomonas campestris pv. raphani 756C, complete genome.	173	3.9E-11	162	31.5
568	334731328	CP000245	<i>Ramlibacter tataouinensis</i> TTB310	Ramlibacter tataouinensis TTB310, complete genome.	173	3.9E-11	160	32.5
569	13422207	AE005673	<i>Caulobacter crescentus</i> CB15	Caulobacter crescentus CB15, complete genome.	180	4E-11	172	32.0
570	312280363	CP002341	<i>Lactobacillus delbrueckii</i> subsp <i>bulgaricus</i> ND02	Lactobacillus delbrueckii subsp. bulgaricus ND02, complete genome.	194	4.2E-11	184	31.0
571	290349764	AB548432	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii gene for phosphinothricin N-acetyltransferase, pat homologue, complete cds, strain: MAFF301158.	199	4.3E-11	172	30.2
572	311888035	FN563149	<i>Rhodococcus equi</i> 103S	Rhodococcus equi 103S chromosome.	162	4.3E-11	159	30.8
573	146402573	CP000697	<i>Acidiphilium cryptum</i> JF-5	Acidiphilium cryptum JF-5, complete genome.	167	4.4E-11	161	32.3
574	325051151	AP012035	<i>Acidiphilium multivorum</i> AIU301	Acidiphilium multivorum AIU301 DNA, complete genome.	167	4.4E-11	161	32.3
575	224468444	CP000857	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Paratyphi C</i> strain	Salmonella enterica subsp. enterica serovar Paratyphi C strain RKS4594, complete genome.	171	4.5E-11	168	33.9
576	337763619	FQ859184	<i>Streptomyces cattleya</i> NRRL 8057	Streptomyces cattleya NRRL 8057 plasmid pSCAT, complete genome.	176	4.6E-11	159	30.8
577	63257091	CP000075	<i>Pseudomonas syringae</i> pv <i>syringae</i> B728a	Pseudomonas syringae pv. syringae B728a, complete genome.	179	4.7E-11	160	31.9
578	116093475	CP000412	<i>Lactobacillus delbrueckii</i> subsp <i>bulgaricus</i> ATCC BAA-365	Lactobacillus delbrueckii subsp. bulgaricus ATCC BAA-365, complete genome.	190	4.9E-11	184	31.0
579	217504374	CP001280	<i>Methylocella silvestris</i> BL2	Methylocella silvestris BL2, complete genome.	195	5E-11	159	34.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
580	268614393	CP001739	<i>Sebaldella termitidis</i> ATCC 33386	Sebaldella termitidis ATCC 33386, complete genome.	165	5.2E-11	156	28.8
581	323374910	CP002521	<i>Acidovorax avenae</i> subsp <i>avenae</i> ATCC 19860	Acidovorax avenae subsp. avenae ATCC 19860, complete genome.	173	5.4E-11	159	31.4
582	312443494	CP002345	<i>Paludibacter propionigenes</i> WB4	Paludibacter propionigenes WB4, complete genome.	175	5.5E-11	170	29.4
583	66575439	CP000050	<i>Xanthomonas campestris</i> pv <i>campestris</i> str 8004	Xanthomonas campestris pv. campestris str. 8004, complete genome.	173	6.4E-11	164	31.7
584	21115015	AE008922	<i>Xanthomonas campestris</i> pv <i>campestris</i> str ATCC 33913	Xanthomonas campestris pv. campestris str. ATCC 33913, complete genome.	173	6.4E-11	164	31.7
585	167735075	AM920689	<i>Xanthomonas campestris</i> pv <i>campestris</i>	Xanthomonas campestris pv. campestris complete genome, strain B100.	173	6.4E-11	164	31.7
586	158304204	CP000828	<i>Acaryochloris marina</i> MBIC11017	Acaryochloris marina MBIC11017, complete genome.	175	6.5E-11	177	29.4
587	161164485	AM746676	<i>Sorangium cellulosum</i> 'So ce 56'	Sorangium cellulosum 'So ce 56' complete genome.	333	6.6E-11	170	34.7
588	334737285	CP002824	<i>Enterobacter aerogenes</i> KCTC 2190	Enterobacter aerogenes KCTC 2190, complete genome.	184	6.7E-11	172	30.2
589	296930089	CP002026	<i>Starkeya novella</i> DSM 506	Starkeya novella DSM 506, complete genome.	194	7E-11	182	30.2
590	290349772	AB548436	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii gene for phosphinothricin N-acetyltransferase, pat homologue, complete cds, strain: SPC9018.	199	7.2E-11	173	31.2
591	226093437	AP008955	<i>Brevibacillus brevis</i> NBRC 100599	Brevibacillus brevis NBRC 100599 DNA, complete genome.	163	7.2E-11	158	28.5
592	218521287	CP001298	<i>Methylobacterium chloromethanicum</i> CM4	Methylobacterium chloromethanicum CM4, complete genome.	204	7.3E-11	178	29.8
593	188521100	CP000967	<i>Xanthomonas oryzae</i> pv <i>oryzae</i> PXO99A	Xanthomonas oryzae pv. oryzae PXO99A, complete genome.	179	7.8E-11	176	30.7
594	58426392	AE013598	<i>Xanthomonas oryzae</i> pv <i>oryzae</i> KACC10331	Xanthomonas oryzae pv. oryzae KACC10331, complete genome.	179	7.8E-11	176	30.7
595	84367641	AP008229	<i>Xanthomonas oryzae</i> pv <i>oryzae</i> MAFF 311018	Xanthomonas oryzae pv. oryzae MAFF 311018 DNA, complete genome.	179	7.8E-11	176	30.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
596	332182099	CP002696	<i>Treponema brennaborense</i> DSM 12168	Treponema brennaborense DSM 12168, complete genome.	195	8.3E-11	179	29.1
597	290349766	AB548433	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii gene for phosphinothricin N-acetyltransferase, pat homologue, complete cds, strain: MAFF302094.	199	8.5E-11	173	31.8
598	222114303	AM946015	<i>Streptococcus uberis</i> 0140J	Streptococcus uberis 0140J complete genome.	202	8.6E-11	164	29.3
599	312912578	AP011957	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Typhimurium str	Salmonella enterica subsp. enterica serovar Typhimurium str. T000240 DNA, complete genome.	171	8.9E-11	168	33.3
600	261246783	FN424405	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Typhimurium str D23580	Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 complete genome.	171	8.9E-11	168	33.3
601	206708718	AM933172	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Enteritidis str	Salmonella enterica subsp. enterica serovar Enteritidis str. P125109 complete genome.	171	8.9E-11	168	33.3
602	267993511	CP001363	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Typhimurium str 14028S	Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S, complete genome.	171	8.9E-11	168	33.3
603	301158118	FQ312003	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Typhimurium str SL1344	Salmonella enterica subsp. enterica serovar Typhimurium SL1344 genome.	171	8.9E-11	168	33.3
604	323129860	CP002487	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Typhimurium str ST4/74	Salmonella enterica subsp. enterica serovar Typhimurium str. ST4/74, complete genome.	171	8.9E-11	168	33.3
605	197093865	FM200053	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Paratyphi A str	Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601 complete genome, strain AKU_12601.	171	8.9E-11	168	33.3
606	194408836	CP001120	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar Heidelberg str SL476	Salmonella enterica subsp. enterica serovar Heidelberg str. SL476, complete genome.	171	8.9E-11	168	33.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
607	197212778	CP001138	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Agona str SL483</i>	Salmonella enterica subsp. enterica serovar Agona str. SL483, complete genome.	171	8.9E-11	168	33.3
608	197939526	CP001144	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Dublin str CT_02021853</i>	Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853, complete genome.	171	8.9E-11	168	33.3
609	205272508	AM933173	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Gallinarum str 287/91</i>	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91 complete genome.	171	8.9E-11	168	33.3
610	332988477	CP002614	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Typhimurium str UK-1</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. UK-1, complete genome.	171	8.9E-11	168	33.3
611	16420114	AE006468	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Typhimurium str LT2</i>	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2, complete genome.	171	8.9E-11	168	33.3
612	194403112	CP001113	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Newport str SL254</i>	Salmonella enterica subsp. enterica serovar Newport str. SL254, complete genome.	171	8.9E-11	168	33.3
613	56127721	CP000026	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Paratyphi A str ATCC</i>	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150, complete genome.	171	8.9E-11	168	33.3
614	194710101	CP001127	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Schwarzengrund str</i>	Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633, complete genome.	171	8.9E-11	168	33.3
615	77966475	CP000151	<i>Burkholderia sp 383</i>	Burkholderia sp. 383 chromosome 1, complete sequence.	182	9.3E-11	178	32.0
616	290349770	AB548435	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii gene for phosphinothricin N-acetyltransferase, pat homologue, complete cds, strain: KH5.	199	1E-10	173	31.2
617	62127790	AE017220	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Choleraesuis str</i>	Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67, complete genome.	171	1E-10	168	33.3
618	187727447	CP001068	<i>Ralstonia pickettii 12J</i>	Ralstonia pickettii 12J chromosome 1, complete sequence.	171	1E-10	170	34.1
619	291556282	FP929059	<i>Eubacterium siraeum V10Sc8a</i>	Eubacterium siraeum V10Sc8a draft genome.	172	1.1E-10	164	29.9

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
620	71555745	CP000058	<i>Pseudomonas syringae</i> pv <i>phaseolicola</i> 1448A	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A, complete genome.	179	1.1E-10	159	32.7
621	334194467	CP002819	<i>Ralstonia solanacearum</i> Po82	<i>Ralstonia solanacearum</i> Po82, complete genome.	182	1.1E-10	165	31.5
622	299070322	FP885897	<i>Ralstonia solanacearum</i> CFBP2957	<i>Ralstonia solanacearum</i> str. CFBP2957 chromosome, complete genome.	182	1.1E-10	165	32.1
623	225701330	FM204884	<i>Streptococcus equi</i> subsp <i>zooepidemicus</i>	<i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> H70, complete genome.	193	1.2E-10	177	32.2
624	21205621	BA000033	<i>Staphylococcus aureus</i> subsp <i>aureus</i> MW2	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2 DNA, complete genome.	163	1.2E-10	161	29.8
625	49245750	BX571857	<i>Staphylococcus aureus</i> subsp <i>aureus</i> MSSA476	<i>Staphylococcus aureus</i> strain MSSA476, complete genome.	163	1.2E-10	161	29.8
626	334095191	CP002781	<i>Sinorhizobium meliloti</i> AK83	<i>Sinorhizobium meliloti</i> AK83 chromosome 1, complete sequence.	169	1.2E-10	171	31.0
627	336033334	CP001830	<i>Sinorhizobium meliloti</i> SM11	<i>Sinorhizobium meliloti</i> SM11, complete genome.	169	1.2E-10	171	31.0
628	15074495	AL591688	<i>Sinorhizobium meliloti</i> 1021	<i>Sinorhizobium meliloti</i> 1021 complete chromosome.	169	1.2E-10	171	31.0
629	333811486	CP002740	<i>Sinorhizobium meliloti</i> BL225C	<i>Sinorhizobium meliloti</i> BL225C, complete genome.	169	1.2E-10	171	31.0
630	9657787	AE003853	<i>Vibrio cholerae</i> O1 biovar <i>El Tor</i> str N16961	<i>Vibrio cholerae</i> O1 biovar <i>eltor</i> str. N16961 chromosome II, complete sequence.	169	1.2E-10	152	32.2
631	239801779	CP001635	<i>Variovorax paradoxus</i> S110	<i>Variovorax paradoxus</i> S110 chromosome 1, complete sequence.	173	1.3E-10	166	32.5
632	283474827	FP565176	<i>Xanthomonas albilineans</i>	<i>Xanthomonas albilineans</i> str. GPE PC73, chromosome, complete genome.	173	1.3E-10	160	31.9
633	260220796	FN543104	<i>Curvibacter putative symbiont of Hydra magnipapillata</i>	<i>Curvibacter putative symbiont of Hydra magnipapillata</i> genomic scaffold HmaUn_WGA69518_1.	174	1.3E-10	173	28.3
634	315594772	CP002417	<i>Variovorax paradoxus</i> EPS	<i>Variovorax paradoxus</i> EPS, complete genome.	174	1.3E-10	169	30.2
635	72122291	CP000091	<i>Ralstonia eutropha</i> JMP134	<i>Ralstonia eutropha</i> JMP134 chromosome 2, complete sequence.	175	1.3E-10	173	34.1

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
636	334729918	CP000245	<i>Ramlibacter tataouinensis</i> TTB310	Ramlibacter tataouinensis TTB310, complete genome.	177	1.3E-10	159	31.4
637	192284476	CP001096	<i>Rhodopseudomonas palustris</i> TIE-1	Rhodopseudomonas palustris TIE-1, complete genome.	180	1.3E-10	176	30.7
638	115519117	CP000463	<i>Rhodopseudomonas palustris</i> BisA53	Rhodopseudomonas palustris BisA53, complete genome.	180	1.3E-10	174	32.2
639	150375439	AP009351	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> str. Newman	Staphylococcus aureus subsp. aureus str. Newman DNA, complete genome.	163	1.4E-10	161	29.8
640	329315208	CP002643	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> T0131	Staphylococcus aureus subsp. aureus T0131, complete genome.	163	1.4E-10	161	29.8
641	269942101	FN433596	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> TW20	Staphylococcus aureus subsp. aureus TW20, complete genome.	163	1.4E-10	161	29.8
642	49242859	BX571856	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MRSA252	Staphylococcus aureus subsp. aureus strain MRSA252, complete genome.	163	1.4E-10	161	29.8
643	57285223	CP000046	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> COL	Staphylococcus aureus subsp. aureus COL, complete genome.	163	1.4E-10	161	29.8
644	87204027	CP000253	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> NCTC 8325	Staphylococcus aureus subsp. aureus NCTC 8325, complete genome.	163	1.4E-10	161	29.8
645	87127742	CP000255	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> USA300_FPR3757	Staphylococcus aureus subsp. aureus USA300_FPR3757, complete genome.	163	1.4E-10	161	29.8
646	298695789	CP001996	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ED133	Staphylococcus aureus subsp. aureus ED133, complete genome.	163	1.4E-10	161	29.8
647	302752389	CP002120	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> str. JKD6008	Staphylococcus aureus subsp. aureus str. JKD6008, complete genome.	163	1.4E-10	161	29.8
648	160369533	CP000730	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> USA300_TCH1516	Staphylococcus aureus subsp. aureus USA300_TCH1516, complete genome.	163	1.4E-10	161	29.8
649	312437053	CP002110	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> TCH60	Staphylococcus aureus subsp. aureus TCH60, complete genome.	163	1.4E-10	161	29.8

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
650	39648972	BX572599	<i>Rhodopseudomonas palustris</i> CGA009	Rhodopseudomonas palustris CGA009 complete genome; segment 7/16.	203	1.4E-10	176	30.7
651	221734944	CP000633	<i>Agrobacterium vitis</i> S4	Agrobacterium vitis S4 chromosome 1, complete sequence.	168	1.4E-10	155	32.3
652	148513984	CP000712	<i>Pseudomonas putida</i> F1	Pseudomonas putida F1, complete genome.	171	1.5E-10	169	32.0
653	166862380	CP000926	<i>Pseudomonas putida</i> GB-1	Pseudomonas putida GB-1, complete genome.	171	1.5E-10	169	31.4
654	300076629	CP002039	<i>Herbaspirillum seropedicae</i> SmR1	Herbaspirillum seropedicae SmR1, complete genome.	173	1.5E-10	161	32.3
655	299065311	FP885895	<i>Ralstonia solanacearum</i> CMR15	Ralstonia solanacearum str. CMR15 chromosome, complete genome.	182	1.5E-10	180	31.7
656	225700396	FM204883	<i>Streptococcus equi</i> subsp <i>equi</i> 4047	Streptococcus equi subsp. equi 4047, complete genome.	193	1.6E-10	178	33.1
657	76574793	DQ168848	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii strain 83-1 pathogenicity island, partial sequence.	199	1.7E-10	173	31.8
658	68446267	AP006716	<i>Staphylococcus haemolyticus</i> JCSC1435	Staphylococcus haemolyticus JCSC1435 DNA, complete genome.	164	1.7E-10	162	28.4
659	240866773	CP001644	<i>Ralstonia pickettii</i> 12D	Ralstonia pickettii 12D chromosome 1, complete sequence.	171	1.7E-10	170	33.5
660	24986609	AE015451	<i>Pseudomonas putida</i> KT2440	Pseudomonas putida KT2440 complete genome.	171	1.7E-10	169	32.0
661	295095764	FP929040	<i>Enterobacter cloacae</i> subsp <i>cloacae</i> NCTC 9394	Enterobacter cloacae subsp. cloacae NCTC 9394 draft genome.	172	1.7E-10	168	32.1
662	221731319	CP001392	<i>Acidovorax ebreus</i> TPSY	Acidovorax ebreus TPSY, complete genome.	173	1.8E-10	159	30.8
663	301633857	CP002116	<i>Spirochaeta smaragdinae</i> DSM 11293	Spirochaeta smaragdinae DSM 11293, complete genome.	173	1.8E-10	167	29.3
664	54015164	AP006618	<i>Nocardia farcinica</i> IFM 10152	Nocardia farcinica IFM 10152 DNA, complete genome.	177	1.8E-10	173	33.5
665	161363323	CP000886	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Paratyphi B</i> str <i>SPB7</i>	Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7, complete genome.	171	2.1E-10	168	32.7

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
666	310759070	CP002287	<i>Achromobacter xylosoxidans</i> A8	Achromobacter xylosoxidans A8, complete genome.	185	2.2E-10	157	33.1
667	221727300	CP000629	<i>Agrobacterium radiobacter</i> K84	Agrobacterium radiobacter K84 chromosome 2, complete sequence.	198	2.3E-10	184	31.5
668	169761802	CP000949	<i>Pseudomonas putida</i> W619	Pseudomonas putida W619, complete genome.	171	2.4E-10	169	31.4
669	313500828	CP002290	<i>Pseudomonas putida</i> BIRD-1	Pseudomonas putida BIRD-1, complete genome.	171	2.4E-10	169	32.0
670	170938977	CU633751	<i>Cupriavidus taiwanensis</i> LMG 19424	Cupriavidus taiwanensis str. LMG19424 plasmid pRALTA, complete genome.	179	2.5E-10	176	30.7
671	160342758	CP000868	<i>Burkholderia multivorans</i> ATCC 17616	Burkholderia multivorans ATCC 17616 chromosome 1, complete sequence.	184	2.6E-10	181	30.4
672	189333956	AP009385	<i>Burkholderia multivorans</i> ATCC 17616	Burkholderia multivorans ATCC 17616 DNA, complete genome, chromosome 1.	184	2.6E-10	181	30.4
673	33574427	BX640433	<i>Bordetella parapertussis</i>	Bordetella parapertussis strain 12822, complete genome; segment 11/14.	184	2.6E-10	163	33.7
674	163259599	AM902716	<i>Bordetella petrii</i>	Bordetella petrii strain DSM 12804, complete genome.	186	2.6E-10	171	32.2
675	339893677	FR870271	<i>Staphylococcus lugdunensis</i> N920143	Staphylococcus lugdunensis N920143 complete genome.	164	2.8E-10	160	30.0
676	289179374	CP001837	<i>Staphylococcus lugdunensis</i> HKU09-01	Staphylococcus lugdunensis HKU09-01, complete genome.	164	2.8E-10	160	30.0
677	333120734	CP002471	<i>Streptococcus parauberis</i> KCTC 11537	Streptococcus parauberis KCTC 11537, complete genome.	206	2.8E-10	180	29.4
678	209534227	CP001191	<i>Rhizobium leguminosarum</i> bv. trifolii WSM2304	Rhizobium leguminosarum bv. trifolii WSM2304, complete genome.	169	2.8E-10	158	31.6
679	339512762	FR877557	<i>Salmonella bongori</i> NCTC 12419	Salmonella bongori NCTC 12419, culture collection SGSC SARC11, complete genome.	172	2.9E-10	168	32.7
680	171992600	CP001025	<i>Burkholderia ambifaria</i> MC40-6	Burkholderia ambifaria MC40-6 chromosome 1, complete sequence.	182	3E-10	178	29.8
681	187728757	CP001069	<i>Ralstonia pickettii</i> 12J	Ralstonia pickettii 12J chromosome 2, complete sequence.	182	3E-10	181	30.9
682	240867359	CP001645	<i>Ralstonia pickettii</i> 12D	Ralstonia pickettii 12D chromosome 2, complete sequence.	182	3E-10	181	30.9

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
683	150955958	CP000647	<i>Klebsiella pneumoniae subsp pneumoniae MGH 78578</i>	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> MGH 78578, complete sequence.	184	3E-10	172	29.7
684	339762852	CP002910	<i>Klebsiella pneumoniae KCTC 2242</i>	<i>Klebsiella pneumoniae</i> KCTC 2242, complete genome.	184	3E-10	172	29.7
685	238548013	AP006725	<i>Klebsiella pneumoniae subsp pneumoniae NTUH-K2044</i>	<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> NTUH-K2044 DNA, complete genome.	184	3E-10	172	29.7
686	146347774	CP000673	<i>Clostridium kluyveri DSM 555</i>	<i>Clostridium kluyveri</i> DSM 555, complete genome.	161	3.2E-10	160	29.4
687	219569087	AP009049	<i>Clostridium kluyveri NBRC 12016</i>	<i>Clostridium kluyveri</i> NBRC 12016 DNA, complete genome.	161	3.2E-10	160	29.4
688	147742031	CP000703	<i>Staphylococcus aureus subsp aureus JH9</i>	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> JH9, complete genome.	163	3.3E-10	161	29.8
689	14248303	BA000017	<i>Staphylococcus aureus subsp aureus Mu50</i>	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> Mu50 DNA, complete genome.	163	3.3E-10	161	29.8
690	156722979	AP009324	<i>Staphylococcus aureus subsp aureus Mu3</i>	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> Mu3 DNA, complete genome.	163	3.3E-10	161	29.8
691	149947491	CP000736	<i>Staphylococcus aureus subsp aureus JH1</i>	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> JH1, complete genome.	163	3.3E-10	161	29.8
692	262076451	CP001781	<i>Staphylococcus aureus subsp aureus ED98</i>	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ED98, complete genome.	163	3.3E-10	161	29.8
693	312830868	FR714927	<i>Staphylococcus aureus subsp aureus ECT-R 2</i>	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> ECT-R 2 complete genome.	163	3.3E-10	161	29.8
694	13702479	BA000018	<i>Staphylococcus aureus subsp aureus N315</i>	<i>Staphylococcus aureus</i> subsp. <i>aureus</i> N315 DNA, complete genome.	163	3.3E-10	161	29.8
695	285818189	CP001844	<i>Staphylococcus aureus 04-02981</i>	<i>Staphylococcus aureus</i> 04-02981, complete genome.	163	3.3E-10	161	29.8
696	27316544	AE015929	<i>Staphylococcus epidermidis ATCC 12228</i>	<i>Staphylococcus epidermidis</i> ATCC 12228, complete genome.	164	3.3E-10	163	28.2
697	190696218	CP001074	<i>Rhizobium etli CIAT 652</i>	<i>Rhizobium etli</i> CIAT 652, complete genome.	171	3.4E-10	170	31.8
698	329311594	CP002657	<i>Alicyclophilus denitrificans K601</i>	<i>Alicyclophilus denitrificans</i> K601, complete genome.	175	3.5E-10	159	29.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
699	317116475	CP002449	<i>Alicyclophilus denitrificans</i> BC	Alicyclophilus denitrificans BC, complete genome.	175	3.5E-10	159	29.6
700	68348435	CP000076	<i>Pseudomonas fluorescens</i> Pf-5	Pseudomonas fluorescens Pf-5, complete genome.	177	3.5E-10	173	33.5
701	325121965	CP002177	<i>Acinetobacter calcoaceticus</i> PHEA-2	Acinetobacter calcoaceticus PHEA-2, complete genome.	181	3.6E-10	173	28.3
702	288889101	CP001891	<i>Klebsiella variicola</i> At-22	Klebsiella variicola At-22, complete genome.	184	3.6E-10	172	29.7
703	206565687	CP000964	<i>Klebsiella pneumoniae</i> 342	Klebsiella pneumoniae 342, complete genome.	184	3.6E-10	172	29.7
704	57636156	CP000029	<i>Staphylococcus epidermidis</i> RP62A	Staphylococcus epidermidis RP62A, complete genome.	164	3.9E-10	163	28.2
705	320085923	FR775221	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Weltevreden</i> str <i>Weltevreden</i> str	Salmonella enterica subsp. enterica serovar Weltevreden str. 2007-60-3289-1 complete genome, contig 34.	171	4E-10	168	32.7
706	221736457	CP000633	<i>Agrobacterium vitis</i> S4	Agrobacterium vitis S4 chromosome 1, complete sequence.	180	4.2E-10	177	29.9
707	229359998	AM181176	<i>Pseudomonas fluorescens</i> SBW25	Pseudomonas fluorescens SBW25 complete genome.	170	4.7E-10	170	30.6
708	29137573	AE014613	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Typhi</i> str <i>Ty2</i>	Salmonella enterica subsp. enterica serovar Typhi Ty2, complete genome.	171	4.8E-10	168	32.7
709	16502584	AL627270	<i>Salmonella enterica</i> subsp <i>enterica</i> serovar <i>Typhi</i> (<i>Salmonella</i> <i>Typhi</i>)	Salmonella enterica serovar Typhi (<i>Salmonella typhi</i>) strain CT18, complete chromosome; segment 6/20.	171	4.8E-10	168	32.7
710	299077104	FP885906	<i>Ralstonia solanacearum</i> PSI07	Ralstonia solanacearum str. PSI07 chromosome, complete genome.	182	5E-10	180	31.1
711	149772266	AM398681	<i>Flavobacterium psychrophilum</i> JIP02/86	Flavobacterium psychrophilum JIP02/86 complete genome.	165	5.5E-10	159	28.3
712	77994748	CP000141	<i>Carboxydotherrmus hydrogenoformans</i> Z-2901	Carboxydotherrmus hydrogenoformans Z-2901, complete genome.	168	5.5E-10	158	29.1
713	291531464	FP929044	<i>Eubacterium siraeum</i> 70/3	Eubacterium siraeum 70/3 draft genome.	172	5.7E-10	164	29.3

PAT/*pat* Protein
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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
714	58003225	CP000009	<i>Gluconobacter oxydans</i> 621H	Gluconobacter oxydans 621H, complete genome.	173	5.7E-10	158	34.2
715	237878608	CP001504	<i>Burkholderia glumae</i> BGR1	Burkholderia glumae BGR1 chromosome 2, complete sequence.	174	5.7E-10	177	32.2
716	33577346	BX640448	<i>Bordetella bronchiseptica</i> RB50	Bordetella bronchiseptica strain RB50, complete genome; segment 12/16.	184	6E-10	163	33.1
717	17430157	AL646052	<i>Ralstonia solanacearum</i> GMI1000	Ralstonia solanacearum GMI1000 chromosome complete sequence.	182	7E-10	181	30.9
718	290349768	AB548434	<i>Pseudomonas cichorii</i>	Pseudomonas cichorii gene for phosphinothricin N-acetyltransferase, pat homologue, complete cds, strain: MAFF730054.	199	7.5E-10	171	30.4
719	56677741	CP000031	<i>Ruegeria pomeroyi</i> DSS-3	Ruegeria pomeroyi DSS-3, complete genome.	164	7.6E-10	160	32.5
720	221722737	CP000628	<i>Agrobacterium radiobacter</i> K84	Agrobacterium radiobacter K84 chromosome 1, complete sequence.	168	7.8E-10	157	29.9
721	115281066	CP000440	<i>Burkholderia ambifaria</i> AMMD	Burkholderia ambifaria AMMD chromosome 1, complete sequence.	182	8.3E-10	178	29.8
722	184194555	CP001044	<i>Burkholderia phymatum</i> STM815	Burkholderia phymatum STM815 chromosome 2, complete sequence.	188	8.5E-10	170	31.8
723	168990271	CP000817	<i>Lysinibacillus sphaericus</i> C3-41	Lysinibacillus sphaericus C3-41, complete genome.	165	9E-10	162	30.9
724	288909503	AP010946	<i>Azospirillum</i> sp B510	Azospirillum sp. B510 DNA, complete genome.	166	9.1E-10	160	33.8
725	315602489	CP002418	<i>Rhodopseudomonas palustris</i> DX-1	Rhodopseudomonas palustris DX-1, complete genome.	180	9.7E-10	167	29.9
726	269093820	CP001820	<i>Veillonella parvula</i> DSM 2008	Veillonella parvula DSM 2008, complete genome.	166	1.1E-9	153	29.4
727	150027976	CP000738	<i>Sinorhizobium medicae</i> WSM419	Sinorhizobium medicae WSM419, complete genome.	169	1.1E-9	163	31.3
728	338840417	CP002870	<i>Pseudomonas putida</i> S16	Pseudomonas putida S16, complete genome.	171	1.1E-9	170	31.8
729	237501160	CP001616	<i>Tolomonas auensis</i> DSM 9187	Tolomonas auensis DSM 9187, complete genome.	173	1.1E-9	163	30.7
730	120607738	CP000539	<i>Acidovorax</i> sp JS42	Acidovorax sp. JS42, complete genome.	173	1.1E-9	159	29.6

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
731	160366362	CP000884	<i>Delftia acidovorans</i> SPH-1	Delftia acidovorans SPH-1, complete genome.	174	1.1E-9	160	31.2
732	89344931	CP000267	<i>Rhodferax ferrireducens</i> T118	Rhodferax ferrireducens T118, complete genome.	174	1.1E-9	169	27.2
733	298700539	CP002080	<i>Acinetobacter</i> sp DR1	Acinetobacter sp. DR1, complete genome.	181	1.2E-9	159	27.7
734	149932450	CP000139	<i>Bacteroides vulgatus</i> ATCC 8482	Bacteroides vulgatus ATCC 8482, complete genome.	161	1.2E-9	161	29.2
735	51103089	AY597279	<i>Pseudomonas viridiflava</i>	Pseudomonas viridiflava strain LP23.1a pathogenicity island PAI-Region-2, partial sequence.	199	1.2E-9	170	30.0
736	294477643	CP001312	<i>Rhodobacter capsulatus</i> SB 1003	Rhodobacter capsulatus SB 1003, complete genome.	167	1.3E-9	168	32.1
737	321167103	CP002505	<i>Rahnella</i> sp Y9602	Rahnella sp. Y9602, complete genome.	175	1.3E-9	160	27.5
738	218322292	FM954972	<i>Vibrio splendidus</i> LGP32	Vibrio splendidus LGP32 chromosome 1.	168	1.5E-9	152	29.6
739	156532330	CP000783	<i>Cronobacter sakazakii</i> ATCC BAA-894	Cronobacter sakazakii ATCC BAA-894, complete genome.	172	1.5E-9	171	31.0
740	213986498	CP001172	<i>Acinetobacter baumannii</i> AB307-0294	Acinetobacter baumannii AB307-0294, complete genome.	181	1.6E-9	164	28.0
741	169149118	CU459141	<i>Acinetobacter baumannii</i> AYE	Acinetobacter baumannii str. AYE, complete genome.	181	1.6E-9	164	28.0
742	213056235	CP001182	<i>Acinetobacter baumannii</i> AB0057	Acinetobacter baumannii AB0057, complete genome.	181	1.6E-9	164	28.0
743	291547815	FP929053	<i>Ruminococcus</i> sp SR1/5	Ruminococcus sp. SR1/5 draft genome.	195	1.7E-9	164	27.4
744	51103190	AY597283	<i>Pseudomonas viridiflava</i>	Pseudomonas viridiflava strain RMX3.1b pathogenicity island PAI-Region-2, partial sequence.	199	1.7E-9	174	29.9
745	238547269	AP006725	<i>Klebsiella pneumoniae</i> subsp <i>pneumoniae</i> NTUH-K2044	Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044 DNA, complete genome.	180	1.9E-9	175	31.4
746	51103107	AY597281	<i>Pseudomonas viridiflava</i>	Pseudomonas viridiflava strain ME3.1b pathogenicity island PAI-Region-2, partial sequence.	199	2.1E-9	170	29.4
747	51103149	AY597282	<i>Pseudomonas viridiflava</i>	Pseudomonas viridiflava strain RMX23.1a pathogenicity island PAI-Region-2, partial sequence.	199	2.1E-9	170	29.4

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
748	333743120	CP002735	<i>Delftia</i> sp Cs1-4	Delftia sp. Cs1-4, complete genome.	174	2.2E-9	160	30.6
749	115421831	AM167904	<i>Bordetella avium</i> 197N	Bordetella avium 197N complete genome.	180	2.2E-9	183	33.3
750	169152486	CU468230	<i>Acinetobacter baumannii</i>	Acinetobacter baumannii str. SDF, complete genome.	181	2.3E-9	164	28.0
751	312202775	CP002330	<i>Caldicellulosiruptor kronotskyensis</i> 2002	Caldicellulosiruptor kronotskyensis 2002, complete genome.	161	2.4E-9	158	27.2
752	306527914	CP002038	<i>Dickeya dadantii</i> 3937	Dickeya dadantii 3937, complete genome.	170	2.5E-9	159	34.6
753	333117523	CP002727	<i>Pseudomonas fulva</i> 12-X	Pseudomonas fulva 12-X, complete genome.	172	2.6E-9	163	33.1
754	226318041	CP001114	<i>Deinococcus deserti</i> VCD115	Deinococcus deserti VCD115, complete genome.	176	2.6E-9	174	27.6
755	345145	A01504	<i>Alcaligenes faecalis</i>	A.faecalis DNA for PTC-resistance protein (PTC=phosphinothricin).	197	2.9E-9	174	28.7
756	219997813	CP001348	<i>Clostridium cellulolyticum</i> H10	Clostridium cellulolyticum H10, complete genome.	164	2.9E-9	159	27.7
757	158333215	AP009384	<i>Azorhizobium caulinodans</i> ORS 571	Azorhizobium caulinodans ORS 571 DNA, complete genome.	171	3E-9	172	32.0
758	339762171	CP002910	<i>Klebsiella pneumoniae</i> KCTC 2242	Klebsiella pneumoniae KCTC 2242, complete genome.	172	3E-9	170	31.8
759	150955316	CP000647	<i>Klebsiella pneumoniae</i> subsp <i>pneumoniae</i> MGH 78578	Klebsiella pneumoniae subsp. pneumoniae MGH 78578, complete sequence.	172	3E-9	170	31.8
760	321169364	CP002505	<i>Rahnella</i> sp Y9602	Rahnella sp. Y9602, complete genome.	173	3E-9	159	28.3
761	77380814	CP000094	<i>Pseudomonas fluorescens</i> Pf0-1	Pseudomonas fluorescens Pf0-1, complete genome.	177	3.1E-9	172	31.4
762	146194607	CU234118	<i>Bradyrhizobium</i> sp ORS278	Bradyrhizobium sp. ORS278, complete sequence.	190	3.3E-9	182	27.5
763	187428000	CP001063	<i>Shigella boydii</i> CDC 3083-94	Shigella boydii CDC 3083-94, complete genome.	193	3.3E-9	174	29.9
764	51103098	AY597280	<i>Pseudomonas viridiflava</i>	Pseudomonas viridiflava strain PNA3.3a pathogenicity island PAI-Region-2, partial sequence.	199	3.4E-9	170	28.8

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
765	296029444	CP001966	<i>Tsukamurella paurometabola</i> DSM 20162	Tsukamurella paurometabola DSM 20162, complete genome.	165	3.5E-9	162	30.9
766	295056679	CP001918	<i>Enterobacter cloacae</i> subsp <i>cloacae</i> ATCC 13047	Enterobacter cloacae subsp. cloacae ATCC 13047, complete genome.	172	3.6E-9	172	29.7
767	167216130	AB378291	<i>Nocardia</i> sp AB2253	Nocardia sp. AB2253 PAT gene for phosphinothricin acetyltransferase, complete cds.	177	3.7E-9	169	30.8
768	33572834	BX640418	<i>Bordetella pertussis</i> Tohama I	Bordetella pertussis strain Tohama I, complete genome; segment 8/12.	180	3.7E-9	163	32.5
769	332382886	CP002695	<i>Bordetella pertussis</i> CS	Bordetella pertussis CS, complete genome.	180	3.7E-9	163	32.5
770	240857624	CP001622	<i>Rhizobium leguminosarum</i> bv <i>trifolii</i> WSM1325	Rhizobium leguminosarum bv. trifolii WSM1325, complete genome.	183	3.8E-9	157	31.2
771	147830231	AM711867	<i>Clavibacter michiganensis</i> subsp <i>michiganensis</i> NCPPB 382	Clavibacter michiganensis subsp. michiganensis NCPPB 382 complete genome.	229	3.8E-9	182	31.3
772	91072265	CP000243	<i>Escherichia coli</i> UTI89	Escherichia coli UTI89, complete genome.	193	3.9E-9	174	29.9
773	333969605	CP002797	<i>Escherichia coli</i> NA114	Escherichia coli NA114, complete genome.	193	3.9E-9	174	29.9
774	26108135	AE014075	<i>Escherichia coli</i> CFT073	Escherichia coli CFT073, complete genome.	193	3.9E-9	174	29.9
775	290762424	CP001846	<i>Escherichia coli</i> O55:H7 str CB9615	Escherichia coli O55:H7 str. CB9615, complete genome.	193	3.9E-9	174	29.9
776	209159058	CP001164	<i>Escherichia coli</i> O157:H7 str EC4115	Escherichia coli O157:H7 str. EC4115, complete genome.	193	3.9E-9	174	29.9
777	157081454	CP000800	<i>Escherichia coli</i> E24377A	Escherichia coli E24377A, complete genome.	193	3.9E-9	174	29.9
778	294490620	CP001969	<i>Escherichia coli</i> IHE3034	Escherichia coli IHE3034, complete genome.	193	3.9E-9	174	29.9
779	311775319	CP002216	<i>Caldicellulosiruptor owensensis</i> OL	Caldicellulosiruptor owensensis OL, complete genome.	161	4E-9	158	27.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
780	256007783	CP001631	<i>Acidimicrobium ferrooxidans</i> DSM 10331	Acidimicrobium ferrooxidans DSM 10331, complete genome.	166	4.1E-9	160	30.6
781	115588235	CP000438	<i>Pseudomonas aeruginosa</i> UCBPP-PA14	Pseudomonas aeruginosa UCBPP-PA14, complete genome.	172	4.2E-9	172	30.8
782	150959082	CP000744	<i>Pseudomonas aeruginosa</i> PA7	Pseudomonas aeruginosa PA7, complete genome.	172	4.2E-9	172	30.8
783	9951139	AE004091	<i>Pseudomonas aeruginosa</i> PAO1	Pseudomonas aeruginosa PAO1, complete genome.	172	4.2E-9	172	30.8
784	218774189	FM209186	<i>Pseudomonas aeruginosa</i> LESB58	Pseudomonas aeruginosa LESB58 complete genome sequence.	172	4.2E-9	172	30.8
785	327482363	CP002622	<i>Pseudomonas stutzeri</i> DSM 4166	Pseudomonas stutzeri DSM 4166, complete genome.	174	4.3E-9	172	29.7
786	197089704	CP001124	<i>Geobacter bemidjiensis</i> Bem	Geobacter bemidjiensis Bem, complete genome.	178	4.4E-9	157	31.2
787	169815714	CP000958	<i>Burkholderia cenocepacia</i> MC0-3	Burkholderia cenocepacia MC0-3 chromosome 1, complete sequence.	184	4.5E-9	162	29.6
788	146406740	CP000494	<i>Bradyrhizobium</i> sp. BTAi1	Bradyrhizobium sp. BTAi1, complete genome.	190	4.6E-9	167	27.5
789	218356353	CU928158	<i>Escherichia fergusonii</i> ATCC 35469	Escherichia fergusonii ATCC 35469 chromosome, complete genome.	249	4.8E-9	174	29.9
790	218351722	CU928145	<i>Escherichia coli</i> 55989	Escherichia coli 55989 chromosome, complete genome.	250	4.9E-9	174	29.9
791	218360742	CU928160	<i>Escherichia coli</i> IA11	Escherichia coli IA11 chromosome, complete genome.	250	4.9E-9	174	29.9
792	206567613	CP000964	<i>Klebsiella pneumoniae</i> 342	Klebsiella pneumoniae 342, complete genome.	172	5E-9	170	31.8
793	288889965	CP001891	<i>Klebsiella variicola</i> At-22	Klebsiella variicola At-22, complete genome.	172	5E-9	170	31.8
794	238685470	EU670845	<i>Acinetobacter nosocomialis</i>	Acinetobacter genomosp. 13TU strain 8488 thermonuclease protein gene, partial cds; transposon ISAb1, complete sequence; beta-lactamase OXA-138 (blaOXA-138), sortase, and predicted transcriptional regulator genes, complete cds; and unknown gene.	181	5.2E-9	164	27.4
795	322508197	CP001921	<i>Acinetobacter baumannii</i> 1656-2	Acinetobacter baumannii 1656-2, complete genome.	181	5.2E-9	164	27.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
796	183209473	CP000863	<i>Acinetobacter baumannii</i> ACICU	Acinetobacter baumannii ACICU, complete genome.	181	5.2E-9	164	27.4
797	323517796	CP002522	<i>Acinetobacter baumannii</i> TCDC-AB0715	Acinetobacter baumannii TCDC-AB0715, complete genome.	181	5.2E-9	164	27.4
798	255076972	GQ352402	<i>Acinetobacter baumannii</i>	Acinetobacter baumannii strain AbSK-17 plasmid pAbSK-OXA-82 replicase, zeta toxin family protein, hypothetical proteins, thermonuclease protein, and hypothetical protein genes, complete cds; insertion sequence ISAb1, complete sequence; and beta-lactamase OXA-51-like protein (blaOXA-82), sortase, and transcriptional regulator genes, complete cds.	181	5.2E-9	164	27.4
799	323517284	CP002522	<i>Acinetobacter baumannii</i> TCDC-AB0715	Acinetobacter baumannii TCDC-AB0715, complete genome.	181	5.2E-9	164	27.4
800	169156403	AM849034	<i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>	Clavibacter michiganensis subsp. sepedonicus complete genome.	229	5.3E-9	173	31.2
801	157066607	CP000802	<i>Escherichia coli</i> HS	Escherichia coli HS, complete genome.	193	5.5E-9	174	29.9
802	169156711	AM849034	<i>Clavibacter michiganensis</i> subsp. <i>sepedonicus</i>	Clavibacter michiganensis subsp. sepedonicus complete genome.	194	5.5E-9	159	32.7
803	338803136	CP002881	<i>Pseudomonas stutzeri</i> ATCC 17588 = LMG 11199	Pseudomonas stutzeri ATCC 17588 = LMG 11199, complete genome.	169	5.9E-9	172	30.2
804	145318632	CP000653	<i>Enterobacter</i> sp. 638	Enterobacter sp. 638, complete genome.	171	5.9E-9	171	30.4
805	282948751	FN543502	<i>Citrobacter rodentium</i> ICC168	Citrobacter rodentium ICC168, complete genome.	172	5.9E-9	172	32.0
806	157082945	CP000822	<i>Citrobacter koseri</i> ATCC BAA-895	Citrobacter koseri ATCC BAA-895, complete genome.	172	5.9E-9	168	31.5
807	170777275	CP001013	<i>Leptothrix cholodnii</i> SP-6	Leptothrix cholodnii SP-6, complete genome.	198	6.7E-9	172	29.7
808	30041493	AE014073	<i>Shigella flexneri</i> 2a str. 2457T	Shigella flexneri 2a str. 2457T, complete genome.	172	7E-9	169	29.6
809	260449426	CP001637	<i>Escherichia coli</i> DH1	Escherichia coli DH1, complete genome.	172	7E-9	169	29.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
810	238862125	CP001396	<i>Escherichia coli</i> BW2952	<i>Escherichia coli</i> BW2952, complete genome.	172	7E-9	169	29.6
811	81245502	CP000036	<i>Shigella boydii</i> Sb227	<i>Shigella boydii</i> Sb227, complete genome.	172	7E-9	169	29.6
812	169888957	CP000948	<i>Escherichia coli</i> str K-12 substr DH10B	<i>Escherichia coli</i> str. K12 substr. DH10B, complete genome.	172	7E-9	169	29.6
813	308748869	CP002272	<i>Enterobacter cloacae</i> SCF1	<i>Enterobacter cloacae</i> SCF1, complete genome.	172	7E-9	168	31.5
814	324025703	CP002541	<i>Spirochaeta</i> sp Buddy	<i>Spirochaeta</i> sp. Buddy, complete genome.	172	7E-9	159	31.4
815	1787719	U00096	<i>Escherichia coli</i> str K-12 substr MG1655	<i>Escherichia coli</i> str. K-12 substr. MG1655, complete genome.	172	7E-9	169	29.6
816	339414823	CP002890	<i>Escherichia coli</i> UMN18	<i>Escherichia coli</i> UMN18, complete genome.	172	7E-9	169	29.6
817	56383511	AE005674	<i>Shigella flexneri</i> 2a str 301	<i>Shigella flexneri</i> 2a str. 301, complete genome.	172	7E-9	169	29.6
818	85674969	AP009048	<i>Escherichia coli</i> str K-12 substr W3110	<i>Escherichia coli</i> str. K12 substr. W3110 DNA, complete genome.	172	7E-9	169	29.6
819	257758906	AP010958	<i>Escherichia coli</i> O103:H2 str 12009	<i>Escherichia coli</i> O103:H2 str. 12009 DNA, complete genome.	172	7E-9	169	29.6
820	315136088	AP012030	<i>Escherichia coli</i> DH1	<i>Escherichia coli</i> DH1 (ME8569) DNA, complete genome.	172	7E-9	169	29.6
821	170518025	CP000970	<i>Escherichia coli</i> SMS-3-5	<i>Escherichia coli</i> SMS-3-5, complete genome.	172	7E-9	169	29.0
822	262208872	CP001220	<i>Comamonas testosteroni</i> CNB-2	<i>Comamonas testosteroni</i> CNB-2, complete genome.	177	7.2E-9	159	30.2
823	115255784	AM236080	<i>Rhizobium leguminosarum</i> bv viciae 3841	<i>Rhizobium leguminosarum</i> bv. viciae chromosome complete genome, strain 3841.	183	7.4E-9	165	31.5
824	281178582	AP009378	<i>Escherichia coli</i> SE15	<i>Escherichia coli</i> SE15 DNA, complete genome.	172	8.3E-9	169	29.6
825	307553456	CP001671	<i>Escherichia coli</i> ABU 83972	<i>Escherichia coli</i> ABU 83972, complete genome.	172	8.3E-9	169	29.6
826	218432014	CU928163	<i>Escherichia coli</i> UMN026	<i>Escherichia coli</i> UMN026 chromosome, complete genome.	172	8.3E-9	169	29.6
827	209770888	EU901210	<i>Escherichia coli</i>	<i>Escherichia coli</i> strain 493/89 putative resistance protein (ECs2052) gene, complete cds.	172	8.3E-9	169	29.6

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
828	215264756	FM180568	<i>Escherichia coli</i> O127:H6 str E2348/69	Escherichia coli O127:H6 E2348/69 complete genome, strain E2348/69.	172	8.3E-9	169	29.6
829	12515251	AE005174	<i>Escherichia coli</i> O157:H7 str EDL933	Escherichia coli O157:H7 EDL933, complete genome.	172	8.3E-9	169	29.6
830	254592393	CP001368	<i>Escherichia coli</i> O157:H7 str TW14359	Escherichia coli O157:H7 str. TW14359, complete genome.	172	8.3E-9	169	29.6
831	209770890	EU901211	<i>Escherichia coli</i>	Escherichia coli strain 86-24 putative resistance protein (ECs2052) gene, complete cds.	172	8.3E-9	169	29.6
832	209770896	EU901214	<i>Escherichia coli</i>	Escherichia coli strain TW14359 putative resistance protein (ECs2052) gene, complete cds.	172	8.3E-9	169	29.6
833	209911981	AP009240	<i>Escherichia coli</i> SE11	Escherichia coli SE11 DNA, complete genome.	172	8.3E-9	169	29.6
834	253973407	CP000819	<i>Escherichia coli</i> B str REL606	Escherichia coli B str. REL606, complete genome.	172	8.3E-9	169	29.6
835	222033196	CU651637	<i>Escherichia coli</i> LF82	Escherichia coli LF82 chromosome, complete sequence.	172	8.3E-9	169	29.6
836	242377201	AM946981	<i>Escherichia coli</i> BL21(DE3)	Escherichia coli BL21(DE3), complete genome.	172	8.3E-9	169	29.6
837	284921334	FN554766	<i>Escherichia coli</i> 042	Escherichia coli 042 complete genome.	172	8.3E-9	169	29.6
838	81241135	CP000034	<i>Shigella dysenteriae</i> Sd197	Shigella dysenteriae Sd197, complete genome.	172	8.3E-9	169	29.6
839	307627034	CP002167	<i>Escherichia coli</i> UM146	Escherichia coli UM146, complete genome.	172	8.3E-9	169	29.6
840	257764249	AP010960	<i>Escherichia coli</i> O111:H- str 11128	Escherichia coli O111:H- str. 11128 DNA, complete genome.	172	8.3E-9	169	29.6
841	257753822	AP010953	<i>Escherichia coli</i> O26:H11 str 11368	Escherichia coli O26:H11 str. 11368 DNA, complete genome.	172	8.3E-9	169	29.6
842	13361518	BA000007	<i>Escherichia coli</i> O157:H7 str Sakai	Escherichia coli O157:H7 str. Sakai DNA, complete genome.	172	8.3E-9	169	29.6
843	253324621	CP001665	<i>Escherichia coli</i> 'BL21-Gold(DE3)pLysS AG'	Escherichia coli 'BL21-Gold(DE3)pLysS AG', complete genome.	172	8.3E-9	169	29.6
844	218426940	CU928162	<i>Escherichia coli</i> ED1a	Escherichia coli ED1a chromosome, complete genome.	172	8.3E-9	169	29.6
845	110343220	CP000247	<i>Escherichia coli</i> 536	Escherichia coli 536, complete genome.	172	8.3E-9	169	29.6

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
846	218365147	CU928161	<i>Escherichia coli</i> S88	Escherichia coli S88 chromosome, complete genome.	172	8.3E-9	169	29.6
847	253977618	CP001509	<i>Escherichia coli</i> BL21(DE3)	Escherichia coli BL21(DE3), complete genome.	172	8.3E-9	169	29.6
848	209770894	EU901213	<i>Escherichia coli</i>	Escherichia coli strain TB182A putative resistance protein (ECs2052) gene, complete cds.	172	8.3E-9	169	29.6
849	115512814	CP000468	<i>Escherichia coli</i> APEC O1	Escherichia coli APEC O1, complete genome.	172	8.3E-9	169	29.6
850	209770892	EU901212	<i>Escherichia coli</i>	Escherichia coli strain 87-14 putative resistance protein (ECs2052) gene, complete cds.	172	8.3E-9	169	29.6
851	332343115	CP002729	<i>Escherichia coli</i> UMNK88	Escherichia coli UMNK88, complete genome.	172	8.3E-9	169	29.6
852	312946030	CP001855	<i>Escherichia coli</i> O83:H1 str NRG 857C	Escherichia coli O83:H1 str. NRG 857C, complete genome.	172	8.3E-9	169	29.6
853	95112815	CT573326	<i>Pseudomonas entomophila</i> L48	Pseudomonas entomophila str. L48 chromosome, complete sequence.	174	8.4E-9	171	31.0
854	198037229	AM747720	<i>Burkholderia cenocepacia</i> J2315	Burkholderia cenocepacia J2315 chromosome 1, complete genome.	182	8.7E-9	177	28.8
855	198035449	AM747720	<i>Burkholderia cenocepacia</i> J2315	Burkholderia cenocepacia J2315 chromosome 1, complete genome.	182	8.7E-9	177	28.8
856	288731456	FN597254	<i>Streptococcus gallolyticus</i> UCN34	Streptococcus gallolyticus UCN34 complete genome.	190	9E-9	183	27.3
857	333111244	CP002739	<i>Thermoanaerobacterium xylanolyticum</i> LX-11	Thermoanaerobacterium xylanolyticum LX-11, complete genome.	161	9.3E-9	157	28.0
858	222456305	CP001393	<i>Caldicellulosiruptor bescii</i> DSM 6725	Caldicellulosiruptor bescii DSM 6725, complete genome.	161	9.3E-9	158	26.6
859	312180786	CP002326	<i>Caldicellulosiruptor kristjanssonii</i> 177R1B	Caldicellulosiruptor kristjanssonii 177R1B, complete genome.	161	9.3E-9	158	27.2
860	262083743	CP001802	<i>Gordonia bronchialis</i> DSM 43247	Gordonia bronchialis DSM 43247, complete genome.	172	9.8E-9	170	29.4
861	105892412	CP000378	<i>Burkholderia cenocepacia</i> AU 1054	Burkholderia cenocepacia AU 1054 chromosome 1, complete sequence.	182	1E-8	177	28.2
862	116647257	CP000458	<i>Burkholderia cenocepacia</i> HI2424	Burkholderia cenocepacia HI2424 chromosome 1, complete sequence.	182	1E-8	177	28.2

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Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
863	114315030	CP000394	<i>Granulibacter bethesdensis</i> CGDNIH1	Granulibacter bethesdensis CGDNIH1, complete genome.	183	1E-8	168	31.5
864	336297132	CP002869	<i>Paenibacillus mucilaginosus</i> KNP414	Paenibacillus mucilaginosus KNP414, complete genome.	161	1.1E-8	157	28.7
865	294802306	CP001982	<i>Bacillus megaterium</i> DSM 319	Bacillus megaterium DSM319, complete genome.	163	1.1E-8	159	26.4
866	254948975	CP001619	<i>Dyadobacter fermentans</i> DSM 18053	Dyadobacter fermentans DSM 18053, complete genome.	167	1.1E-8	159	23.3
867	169755150	CP000946	<i>Escherichia coli</i> ATCC 8739	Escherichia coli ATCC 8739, complete genome.	172	1.2E-8	169	29.6
868	315060726	CP002185	<i>Escherichia coli</i> W	Escherichia coli W, complete genome.	172	1.2E-8	169	29.6
869	323378708	CP002516	<i>Escherichia coli</i> KO11FL	Escherichia coli KO11, complete genome.	172	1.2E-8	169	29.6
870	73855674	CP000038	<i>Shigella sonnei</i> Ss046	Shigella sonnei Ss046, complete genome.	172	1.2E-8	169	29.6
871	134138332	CP000614	<i>Burkholderia vietnamiensis</i> G4	Burkholderia vietnamiensis G4 chromosome 1, complete sequence.	182	1.2E-8	163	29.4
872	336308489	CP002859	<i>Runella slithyformis</i> DSM 19594	Runella slithyformis DSM 19594, complete genome.	163	1.3E-8	160	26.9
873	334279805	AP012053	<i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> ATCC 43143	Streptococcus gallolyticus subsp. gallolyticus ATCC 43143 DNA, complete genome.	190	1.5E-8	183	27.3
874	325177576	FR824043	<i>Streptococcus gallolyticus</i> subsp. <i>gallolyticus</i> ATCC BAA-2069	Streptococcus gallolyticus subsp. gallolyticus ATCC BAA-2069 complete chromosome sequence, strain ATCC BAA-2069.	190	1.5E-8	183	27.3
875	302195463	CP002109	<i>Clostridium saccharolyticum</i> WM1	Clostridium saccharolyticum WM1, complete genome.	163	1.6E-8	160	30.0
876	309701715	FN649414	<i>Escherichia coli</i> ETEC H10407	Escherichia coli ETEC H10407, complete genome.	172	1.6E-8	169	29.0
877	302394872	CP001810	<i>Butyrivibrio proteoclasticus</i> B316	Butyrivibrio proteoclasticus B316 chromosome 1, complete sequence.	190	1.8E-8	184	29.9
878	49530771	CR543861	<i>Acinetobacter</i> sp. ADP1	Acinetobacter sp. ADP1 complete genome.	182	2E-8	160	28.1

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Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
879	334281966	AP012054	<i>Streptococcus pasteurianus</i> ATCC 43144	Streptococcus pasteurianus ATCC 43144 DNA, complete genome.	212	2.3E-8	183	27.3
880	184197471	CP001045	<i>Burkholderia phymatum</i> STM815	Burkholderia phymatum STM815 plasmid pBPHY01, complete sequence.	175	2.3E-8	174	30.5
881	334736548	CP002824	<i>Enterobacter aerogenes</i> KCTC 2190	Enterobacter aerogenes KCTC 2190, complete genome.	172	2.7E-8	170	31.2
882	311777500	CP002219	<i>Caldicellulosiruptor hydrothermalis</i> 108	Caldicellulosiruptor hydrothermalis 108, complete genome.	161	3E-8	158	25.3
883	330433185	CP002667	<i>Gallibacterium anatis</i> UMN179	Gallibacterium anatis UMN179, complete genome.	166	3.1E-8	160	28.8
884	333474668	CP002773	<i>Serratia</i> sp AS9	Serratia sp. AS9, complete genome.	172	3.2E-8	174	31.6
885	333962265	CP002775	<i>Serratia</i> sp AS13	Serratia sp. AS13, complete genome.	172	3.2E-8	174	31.6
886	333492168	CP002774	<i>Serratia</i> sp AS12	Serratia sp. AS12, complete genome.	172	3.2E-8	174	31.6
887	6458918	AE000513	<i>Deinococcus radiodurans</i> R1	Deinococcus radiodurans R1 chromosome 1, complete sequence.	174	3.2E-8	167	27.5
888	327393598	AP012032	<i>Pantoea ananatis</i> AJ13355	Pantoea ananatis AJ13355 DNA, complete genome.	176	3.2E-8	172	28.5
889	147830650	AM711867	<i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> NCPPB 382	Clavibacter michiganensis subsp. michiganensis NCPPB 382 complete genome.	177	3.3E-8	152	31.6
890	327375395	CP002585	<i>Pseudomonas brassicacearum</i> subsp. <i>brassicacearum</i> NFM421	Pseudomonas brassicacearum subsp. brassicacearum NFM421, complete genome.	177	3.3E-8	173	30.6
891	63258367	CP000075	<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a	Pseudomonas syringae pv. syringae B728a, complete genome.	185	3.4E-8	181	29.3
892	218756521	CP001197	<i>Desulfovibrio vulgaris</i> str. 'Miyazaki F'	Desulfovibrio vulgaris str. 'Miyazaki F', complete genome.	178	3.9E-8	179	30.7
893	310866426	CP001840	<i>Bifidobacterium bifidum</i> PRL2010	Bifidobacterium bifidum PRL2010, complete genome.	180	3.9E-8	161	29.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
894	309251194	CP002220	<i>Bifidobacterium bifidum</i> S17	Bifidobacterium bifidum S17, complete genome.	184	4E-8	161	29.2
895	302777160	CP002171	<i>Thermoanaerobacterium thermosaccharolyticum</i> DSM 571	Thermoanaerobacterium thermosaccharolyticum DSM 571, complete genome.	161	4.2E-8	157	27.4
896	316952279	CP002434	<i>Pantoea</i> sp. At-9b	Pantoea sp. At-9b plasmid pPAT9B01, complete sequence.	169	4.4E-8	172	30.8
897	27349367	BA000040	<i>Bradyrhizobium japonicum</i> USDA 110	Bradyrhizobium japonicum USDA 110 DNA, complete genome.	171	5.2E-8	170	29.4
898	510453	X79980	<i>Streptomyces griseus</i>	S.griseus genes nat, hrdD and ORF1.	194	6.9E-8	179	26.8
899	163675956	CP000912	<i>Brucella suis</i> ATCC 23445	Brucella suis ATCC 23445 chromosome II, complete sequence.	164	7.1E-8	160	28.1
900	294349230	CP001983	<i>Bacillus megaterium</i> QM B1551	Bacillus megaterium QM B1551, complete genome.	163	8.4E-8	159	26.4
901	325060136	CP002248	<i>Agrobacterium</i> sp. H13-3	Agrobacterium sp. H13-3 circular chromosome, complete sequence.	165	8.4E-8	158	28.5
902	20906433	AE008384	<i>Methanosarcina mazei</i> Go1	Methanosarcina mazei strain Goe1, complete genome.	163	9.9E-8	156	26.9
903	326415084	CP002568	<i>Polymorphum gilvum</i> SL003B-26A1	Polymorphum gilvum SL003B-26A1, complete genome.	172	1E-7	166	28.3
904	109455435	CP000362	<i>Roseobacter denitrificans</i> OCh 114	Roseobacter denitrificans OCh 114, complete genome.	158	1.1E-7	159	27.0
905	17982280	AE008917	<i>Brucella melitensis</i> bv 1 str 16M	Brucella melitensis bv. 1 str. 16M chromosome I, complete sequence.	164	1.2E-7	160	27.5
906	340559709	CP002078	<i>Brucella pinnipedialis</i> B2/94	Brucella pinnipedialis B2/94 chromosome 1, complete sequence.	164	1.6E-7	160	27.5
907	256000224	CP001578	<i>Brucella microti</i> CCM 4915	Brucella microti CCM 4915 chromosome 1, complete sequence.	164	1.6E-7	160	27.5
908	225641480	CP001488	<i>Brucella melitensis</i> ATCC 23457	Brucella melitensis ATCC 23457 chromosome I, complete sequence.	164	1.6E-7	160	27.5
909	62196657	AE017223	<i>Brucella abortus</i> bv 1 str 9-941	Brucella abortus biovar 1 str. 9-941 chromosome I, complete sequence.	164	1.6E-7	160	27.5
910	82616542	AM040264	<i>Brucella melitensis</i> biovar Abortus 2308	Brucella melitensis biovar Abortus 2308 chromosome I, complete sequence, strain 2308.	164	1.6E-7	160	27.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
911	242391628	AP010935	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> GGS_124	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> GGS_124 DNA, complete genome.	206	1.7E-7	186	26.9
912	326409661	CP002459	<i>Brucella melitensis</i> M28	<i>Brucella melitensis</i> M28 chromosome 1, complete sequence.	195	1.9E-7	160	27.5
913	326539368	CP001851	<i>Brucella melitensis</i> M5-90	<i>Brucella melitensis</i> M5-90 chromosome I, complete sequence.	196	1.9E-7	160	27.5
914	189020319	CP000887	<i>Brucella abortus</i> S19	<i>Brucella abortus</i> S19 chromosome 1, complete sequence.	202	1.9E-7	160	27.5
915	148370175	CP000708	<i>Brucella ovis</i> ATCC 25840	<i>Brucella ovis</i> ATCC 25840 chromosome I, complete sequence.	202	1.9E-7	160	27.5
916	119766127	CP000507	<i>Shewanella amazonensis</i> SB2B	<i>Shewanella amazonensis</i> SB2B, complete genome.	165	2E-7	151	30.5
917	295098790	FP929041	<i>Eubacterium cylindroides</i> T2-87	<i>Eubacterium cylindroides</i> T2-87 draft genome.	182	2.1E-7	159	24.5
918	82470800	AY603069	<i>Mitsuokella multacida</i>	<i>Mitsuokella multacida</i> flavoredoxin, acetyl- or acyltransferase, and tetracycline resistance protein (<i>tetW</i>) genes, complete cds; and unknown gene.	148	2.1E-7	137	29.9
919	161336395	CP000872	<i>Brucella canis</i> ATCC 23365	<i>Brucella canis</i> ATCC 23365 chromosome I, complete sequence.	164	2.3E-7	160	27.5
920	23348505	AE014291	<i>Brucella suis</i> 1330	<i>Brucella suis</i> 1330 chromosome I, complete sequence.	164	2.3E-7	160	27.5
921	343383475	CP002997	<i>Brucella suis</i> 1330	<i>Brucella suis</i> 1330 chromosome I, complete sequence.	164	2.3E-7	160	27.5
922	28855260	AE016853	<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000	<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000, complete genome.	180	2.5E-7	178	28.7
923	323127806	CP002215	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> ATCC 12394	<i>Streptococcus dysgalactiae</i> subsp. <i>equisimilis</i> ATCC 12394, complete genome.	194	3.7E-7	186	26.3
924	15155901	AE007869	<i>Agrobacterium tumefaciens</i> str. C58	<i>Agrobacterium tumefaciens</i> str. C58 circular chromosome, complete sequence.	165	3.8E-7	158	27.8
925	296091122	CP001874	<i>Thermobispora bispora</i> DSM 43833	<i>Thermobispora bispora</i> DSM 43833, complete genome.	177	4E-7	159	30.8
926	301639443	CP002085	<i>Desulfarculus baarsii</i> DSM 2075	<i>Desulfarculus baarsii</i> DSM 2075, complete genome.	365	5.2E-7	159	27.0

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
927	148571524	CP000713	<i>Psychrobacter sp PRwf-1</i>	Psychrobacter sp. PRwf-1, complete genome.	202	5.3E-7	164	26.8
928	150958278	CP000648	<i>Klebsiella pneumoniae subsp pneumoniae MGH 78578</i>	Klebsiella pneumoniae subsp. pneumoniae MGH 78578 plasmid pKPN3, complete sequence.	175	5.6E-7	164	31.1
929	93357842	CP000353	<i>Cupriavidus metallidurans CH34</i>	Cupriavidus metallidurans CH34 megaplasmid, complete sequence.	164	6.3E-7	162	26.5
930	71554182	CP000058	<i>Pseudomonas syringae pv phaseolicola 1448A</i>	Pseudomonas syringae pv. phaseolicola 1448A, complete genome.	180	6.8E-7	178	28.7
931	260219397	FN543096	<i>Cronobacter turicensis z3032</i>	Cronobacter turicensis z3032 plasmid pCTU3, complete sequence.	175	7.9E-7	164	31.1
932	119376983	CP000490	<i>Paracoccus denitrificans PD1222</i>	Paracoccus denitrificans PD1222 chromosome 2, complete sequence.	162	8.7E-7	160	27.5
933	145573930	CP000680	<i>Pseudomonas mendocina ymp</i>	Pseudomonas mendocina ymp, complete genome.	166	8.9E-7	158	29.1
934	260217055	FN543093	<i>Cronobacter turicensis z3032</i>	Cronobacter turicensis z3032 complete genome.	156	0.000001	121	33.1
935	291535424	FP929049	<i>Roseburia intestinalis M50/1</i>	Roseburia intestinalis M50/1 draft genome.	170	0.0000013	150	28.7
936	291537931	FP929050	<i>Roseburia intestinalis XB6B4</i>	Roseburia intestinalis XB6B4 draft genome.	170	0.0000013	150	28.7
937	297141190	CP001791	<i>Bacillus selenitireducens MLS10</i>	Bacillus selenitireducens MLS10, complete genome.	174	0.0000013	172	26.7
938	338756724	CP002623	<i>Roseobacter litoralis Och 149</i>	Roseobacter litoralis Och 149, complete genome.	158	0.0000014	159	25.2
939	157911048	CP000830	<i>Dinoroseobacter shibae DFL 12</i>	Dinoroseobacter shibae DFL 12, complete genome.	161	0.0000014	153	27.5
940	328915980	CP002620	<i>Pseudomonas mendocina NK-01</i>	Pseudomonas mendocina NK-01, complete genome.	166	0.0000015	161	28.0
941	151560487	CP000758	<i>Ochrobactrum anthropi ATCC 49188</i>	Ochrobactrum anthropi ATCC 49188 chromosome 1, complete sequence.	164	0.0000017	160	26.2
942	296922564	FN806773	<i>Propionibacterium freudenreichii subsp shermanii CIRM-BIA1</i>	Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1, complete genome.	170	0.0000018	156	29.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
943	169813534	CP000961	<i>Shewanella woodyi</i> ATCC 51908	Shewanella woodyi ATCC 51908, complete genome.	162	0.000002	161	29.2
944	308047292	CP002222	<i>Lactobacillus plantarum</i> subsp. <i>plantarum</i> ST-III	Lactobacillus plantarum subsp. plantarum ST-III, complete genome.	165	0.0000029	166	27.1
945	254046643	CP001617	<i>Lactobacillus plantarum</i> JDM1	Lactobacillus plantarum JDM1, complete genome.	165	0.0000029	166	27.1
946	342242981	AL935263	<i>Lactobacillus plantarum</i> WCFS1	Lactobacillus plantarum WCFS1 complete genome.	165	0.0000029	166	27.1
947	219547281	CP001338	<i>Methanosphaerula palustris</i> E1-9c	Candidatus Methanosphaerula palustris E1-9c, complete genome.	167	0.0000057	155	28.4
948	298361361	CP001895	<i>Pantoea vagans</i> C9-1	Pantoea vagans C9-1 plasmid pPag3, complete sequence.	127	0.0000064	104	37.5
949	326548430	CP002584	<i>Sphingobacterium</i> sp 21	Sphingobacterium sp. 21, complete genome.	163	0.0000078	160	28.8
950	343097828	HE577054	<i>Paenibacillus polymyxa</i> M1	Paenibacillus polymyxa M1 main chromosome, complete genome.	164	0.0000078	162	25.9
951	343463978	CP002018	<i>Ketogulonigenium vulgare</i> WSH-001	Ketogulonigenium vulgare WSH-001, complete genome.	176	0.0000083	171	25.7
952	308753485	CP002224	<i>Ketogulonicigenium vulgare</i> Y25	Ketogulonicigenium vulgare Y25, complete genome.	176	0.0000083	171	25.7
953	297165304	CP002049	<i>Truepera radiovictrix</i> DSM 17093	Truepera radiovictrix DSM 17093, complete genome.	179	0.0000084	164	28.0
954	294475182	CP001312	<i>Rhodobacter capsulatus</i> SB 1003	Rhodobacter capsulatus SB 1003, complete genome.	161	0.000011	159	28.9
955	328555361	CP002627	<i>Bacillus amyloliquefaciens</i> TA208	Bacillus amyloliquefaciens TA208, complete genome.	165	0.000011	161	28.6
956	307608252	FN597644	<i>Bacillus amyloliquefaciens</i> DSM 7	Bacillus amyloliquefaciens DSM7 complete genome.	165	0.000011	161	28.6
957	328913731	CP002634	<i>Bacillus amyloliquefaciens</i> LL3	Bacillus amyloliquefaciens LL3, complete genome.	165	0.000011	161	28.6
958	154353624	CP000560	<i>Bacillus amyloliquefaciens</i> FZB42	Bacillus amyloliquefaciens FZB42, complete genome.	165	0.000011	161	29.2
959	341829649	CP002927	<i>Bacillus amyloliquefaciens</i> XH7	Bacillus amyloliquefaciens XH7, complete genome.	165	0.000011	161	28.6

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
960	339638395	FR874854	<i>Lactobacillus pentosus</i> IG1	Lactobacillus pentosus IG1, annotated genomic scaffold00001.	165	0.000013	166	27.7
961	336102126	CP002857	<i>Corynebacterium resistens</i> DSM 45100	Corynebacterium resistens DSM 45100, complete genome.	189	0.000015	169	27.8
962	339284200	CP002901	<i>Sulfobacillus acidophilus</i> TPY	Sulfobacillus acidophilus TPY, complete genome.	174	0.000016	160	28.8
963	302199811	CP002131	<i>Thermosediminibacter oceani</i> DSM 16646	Thermosediminibacter oceani DSM 16646, complete genome.	164	0.000018	161	27.3
964	52005391	CP000002	<i>Bacillus licheniformis</i> ATCC 14580	Bacillus licheniformis ATCC 14580, complete genome.	165	0.000018	156	26.9
965	52350073	AE017333	<i>Bacillus licheniformis</i> ATCC 14580	Bacillus licheniformis DSM 13, complete genome.	165	0.000018	156	26.9
966	334882980	FR871837	<i>Lactobacillus pentosus</i> MP-10	Lactobacillus pentosus MP-10 draft genome, annotated contig00023.	165	0.000018	166	27.7
967	226714443	CP001154	<i>Laribacter hongkongensis</i> HLHK9	Laribacter hongkongensis HLHK9, complete genome.	179	0.000019	168	26.8
968	77388776	CP000143	<i>Rhodobacter sphaeroides</i> 241	Rhodobacter sphaeroides 2.4.1 chromosome 1, complete sequence.	158	0.000021	158	28.5
969	189340824	CP001097	<i>Chlorobium limicola</i> DSM 245	Chlorobium limicola DSM 245, complete genome.	163	0.000021	160	25.6
970	49179553	AE017225	<i>Bacillus anthracis</i> str Sterne	Bacillus anthracis str. Sterne, complete genome.	87	0.000025	87	32.2
971	254947402	CP001619	<i>Dyadobacter fermentans</i> DSM 18053	Dyadobacter fermentans DSM 18053, complete genome.	165	0.000025	157	28.0
972	254042086	CP001678	<i>Hirschia baltica</i> ATCC 49814	Hirschia baltica ATCC 49814, complete genome.	165	0.000025	161	26.7
973	269096968	CP001819	<i>Sanguibacter keddiei</i> DSM 10542	Sanguibacter keddiei DSM 10542, complete genome.	166	0.000026	171	28.7
974	146156569	CP000685	<i>Flavobacterium johnsoniae</i> UW101	Flavobacterium johnsoniae UW101, complete genome.	168	0.000026	163	27.0
975	254948456	CP001619	<i>Dyadobacter fermentans</i> DSM 18053	Dyadobacter fermentans DSM 18053, complete genome.	164	0.00003	160	28.1
976	88188189	CP000254	<i>Methanospirillum hungatei</i> JF-1	Methanospirillum hungatei JF-1, complete genome.	166	0.00003	155	25.2

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
977	140845069	AP009044	<i>Corynebacterium glutamicum R</i>	Corynebacterium glutamicum R DNA, complete genome.	176	0.000032	174	25.9
978	311894634	AP010968	<i>Kitasatospora setae KM-6054</i>	Kitasatospora setae KM-6054 DNA, complete genome.	167	0.000036	165	30.3
979	163669824	CP000909	<i>Chloroflexus aurantiacus J-10-fl</i>	Chloroflexus aurantiacus J-10-fl, complete genome.	168	0.000036	162	25.9
980	222450348	CP001364	<i>Chloroflexus sp Y-400-fl</i>	Chloroflexus sp. Y-400-fl, complete genome.	168	0.000036	162	25.9
981	146155243	CP000685	<i>Flavobacterium johnsoniae UW101</i>	Flavobacterium johnsoniae UW101, complete genome.	168	0.000043	163	27.0
982	219544619	CP001337	<i>Chloroflexus aggregans DSM 9485</i>	Chloroflexus aggregans DSM 9485, complete genome.	170	0.000043	162	25.3
983	311906210	CP002305	<i>Leadbetterella byssophila DSM 17132</i>	Leadbetterella byssophila DSM 17132, complete genome.	163	0.000049	146	26.0
984	83637586	CP000155	<i>Hahella chejuensis KCTC 2396</i>	Hahella chejuensis KCTC 2396, complete genome.	171	0.000051	140	29.3
985	296930838	CP002026	<i>Starkeya novella DSM 506</i>	Starkeya novella DSM 506, complete genome.	162	0.000058	163	27.0
986	126104864	CP000577	<i>Rhodobacter sphaeroides ATCC 17029</i>	Rhodobacter sphaeroides ATCC 17029 chromosome 1, complete sequence.	158	0.000067	158	27.8
987	221161026	CP001150	<i>Rhodobacter sphaeroides KD131</i>	Rhodobacter sphaeroides KD131 chromosome 1, complete sequence.	158	0.000067	158	27.8
988	196478326	CP000747	<i>Phenylobacterium zucineum HLK1</i>	Phenylobacterium zucineum HLK1, complete genome.	169	0.000071	178	27.0
989	311905796	CP002305	<i>Leadbetterella byssophila DSM 17132</i>	Leadbetterella byssophila DSM 17132, complete genome.	166	0.000083	152	25.0
990	290569895	CP001778	<i>Stackebrandtia nassauensis DSM 44728</i>	Stackebrandtia nassauensis DSM 44728, complete genome.	163	0.000097	160	28.1
991	315590407	CP002343	<i>Intrasporangium calvum DSM 43043</i>	Intrasporangium calvum DSM 43043, complete genome.	162	0.00011	160	31.9
992	52209488	BX571965	<i>Burkholderia pseudomallei K96243</i>	Burkholderia pseudomallei strain K96243, chromosome 1, complete sequence.	168	0.00012	141	30.5
993	126225306	CP000572	<i>Burkholderia pseudomallei 1106a</i>	Burkholderia pseudomallei 1106a chromosome I, complete sequence.	168	0.00012	141	30.5

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
994	126218493	CP000570	<i>Burkholderia pseudomallei</i> 668	Burkholderia pseudomallei 668 chromosome I, complete sequence.	168	0.00012	141	30.5
995	134268020	CP000557	<i>Geobacillus thermodenitrificans</i> NG80-2	Geobacillus thermodenitrificans NG80-2, complete genome.	173	0.00012	140	27.1
996	76577976	CP000124	<i>Burkholderia pseudomallei</i> 1710b	Burkholderia pseudomallei 1710b chromosome I, complete sequence.	179	0.00012	141	30.5
997	119947506	CP000474	<i>Arthrobacter aurescens</i> TC1	Arthrobacter aurescens TC1, complete genome.	169	0.00014	165	29.1
998	257779088	CP001720	<i>Desulfotomaculum acetoxidans</i> DSM 771	Desulfotomaculum acetoxidans DSM 771, complete genome.	163	0.00019	151	24.5
999	183224758	AP007281	<i>Lactobacillus reuteri</i> JCM 1112	Lactobacillus reuteri JCM 1112 DNA, complete genome.	164	0.00019	160	24.4
1000	257152480	FM179323	<i>Lactobacillus rhamnosus</i> Lc 705	Lactobacillus rhamnosus Lc 705 whole genome sequence, strain Lc 705.	164	0.00019	162	25.3

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

6.6. Table 6 - Bayer Toxin database

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
1	FP885891_338	FP885891_338	<i>Ralstonia solanacearum</i> PSI07	<i>Ralstonia solanacearum</i> str. PSI07 megaplasmid, complete genome.	183	4.9E-22	164	39.6
2	CP001805_1611	CP001805_1611	<i>Vibrio</i> sp Ex25	<i>Vibrio</i> sp. Ex25 chromosome 1, complete sequence.	169	5.5E-17	166	34.3
3	CP000626_930	CP000626_930	<i>Vibrio cholerae</i> O395	<i>Vibrio cholerae</i> O395 chromosome 1, complete genome.	169	1.1E-16	152	36.2
4	CP001486_892	CP001486_892	<i>Vibrio cholerae</i> MJ-1236	<i>Vibrio cholerae</i> MJ-1236 chromosome 2, complete sequence.	169	2.1E-16	152	36.2
5	AE003853_379	AE003853_379	<i>Vibrio cholerae</i> O1 biovar El Tor str N16961	<i>Vibrio cholerae</i> O1 biovar eltor str. N16961 chromosome II, complete sequence.	169	7.9E-16	152	35.5
6	FP885897_294	FP885897_294	<i>Ralstonia solanacearum</i> CFBP2957	<i>Ralstonia solanacearum</i> str. CFBP2957 chromosome, complete genome.	182	4.5E-15	164	34.1
7	CU928158_1385	CU928158_1385	<i>Escherichia fergusonii</i> ATCC 35469	<i>Escherichia fergusonii</i> ATCC 35469 chromosome, complete genome.	249	5.2E-15	174	33.3
8	CU928145_1549	CU928145_1549	<i>Escherichia coli</i> 55989	<i>Escherichia coli</i> 55989 chromosome, complete genome.	250	5.2E-15	174	33.3
9	FP885895_265	FP885895_265	<i>Ralstonia solanacearum</i> CMR15	<i>Ralstonia solanacearum</i> str. CMR15 chromosome, complete genome.	182	6.3E-15	179	33.5
10	FP885906_344	FP885906_344	<i>Ralstonia solanacearum</i> PSI07	<i>Ralstonia solanacearum</i> str. PSI07 chromosome, complete genome.	182	2E-14	179	33.0
11	GQ352402_11	GQ352402_11	<i>Acinetobacter baumannii</i>	<i>Acinetobacter baumannii</i> strain AbSK-17 plasmid pAbSK-OXA-82 replicase, zeta toxin family protein, hypothetical proteins, thermonuclease protein, and hypothetical protein genes, complete cds; insertion sequence ISAbA1, complete sequence; and beta-lactamase OXA-51-like protein (blaOXA-82), sortase, and transcriptional regulator genes, complete cds.	181	2.5E-13	164	29.3
12	CP000764_3271	CP000764_3271	<i>Bacillus cytotoxicus</i> NVH 391-98	<i>Bacillus cereus</i> subsp. cytotoxis NVH 391-98, complete genome.	174	0.019	83	24.1

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
13	CP000764_1936	CP000764_1936	<i>Bacillus cytotoxicus</i> NVH 391-98	Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome.	156	0.054	83	25.3
14	CP000764_1506	CP000764_1506	<i>Bacillus cytotoxicus</i> NVH 391-98	Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome.	188	0.29	130	26.2
15	GUAA_BACCN	A7GKG1	<i>Bacillus cereus subsp. cytotoxis</i> (strain NVH 391-98)	RecName: Full=GMP synthase [glutamine-hydrolyzing]; EC=6.3.5.2; AltName: Full=GMP synthetase; AltName: Full=Glutamine amidotransferase;	512	0.39	81	32.1
16	GUAA_STRP3	Q8K7E6	<i>Streptococcus pyogenes</i> serotype M3	RecName: Full=GMP synthase [glutamine-hydrolyzing]; EC=6.3.5.2; AltName: Full=GMP synthetase; AltName: Full=Glutamine amidotransferase;	520	0.4	76	34.2
17	GUAA_BACWK	A9VQG9	<i>Bacillus weihenstephanensis</i> (strain KBAB4)	RecName: Full=GMP synthase [glutamine-hydrolyzing]; EC=6.3.5.2; AltName: Full=GMP synthetase; AltName: Full=Glutamine amidotransferase;	512	0.47	81	32.1
18	CP000764_478	CP000764_478	<i>Bacillus cytotoxicus</i> NVH 391-98	Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome.	170	0.72	110	23.6
19	CP000764_1617	CP000764_1617	<i>Bacillus cytotoxicus</i> NVH 391-98	Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome.	284	1	168	22.6
20	CP000764_1903	CP000764_1903	<i>Bacillus cytotoxicus</i> NVH 391-98	Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome.	166	1.2	70	21.4
21	CP000076_623	CP000076_623	<i>Pseudomonas fluorescens</i> Pf-5	Pseudomonas fluorescens Pf-5, complete genome.	177	1.7	90	27.8
22	CP000764_2507	CP000764_2507	<i>Bacillus cytotoxicus</i> NVH 391-98	Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome.	1148	3.3	164	28.7
23	FN392235_2551	FN392235_2551	<i>Erwinia pyrifoliae</i> DSM 12163	Erwinia pyrifoliae DSM 12163 complete genome, culture collection DSM:12163.	172	3.3	150	22.0
24	CP000764_1020	CP000764_1020	<i>Bacillus cytotoxicus</i> NVH 391-98	Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome.	192	3.7	68	26.5
25	AY092402_18	AY092402_18	<i>Aspergillus ochraceoroseus</i>	Aspergillus ochraceoroseus strain SRRC 1432 aflatoxin/sterigmatocystin gene cluster, complete sequence.	1583	4.5	52	42.3
26	AM270106_54	AM270106_54	<i>Aspergillus niger</i>	Aspergillus niger contig An05c0060, complete genome.	719	4.8	124	23.4
27	GUAA_CLOBK	B11FD1	<i>Clostridium botulinum</i> (strain Okra / Type B1)	RecName: Full=GMP synthase [glutamine-hydrolyzing]; EC=6.3.5.2; AltName: Full=GMP synthetase; AltName: Full=Glutamine amidotransferase;	510	4.8	81	28.4

PAT/*pat* Protein
Amino acid sequence homology search with known toxins

Hit number	Name	Locus	Species	Description	Matching sequence length	E-value	Length of alignment	% Identity
28	GUAA_CLOBM	B1L1J7	<i>Clostridium botulinum</i> (strain Loch Maree / Type A3)	RecName: Full=GMP synthase [glutamine-hydrolyzing]; EC=6.3.5.2; AltName: Full=GMP synthetase; AltName: Full=Glutamine amidotransferase;	510	4.8	81	28.4
29	GUAA_CLOB1	A7FYP0	<i>Clostridium botulinum</i> (strain ATCC 19397 / Type A)	RecName: Full=GMP synthase [glutamine-hydrolyzing]; EC=6.3.5.2; AltName: Full=GMP synthetase; AltName: Full=Glutamine amidotransferase;	510	4.8	81	28.4
30	Y18930_261	Y18930_261	<i>Sulfolobus solfataricus</i> P2	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.	267	7	100	24.0

FINAL REPORT AMENDMENT

There is no final report amendment at this time.