

SUMMARY

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STUDY TITLE

Sequence Similarity Assessment of PAT Protein to Known Toxins by Bioinformatics Analysis
(Update, February, 2011)

DATA REQUIREMENTS

N/A

AUTHOR(S)

P. Song

STUDY COMPLETED ON

20 – April – 2011

PERFORMING LABORATORY

Regulatory Sciences and Government Affairs—Indianapolis Lab
Dow AgroSciences LLC
9330 Zionsville Road
Indianapolis, Indiana 46268-1054

LABORATORY STUDY ID

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Sequence Similarity Assessment of PAT Protein to Known Toxins by Bioinformatics Analysis
(Update, February, 2011)

SUMMARY

Phosphinothricin *N*-acetyltransferase (PAT) protein, encoded by the *pat* gene originally derived from soil bacterium *Streptomyces viridochromogenes*, acetylates phosphinothricin and thus confers tolerance to chemically synthesized phosphinothricin such as glufosinate-ammonium based herbicides. For that reason, the gene has been widely used in the production of events carrying an herbicide tolerance trait or as a selectable marker during plant transformation. The *pat* gene has been integrated into many transgenic events produced by Dow AgroSciences, including corn (*Zea mays* L.) events TC1507, DAS-59122-7, and DAS-40278-9, cotton (*Gossypium hirsutum* L.) events 281-24-236 and 3006-210-23, and soybean (*Glycine max* L.) events DAS-68416-4 and DAS-44406-6. In this study, the amino acid sequence of the PAT protein was evaluated for sequence similarity to known protein toxins using a BLASTp search against an up-to-date GenBank non-redundant protein database (update to February 18, 2011). All the sequence alignments returned by the search were associated with phosphinothricin *N*-acetyltransferase and *N*-acetyltransferase or similar proteins. The results indicated that the PAT protein expressed in maize, cotton, and soybean transgenic events contains no significant sequence similarity with any known toxic protein that is harmful to humans or animals.

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N/A

AUTHOR(S)

P. Song 317-337-3434
[psong@dow.com]

STUDY COMPLETED ON

20 – April – 2011

PERFORMING LABORATORY

Regulatory Sciences and Government Affairs—Indianapolis Lab
Dow AgroSciences LLC
9330 Zionsville Road
Indianapolis, Indiana 46268-1054

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Compound: PAT (phosphinothricin acetyl transferase) Protein

Title: Sequence Similarity Assessment of PAT Protein to Known Toxins by
Bioinformatics Analysis
(Update, February, 2011)

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Company: Dow AgroSciences LLC

Company Agent: M. Kieger

Title: Regulatory Manager

Signature: 

Date: 19 April 2011

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(Update, February, 2011)

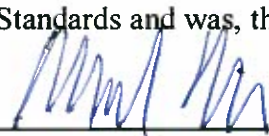
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United States Environmental Protection Agency
Title 40 Code of Federal Regulations Part 160
FEDERAL REGISTER, August 17, 1989

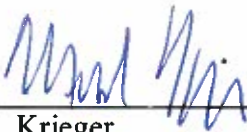
Organisation for Economic Co-Operation and Development
ENV/MC/CHEM(98)17, Paris January 26, 1998

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M. Krieger
Sponsor
Dow AgroSciences LLC

19 April 2011
Date



M. Krieger
Submitter
Dow AgroSciences LLC

19 April 2011
Date



P. Song
Study Director/Author
Dow AgroSciences LLC

20-April-2011
Study Completion Date

QUALITY ASSURANCE STATEMENT

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NON-GLP STUDY

SIGNATURE PAGE



P. Song
Author
Dow AgroSciences LLC

20 April - 2011

Date



M. Zhuang
Peer Reviewer
Dow AgroSciences LLC

8 - Apr - 2011

Date



R. Herman
Peer Reviewer
Dow AgroSciences LLC

8 - Apr - 2011

Date



S. Guttikonda
Peer Reviewer
Dow AgroSciences LLC

8 - Apr - 2011

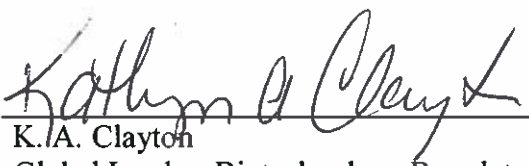
Date



G. Shan
Science Leader
Dow AgroSciences LLC

19 Apr 2011

Date



K.A. Clayton
Global Leader, Biotechnology Regulatory
Sciences
Dow AgroSciences LLC

19 APR 2011

Date

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Sequence Similarity Assessment of PAT Protein to Known Toxins by Bioinformatics Analysis
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ABSTRACT

Phosphinothricin *N*-acetyltransferase (PAT) protein, encoded by the *pat* gene originally derived from soil bacterium *Streptomyces viridochromogenes*, acetylates phosphinothricin and thus confers tolerance to chemically synthesized phosphinothricin such as glufosinate-ammonium based herbicides. For that reason, the gene has been widely used in the production of events carrying an herbicide tolerance trait or as a selectable marker during plant transformation. The *pat* gene has been integrated into many transgenic events produced by Dow AgroSciences, including corn (*Zea mays* L.) events TC1507, DAS-59122-7, and DAS-40278-9, cotton (*Gossypium hirsutum* L.) events 281-24-236 and 3006-210-23, and soybean (*Glycine max* L.) events DAS-68416-4 and DAS-44406-6. In this study, the amino acid sequence of the PAT protein was evaluated for sequence similarity to known protein toxins using a BLASTp search against an up-to-date GenBank non-redundant protein database (update to February 18, 2011). All the sequence alignments returned by the search were associated with phosphinothricin *N*-acetyltransferase and *N*-acetyltransferase or similar proteins. The results indicated that the PAT protein expressed in maize, cotton, and soybean transgenic events contains no significant sequence similarity with any known toxic protein that is harmful to humans or animals.

INTRODUCTION

Phosphinothricin *N*-acetyltransferase (PAT) enzyme, encoded by the *pat* gene originally derived from soil bacterium *Streptomyces viridochromogenes*, acetylates phosphinothricin and thus confers tolerance to chemically synthesized phosphinothricin such as glufosinate-ammonium based herbicides. For that reason, the gene has been widely used in the production of events carrying an herbicide tolerance trait or as a selectable marker during plants transformation. The *pat* gene has been integrated into many transgenic events produced by Dow AgroSciences, including corn (*Zea mays* L.) events TC1507, DAS-59122-7, and DAS-40278-9, cotton (*Gossypium hirsutum* L.) events 281-24-236 and 3006-210-23, and soybean (*Glycine max* L.) events DAS-68416-4 and DAS-44406-6.

The safety assessment of proteins expressed in transgenic plants may include an evaluation of whether or not the protein can function as a potential toxin when present in the human diet. It has been reported that assessing the potential toxicity of a protein may include comparison of the protein sequence to known protein toxin sequences (¹). Since there is no commonly recognized definition of a protein toxin based on its sequence, a comparison should be made to a database of all available protein sequences as a conservative approach. Proteins identified with statistically significant similarity using a local alignment algorithm should then be evaluated for their relevance as potential toxins. For small-scale analyses, such as a single search of a query protein against a large database, a statistically significant similarity that ensures avoidance of false positives (labeling a sequence as related to something in the database when it is not) typically employs an expectation value (E-value) threshold between 0.001 and 0.01. The E-value corresponds to the frequency one would expect to see a match of equal or greater quality by chance (false positive) in a search of the database. For E-values of 0.001 or 0.01, one would expect to find a false positive result once in 1000 or 100 searches, respectively (²). For E()= 1, there is a statistically equal chance of a hit occurring due to homology or by random chance in a search of a given database. Although little can be done to avoid false negatives (labeling a

sequence as unrelated to something in the database when in fact a homolog is present), visual inspection of the quality of less conservative alignments with $E() < 1$ may minimize false negative results (²).

The objective of this study was to compare the amino acid sequences of the PAT protein expressed in transgenic events with known protein toxins in the public protein sequence database.

METHODS

Query Sequence Preparation

The PAT protein sequence was prepared in FASTA format accepted by BLASTp search program (Appendix 1).

Toxicity Assessment

To assess potential toxicity of the PAT protein expressed in maize, cotton, and soybean transgenic events, a search for similarity of protein sequences was conducted using the BLASTp program (³). The amino acid sequence of the PAT was queried using the BLASTp (Version 2.2.22+) against a non-redundant protein dataset (update to February 18, 2011), which incorporates non-redundant entries from all GenBank and RefSeq nucleotide translations (Genpept "nr") along with protein sequences from SWISS-PROT (<http://www.expasy.org/sprot/>), PIR (<http://pir.georgetown.edu/>), PRF (<http://www.prf.or.jp/aboutdb-e.html>), and PDB (<http://www.wwpdb.org/>). The search was done through the BLAST program installed in an internal UNIX computer with default settings (Matrix = BLOSUM62, Gap Costs = Existence: 11, Extension: 1) except that a cutoff expectation E-value of 1.0 was used to generate biologically meaningful similarity between the

query sequences and proteins in the database, the low complexity filtering was turned off, and the sequence description and alignment display were set to 2000 alignments. Although a statistically significant sequence similarity generally requires a match with an expectation value less than 0.01, a cutoff of $E() < 1.0$ ensures that proteins with even limited similarity will not be overlooked in the search (2).

RESULTS AND DISCUSSION

The search of the PAT protein sequence against GenBank non-redundant protein dataset returned a total of 1063 hits, including 941 with $E() < 0.01$ (Table 1, Appendix 2). Among the 941 hits, 712 are related to the same class of phosphinothricin *N*-acetyltransferase enzyme, GCN5 related *N*-acetyltransferase and GNAT family *N*-acetyltransferase from various bacteria. Five alignments are with ArsR family transcriptional regulator from *Rhodococcus* species. Those transcriptional regulators contain regions highly similar to GCN5 related *N*-acetyltransferase. In addition, there are 102 alignments associated with sortase-like acyltransferase from various bacteria and another 110 alignments with hypothetical proteins that are generated by genomic sequencing of various bacteria and similar to either phosphinothricin *N*-acetyltransferase or GCN5 related *N*-acetyltransferase or GNAT family *N*-acetyltransferase. The other 12 alignments are associated with the protein family of acyltransferase. None of the significant sequence alignments are related to any known protein toxins (Appendix 2). The results is consistency with a previous study using BLASTp search with PAT protein sequence against the NCBI protein nr database generated very similar results with the majority of the statistically significant hits associated with proteins like phosphinothricin acetyltransferase, other acetyltransferases, and hypothetical proteins without assigned function. Furthermore, most of the non-significant alignments are related with phosphinothricin *N*-acetyltransferase or GCN5 related *N*-acetyltransferase, and none of them were associated with known protein toxins.

CONCLUSION

Bioinformatics analysis of the PAT protein expressed in transgenic events using BLASTp search against an up-to-date GenBank non redundant protein database did not generate any significant sequence similarity with any known proteins that are harmful to humans or animals.

Table 1. Summary of Alignments (E() <0.01) Returned by BLASTp Search of PAT Protein Sequence

Description	Number of Returned Alignments	E-Value
<i>N</i> -acetyltransferase family proteins including phosphinothricin <i>N</i> -acetyltransferase, GCN5-related <i>N</i> -acetyltransferase, GNAT family <i>N</i> -acetyltransferase	712	$0.009 - 4.00 \times 10^{-105}$
Hypothetical protein	110	$0.005 - 4.00 \times 10^{-26}$
(Putative) sortase and related acyltransferase	102	$0.005 - 4.00 \times 10^{-32}$
ArsR family transcriptional regulators	5	$2.00 \times 10^{-5} - 5.00 \times 10^{-9}$
Other acyltransferase superfamily protein	12	$0.004 - 2.00 \times 10^{-88}$

REFERENCES

1. Codex Alimentarius, C. GUIDELINE FOR THE CONDUCT OF FOOD SAFETY ASSESSMENT OF FOODS DERIVED FROM RECOMBINANT-DNA PLANTS; 2009; pp 20-22.
2. Pearson, W. R., Flexible sequence similarity searching with the FASTA3 program package. *Methods Mol Biol* **2000**, *132*, 185-219.
3. Altschul, S. F., W. Gish, W. Miller, E. W. Myers, and D. J. Lipman, Basic local alignment search tool. *J. Mol. Biol.*, 1990. **215**: p. 403-10

APPENDIX

1. Amino Acid Sequence of PAT

```
1  MSPERRPVEI  RPATAADMAA  VCDIVNHYIE  TSTVNFRTPE  QTPQEWIDDL
51  ERLQDRYPWL  VAEVEGVVAG  IAYAGPWKAR  NAYDWTVEST  VYVSHRHQRL
101 GLGSTLYTHL  LKSMEAQGFK  SVVAVIGLPN  DPSVRLHEAL  GYTARGTLRA
151 AGYKHGGWHD  VGFWQRDFEL  PAPPRPVRPV  TQI
```

2. BLASTp Search Output of PAT Protein Sequence

BLASTp search of PAT protein generated an output file with more than 300 pages. The file is electronically stored in a secured computer in Dow AgroSciences and available for viewing in PDF format.

Appendix of Report 110331

Blastp search outputs of PAT protein

BLASTP 2.2.21 [Jun-14-2009]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference for compositional score matrix adjustment: Altschul, Stephen F., John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Query= PAT
(183 letters)

Database: /usr/local/blast/db/blastlibs/nr
13,473,798 sequences; 4,621,495,809 total letters

Searching.....done

Sequences producing significant alignments:	Score (bits)	E Value
ref ZP_07302142.1 phosphinothricin-N-acetyltransferase [Strepto...	378	e-103
gb AAF15587.1 AF187951_1 promotes resistance to glutamine synthe...	301	4e-80
sp P16426.1 PAT_STRHY RecName: Full=Phosphinothricin N-acetyltra...	300	4e-80
gb ABU39932.1 bialaphos/phosphinothricin resistance protein [Cl...	299	8e-80
gb ADN51987.1 phosphinothricin acetyltransferase [Binary vector...	299	9e-80
gb ABB52512.1 editing-dependent chimeric phosphinothricin acety...	299	1e-79
gb ABB52513.1 phosphinothricin acetyltransferase [synthetic con...	299	1e-79
gb ADF81054.1 phosphinothricin acetyltransferase [Tobacco plast...	299	1e-79
gb AAR86773.1 phosphinothricin acetyl transferase [synthetic co...	299	1e-79
gb AAO85360.1 phosphinothricin acetyl transferase [Binary vecto...	298	2e-79
gb AAK21981.1 phosphinothricin acetyltransferase [synthetic con...	298	2e-79
prf 1311256A gene bar,herbicide resistance	296	7e-79
gb ABK32772.1 BastaR [Silencing vector pFE12860S] >gi 117209779...	287	4e-76
gb ABA55625.1 phosphinothricin acetyltransferase [synthetic con...	228	3e-58
ref YP_001156945.1 GCN5-related N-acetyltransferase [Salinispor...	190	9e-47
ref YP_234588.1 GCN5-related N-acetyltransferase [Pseudomonas s...	149	2e-34
ref YP_003776508.1 phosphinothricin N-acetyltransferase [Herbas...	144	4e-33
ref YP_327183.1 N-acetyltransferase [Natronomonas pharaonis DSM...	143	1e-32
ref ZP_08023172.1 phosphinothricin acetyltransferase, putative ...	142	3e-32
ref NP_925472.1 phosphinothricin N-acetyltransferase [Gloeobact...	137	5e-31
ref YP_003130042.1 GCN5-related N-acetyltransferase [Halorhabdu...	136	1e-30
ref ZP_06174053.1 hypothetical protein VME_04370 [Vibrio harvey...	135	2e-30
ref YP_001546382.1 GCN5-related N-acetyltransferase [Herpetosip...	133	1e-29
ref ZP_07277001.1 phosphinothricin N-acetyltransferase [Strepto...	131	4e-29
ref ZP_01235017.1 Phosphinothricin N-acetyltransferase, putativ...	130	7e-29
ref YP_675890.1 GCN5-related N-acetyltransferase [Mesorhizobium...	129	2e-28
ref YP_003479949.1 Phosphinothricin acetyltransferase [Natrialb...	128	4e-28
ref ZP_07864612.1 acetyltransferase, GNAT family [Streptococcus...	128	4e-28
ref ZP_00994644.1 GCN5-related N-acetyltransferase [Janibacter ...	128	4e-28
ref YP_003536939.1 Phosphinothricin N-acetyltransferase [Halofe...	127	4e-28
ref ZP_08119923.1 phosphinothricin acetyltransferase [Pseudonoc...	127	4e-28

ref	ZP_01869333.1	Phosphinothricin N-acetyltransferase, putativ...	127	5e-28
ref	YP_001198067.1	sortase and related acyltransferase [Strepto...	127	5e-28
ref	ZP_08069452.1	phosphinothricin acetyltransferase [Streptoco...	127	5e-28
ref	YP_001261029.1	GCN5-like N-acetyltransferase [Sphingomonas ...	127	5e-28
ref	YP_820655.1	phosphinothricin acetyltransferase, putative [S...	127	6e-28
ref	YP_141658.1	phosphinothricin acetyltransferase [Streptococc...	126	2e-27
ref	ZP_07832184.1	putative phosphinothricin N-acetyltransferase...	125	3e-27
ref	YP_003401819.1	GCN5-related N-acetyltransferase [Haloterrig...	124	4e-27
gb	ADQ63288.1	Sortase acyltransferase-like protein [Streptococc...	124	4e-27
ref	ZP_08021317.1	phosphinothricin acetyltransferase [Streptoco...	124	5e-27
ref	ZP_04062352.1	phosphinothricin N-acetyltransferase [Strepto...	124	5e-27
ref	ZP_08098012.1	phosphinothricin N-acetyltransferase, putativ...	124	5e-27
ref	YP_003409278.1	phosphinothricin acetyltransferase [Geoderma...	124	5e-27
gb	ADZ90538.1	Phosphinothricin acetyltransferase [Marinomonas m...	124	6e-27
ref	YP_139746.1	phosphinothricin acetyltransferase, putative [S...	124	6e-27
ref	ZP_03399908.1	phosphinothricin N-acetyltransferase [Pseudom...	123	1e-26
ref	ZP_06060563.1	acyltransferase [Streptococcus sp. 2_1_36FAA]...	123	1e-26
ref	ZP_05877484.1	phosphinothricin N-acetyltransferase putative...	123	1e-26
ref	ZP_07837484.1	Phosphinothricin acetyltransferase [Eubacteri...	123	1e-26
ref	ZP_07726783.1	putative phosphinothricin N-acetyltransferase...	122	2e-26
ref	YP_003074738.1	phosphinothricin N-acetyltransferase [Teredi...	122	2e-26
ref	ZP_03624439.1	GCN5-related N-acetyltransferase [Streptococc...	122	2e-26
ref	YP_001354135.1	phosphinothricin N-acetyltransferase [Janthi...	122	2e-26
ref	ZP_05645407.1	conserved hypothetical protein [Enterococcus ...	122	2e-26
ref	ZP_05655037.1	conserved hypothetical protein [Enterococcus ...	122	3e-26
ref	YP_927219.1	phosphinothricin N-acetyltransferase [Shewanell...	121	4e-26
ref	YP_001758117.1	GCN5-related N-acetyltransferase [Methylobac...	121	4e-26
ref	YP_001893235.1	GCN5-related N-acetyltransferase [Ralstonia ...	120	6e-26
ref	YP_001601101.1	putative phosphinothricin N-acetyltransferas...	120	7e-26
gb	ADI12131.1	Phosphinothricin acetyltransferase [Streptomyces ...	120	7e-26
gb	EGC23067.1	phosphinothricin acetyltransferase [Streptococcus...	120	1e-25
ref	ZP_04747260.1	GCN5-related N-acetyltransferase [Mycobacteri...	120	1e-25
ref	YP_002275595.1	GCN5-like N-acetyltransferase [Gluconacetoba...	120	1e-25
ref	ZP_08145758.1	phosphinothricin acetyltransferase [Enterococ...	119	1e-25
gb	EGD36393.1	phosphinothricin acetyltransferase [Streptococcus...	119	1e-25
gb	EGC26393.1	phosphinothricin acetyltransferase [Streptococcus...	119	1e-25
gb	EGC24800.1	phosphinothricin acetyltransferase [Streptococcus...	119	1e-25
ref	YP_001450496.1	acyltransferase [Streptococcus gordonii str....	119	2e-25
gb	EGD29501.1	phosphinothricin acetyltransferase [Streptococcus...	119	2e-25
ref	YP_004016335.1	phosphinothricin acetyltransferase [Frankia ...	119	2e-25
ref	ZP_08087207.1	phosphinothricin acetyltransferase [Streptoco...	119	2e-25
gb	EGD38415.1	phosphinothricin acetyltransferase [Streptococcus...	119	2e-25
ref	YP_004140179.1	phosphinothricin acetyltransferase [Mesorhiz...	119	2e-25
ref	YP_001035153.1	phosphinothricin acetyltransferase, putative...	119	2e-25
ref	ZP_06895655.1	phosphinothricin acetyltransferase [Roseomona...	119	3e-25
ref	YP_463756.1	GCN5-related N-acetyltransferase [Anaeromyxobac...	118	3e-25
ref	ZP_08047697.1	phosphinothricin N-acetyltransferase [Strepto...	118	3e-25
ref	ZP_05648693.1	phosphinothricin N-acetyltransferase [Enteroc...	118	3e-25
ref	ZP_01131943.1	phosphinothricin N-acetyltransferase [Pseudoa...	118	4e-25
gb	EGD31687.1	phosphinothricin acetyltransferase [Streptococcus...	118	4e-25
ref	YP_155176.1	phosphinothricin N-acetyltransferase, putative ...	117	5e-25
ref	ZP_06900531.1	phosphinothricin acetyltransferase [Streptoco...	117	6e-25
ref	ZP_05813493.1	GCN5-related N-acetyltransferase [Mesorhizobi...	117	6e-25
ref	YP_550242.1	GCN5-related N-acetyltransferase [Polaromonas s...	117	8e-25
ref	ZP_01898379.1	Phosphinothricin N-acetyltransferase, putativ...	117	8e-25
ref	YP_003914549.1	phosphinothricin acetyltransferase [Ferrimon...	116	1e-24
ref	ZP_05981641.1	phosphinothricin N-acetyltransferase [Subdoli...	116	1e-24
ref	YP_004104996.1	phosphinothricin acetyltransferase [Ruminoco...	116	1e-24
emb	CAM78141.1	phosphinothricin acetyltransferase [Magnetospi...	116	1e-24
ref	ZP_07453833.1	phosphinothricin acetyltransferase [Eubacteri...	116	1e-24
ref	YP_002132943.1	GCN5-related N-acetyltransferase [Anaeromyxo...	116	1e-24
ref	ZP_07296464.1	GNAT family toxin-antitoxin system, toxin com...	116	1e-24
ref	YP_269286.1	phosphinothricin N-acetyltransferase [Colwellia...	115	2e-24

ref	YP_003679970.1	phosphinothricin acetyltransferase [Nocardio...	115	2e-24
ref	YP_003484882.1	putative acetyltransferase [Streptococcus mu...	115	2e-24
ref	YP_003749344.1	phosphinothricin n-acetyltransferase (ppt n-...	115	2e-24
ref	YP_002551041.1	acetyltransferase [Agrobacterium vitis S4] >...	115	3e-24
ref	ZP_08044113.1	GCN5-related N-acetyltransferase [Haladaptatu...	115	4e-24
ref	ZP_07343113.1	phosphinothricin N-acetyltransferase [Burkhol...	114	4e-24
ref	ZP_03755566.1	hypothetical protein ROSEINA2194_04006 [Roseb...	114	4e-24
ref	ZP_08196974.1	phosphinothricin N-acetyltransferase [Nocardi...	114	5e-24
ref	YP_003766886.1	acetyltransferase [Amycolatopsis mediterrane...	114	7e-24
ref	ZP_03797973.1	hypothetical protein COPCOM_00226 [Coprococcu...	114	7e-24
ref	ZP_02434166.1	hypothetical protein BACSTE_00385 [Bacteroid...	113	8e-24
ref	YP_003392558.1	GCN5-related N-acetyltransferase [Conexibact...	113	9e-24
ref	YP_001913381.1	phosphinothricin N-acetyltransferase [Xantho...	113	9e-24
ref	YP_003388108.1	GCN5-related N-acetyltransferase [Spirosoma ...	113	9e-24
ref	ZP_05034621.1	acetyltransferase, GNAT family [Brevundimonas...	113	1e-23
ref	YP_003268792.1	phosphinothricin acetyltransferase [Haliangi...	113	1e-23
ref	ZP_02041092.1	hypothetical protein RUMGNA_01858 [Ruminococc...	113	1e-23
ref	ZP_08157709.1	putative phosphinothricin N-acetyltransferase...	113	1e-23
ref	YP_003178172.1	GCN5-related N-acetyltransferase [Halomicrob...	113	1e-23
ref	ZP_07669863.1	phosphinothricin N-acetyltransferase [Erysipe...	113	1e-23
ref	YP_002490995.1	GCN5-related N-acetyltransferase [Anaeromyxo...	112	2e-23
ref	YP_001523874.1	GCN5-related N-acetyltransferase [Azorhizobi...	112	2e-23
ref	YP_001363663.1	GCN5-related N-acetyltransferase [Kineococcu...	112	2e-23
ref	ZP_08014935.1	hypothetical protein HMPREF9464_00154 [Sutter...	112	2e-23
ref	YP_003383991.1	phosphinothricin acetyltransferase [Kribbell...	112	2e-23
ref	YP_002720780.1	Sortase related acyltransferase [Brachyspira...	112	2e-23
ref	YP_567667.1	GCN5-related N-acetyltransferase [Rhodopseudomo...	112	2e-23
emb	CBK80336.1	Sortase and related acyltransferases [Coprococcu...	112	2e-23
ref	NP_347494.1	phosphinothricin acetyltransferase [Clostridium...	112	3e-23
ref	ZP_07458488.1	phosphinothricin acetyltransferase [Streptoco...	112	3e-23
ref	ZP_04115199.1	Phosphinothricin N-acetyltransferase [Bacillu...	111	3e-23
ref	YP_001033220.1	phosphinothricin N-acetyltransferase [Lactoc...	111	5e-23
ref	ZP_04186528.1	Phosphinothricin N-acetyltransferase [Bacillu...	111	5e-23
ref	YP_779246.1	GCN5-related N-acetyltransferase [Rhodopseudomo...	110	6e-23
ref	YP_001557413.1	GCN5-related N-acetyltransferase [Clostridiu...	110	6e-23
ref	ZP_02027156.1	hypothetical protein EUBVEN_02425 [Eubacteriu...	110	6e-23
ref	ZP_03110621.1	acetyltransferase, GNAT family [Bacillus cere...	110	6e-23
ref	NP_721464.1	putative acetyltransferase [Streptococcus mutan...	110	7e-23
ref	NP_105235.1	phosphinothricin acetyltransferase [Mesorhizobiu...	110	7e-23
ref	YP_002559467.1	acetyltransferase family protein [Macrococcu...	110	7e-23
ref	ZP_04084797.1	Phosphinothricin N-acetyltransferase [Bacillu...	110	7e-23
ref	ZP_04671490.1	phosphinothricin N-acetyltransferase [Clostri...	110	8e-23
ref	ZP_02188752.1	GCN5-related N-acetyltransferase [alpha prote...	110	8e-23
ref	ZP_03234565.1	acetyltransferase, GNAT family [Bacillus cere...	110	9e-23
ref	YP_713648.1	putative N-acetyltransferase [Frankia alni ACN1...	110	9e-23
ref	YP_003340665.1	phosphinothricin acetyltransferase [Streptos...	110	1e-22
ref	NP_744077.1	phosphinothricin N-acetyltransferase, putative ...	110	1e-22
ref	ZP_04174994.1	Phosphinothricin N-acetyltransferase [Bacillu...	110	1e-22
ref	YP_003738151.1	phosphinothricin N-acetyltransferase [Halalk...	109	1e-22
ref	ZP_05136289.1	phosphinothricin N-acetyltransferase [Stenotr...	109	1e-22
ref	ZP_06897931.1	phosphinothricin acetyltransferase [Roseomona...	109	1e-22
ref	ZP_04120739.1	Phosphinothricin N-acetyltransferase [Bacillu...	109	1e-22
ref	YP_811544.1	sortase related acyltransferase [Lactococcus la...	109	1e-22
ref	ZP_04169245.1	Phosphinothricin N-acetyltransferase [Bacillu...	109	1e-22
ref	NP_959023.1	hypothetical protein MAP0089 [Mycobacterium avi...	109	1e-22
ref	YP_002367523.1	acetyltransferase, GNAT family [Bacillus cer...	109	2e-22
ref	ZP_05130852.1	phosphinothricin acetyltransferase [Clostridi...	109	2e-22
ref	ZP_05346405.1	phosphinothricin N-acetyltransferase [Bryante...	109	2e-22
ref	YP_004267013.1	Phosphinothricin acetyltransferase [Syntroph...	109	2e-22
ref	ZP_04126827.1	Phosphinothricin N-acetyltransferase [Bacillu...	108	2e-22
emb	CAM74335.1	GCN5-related N-acetyltransferase [Magnetospirill...	108	2e-22
ref	NP_832560.1	phosphinothricin N-acetyltransferase [Bacillus ...	108	2e-22
emb	CBK99483.1	Sortase and related acyltransferases [Faecalibac...	108	2e-22

ref YP_003354349.1	GNAT family acetyltransferase [Lactococcus l...	108	2e-22
ref YP_004106813.1	phosphinothricin acetyltransferase [Rhodopse...	108	3e-22
ref ZP_03232858.1	acetyltransferase, GNAT family [Bacillus cere...	108	3e-22
ref ZP_02075451.1	hypothetical protein CLOL250_02227 [Clostridi...	108	3e-22
ref ZP_04146050.1	Phosphinothricin N-acetyltransferase [Bacillu...	108	3e-22
ref YP_002028028.1	GCN5-related N-acetyltransferase [Stenotroph...	108	3e-22
ref ZP_03011953.1	hypothetical protein BACCOP_03879 [Bacteroid...	108	3e-22
ref YP_001971847.1	putative acetyltransferase [Stenotrophomonas...	108	3e-22
ref ZP_08127907.1	phosphinothricin N-acetyltransferase [Clostri...	108	4e-22
gb EFV98070.1	phosphinothricin acetyltransferase [Streptococcus...	108	4e-22
ref YP_001591522.1	hypothetical protein SPAB_05416 [Salmonella ...	108	4e-22
ref ZP_04102502.1	Phosphinothricin N-acetyltransferase [Bacillu...	108	4e-22
ref YP_003399412.1	GCN5-related N-acetyltransferase [Acidaminoc...	108	4e-22
ref ZP_02213075.1	acetyltransferase, GNAT family [Bacillus anth...	108	4e-22
ref ZP_04301002.1	Phosphinothricin N-acetyltransferase [Bacillu...	108	5e-22
ref ZP_04262522.1	Phosphinothricin N-acetyltransferase [Bacillu...	108	5e-22
ref ZP_04223012.1	Phosphinothricin N-acetyltransferase [Bacillu...	107	5e-22
emb CBL02997.1	Sortase and related acyltransferases [Faecalibac...	107	5e-22
ref ZP_04273770.1	Phosphinothricin N-acetyltransferase [Bacillu...	107	5e-22
ref ZP_04323719.1	Phosphinothricin N-acetyltransferase [Bacillu...	107	5e-22
ref ZP_04197844.1	Phosphinothricin N-acetyltransferase [Bacillu...	107	5e-22
ref YP_001645441.1	GCN5-related N-acetyltransferase [Bacillus w...	107	5e-22
ref YP_003550782.1	GCN5-like N-acetyltransferase [Candidatus Pu...	107	5e-22
ref YP_895314.1	phosphinothricin N-acetyltransferase acetyltran...	107	5e-22
ref YP_001202590.1	phosphinothricin acetyltransferase (PPT N-ac...	107	5e-22
ref YP_421541.1	phosphinothricin N-acetyltransferase [Magnetosp...	107	6e-22
ref YP_818802.1	sortase related acyltransferase [Leuconostoc me...	107	6e-22
ref ZP_04072392.1	Phosphinothricin N-acetyltransferase [Bacillu...	107	6e-22
ref ZP_02948867.1	phosphinothricin N-acetyltransferase [Clostri...	107	6e-22
ref ZP_01962684.1	hypothetical protein RUMOB_00397 [Ruminococc...	107	6e-22
ref ZP_00743946.1	Phosphinothricin N-acetyltransferase [Bacillu...	107	7e-22
ref YP_001477588.1	GCN5-related N-acetyltransferase [Serratia p...	107	7e-22
ref NP_267934.1	acyltransferase [Lactococcus lactis subsp. lact...	107	7e-22
ref YP_003211166.1	phosphinothricin N-acetyltransferase [Cronob...	107	7e-22
ref ZP_03913843.1	possible Phosphinothricin acetyltransferase [...	107	7e-22
ref NP_945552.1	GCN5-related N-acetyltransferase [Rhodopseudomo...	107	7e-22
ref ZP_07674254.1	toxin-antitoxin system, toxin component, GNAT...	107	8e-22
ref YP_002235706.1	putative phosphinothricin N-acetyltransferas...	107	8e-22
ref YP_003602596.1	putative phosphinothricin N-acetyltransferas...	107	8e-22
ref ZP_04454120.1	hypothetical protein GCWU000342_00100 [Shuttl...	107	9e-22
ref ZP_05851266.1	phosphinothricin N-acetyltransferase [Granuli...	107	9e-22
ref ZP_04079000.1	Phosphinothricin N-acetyltransferase [Bacillu...	107	9e-22
ref NP_521958.1	phosphinothricin acetyltransferase protein [Ral...	107	9e-22
ref YP_003792542.1	putative phosphinothricin N-acetyltransferas...	107	9e-22
ref ZP_02234915.1	hypothetical protein DORFOR_01789 [Dorea form...	107	9e-22
ref YP_760389.1	acetyltransferase [Hyphomonas neptunium ATCC 15...	106	1e-21
ref YP_003101109.1	GCN5-related N-acetyltransferase [Actinosynn...	106	1e-21
ref YP_001633138.1	acetyltransferase [Bordetella petrii DSM 128...	106	1e-21
ref ZP_04579325.1	conserved hypothetical protein [Oxalobacter f...	106	1e-21
ref ZP_01168931.1	probable phosphinothricin acetyltransferase (...	106	1e-21
ref NP_688817.1	phosphinothricin N-acetyltransferase [Streptoco...	106	1e-21
ref YP_003163209.1	GCN5-related N-acetyltransferase [Leptotrich...	106	1e-21
ref ZP_08010212.1	phosphinothricin N-acetyltransferase [Coproba...	106	1e-21
ref YP_004259793.1	Phosphinothricin acetyltransferase [Bacteroi...	106	1e-21
ref ZP_03210120.1	hypothetical protein BACPLE_03811 [Bacteroid...	106	1e-21
ref ZP_02868381.1	hypothetical protein CLOSPI_02223 [Clostridiu...	106	1e-21
ref ZP_04947527.1	hypothetical protein BDAG_03502 [Burkholderia...	106	2e-21
ref ZP_03297278.1	hypothetical protein COLSTE_01172 [Collinsell...	106	2e-21
ref YP_483910.1	GCN5-related N-acetyltransferase [Rhodopseudomo...	106	2e-21
ref ZP_04289658.1	Phosphinothricin N-acetyltransferase [Bacillu...	105	2e-21
ref ZP_04192159.1	Phosphinothricin N-acetyltransferase [Bacillu...	105	2e-21
ref YP_775946.1	GCN5-related N-acetyltransferase [Burkholderia ...	105	2e-21
ref ZP_04228286.1	Phosphinothricin N-acetyltransferase [Bacillu...	105	2e-21

ref	ZP_03682824.1	hypothetical protein CATMIT_01460 [Catenibact...	105	2e-21
ref	ZP_04889981.1	phosphinothricin N-acetyltransferase [Burkhol...	105	2e-21
ref	ZP_04317895.1	Phosphinothricin N-acetyltransferase [Bacillu...	105	2e-21
ref	YP_003634998.1	GCN5-related N-acetyltransferase [Brachyspir...	105	2e-21
ref	NP_979141.1	acetyltransferase [Bacillus cereus ATCC 10987] ...	105	2e-21
ref	YP_330444.1	phosphinothricin N-acetyltransferase, putative ...	105	2e-21
ref	ZP_03777241.1	hypothetical protein CLOHYLEM_04290 [Clostrid...	105	2e-21
ref	ZP_03715013.1	hypothetical protein EUBHAL_00046 [Eubacteriu...	105	2e-21
ref	ZP_01438277.1	putative phosphinothricin N-acetyltransferase...	105	3e-21
ref	YP_001583998.1	GCN5-related N-acetyltransferase [Burkholder...	105	3e-21
ref	ZP_02084880.1	hypothetical protein CLOBOL_02410 [Clostridiu...	105	3e-21
ref	ZP_04295105.1	Phosphinothricin N-acetyltransferase [Bacillu...	105	3e-21
ref	YP_001772764.1	GCN5-related N-acetyltransferase [Methylobac...	105	3e-21
ref	YP_535527.1	phosphinothricin N-acetyltransferase [Lactobaci...	105	3e-21
ref	YP_036893.1	phosphinothricin N-acetyltransferase [Bacillus ...	105	3e-21
emb	CBL41830.1	Sortase and related acyltransferases [butyrate-p...	105	3e-21
ref	YP_001703771.1	phosphinothricin N-acetyltransferase [Mycoba...	105	3e-21
ref	ZP_00785183.1	phosphinothricin N-acetyltransferase [Strepto...	105	3e-21
ref	ZP_04234094.1	Phosphinothricin N-acetyltransferase [Bacillu...	105	3e-21
ref	YP_001412546.1	GCN5-like N-acetyltransferase [Parvibaculum ...	105	3e-21
gb	ADI12551.1	GCN5-related N-acetyltransferase [Streptomyces bi...	105	4e-21
ref	ZP_06645478.1	phosphinothricin N-acetyltransferase [Erysipe...	105	4e-21
ref	YP_001437209.1	hypothetical protein ESA_01105 [Cronobacter ...	104	4e-21
ref	ZP_01992495.1	phosphinothricin N-acetyltransferase [Vibrio ...	104	4e-21
ref	ZP_02886944.1	GCN5-related N-acetyltransferase [Burkholderi...	104	4e-21
gb	ADJ78841.1	Phosphinothricin N-acetyltransferase [Lactobacill...	104	4e-21
gb	EFV81785.1	acetyltransferase [Achromobacter xylosoxidans C54]	104	4e-21
ref	YP_004148646.1	Phosphinothricin N-acetyltransferase [Staphy...	104	5e-21
ref	YP_002360568.1	GCN5-related N-acetyltransferase [Methylocel...	104	5e-21
ref	ZP_02406525.1	phosphinothricin N-acetyltransferase [Burkhol...	104	5e-21
ref	ZP_00054060.1	COG1247: Sortase and related acyltransferases...	104	5e-21
ref	YP_084124.1	phosphinothricin N-acetyltransferase [Bacillus ...	104	5e-21
ref	YP_004232049.1	phosphinothricin acetyltransferase [Burkhold...	104	5e-21
ref	YP_001878529.1	GCN5-related N-acetyltransferase [Akkermansi...	104	6e-21
ref	ZP_04446277.1	hypothetical protein COLINT_03009 [Collinsell...	104	6e-21
ref	ZP_04096923.1	Phosphinothricin N-acetyltransferase [Bacillu...	104	6e-21
ref	ZP_02384866.1	phosphinothricin N-acetyltransferase [Burkhol...	104	6e-21
ref	YP_371912.1	GCN5-related N-acetyltransferase [Burkholderia ...	104	7e-21
ref	ZP_06074266.1	conserved hypothetical protein [Bacteroides s...	103	7e-21
ref	ZP_03569168.1	phosphinothricin N-acetyltransferase (PPT N-a...	103	8e-21
ref	ZP_02370975.1	phosphinothricin N-acetyltransferase [Burkhol...	103	8e-21
ref	YP_003781205.1	putative acetyltransferase [Clostridium ljun...	103	8e-21
ref	ZP_07634831.1	Sortase related acyltransferase [Ruminococcac...	103	8e-21
ref	YP_548523.1	GCN5-related N-acetyltransferase [Polaromonas s...	103	8e-21
ref	ZP_02415035.1	phosphinothricin N-acetyltransferase [Burkhol...	103	9e-21
ref	ZP_07966268.1	acetyltransferase [Segniliparus rugosus ATCC ...	103	9e-21
ref	YP_002131561.1	phosphinothricin N-acetyltransferase [Phenyl...	103	9e-21
gb	ACO70893.1	putative acetyltransferase [uncultured Verrucomic...	103	9e-21
ref	YP_001301874.1	phosphinothricin N-acetyltransferase [Paraba...	103	9e-21
ref	ZP_05287381.1	phosphinothricin N-acetyltransferase, putativ...	103	1e-20
ref	YP_003308709.1	phosphinothricin acetyltransferase [Sebaldel...	103	1e-20
ref	YP_001308116.1	GCN5-related N-acetyltransferase [Clostridiu...	103	1e-20
ref	ZP_04521588.1	phosphinothricin N-acetyltransferase (PPT N-a...	103	1e-20
ref	YP_001062349.1	phosphinothricin N-acetyltransferase [Burkho...	103	1e-20
ref	ZP_02501639.1	phosphinothricin N-acetyltransferase [Burkhol...	103	1e-20
ref	ZP_02493429.1	phosphinothricin N-acetyltransferase [Burkhol...	103	1e-20
ref	ZP_02451118.1	phosphinothricin N-acetyltransferase [Burkhol...	103	1e-20
ref	ZP_04967733.1	phosphinothricin N-acetyltransferase [Burkhol...	103	1e-20
ref	YP_337680.1	phosphinothricin N-acetyltransferase [Burkholde...	103	1e-20
ref	ZP_07894787.1	phosphinothricin acetyltransferase [Enterococ...	103	1e-20
ref	ZP_01765750.1	phosphinothricin N-acetyltransferase [Burkhol...	103	1e-20
ref	YP_439663.1	phosphinothricin N-acetyltransferase [Burkholde...	103	1e-20
ref	YP_001180792.1	GCN5-related N-acetyltransferase [Caldicellu...	103	1e-20

ref	ZP_02737400.1	putative acetyltransferase [Gemmata obscurigl...	103	1e-20
ref	YP_003981951.1	GNAT family acetyltransferase 28 [Achromobac...	102	1e-20
ref	ZP_06987509.1	phosphinothricin N-acetyltransferase [Bactero...	102	2e-20
ref	YP_001236578.1	phosphinothricin acetyltransferase (PPT N-ac...	102	2e-20
ref	ZP_02426951.1	hypothetical protein CLOPAM_00328 [Clostridiu...	102	2e-20
ref	YP_001414928.1	GCN5-related N-acetyltransferase [Xanthobact...	102	2e-20
ref	ZP_06189127.1	putative N-acetyltransferase [Serratia odorif...	102	2e-20
ref	ZP_02459278.1	phosphinothricin N-acetyltransferase [Burkhol...	102	2e-20
ref	ZP_02211453.1	hypothetical protein CLOBAR_01066 [Clostridiu...	102	2e-20
ref	NP_767103.1	acetyltransferase [Bradyrhizobium japonicum USD...	102	2e-20
ref	ZP_03450133.1	phosphinothricin N-acetyltransferase [Burkhol...	102	2e-20
ref	YP_001908169.1	Putative N-acetyltransferase [Erwinia tasman...	102	2e-20
ref	ZP_02907912.1	GCN5-related N-acetyltransferase [Burkholderi...	102	2e-20
ref	YP_001811189.1	GCN5-related N-acetyltransferase [Burkholder...	102	2e-20
ref	YP_110939.1	phosphinothricin N-acetyltransferase [Burkholde...	102	2e-20
ref	YP_989894.1	phosphinothricin N-acetyltransferase [Burkholde...	102	3e-20
ref	YP_003285848.1	toxin resistance protein [Vibrio sp. Ex25] >...	102	3e-20
ref	ZP_03758704.1	hypothetical protein CLOSTASPAR_02725 [Clostr...	102	3e-20
ref	ZP_07357026.1	phosphinothricin N-acetyltransferase [Desulfo...	102	3e-20
ref	ZP_04565925.1	phosphinothricin N-acetyltransferase [Mollicu...	102	3e-20
ref	ZP_03643045.1	hypothetical protein BACCOPRO_01407 [Bacteroi...	102	3e-20
ref	ZP_03475670.1	hypothetical protein PRABACTJOHN_01332 [Parab...	102	3e-20
ref	ZP_08063150.1	phosphinothricin acetyltransferase [Streptoco...	102	3e-20
ref	YP_003452959.1	acetyltransferase [Azospirillum sp. B510] >g...	102	3e-20
ref	ZP_07312487.1	phosphinothricin N-acetyltransferase [Strepto...	102	3e-20
ref	YP_003151289.1	sortase-like acyltransferase [Cryptobacteriu...	101	3e-20
ref	ZP_03793115.1	phosphinothricin N-acetyltransferase [Burkhol...	101	4e-20
ref	ZP_07954371.1	acetyltransferase [Gemella moribillum M424] >...	101	4e-20
ref	ZP_02164455.1	putative phosphinothricin N-acetyltransferase...	101	4e-20
ref	YP_003332566.1	phosphinothricin acetyltransferase [Dickeya ...	101	4e-20
ref	YP_575598.1	GCN5-related N-acetyltransferase [Nitrobacter h...	101	4e-20
ref	ZP_07945011.1	acetyltransferase [Bilophila wadsworthia 3_1_...	101	4e-20
ref	ZP_06053422.1	GCN5-related N-acetyltransferase [Grimontia h...	101	4e-20
ref	YP_879394.1	phosphinothricin N-acetyltransferase [Mycobacte...	101	4e-20
ref	YP_003784563.1	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-a...	101	4e-20
ref	YP_105922.1	phosphinothricin N-acetyltransferase [Burkholde...	101	4e-20
ref	YP_001195120.1	GCN5-related N-acetyltransferase [Flavobacte...	101	5e-20
ref	YP_003607239.1	Phosphinothricin acetyltransferase [Burkhold...	101	5e-20
ref	ZP_02466216.1	phosphinothricin N-acetyltransferase [Burkhol...	101	5e-20
ref	ZP_02926674.1	putative acetyltransferase [Verrucomicrobium ...	101	5e-20
ref	ZP_06641431.1	phosphinothricin acetyltransferase [Serratia ...	101	5e-20
ref	NP_387329.1	putative acetyltransferase (antibiotic resistan...	101	5e-20
ref	ZP_07376830.1	Phosphinothricin acetyltransferase [Pantoea s...	101	5e-20
ref	ZP_07028623.1	Phosphinothricin acetyltransferase [Afipia sp...	101	5e-20
ref	YP_001078206.1	phosphinothricin N-acetyltransferase [Burkho...	101	5e-20
ref	ZP_02358538.1	phosphinothricin N-acetyltransferase [Burkhol...	100	6e-20
ref	ZP_02365602.1	phosphinothricin N-acetyltransferase [Burkhol...	100	6e-20
ref	ZP_02080264.1	hypothetical protein CLOLEP_01716 [Clostridiu...	100	6e-20
ref	YP_981695.1	GCN5-related N-acetyltransferase [Polaromonas n...	100	6e-20
ref	ZP_05546015.1	conserved hypothetical protein [Parabacteroid...	100	6e-20
ref	YP_001338532.1	putative acetyltransferase [Klebsiella pneum...	100	7e-20
ref	ZP_07304405.1	phosphinothricin N-acetyltransferase [Strepto...	100	7e-20
ref	ZP_03679607.1	hypothetical protein BACCELL_03968 [Bacteroid...	100	7e-20
ref	ZP_02032877.1	hypothetical protein PARMER_02897 [Parabacter...	100	7e-20
ref	YP_004153830.1	phosphinothricin acetyltransferase [Variovor...	100	8e-20
ref	ZP_08076595.1	putative phosphinothricin N-acetyltransferase...	100	8e-20
ref	ZP_05093745.1	acetyltransferase, GNAT family [marine gamma ...	100	8e-20
ref	YP_001117611.1	GCN5-related N-acetyltransferase [Burkholder...	100	9e-20
ref	ZP_06944043.1	toxin resistance protein [Vibrio cholerae RC3...	100	9e-20
ref	ZP_02891871.1	GCN5-related N-acetyltransferase [Burkholderi...	100	9e-20
emb	CBL25177.1	Sortase and related acyltransferases [Ruminococc...	100	9e-20
ref	YP_003881883.1	Phosphinothricin N-acetyltransferase [Dickey...	100	1e-19
ref	YP_003450289.1	acetyltransferase [Azospirillum sp. B510] >g...	100	1e-19

ref	YP_004223325.1	sortase [Microbacterium testaceum StLB037]	>...	100	1e-19
ref	YP_001215771.1	toxin resistance protein [Vibrio cholerae O3...		100	1e-19
ref	ZP_07475281.1	phosphinothricin N-acetyltransferase [Brucell...		100	1e-19
ref	ZP_03313133.1	hypothetical protein DESPIG_03073 [Desulfovib...		100	1e-19
ref	ZP_07478906.1	phosphinothricin N-acetyltransferase [Brucell...		100	1e-19
ref	YP_003620615.1	hypothetical protein LKI_00515 [Leuconostoc ...		100	1e-19
ref	NP_353896.2	acetyltransferase [Agrobacterium tumefaciens st...		100	1e-19
ref	YP_002988528.1	Phosphinothricin acetyltransferase [Dickeya ...		100	1e-19
ref	YP_001258130.1	phosphinothricin N-acetyltransferase [Brucel...		100	1e-19
ref	YP_001888617.1	GCN5-related N-acetyltransferase [Burkholder...		100	1e-19
ref	YP_585578.1	GCN5-related N-acetyltransferase [Cupriavidus m...		100	1e-19
ref	NP_540775.1	phosphinothricin N-acetyltransferase [Brucella ...		100	1e-19
ref	YP_003005423.1	Phosphinothricin acetyltransferase [Dickeya ...		100	1e-19
ref	YP_553531.1	putative phosphinothricin N-acetyltransferase [...		100	1e-19
ref	YP_935194.1	putative N-acetyltransferase [Azoarcus sp. BH72...		100	1e-19
ref	ZP_04761786.1	GCN5-related N-acetyltransferase [Acidovorax ...		100	1e-19
ref	YP_364233.1	putative phosphinothricin N-acetyltransferase [...		99	2e-19
ref	YP_004278115.1	GCN5-related N-acetyltransferase [Agrobacter...		99	2e-19
ref	ZP_04858262.1	conserved hypothetical protein [Ruminococcus ...		99	2e-19
ref	YP_297475.1	GCN5-related N-acetyltransferase [Ralstonia eut...		99	2e-19
ref	ZP_07217130.1	phosphinothricin N-acetyltransferase [Bactero...		99	2e-19
ref	ZP_08079711.1	phosphinothricin acetyltransferase [Lactobaci...		99	2e-19
ref	YP_003594410.1	phosphinothricin acetyltransferase [Caulobac...		99	2e-19
ref	NP_879101.1	putative acetyltransferase [Bordetella pertussi...		99	2e-19
ref	NP_882772.1	putative acetyltransferase [Bordetella parapert...		99	2e-19
ref	YP_530095.1	GCN5-related N-acetyltransferase [Rhodopseudomo...		99	2e-19
emb	CBL24674.1	Sortase and related acyltransferases [Ruminococc...		99	2e-19
ref	YP_001368661.1	GCN5-like N-acetyltransferase [Ochrobactrum ...		99	2e-19
ref	ZP_08188723.1	sortase-like acyltransferase [Xanthomonas per...		99	2e-19
ref	ZP_06843515.1	Phosphinothricin acetyltransferase [Burkholde...		99	2e-19
ref	YP_003819401.1	Phosphinothricin acetyltransferase [Brevundi...		99	3e-19
emb	CBL06841.1	Sortase and related acyltransferases [Megamonas ...		99	3e-19
ref	YP_001682970.1	GCN5-like N-acetyltransferase [Caulobacter s...		99	3e-19
ref	ZP_03265218.1	GCN5-related N-acetyltransferase [Burkholderi...		99	3e-19
ref	YP_002234420.1	putative acetyltransferase [Burkholderia cen...		99	3e-19
ref	YP_002885911.1	GCN5-related N-acetyltransferase [Exiguobact...		99	3e-19
ref	ZP_06896375.1	phosphinothricin acetyltransferase [Roseomona...		99	3e-19
ref	YP_002502279.1	GCN5-related N-acetyltransferase [Methylobac...		99	3e-19
ref	ZP_07957845.1	acetyltransferase [Lachnospiraceae bacterium ...		99	3e-19
ref	ZP_01675773.1	toxin resistance protein [Vibrio cholerae 274...		99	4e-19
ref	YP_001779246.1	GCN5-related N-acetyltransferase [Burkholder...		99	4e-19
ref	YP_998663.1	GCN5-related N-acetyltransferase [Verminephroba...		99	4e-19
ref	YP_623564.1	GCN5-related N-acetyltransferase [Burkholderia ...		98	4e-19
ref	ZP_05180120.1	phosphinothricin N-acetyltransferase [Brucell...		98	4e-19
ref	YP_002287583.1	phosphinothricin N-acetyltransferase [Oligot...		98	4e-19
ref	NP_900042.1	resistance protein [Chromobacterium violaceum A...		98	4e-19
ref	YP_004012611.1	phosphinothricin acetyltransferase [Rhodomic...		98	4e-19
ref	YP_002123860.1	Phosphinothricin N-acetyltransferase [Strept...		98	5e-19
ref	ZP_02438997.1	hypothetical protein CLOSS21_01461 [Clostridi...		98	5e-19
ref	ZP_05456648.1	phosphinothricin N-acetyltransferase [Brucell...		98	5e-19
ref	NP_793104.1	phosphinothricin N-acetyltransferase [Pseudomon...		98	6e-19
ref	YP_001832727.1	GCN5-related N-acetyltransferase [Beijerinck...		98	6e-19
ref	NP_642621.1	phosphinothricin N-acetyltransferase [Xanthomon...		98	6e-19
ref	ZP_02376770.1	GCN5-related N-acetyltransferase [Burkholderi...		98	6e-19
ref	YP_417853.1	phosphinothricin N-acetyltransferase [Staphyloc...		97	6e-19
ref	NP_863380.1	hypothetical protein R64_p025 [Salmonella enter...		97	6e-19
ref	YP_002562667.1	GNAT family acetyltransferase [Streptococcus...		97	7e-19
ref	ZP_07093254.1	acetyltransferase, GNAT family [Lactobacillus...		97	7e-19
ref	NP_627417.1	phosphinothricin acetyltransferase [Streptomyce...		97	7e-19
ref	ZP_07904920.1	phosphinothricin acetyltransferase [Eubacteri...		97	8e-19
ref	NP_637556.1	phosphinothricin N-acetyltransferase [Xanthomon...		97	8e-19
ref	YP_003941113.1	Phosphinothricin acetyltransferase [Enteroba...		97	8e-19
ref	NP_824872.1	phosphinothricin N-acetyltransferase [Streptomy...		97	8e-19

ref ZP_01114119.1	putative phosphinothricin N-acetyltransferase...	97	8e-19
ref YP_002283223.1	GCN5-related N-acetyltransferase [Rhizobium ...	97	9e-19
ref YP_001328738.1	GCN5-related N-acetyltransferase [Sinorhizob...	97	9e-19
emb CBL33399.1	Sortase and related acyltransferases [Eubacteriu...	97	9e-19
ref YP_001757052.1	GCN5-related N-acetyltransferase [Methylobac...	97	9e-19
ref YP_001339364.1	GCN5-like N-acetyltransferase [Marinomonas s...	97	1e-18
ref YP_002961972.1	phosphinothricin N-acetyltransferase [Methylo...	97	1e-18
ref YP_002007021.1	phosphinothricin n-acetyltransferase [Cupria...	97	1e-18
ref ZP_04996481.1	conserved hypothetical protein [Streptomyces ...	97	1e-18
gb ADL24342.1	acetyltransferase, GNAT family [Staphylococcus au...	97	1e-18
gb ADY85178.1	Phosphinothricin acetyltransferase [Lactobacillus...	97	1e-18
ref ZP_01259639.1	toxin resistance protein [Vibrio alginolyticu...	97	1e-18
ref ZP_03301026.1	hypothetical protein BACDOR_02398 [Bacteroides...	97	1e-18
ref YP_001339360.1	GCN5-like N-acetyltransferase [Marinomonas s...	97	1e-18
ref YP_300460.1	putative acetyltransferase [Staphylococcus sapr...	97	1e-18
ref YP_002731861.1	phosphinothricin N-acetyltransferase [Brucel...	97	1e-18
ref ZP_02243592.1	phosphinothricin N-acetyltransferase [Xanthom...	97	1e-18
ref ZP_04540039.1	conserved hypothetical protein [Bacteroides s...	97	1e-18
ref ZP_06412786.1	Phosphinothricin acetyltransferase [Frankia s...	96	1e-18
ref YP_728012.1	phosphinothricin N-acetyltransferase [Ralstonia...	96	1e-18
ref NP_769816.1	acetyltransferase [Bradyrhizobium japonicum USD...	96	1e-18
ref ZP_04941465.1	GCN5-related N-acetyltransferase [Burkholderi...	96	1e-18
ref YP_004088834.1	phosphinothricin acetyltransferase [Asticcac...	96	2e-18
ref ZP_02919852.1	hypothetical protein STRINF_00704 [Streptococ...	96	2e-18
ref YP_002770383.1	phosphinothricin acetyltransferase [Brevibac...	96	2e-18
ref YP_001638468.1	GCN5-related N-acetyltransferase [Methylobac...	96	2e-18
ref ZP_07726498.1	acetyltransferase, GNAT family [Streptococcus...	96	2e-18
ref YP_003638725.1	Phosphinothricin acetyltransferase [Cellulom...	96	2e-18
ref YP_200814.1	phosphinothricin N-acetyltransferase [Xanthomon...	96	2e-18
ref YP_003968115.1	Phosphinothricin acetyltransferase [Ilyobact...	96	2e-18
ref ZP_06089820.1	conserved hypothetical protein [Bacteroides s...	96	2e-18
ref NP_232781.1	toxin resistance protein [Vibrio cholerae O1 bi...	96	2e-18
gb EFA85466.1	hypothetical protein PPL_01423 [Polysphondylium p...	96	2e-18
ref YP_619073.1	acyltransferase [Lactobacillus delbrueckii subs...	96	2e-18
ref YP_004006032.1	gnat acetyltransferase [Rhodococcus equi 103...	96	2e-18
gb EGD28189.1	phosphinothricin acetyltransferase [Lactobacillus...	96	2e-18
ref ZP_05736877.1	phosphinothricin N-acetyltransferase [Granuli...	96	2e-18
ref ZP_04449569.1	hypothetical protein GCWU000282_00798 [Catone...	96	3e-18
ref YP_001903385.1	Putative phosphinothricin N-acetyltransferas...	96	3e-18
ref ZP_06684576.1	phosphinothricin N-acetyltransferase [Achromo...	96	3e-18
ref YP_003144489.1	sortase-like acyltransferase [Slackia heliot...	96	3e-18
emb CAQ50959.1	hypothetical acetyltransferase YncA [Staphylococ...	96	3e-18
ref YP_784856.1	acetyltransferase [Bordetella avium 197N] >gi 1...	96	3e-18
emb CBA28717.1	Phosphinothricin N-acetyltransferase [Curvibacte...	96	3e-18
ref YP_003830359.1	GNAT family acetyltransferase [Butyrivibrio ...	96	3e-18
emb CBK74492.1	Sortase and related acyltransferases [Butyrivibr...	96	3e-18
ref YP_003101768.1	GCN5-related N-acetyltransferase [Actinosynn...	96	3e-18
ref ZP_01996698.1	hypothetical protein DORLON_02716 [Dorea long...	95	3e-18
ref ZP_02862900.1	hypothetical protein ANASTE_02127 [Anaerofust...	95	3e-18
ref ZP_08185887.1	sortase-like acyltransferase [Xanthomonas gar...	95	3e-18
ref YP_003910913.1	phosphinothricin acetyltransferase [Burkhold...	95	4e-18
ref ZP_07818891.1	acetyltransferase, GNAT family [Eremococcus c...	95	4e-18
ref YP_002516357.1	phosphinothricin N-acetyltransferase [Caulob...	95	4e-18
ref YP_003613927.1	GCN5-related N-acetyltransferase [Enterobact...	95	4e-18
ref YP_004034059.1	sortase related acyltransferase [Lactobacill...	95	4e-18
ref ZP_04676812.1	phosphinothricin acetyltransferase [Staphyloc...	95	4e-18
ref YP_002943286.1	phosphinothricin acetyltransferase [Variovor...	95	4e-18
ref YP_062723.1	phosphinothricin acetyltransferase protein [Lei...	95	4e-18
ref YP_002637715.1	acetyltransferase [Salmonella enterica subsp...	95	4e-18
ref YP_003695517.1	phosphinothricin acetyltransferase [Starkeya...	95	5e-18
ref YP_002943389.1	phosphinothricin acetyltransferase [Variovor...	95	5e-18
ref YP_813066.1	sortase related acyltransferase [Lactobacillus ...	95	5e-18
ref YP_001570427.1	hypothetical protein SARI_01387 [Salmonella ...	95	5e-18

ref YP_004155971.1	phosphinothricin acetyltransferase [Variovor...	94	5e-18
ref YP_002744002.1	acetyltransferase (GNAT) family protein [Str...	94	5e-18
ref YP_004255451.1	Phosphinothricin acetyltransferase [Deinococ...	94	6e-18
ref NP_419751.1	phosphinothricin N-acetyltransferase [Caulobact...	94	6e-18
ref ZP_06703408.1	phosphinothricin N-acetyltransferase [Xanthom...	94	6e-18
ref ZP_03398208.1	phosphinothricin N-acetyltransferase [Pseudom...	94	6e-18
ref YP_002746939.1	acetyltransferase (GNAT) family protein [Str...	94	7e-18
gb ADW05103.1	Phosphinothricin acetyltransferase [Streptomyces ...	94	7e-18
ref ZP_08156293.1	phosphinothricin acetyltransferase [Rhodococc...	94	8e-18
emb CBK97049.1	Sortase and related acyltransferases [Eubacteriu...	94	8e-18
ref ZP_04589637.1	phosphinothricin N-acetyltransferase [Pseudom...	94	8e-18
ref YP_427494.1	GCN5-related N-acetyltransferase [Rhodospirillu...	94	8e-18
ref ZP_04560308.1	yceA [Citrobacter sp. 30_2] >gi 226908433 gb ...	94	8e-18
ref ZP_04776030.1	phosphinothricin N-acetyltransferase [Gemella...	94	9e-18
ref YP_003766391.1	acetyltransferase [Amycolatopsis mediterrane...	94	9e-18
ref ZP_06492287.1	putative phosphinothricin N-acetyltransferase...	94	9e-18
ref YP_003518666.1	Pat [Pantoea ananatis LMG 20103] >gi 2911509...	94	9e-18
emb CBL38504.1	Sortase and related acyltransferases [butyrate-p...	94	1e-17
ref YP_002548913.1	Phosphinothricin acetyltransferase [Agrobact...	94	1e-17
gb EFZ06201.1	putative acyltransferase [Salmonella enterica sub...	94	1e-17
ref ZP_07603383.1	Phosphinothricin acetyltransferase [Streptomy...	94	1e-17
ref YP_468767.1	phosphinothricin acetyltransferase (antibiotic ...	94	1e-17
ref ZP_01772202.1	Hypothetical protein COLAER_01204 [Collinsell...	94	1e-17
ref YP_002827727.1	putative GCN5-related N-acetyltransferase [S...	93	1e-17
ref YP_275243.1	phosphinothricin N-acetyltransferase [Pseudomon...	93	1e-17
ref YP_001020299.1	putative phosphinothricin acetyltransferase ...	93	1e-17
gb ADI99011.1	probable phosphinothricin N-acetyltransferase [St...	93	1e-17
dbj BAI77989.1	phosphinothricin N-acetyltransferase [Pseudomona...	93	2e-17
ref ZP_05687808.1	acetyltransferase [Staphylococcus aureus A963...	93	2e-17
ref ZP_03290892.1	hypothetical protein CLONEX_03111 [Clostridiu...	93	2e-17
ref YP_216574.1	putative acyltransferase [Salmonella enterica s...	93	2e-17
ref YP_002363145.1	GCN5-related N-acetyltransferase [Methylocel...	93	2e-17
ref YP_041954.1	acetyltransferase (GNAT) family protein [Staphy...	93	2e-17
ref ZP_06458335.1	phosphinothricin N-acetyltransferase [Pseudom...	93	2e-17
ref ZP_07291989.1	GNAT family toxin-antitoxin system, toxin com...	93	2e-17
ref ZP_05613409.1	phosphinothricin N-acetyltransferase [Faecali...	93	2e-17
ref YP_002419800.1	GCN5-related N-acetyltransferase [Methylobac...	93	2e-17
gb EGC37188.1	hypothetical protein DICPUDRAFT_150275 [Dictyoste...	92	2e-17
ref YP_004153949.1	phosphinothricin acetyltransferase [Variovor...	92	2e-17
ref YP_970241.1	GCN5-related N-acetyltransferase [Acidovorax av...	92	2e-17
ref ZP_07735846.1	GCN5-related N-acetyltransferase [Caldicellul...	92	2e-17
ref ZP_06586877.1	conserved hypothetical protein [Streptomyces ...	92	2e-17
ref NP_647266.1	hypothetical protein MW2449 [Staphylococcus aur...	92	2e-17
ref YP_001923646.1	GCN5-related N-acetyltransferase [Methylobac...	92	2e-17
ref ZP_07005548.1	GCN5-related N-acetyltransferase [Pseudomonas...	92	2e-17
ref YP_003658700.1	GCN5-related N-acetyltransferase [Segnilipar...	92	2e-17
ref YP_236225.1	GCN5-related N-acetyltransferase [Pseudomonas s...	92	3e-17
ref ZP_07047827.1	acetyltransferase yncA [Lysinibacillus fusifo...	92	3e-17
ref ZP_06325630.1	acetyltransferase [Staphylococcus aureus subs...	92	3e-17
ref YP_003930830.1	acetyltransferase [Pantoea vagans C9-1] >gi ...	92	3e-17
ref ZP_04711138.1	GCN5-related N-acetyltransferase [Streptomyce...	92	3e-17
ref YP_002977838.1	GCN5-related N-acetyltransferase [Rhizobium ...	92	3e-17
ref YP_187333.1	acetyltransferase [Staphylococcus aureus subsp....	92	3e-17
ref ZP_07379546.1	Phosphinothricin acetyltransferase [Pantoea s...	92	3e-17
ref ZP_01857922.1	hypothetical acetyltransferase YncA [Planctom...	92	3e-17
ref ZP_04695956.1	GCN5-related N-acetyltransferase [Streptomyce...	92	3e-17
ref ZP_04839299.1	hypothetical protein SauraC_08067 [Staphyloco...	92	4e-17
ref YP_003597722.1	GNAT family acetyltransferase [Bacillus mega...	92	4e-17
ref YP_003447536.1	acetyltransferase [Azospirillum sp. B510] >g...	92	4e-17
ref YP_049065.1	putative acetyltransferase [Pectobacterium atro...	92	4e-17
ref YP_001977481.1	probable phosphinothricin acetyltransferase ...	92	4e-17
ref YP_004235746.1	phosphinothricin acetyltransferase [Acidovor...	92	4e-17
ref YP_001177449.1	GCN5-related N-acetyltransferase [Enterobact...	92	4e-17

ref ZP_08176212.1	sortase-like acyltransferase [Xanthomonas ves...	92	4e-17
ref YP_004023921.1	Gcn5-like N-acetyltransferase [Caldicellulos...	92	4e-17
ref YP_002280388.1	Gcn5-related N-acetyltransferase [Rhizobium ...	91	5e-17
ref NP_460549.1	acyltransferase [Salmonella enterica subsp. ent...	91	5e-17
ref YP_770098.1	acetyltransferase [Rhizobium leguminosarum bv. ...	91	5e-17
ref YP_004118289.1	phosphinothricin acetyltransferase [Pantoea ...	91	5e-17
emb CBK84854.1	Sortase and related acyltransferases [Enterobact...	91	5e-17
ref ZP_04868204.1	possible Phosphinothricin acetyltransferase [...	91	6e-17
ref ZP_07374561.1	toxin-antitoxin system, toxin component, gnat...	91	6e-17
ref YP_002299686.1	phosphinothricin N-acetyltransferase [Rhodos...	91	6e-17
ref YP_003490867.1	N-acetyltransferase [Streptomyces scabiei 87...	91	6e-17
ref YP_001298770.1	putative sortase and related acyltransferase...	91	6e-17
ref NP_373053.1	N-acetyltransferase [Staphylococcus aureus subs...	91	6e-17
ref ZP_07922338.1	phosphinothricin acetyltransferase [Pseudoram...	91	7e-17
ref ZP_06258790.1	toxin-antitoxin system, toxin component, GNAT...	91	7e-17
ref YP_002554139.1	gcn5-like n-acetyltransferase [Acidovorax eb...	91	7e-17
ref YP_002944112.1	Gcn5-related N-acetyltransferase [Variovorax...	91	7e-17
emb CAJ88465.1	putative acetyltransferase [Streptomyces ambofac...	91	7e-17
ref ZP_07261654.1	Gcn5-related N-acetyltransferase [Pseudomonas...	91	7e-17
ref ZP_04679268.1	Phosphinothricin N-acetyltransferase [Ochroba...	91	8e-17
ref ZP_08078774.1	acetyltransferase, GNAT family [Succinatimona...	91	8e-17
ref ZP_08091588.1	GNAT family Toxin-antitoxin system [Clostridi...	91	9e-17
ref ZP_04826272.1	possible Phosphinothricin acetyltransferase [...	91	9e-17
dbj BAI77993.1	phosphinothricin N-acetyltransferase [Pseudomona...	91	9e-17
ref ZP_06709676.1	GNAT family toxin-antitoxin system, toxin com...	91	9e-17
dbj BAI77992.1	phosphinothricin N-acetyltransferase [Pseudomona...	91	9e-17
ref YP_004042835.1	gcn5-related N-acetyltransferase [Paludibact...	91	1e-16
gb ADY39465.1	Gcn5-related N-acetyltransferase [bacterium enric...	91	1e-16
ref YP_471413.1	putative phosphinothricin N-acetyltransferase (...	90	1e-16
ref YP_117898.1	putative acetyltransferase [Nocardia farcinica ...	90	1e-16
ref NP_765632.1	N-acetyltransferase [Staphylococcus epidermidis...	90	1e-16
ref ZP_00943431.1	Phosphinothricin N-acetyltransferase [Ralston...	90	1e-16
ref XP_003088197.1	hypothetical protein CRE_05355 [Caenorhabdit...	90	1e-16
ref ZP_02421681.1	hypothetical protein EUBSIR_00512 [Eubacteriu...	90	1e-16
ref YP_003182713.1	Gcn5-related N-acetyltransferase [Eggerthell...	90	1e-16
ref YP_001616270.1	putative acetyltransferase [Sorangium cellul...	90	1e-16
ref XP_002416063.1	phosphinothricin N-acetyltransferase, putati...	90	1e-16
ref YP_189646.1	phosphinothricin acetyltransferase, putative [S...	90	1e-16
ref ZP_07947262.1	acetyltransferase [Eggerthella sp. 1_3_56FAA]...	90	1e-16
ref YP_002573340.1	Gcn5-like N-acetyltransferase [Caldicellulos...	90	1e-16
ref YP_001587924.1	hypothetical protein SPAB_01697 [Salmonella ...	90	1e-16
ref YP_002543819.1	phosphinothricin acetyltransferase (antibiot...	90	1e-16
ref YP_001832067.1	Gcn5-related N-acetyltransferase [Beijerinck...	90	1e-16
ref YP_002252427.1	antibiotic resistance (acetyltransferase) pr...	90	1e-16
ref ZP_06355097.1	toxin-antitoxin system, toxin component, GNAT...	90	1e-16
ref ZP_07842937.1	toxin-antitoxin system, toxin component, GNAT...	90	2e-16
ref ZP_07743896.1	putative acetyltransferase [Vibrio caribbenth...	90	2e-16
ref ZP_06917734.1	phosphinothricin N-acetyltransferase [Strepto...	90	2e-16
ref ZP_01721887.1	hypothetical protein BB14905_06898 [Bacillus ...	90	2e-16
ref YP_166358.1	phosphinothricin N-acetyltransferase, putative ...	90	2e-16
dbj BAI77990.1	phosphinothricin N-acetyltransferase [Pseudomona...	90	2e-16
ref ZP_08164878.1	putative phosphinothricin N-acetyltransferase...	90	2e-16
ref ZP_01915320.1	phosphinothricin N-acetyltransferase [Limnoba...	89	2e-16
ref ZP_04060141.1	phosphinothricin acetyltransferase [Staphyloco...	89	2e-16
ref YP_004026569.1	Gcn5-like N-acetyltransferase [Caldicellulos...	89	2e-16
ref NP_639084.1	phosphinothricin acetyltransferase [Xanthomonas...	89	2e-16
ref YP_001796181.1	putative acyltransferase with acyl-CoA N-acy...	89	2e-16
ref ZP_03500072.1	Gcn5-related N-acetyltransferase [Rhizobium e...	89	2e-16
ref YP_001695941.1	acetyltransferase yncA [Lysinibacillus sphae...	89	2e-16
ref YP_003365800.1	putative acetyltransferase [Citrobacter rode...	89	2e-16
gb ABA47267.1	phosphinothricin N-acetyltransferase [Pseudomonas...	89	2e-16
ref ZP_07289232.1	phosphinothricin n-acetyltransferase [Strep...	89	2e-16
emb CBL20923.1	Sortase and related acyltransferases [Ruminococc...	89	2e-16

ref	ZP_06758377.1	acetyltransferase, GNAT family [Veillonella s...	89	2e-16
ref	YP_003741598.1	Phosphinothricin N-acetyltransferase [Erwini...	89	2e-16
ref	YP_001525936.1	acetyltransferase [Azorhizobium caulinodans ...	89	2e-16
ref	ZP_06729691.1	phosphinothricin N-acetyltransferase [Xanthom...	89	2e-16
ref	YP_002541986.1	phosphinothricin N-acetyltransferase (antibi...	89	2e-16
ref	YP_252457.1	hypothetical protein SH0542 [Staphylococcus hae...	89	2e-16
gb	EFV88451.1	acetyltransferase, GNAT family [Staphylococcus ep...	89	2e-16
ref	ZP_01694880.1	acetyltransferase, gnat family [Microscilla m...	89	2e-16
ref	ZP_08192665.1	GCN5-related N-acetyltransferase [Clostridium...	89	3e-16
ref	YP_001980331.1	putative phosphinothricin N-acetyltransferas...	89	3e-16
ref	YP_003311091.1	GCN5-related N-acetyltransferase [Veillonell...	89	3e-16
ref	ZP_08040600.1	phosphinothricin acetyltransferase [Streptoco...	89	3e-16
emb	CBK87248.1	Sortase and related acyltransferases [Enterobact...	89	3e-16
ref	YP_003562993.1	GNAT family acetyltransferase [Bacillus mega...	89	3e-16
pdb	3DR8 A Chain A, Structure Of Ynca, A Putative Acetyltransfer...		89	3e-16
ref	YP_001415549.1	GCN5-related N-acetyltransferase [Xanthobact...	89	3e-16
ref	YP_003086840.1	GCN5-related N-acetyltransferase [Dyadobacte...	89	3e-16
ref	YP_001901044.1	GCN5-related N-acetyltransferase [Ralstonia ...	89	3e-16
ref	YP_001859565.1	GCN5-related N-acetyltransferase [Burkholder...	89	3e-16
ref	ZP_02831369.1	phosphinothricin acetyltransferase [Salmonell...	89	4e-16
ref	NP_455906.1	acetyltransferase [Salmonella enterica subsp. e...	88	4e-16
ref	YP_002974830.1	GCN5-related N-acetyltransferase [Rhizobium ...	88	4e-16
ref	ZP_03518748.1	probable phosphinothricin acetyltransferase (...)	88	4e-16
ref	YP_003777936.1	sortase/acetyltransferase [Herbaspirillum se...	88	4e-16
ref	ZP_02902668.1	acetyltransferase, GNAT family [Escherichia a...	88	4e-16
ref	YP_004002606.1	GCN5-like N-acetyltransferase [Caldicellulos...	88	4e-16
ref	ZP_01619614.1	putative phosphinothricin N-acetyltransferase...	88	4e-16
ref	ZP_05902359.1	phosphinothricin N-acetyltransferase [Leptotr...	88	5e-16
ref	YP_782081.1	GCN5-related N-acetyltransferase [Rhodopseudomo...	88	5e-16
ref	YP_001515135.1	acetyltransferase, putative [Acaryochloris m...	88	5e-16
ref	ZP_08139853.1	GCN5-related N-acetyltransferase [Pseudomonas...	88	5e-16
ref	YP_002504394.1	GCN5-related N-acetyltransferase [Clostridiu...	88	5e-16
ref	ZP_06274580.1	Phosphinothricin acetyltransferase [Streptomy...	88	6e-16
ref	ZP_01064186.1	toxin resistance protein [Vibrio sp. MED222] ...	88	6e-16
ref	ZP_07360833.1	acetyltransferase [Actinomyces viscosus C505]	88	6e-16
ref	YP_003610973.1	putative acetyltransferase [Enterobacter clo...	88	6e-16
ref	ZP_03527994.1	GCN5-related N-acetyltransferase [Rhizobium e...	88	6e-16
dbj	BAG06876.1	phosphinothricin acetyltransferase [Nocardia sp....	88	6e-16
ref	ZP_06743498.1	acetyltransferase, GNAT family [Bacteroides v...	88	6e-16
ref	ZP_04798151.1	possible Phosphinothricin acetyltransferase [...]	87	7e-16
ref	NP_885641.1	hypothetical protein BPP3481 [Bordetella parape...	87	7e-16
ref	ZP_03928954.1	acyltransferase [Acidaminococcus sp. D21] >gi...	87	7e-16
ref	ZP_05968426.2	toxin-antitoxin system, toxin component, GNAT...	87	8e-16
ref	ZP_05036885.1	acetyltransferase, GNAT family [Synechococcus...	87	8e-16
ref	ZP_08034621.1	toxin-antitoxin system, toxin component, GNAT...	87	9e-16
ref	YP_003638540.1	Phosphinothricin acetyltransferase [Cellulom...	87	9e-16
ref	YP_001235019.1	GCN5-related N-acetyltransferase [Acidiphili...	87	9e-16
ref	ZP_02382636.1	putative antibiotic resistance (acetyltransfe...	87	1e-15
ref	YP_987554.1	GCN5-related N-acetyltransferase [Acidovorax sp...	87	1e-15
ref	ZP_03699912.1	GCN5-related N-acetyltransferase [Lutiella ni...	87	1e-15
ref	ZP_07675196.1	toxin-antitoxin system, toxin component, GNAT...	87	1e-15
ref	YP_003470746.1	Phosphinothricin N-acetyltransferase [Staphy...	87	1e-15
ref	YP_766974.1	phosphinothricin N-acetyltransferase [Rhizobium...	87	1e-15
ref	YP_001710475.1	putative acetyltransferase [Clavibacter mich...	87	1e-15
ref	ZP_07912391.1	acetyltransferase [Staphylococcus lugdunensis...	87	1e-15
ref	ZP_06690604.1	conserved hypothetical protein [Acinetobacter...	87	1e-15
ref	ZP_03523576.1	probable phosphinothricin acetyltransferase (...)	87	1e-15
ref	YP_199234.1	phosphinothricin acetyltransferase [Xanthomonas...	87	1e-15
ref	YP_192775.1	putative acetyltransferase (antibiotic resistan...	87	1e-15
ref	XP_645686.1	hypothetical protein DDB_G0271268 [Dictyosteliu...	86	1e-15
ref	YP_003744261.1	antibiotic resistance protein (acetyltransfe...	86	1e-15
ref	YP_003109023.1	GCN5-related N-acetyltransferase [Acidimicro...	86	2e-15
dbj	BAI77991.1	phosphinothricin N-acetyltransferase [Pseudomona...	86	2e-15

ref YP_002550431.1	acetyltransferase [Agrobacterium vitis S4] >...	86	2e-15
ref YP_001336218.1	acetyltransferase [Klebsiella pneumoniae sub...	86	2e-15
ref YP_003992355.1	GCN5-like N-acetyltransferase [Caldicellulos...	86	2e-15
ref ZP_07182496.1	toxin-antitoxin system, toxin component, GNAT...	86	2e-15
ref YP_001222281.1	putative N-acetyltransferase [Clavibacter mi...	86	2e-15
ref YP_001395681.1	acetyltransferase [Clostridium kluyveri DSM ...	86	2e-15
ref YP_002237448.1	putative phosphinothricin N-acetyltransferas...	86	2e-15
ref YP_001296551.1	phosphinothricin N-acetyltransferase YncA [F...	86	2e-15
ref YP_002382603.1	acyl-CoA N-acyltransferase [Escherichia ferg...	86	2e-15
ref ZP_03000532.1	acetyltransferase, GNAT family [Escherichia c...	86	2e-15
gb EGC95077.1	acyl-CoA N-acyltransferase [Escherichia fergusonii...	86	2e-15
ref YP_003377320.1	N-acetyltransferase [Xanthomonas albilineans...	86	2e-15
ref ZP_02799324.2	acetyltransferase, GNAT family [Escherichia c...	86	2e-15
ref YP_002386887.1	putative acyl-CoA N-acyltransferase [Escheri...	86	2e-15
ref ZP_05119263.1	phosphinothricin N-acetyltransferase [Vibrio ...	86	2e-15
ref ZP_07477230.1	acetyltransferase [Brucella sp. B01] >gi 3062...	86	2e-15
ref NP_753773.1	acetyltransferase yncA [Escherichia coli CFT073...	86	2e-15
ref YP_001566360.1	GCN5-like N-acetyltransferase [Delftia acido...	86	2e-15
ref YP_449585.1	phosphinothricin acetyltransferase [Xanthomonas...	86	2e-15
ref YP_002893339.1	GCN5-related N-acetyltransferase [Tolomonas ...	86	3e-15
ref ZP_07827503.1	toxin-antitoxin system, toxin component, GNAT...	86	3e-15
ref ZP_06703884.1	N-acetyltransferase [Xanthomonas fuscans subs...	86	3e-15
gb EGC07342.1	acetyltransferase [Escherichia fergusonii B253]	86	3e-15
ref ZP_07823528.1	acetyltransferase, GNAT family [Streptococcus...	86	3e-15
ref YP_001743779.1	acetyltransferase [Escherichia coli SMS-3-5]...	86	3e-15
ref NP_890464.1	hypothetical protein BB3930 [Bordetella bronchi...	86	3e-15
ref ZP_07623784.1	putative acyl-CoA N-acyltransferase [Escheric...	86	3e-15
ref YP_003820657.1	Phosphinothricin acetyltransferase [Clostrid...	86	3e-15
ref ZP_07463894.1	Phosphinothricin N-acetyltransferase [Strepto...	86	3e-15
ref YP_003429952.1	acetyltransferase (GNAT) family [Streptococc...	86	3e-15
ref YP_001880295.1	acetyltransferase, GNAT family [Shigella boy...	86	3e-15
ref YP_002919687.1	hypothetical acetyltransferase [Klebsiella p...	86	3e-15
gb EGB59486.1	acetyltransferase [Escherichia coli M863] >gi 323...	86	3e-15
ref ZP_07618583.1	putative acyltransferase with acyl-CoA N-acyl...	86	3e-15
ref ZP_07162231.1	toxin-antitoxin system, toxin component, GNAT...	86	3e-15
ref ZP_06486378.1	phosphinothricin acetyltransferase [Xanthomon...	86	3e-15
ref ZP_08029282.1	acetyltransferase, GNAT family [Solobacterium...	86	3e-15
emb CAZ87971.1	Phosphinothricin N-acetyltransferase (PPT N-acet...	85	3e-15
ref ZP_08187501.1	sortase-like acyltransferase [Xanthomonas per...	85	3e-15
gb EFW57438.1	Putative acetyltransferase [Shigella boydii ATCC ...	85	3e-15
ref YP_299321.1	GCN5-related N-acetyltransferase [Ralstonia eut...	85	3e-15
ref NP_644097.1	phosphinothricin acetyltransferase [Xanthomonas...	85	3e-15
ref ZP_06488940.1	phosphinothricin acetyltransferase [Xanthomon...	85	3e-15
ref YP_002546043.1	phosphinothricin N-acetyltransferase (antibi...	85	3e-15
ref YP_365646.1	N-acetyltransferase [Xanthomonas campestris pv...	85	3e-15
ref ZP_06352816.1	toxin-antitoxin system, toxin component, GNAT...	85	4e-15
ref NP_837412.1	putative resistance protein [Shigella flexneri ...	85	4e-15
ref ZP_07825890.1	acetyltransferase, GNAT family [Dialister mic...	85	4e-15
ref ZP_01734503.1	hypothetical protein FBBAL38_09159 [Flavobact...	85	4e-15
ref NP_287713.1	putative resistance protein [Escherichia coli O...	85	4e-15
ref NP_385668.1	putative acetyltransferase (antibiotic resistanc...	85	4e-15
gb EFW74048.1	Putative acetyltransferase [Escherichia coli EC41...	85	4e-15
gb EFW52005.1	putative acetyltransferase [Shigella dysenteriae ...	85	4e-15
ref ZP_05077427.1	phosphinothricin acetyltransferase [Rhodobact...	85	4e-15
gb AAT96234.1	phosphinothricin N-acetyltransferase [Pseudomonas...	85	4e-15
emb CBJ36480.1	putative antibiotic resistance protein (Acetyltr...	85	4e-15
ref ZP_05626426.1	phosphinothricin N-acetyltransferase [Campylo...	85	4e-15
ref YP_001458245.1	acetyltransferase [Escherichia coli HS] >gi ...	85	4e-15
ref YP_004287364.1	phosphinothricin acetyltransferase [Streptoc...	85	4e-15
ref YP_408038.1	resistance protein [Shigella boydii Sb227] >gi ...	85	5e-15
ref ZP_04562062.1	conserved hypothetical protein [Citrobacter s...	85	5e-15
ref ZP_05639427.1	phosphinothricin N-acetyltransferase [Pseudom...	85	5e-15
ref ZP_05056656.1	acetyltransferase, GNAT family [Verrucomicrob...	85	5e-15

sp P31668.1 PAT_ALCFA RecName: Full=Phosphinothricin N-acetyltra...	85	5e-15
ref NP_415965.1 predicted acyltransferase with acyl-CoA N-acylt...	85	5e-15
ref YP_003648553.1 GCN5-related N-acetyltransferase [Tsukamurel...	85	5e-15
ref YP_003801878.1 GCN5-related N-acetyltransferase [Spirochaet...	85	5e-15
ref YP_003036408.1 GCN5-related N-acetyltransferase [Escherichi...	84	6e-15
ref YP_001991332.1 GCN5-related N-acetyltransferase [Rhodopseud...	84	6e-15
ref ZP_06934756.1 predicted acyltransferase with acyl-CoA N-acy...	84	6e-15
ref ZP_04661553.1 Acetyltransferase (GNAT) family protein [Acin...	84	6e-15
ref YP_002544927.1 phosphinothricin acetyltransferase (antibiot...	84	6e-15
ref YP_001335576.1 acetyltransferase [Klebsiella pneumoniae sub...	84	7e-15
ref YP_001453059.1 hypothetical protein CKO_01490 [Citrobacter ...	84	7e-15
ref YP_004109757.1 GCN5-like N-acetyltransferase [Rhodopseudomo...	84	7e-15
ref YP_310616.1 putative resistance protein [Shigella sonnei Ss...	84	7e-15
gb AAT96250.1 phosphinothricin N-acetyltransferase [Pseudomonas...	84	8e-15
gb AAT96331.1 phosphinothricin N-acetyltransferase [Pseudomonas...	84	8e-15
gb AAT96291.1 phosphinothricin N-acetyltransferase [Pseudomonas...	84	8e-15
ref NP_947397.1 putative phosphinothricin N-acetyltransferase [R...	84	8e-15
ref ZP_07153818.1 toxin-antitoxin system, toxin component, GNAT...	84	8e-15
ref YP_001630169.1 acetyltransferase [Bordetella petrii DSM 128...	84	8e-15
ref YP_003365162.1 putative acetyltransferase [Citrobacter rode...	84	9e-15
ref YP_004214190.1 GCN5-related N-acetyltransferase [Rahnella s...	84	9e-15
ref ZP_02244935.1 phosphinothricin acetyltransferase [Xanthomon...	84	9e-15
ref YP_002983106.1 GCN5-like N-acetyltransferase [Ralstonia pic...	84	9e-15
ref ZP_04600234.1 hypothetical protein VEIDISOL_01683 [Veillone...	84	1e-14
gb ADY81488.1 putative antibiotic resistance (acetyltransferase...	84	1e-14
ref YP_001622888.1 hypothetical protein BSUIS_B1127 [Brucella s...	84	1e-14
ref YP_001270028.1 GCN5-related N-acetyltransferase [Pseudomona...	84	1e-14
emb CBJ01023.1 putative acetyltransferase [Escherichia coli ETE...	84	1e-14
ref YP_001893348.1 GCN5-related N-acetyltransferase [Ralstonia ...	84	1e-14
ref ZP_03043698.1 acetyltransferase, GNAT family [Escherichia c...	83	1e-14
ref ZP_07466039.1 phosphinothricin N-acetyltransferase [Strepto...	83	1e-14
ref ZP_00049330.1 COG1247: Sortase and related acyltransferases...	83	1e-14
ref ZP_03629351.1 GCN5-related N-acetyltransferase [bacterium E...	83	1e-14
ref ZP_02691607.1 Phosphinothricin N-acetyltransferase [Epulopi...	83	1e-14
ref YP_001239152.1 putative phosphinothricin N-acetyltransferas...	83	1e-14
ref ZP_05827462.1 sortase [Acinetobacter baumannii ATCC 19606] ...	83	1e-14
ref NP_881122.1 hypothetical protein BP2495 [Bordetella pertuss...	83	1e-14
ref ZP_07507612.1 putative acyl-CoA N-acyltransferase [Escheric...	83	1e-14
ref YP_003635502.1 Phosphinothricin acetyltransferase [Cellulom...	83	1e-14
ref NP_746951.1 GCN5-related N-acetyltransferase [Pseudomonas p...	83	1e-14
ref YP_003612366.1 GCN5-related N-acetyltransferase [Enterobact...	83	2e-14
ref YP_003882401.1 GCN5-related N-acetyltransferase [Dickeya da...	83	2e-14
gb AAT96242.1 phosphinothricin N-acetyltransferase [Pseudomonas...	83	2e-14
ref YP_001671123.1 GCN5-related N-acetyltransferase [Pseudomona...	83	2e-14
ref ZP_03786255.1 acetyltransferase [Brucella ceti str. Cudo] >...	83	2e-14
ref YP_001259507.1 acetyltransferase [Brucella ovis ATCC 25840]...	83	2e-14
gb ADZ87583.1 GCN5-related N-acetyltransferase [Brucella melite...	83	2e-14
ref ZP_01816180.1 toxin resistance protein [Vibrionales bacteri...	83	2e-14
ref YP_368499.1 GCN5-related N-acetyltransferase [Burkholderia ...	83	2e-14
gb ADZ66726.1 GCN5-related N-acetyltransferase [Brucella melite...	83	2e-14
ref YP_003221537.1 putative acyltransferase [Escherichia coli O...	83	2e-14
ref NP_539296.1 phosphinothricin N-acetyltransferase [Brucella ...	83	2e-14
ref YP_001221862.1 putative acetyltransferase [Clavibacter mich...	83	2e-14
ref YP_001713984.1 putative antibiotic resistance (phosphinothr...	83	2e-14
ref YP_359127.1 putative phosphinothricin N-acetyltransferase [...	83	2e-14
ref ZP_05824268.1 sortase [Acinetobacter sp. RUH2624] >gi 26040...	82	2e-14
ref YP_003751039.1 antibiotic resistance protein (acetyltransfe...	82	2e-14
ref ZP_01984684.1 phosphinothricin N-acetyltransferase [Vibrio ...	82	2e-14
gb ADR62194.1 GCN5-related N-acetyltransferase [Pseudomonas put...	82	2e-14
ref ZP_08178282.1 sortase-like acyltransferase [Xanthomonas ves...	82	2e-14
ref YP_001792179.1 GCN5-like N-acetyltransferase [Leptothrix ch...	82	2e-14
ref ZP_04595027.1 GCN5-related N-acetyltransferase [Brucella ab...	82	2e-14
ref ZP_05967781.1 toxin-antitoxin system, toxin component, GNAT...	82	2e-14

ref YP_001176830.1	GCN5-related N-acetyltransferase [Enterobact...	82	2e-14
ref YP_001935515.1	GCN5-related N-acetyltransferase [Brucella a...	82	3e-14
ref YP_001707430.1	putative antibiotic resistance (phosphinothr...	82	3e-14
ref ZP_02188651.1	phosphinothricin N-acetyltransferase [alpha p...	82	3e-14
ref ZP_06487360.1	putative phosphinothricin N-acetyltransferase...	82	3e-14
ref ZP_08117889.1	GCN5-related N-acetyltransferase [Thermoanaer...	82	3e-14
ref YP_002733348.1	GCN5-related N-acetyltransferase [Brucella m...	82	3e-14
ref YP_001580341.1	GCN5-related N-acetyltransferase [Burkholder...	82	3e-14
gb EFZ55752.1	acetyltransferase family protein [Escherichia col...	82	3e-14
ref ZP_07773233.1	acetyltransferase [Pseudomonas fluorescens WH...	82	3e-14
gb EFZ70777.1	acetyltransferase family protein [Escherichia col...	82	3e-14
ref NP_521254.1	putative antibiotic resistance (acetyltransfera...	82	3e-14
ref ZP_06348055.1	toxin-antitoxin system, toxin component, GNAT...	82	3e-14
ref YP_001710167.1	putative toxin resistance acetyltransferase ...	82	4e-14
ref ZP_06548680.1	acetyltransferase [Klebsiella sp. 1_1_55] >gi...	82	4e-14
ref YP_002997301.1	phosphinothricin N-acetyltransferase [Strept...	82	4e-14
ref ZP_03543324.1	GCN5-related N-acetyltransferase [Comamonas t...	82	4e-14
ref YP_002238268.1	acetyltransferase, GNAT family [Klebsiella p...	82	4e-14
ref YP_002140771.1	GNAT family acetyltransferase [Geobacter bem...	82	4e-14
ref YP_222318.1	acetyltransferase [Brucella abortus bv. 1 str. ...	82	4e-14
gb EFA85320.1	hypothetical protein PPL_02321 [Polysphondylium p...	82	5e-14
gb EFY03230.1	acetyltransferase (GNAT) family protein [Streptoc...	81	5e-14
ref YP_001527618.1	putative acetyltransferase protein [Azorhizo...	81	5e-14
ref NP_698636.1	acetyltransferase [Brucella suis 1330] >gi 1616...	81	5e-14
ref YP_003977234.1	GNAT family acetyltransferase 4 [Achromobact...	81	5e-14
ref ZP_08127446.1	hypothetical protein AoriK_13175 [Actinomyces...	81	5e-14
ref YP_003271604.1	GCN5-like N-acetyltransferase [Gordonia bron...	81	5e-14
ref YP_001206849.1	putative phosphinothricin N-acetyltransferas...	81	5e-14
ref ZP_06911259.1	phosphinothricin N-acetyltransferase [Strepto...	81	6e-14
ref NP_662156.1	acetyltransferase [Chlorobium tepidum TLS] >gi ...	81	6e-14
ref ZP_01229015.1	phosphinothricin N-acetyltransferase [Auranti...	81	7e-14
ref YP_001846218.1	sortase [Acinetobacter baumannii ACICU] >gi ...	81	8e-14
ref YP_001751487.1	GCN5-related N-acetyltransferase [Pseudomona...	80	8e-14
ref YP_003642748.1	Phosphinothricin acetyltransferase [Thiomona...	80	8e-14
ref YP_003732477.1	putative antibiotic resistance (phosphinothr...	80	9e-14
gb ACR54770.1	sortase [Acinetobacter genomosp. 13TU]	80	9e-14
ref YP_522665.1	GCN5-related N-acetyltransferase [Rhodoferax fe...	80	9e-14
ref YP_004278147.1	GCN5-related N-acetyltransferase [Agrobacter...	80	9e-14
ref ZP_07471113.1	acetyltransferase [Brucella sp. NF 2653] >gi ...	80	1e-13
ref ZP_06808016.1	phosphinothricin acetyltransferase [Aerococcu...	80	1e-13
ref YP_003308692.1	phosphinothricin acetyltransferase [Sebaldel...	80	1e-13
ref YP_046305.1	putative phosphinothricin N-acetyltransferase [...	80	1e-13
ref ZP_04681054.1	acetyltransferase [Ochrobactrum intermedium L...	80	1e-13
ref ZP_06686178.1	acetyltransferase [Achromobacter piechaudii A...	80	1e-13
ref YP_003807359.1	GCN5-related N-acetyltransferase [Desulfarcu...	80	1e-13
gb ADX25103.1	acetyltransferase (GNAT) family protein [Streptoc...	80	1e-13
ref YP_001326928.1	GCN5-related N-acetyltransferase [Sinorhizob...	80	1e-13
emb CBK87879.1	Sortase and related acyltransferases [Eubacteriu...	80	1e-13
gb ABB77438.1	acetyl- or acyltransferase [Mitsuokella multacida]	80	1e-13
ref ZP_01158185.1	phosphinothricin N-acetyltransferase, putativ...	80	1e-13
ref ZP_06113675.1	toxin-antitoxin system, toxin component, GNAT...	80	1e-13
ref ZP_05181470.1	hypothetical protein Bru83_08976 [Brucella sp...	80	1e-13
ref ZP_07474073.1	acetyltransferase [Brucella sp. B02] >gi 3062...	80	2e-13
ref YP_001764419.1	GCN5-related N-acetyltransferase [Burkholder...	80	2e-13
ref YP_744013.1	phosphinothricin N-acetyltransferase [Granuliba...	80	2e-13
ref NP_253553.1	hypothetical protein PA4866 [Pseudomonas aerugi...	80	2e-13
ref YP_002908175.1	GCN5-related N-acetyltransferase [Burkholder...	80	2e-13
ref ZP_04931736.1	conserved hypothetical protein [Pseudomonas a...	80	2e-13
ref ZP_01367883.1	hypothetical protein PaerPA_01005037 [Pseudom...	80	2e-13
ref YP_001350908.1	hypothetical protein PSPA7_5587 [Pseudomonas...	79	2e-13
ref ZP_01442088.1	phosphinothricin N-acetyltransferase, putativ...	79	2e-13
ref ZP_06881175.1	putative phosphinothricin N-acetyltransferase...	79	2e-13
ref NP_294906.1	phosphinothricin acetyltransferase [Deinococcus...	79	2e-13

ref XP_002536396.1	conserved hypothetical protein [Ricinus comm...	79	2e-13
ref ZP_06825188.1	phosphinothricin N-acetyltransferase [Strepto...	79	2e-13
ref ZP_03520117.1	putative phosphinothricin N-acetyltransferase...	79	3e-13
gb EGD02187.1	GCN5-related N-acetyltransferase [Burkholderia sp...	79	3e-13
ref ZP_06056650.1	sortase [Acinetobacter calcoaceticus RUH2202]...	79	3e-13
ref ZP_05341911.1	acetyltransferase, gnat family [Thalassiosira...	79	3e-13
ref YP_003850803.1	GCN5-related N-acetyltransferase [Thermoanaer...	79	3e-13
ref XP_001617616.1	hypothetical protein NEMVEDRAFT_vlg225937 [N...	79	3e-13
ref YP_001437992.1	hypothetical protein ESA_01902 [Cronobacter ...	79	3e-13
ref YP_004125851.1	phosphinothricin acetyltransferase [Alicyclobac...	79	3e-13
ref YP_003278266.1	GCN5-related N-acetyltransferase [Comamonas ...	79	4e-13
ref ZP_01547046.1	phosphinothricin N-acetyltransferase, putativ...	78	4e-13
ref YP_257776.1	acetyltransferase [Pseudomonas fluorescens Pf-5...	78	4e-13
ref ZP_03127829.1	GCN5-related N-acetyltransferase [Chthoniobac...	78	5e-13
ref ZP_02153326.1	phosphinothricin N-acetyltransferase, putativ...	78	5e-13
ref ZP_07975671.1	phosphinothricin N-acetyltransferase [Strepto...	78	5e-13
gb EFV82779.1	acetyltransferase [Achromobacter xylosoxidans C54]	78	5e-13
ref ZP_05162143.1	hypothetical protein Bsuib55_05592 [Brucella ...	78	5e-13
ref YP_002870251.1	putative acetyltransferase [Pseudomonas fluo...	78	5e-13
ref YP_004211929.1	Phosphinothricin acetyltransferase [Rahnella...	78	5e-13
ref YP_002230172.1	acetyltransferase (GNAT) family protein [Bur...	77	9e-13
ref YP_620550.1	GCN5-related N-acetyltransferase [Burkholderia ...	77	9e-13
ref ZP_06833815.1	putative acetyltransferase (antibiotic resist...	77	9e-13
ref YP_001369814.1	GCN5-like N-acetyltransferase [Ochrobactrum ...	77	1e-12
ref YP_003938516.1	Phosphinothricin N-acetyltransferase [Bifido...	77	1e-12
ref ZP_03129084.1	GCN5-related N-acetyltransferase [Chthoniobac...	77	1e-12
ref ZP_07272181.1	phosphinothricin N-acetyltransferase [Strepto...	77	1e-12
ref ZP_04744486.1	toxin-antitoxin system, toxin component, GNAT...	77	1e-12
pdb 2BL1 A Chain A, Crystal Structure Of A Putative Phosphinothr...		77	1e-12
ref ZP_07316760.1	toxin-antitoxin system, toxin component, GNAT...	77	1e-12
pdb 1YVO A Chain A, Hypothetical Acetyltransferase From P.Aerugi...		77	1e-12
ref ZP_07986020.1	phosphinothricin N-acetyltransferase [Strepto...	77	1e-12
ref ZP_06898706.1	phosphinothricin acetyltransferase [Roseomonas...	77	1e-12
ref ZP_05087661.1	phosphinothricin N-acetyltransferase, putativ...	77	1e-12
ref YP_003970832.1	phosphinothricin N-acetyltransferase [Bifido...	77	1e-12
ref NP_353926.1	phosphinothricin acetyltransferase [Agrobacteri...	77	1e-12
ref ZP_01755850.1	phosphinothricin N-acetyltransferase, putativ...	77	1e-12
ref YP_001862480.1	GCN5-related N-acetyltransferase [Burkholder...	76	2e-12
ref YP_003579438.1	GNAT family acetyltransferase [Rhodobacter c...	76	2e-12
ref ZP_08184514.1	sortase-like acyltransferase [Xanthomonas gar...	76	2e-12
ref ZP_04817732.1	possible Phosphinothricin acetyltransferase [...	76	2e-12
ref ZP_05117294.1	acetyltransferase, GNAT family [Labrenzia ale...	76	2e-12
gb ADZ72147.1	Phosphinothricin N-acetyltransferase, putative [P...	76	2e-12
pdb 1YR0 A Chain A, Crystal Structure Of Phosphinothricin Acetyl...		76	2e-12
ref YP_587199.1	putative GNAT family acetyltransferase [Cupriav...	76	2e-12
ref YP_610326.1	acetyltransferase [Pseudomonas entomophila L48]...	75	3e-12
ref YP_002434888.1	GCN5-related N-acetyltransferase [Desulfovib...	75	3e-12
ref ZP_06067059.1	predicted protein [Acinetobacter junii SH205]...	75	4e-12
ref NP_633926.1	hypothetical protein MM_1902 [Methanosarcina ma...	75	4e-12
ref ZP_02081461.1	hypothetical protein CLOLEP_02937 [Clostridiu...	75	4e-12
ref ZP_05780450.1	acetyltransferase, gnat family [Citricella s...	75	6e-12
ref ZP_01056746.1	phosphinothricin N-acetyltransferase, putativ...	74	6e-12
ref ZP_04704159.1	phosphinothricin N-acetyltransferase [Strepto...	74	6e-12
ref YP_001789720.1	GCN5-like N-acetyltransferase [Leptothrix ch...	74	6e-12
ref YP_682326.1	acetyltransferase, putative [Roseobacter denitr...	74	6e-12
ref ZP_05091057.1	phosphinothricin acetyltransferase [Ruegeria ...	74	7e-12
ref YP_346316.1	GCN5-related N-acetyltransferase [Pseudomonas f...	74	8e-12
ref YP_926367.1	N-acetyltransferase [Shewanella amazonensis SB2...	74	9e-12
ref ZP_06070386.1	conserved hypothetical protein [Acinetobacter...	74	9e-12
ref YP_004246656.1	GCN5-related N-acetyltransferase [Spirochaet...	74	1e-11
ref ZP_06729221.1	phosphinothricin acetyltransferase [Acinetoba...	74	1e-11
ref YP_003576977.1	GNAT family acetyltransferase [Rhodobacter c...	74	1e-11
ref ZP_03612639.1	acetyltransferase, gnat family [Staphylococcu...	74	1e-11

ref	ZP_03646126.1	GCN5-related N-acetyltransferase [Bifidobacte...	73	1e-11
ref	ZP_07802156.1	conserved hypothetical protein [Bifidobacteri...	73	1e-11
ref	ZP_05740840.1	phosphinothricin n-acetyltransferase [Silicib...	73	2e-11
ref	ZP_03528901.1	GCN5-related N-acetyltransferase [Rhizobium e...	73	2e-11
ref	ZP_07841923.1	toxin-antitoxin system, toxin component, GNAT...	73	2e-11
gb	EFV00086.1	acetyltransferase family protein [Escherichia col...	72	2e-11
ref	YP_003698513.1	GCN5-like N-acetyltransferase [Bacillus sele...	72	2e-11
ref	ZP_03574401.1	acetyltransferase, gnat family [Burkholderia ...	72	2e-11
ref	YP_004118309.1	GCN5-related N-acetyltransferase [Pantoea sp...	72	2e-11
ref	YP_237501.1	GCN5-related N-acetyltransferase [Pseudomonas s...	72	3e-11
ref	ZP_01092054.1	GCN5-related N-acetyltransferase [Blastopirel...	72	3e-11
ref	ZP_03823828.1	acetyltransferase [Acinetobacter sp. ATCC 272...	72	3e-11
ref	ZP_07250854.1	phosphinothricin N-acetyltransferase, putativ...	72	3e-11
ref	ZP_03972494.1	Phosphinothricin acetyltransferase [Corynebac...	72	4e-11
ref	ZP_03396120.1	phosphinothricin N-acetyltransferase [Pseudom...	72	4e-11
ref	ZP_03587049.1	acetyltransferase, gnat family [Burkholderia ...	72	4e-11
sp	Q54225.1	NAT_STRGR RecName: Full=N-acetyltransferase >gi 5104...	72	5e-11
ref	YP_917443.1	GCN5-related N-acetyltransferase [Paracoccus de...	71	5e-11
ref	NP_691255.1	phosphinothricin N-acetyltransferase [Oceanobac...	71	6e-11
ref	NP_767756.1	phosphinothricin acetyltransferase [Bradyrhizob...	71	6e-11
ref	YP_003210449.1	N-acetyltransferase YncA [Cronobacter turice...	71	6e-11
ref	ZP_07232129.1	phosphinothricin N-acetyltransferase, putativ...	71	7e-11
ref	YP_003922093.1	phosphinothricin acetyltransferase [Bacillus...	71	7e-11
ref	ZP_05637338.1	phosphinothricin N-acetyltransferase, putativ...	71	7e-11
ref	YP_001998872.1	GCN5-related N-acetyltransferase [Chlorobacu...	71	7e-11
ref	YP_001338537.1	N-acetyltransferase-like protein [Klebsiella...	70	8e-11
ref	ZP_06042260.1	GCN5-related N-acetyltransferase [Corynebacte...	70	8e-11
ref	NP_794626.1	phosphinothricin N-acetyltransferase [Pseudomon...	70	9e-11
ref	ZP_07317215.1	toxin-antitoxin system, toxin component, GNAT...	70	9e-11
ref	YP_003212788.1	hypothetical protein Ctu_3p00440 [Cronobacte...	70	1e-10
ref	YP_003559670.1	putative acetyltransferase [Sphingobium japo...	70	1e-10
ref	YP_001422934.1	YwnH [Bacillus amyloliquefaciens FZB42] >gi ...	70	1e-10
ref	YP_001762213.1	GCN5-like N-acetyltransferase [Shewanella wo...	70	1e-10
ref	ZP_03394589.1	acetyltransferase, gnat family [Corynebacteri...	70	1e-10
ref	YP_001807735.1	GCN5-related N-acetyltransferase [Burkholder...	70	1e-10
ref	ZP_01910089.1	PHOSPHINOTHRICIN N-ACETYLTRANSFERASE [Plesioc...	70	1e-10
ref	YP_003941905.1	Phosphinothricin acetyltransferase [Enteroba...	70	2e-10
ref	YP_613856.1	GCN5-related N-acetyltransferase [Ruegeria sp. ...	70	2e-10
ref	YP_001943206.1	GCN5-related N-acetyltransferase [Chlorobium...	70	2e-10
ref	YP_003688562.1	Acetyltransferase [Propionibacterium freuden...	70	2e-10
ref	ZP_07050608.1	phosphinothricin N-acetyltransferase [Lysinib...	69	2e-10
ref	ZP_05964895.1	N-acetyltransferase [Brucella neotomae 5K33] ...	69	2e-10
ref	YP_003825004.1	GCN5-related N-acetyltransferase [Thermosedi...	69	2e-10
ref	ZP_06538070.1	putative acetyltransferase [Salmonella enteri...	69	2e-10
ref	ZP_03226282.1	acetyltransferase [Bacillus coahuilensis m4-4]	69	2e-10
ref	YP_002785791.1	acetyltransferase [Deinococcus deserti VCD11...	69	2e-10
ref	ZP_03697450.1	GCN5-related N-acetyltransferase [Lutiella ni...	69	2e-10
ref	ZP_02906179.1	GCN5-related N-acetyltransferase [Burkholderi...	69	2e-10
ref	ZP_00238331.1	acetyltransferase, GNAT family [Bacillus cere...	69	2e-10
ref	ZP_02890613.1	GCN5-related N-acetyltransferase [Burkholderi...	69	3e-10
ref	ZP_08079389.1	acetyltransferase, GNAT family [Succinatimona...	69	3e-10
ref	ZP_08019786.1	phosphinothricin acetyltransferase [Lautropia...	69	3e-10
ref	ZP_06458223.1	phosphinothricin N-acetyltransferase, putativ...	69	3e-10
ref	YP_003705558.1	GCN5-related N-acetyltransferase [Truepera r...	69	3e-10
ref	YP_772917.1	GCN5-related N-acetyltransferase [Burkholderia ...	69	3e-10
ref	ZP_05780962.1	phosphinothricin N-acetyltransferase [Citreic...	69	4e-10
ref	ZP_07006942.1	GCN5-related N-acetyltransferase [Pseudomonas...	68	4e-10
ref	ZP_02161988.1	Phosphinothricin N-acetyltransferase [Kordia ...	68	5e-10
ref	YP_001186194.1	GCN5-related N-acetyltransferase [Pseudomona...	68	5e-10
ref	YP_001279533.1	GCN5-related N-acetyltransferase [Psychrobac...	68	5e-10
ref	YP_002467454.1	GCN5-related N-acetyltransferase [Methanosph...	68	5e-10
ref	ZP_01858609.1	hypothetical protein BSG1_03775 [Bacillus sp....	68	6e-10
gb	EFW78864.1	phosphinothricin N-acetyltransferase, putative [P...	68	6e-10

ref ZP_01386326.1	GCN5-related N-acetyltransferase [Chlorobium ...	68	6e-10
ref YP_003840370.1	GCN5-related N-acetyltransferase [Caldicellu...	68	6e-10
ref YP_003696266.1	GCN5-related N-acetyltransferase [Starkeya n...	68	6e-10
ref ZP_05843895.1	GCN5-related N-acetyltransferase [Rhodobacter...	68	6e-10
ref ZP_06064160.1	acetyltransferase [Acinetobacter johnsonii SH...	68	7e-10
ref ZP_04635815.1	hypothetical protein yinte0001_16760 [Yersini...	68	7e-10
ref ZP_06496516.1	GCN5-related N-acetyltransferase [Pseudomonas...	67	7e-10
ref YP_003997004.1	gcn5-related N-acetyltransferase [Leadbetter...	67	7e-10
ref YP_502905.1	GCN5-related N-acetyltransferase [Methanospiril...	67	7e-10
ref ZP_07048308.1	phosphinothricin N-acetyltransferase [Lysinib...	67	8e-10
ref ZP_08206859.1	sortase [Gordonia neofelifaecis NRRL B-59395]...	67	9e-10
ref YP_785269.1	N-acetyltransferase [Bordetella avium 197N] >gi...	67	9e-10
gb ADZ76815.1	GCN5-related N-acetyltransferase [Sphingobacteriu...	67	1e-09
ref YP_001532082.1	GCN5-like N-acetyltransferase [Dinoroseobact...	67	1e-09
ref ZP_05366549.1	phosphinothricin N-acetyltransferase [Coryneb...	67	1e-09
ref ZP_07377158.1	GCN5-related N-acetyltransferase [Pantoea sp....	67	1e-09
ref ZP_00958271.1	putative acetyltransferase, GNAT family prote...	67	1e-09
ref YP_0023962714.1	N-acetyltransferase yncA [Ketogulonicigenium...	67	1e-09
ref ZP_07714681.1	phosphinothricin acetyltransferase [Corynebac...	66	2e-09
ref YP_080971.1	putative phosphinothricin acetyltransferase [Ba...	66	2e-09
ref NP_786466.1	phosphinothricin N-acetyltransferase [Lactobaci...	66	2e-09
ref ZP_07265426.1	GCN5-related N-acetyltransferase [Pseudomonas...	66	2e-09
gb EFW79832.1	phosphinothricin N-acetyltransferase [Pseudomonas...	66	2e-09
ref ZP_06884360.1	GCN5-related N-acetyltransferase [Clostridium...	66	2e-09
ref YP_003064133.1	phosphinothricin N-acetyltransferase [Lactob...	66	2e-09
ref XP_756087.1	GNAT family N-acetyltransferase [Aspergillus fu...	66	2e-09
gb EDP55256.1	GNAT family N-acetyltransferase, putative [Asperg...	66	2e-09
ref NP_615734.1	phosphinothricin acetyltransferase [Methanosarc...	66	2e-09
ref YP_003194019.1	phosphinothricin N-acetyltransferase [Robigi...	66	3e-09
ref YP_276592.1	phosphinothricin N-acetyltransferase [Pseudomon...	65	3e-09
ref ZP_07388746.1	Phosphinothricin acetyltransferase [Paenibaci...	65	3e-09
ref YP_003650967.1	GCN5-related N-acetyltransferase [Thermobisp...	65	3e-09
ref YP_002778658.1	acetyltransferase [Rhodococcus opacus B4] >g...	65	4e-09
ref YP_001118910.1	GCN5-related N-acetyltransferase [Burkholder...	65	4e-09
ref ZP_01447778.1	phosphinothricin N-acetyltransferase [alpha p...	65	4e-09
ref YP_001196742.1	GCN5-related N-acetyltransferase [Flavobacte...	65	4e-09
ref YP_100962.1	putative acetyltransferase [Bacteroides fragili...	65	4e-09
ref YP_003085267.1	GCN5-related N-acetyltransferase [Dyadobacte...	65	4e-09
ref YP_003191605.1	GCN5-related N-acetyltransferase [Desulfotom...	65	4e-09
ref ZP_01059494.1	phosphinothricin N-acetyltransferase [Leeuwen...	65	4e-09
ref ZP_05122029.1	phosphinothricin acetyltransferase [Rhodobact...	65	4e-09
ref ZP_04586796.1	GCN5-related N-acetyltransferase [Pseudomonas...	65	5e-09
ref ZP_03489074.1	hypothetical protein EUBIFOR_01660 [Eubacteri...	65	5e-09
ref YP_213080.1	putative acetyltransferase [Bacteroides fragili...	65	5e-09
ref ZP_07087704.1	phosphinothricin acetyltransferase [Chryseoba...	65	6e-09
ref ZP_03934219.1	possible Phosphinothricin acetyltransferase [...	64	6e-09
ref ZP_08002273.1	YwnH protein [Bacillus sp. BT1B_CT2] >gi 3173...	64	6e-09
emb CBW23960.1	putative acetyltransferase [Bacteroides fragilis...	64	6e-09
ref ZP_04244771.1	GCN5-related N-acetyltransferase [Bacillus ce...	64	7e-09
ref YP_437978.1	sortase and related acyltransferase [Hahella ch...	64	7e-09
ref ZP_05283241.1	putative acetyltransferase [Bacteroides fragi...	64	8e-09
ref ZP_07991612.1	acetyltransferase [Corynebacterium variabile ...	64	9e-09
ref YP_001195416.1	GCN5-related N-acetyltransferase [Flavobacte...	64	9e-09
ref ZP_01902912.1	phosphinothricin N-acetyltransferase, putativ...	64	9e-09
ref YP_003059578.1	GCN5-related N-acetyltransferase [Hirschia b...	64	1e-08
ref YP_001678727.1	phosphinothricin n-acetyltransferase, putati...	64	1e-08
ref ZP_06898661.1	acetyltransferase [Roseomonas cervicalis ATCC...	64	1e-08
ref ZP_07329309.1	GCN5-related N-acetyltransferase [Acetivibrio...	63	2e-08
ref YP_028878.1	hypothetical protein BAS2619 [Bacillus anthraci...	63	2e-08
ref ZP_08109933.1	Phosphinothricin acetyltransferase [Desulfovi...	63	2e-08
ref ZP_03338523.1	putative acetyltransferase [Salmonella enteri...	63	2e-08
ref XP_003034026.1	hypothetical protein SCHCODRAFT_107275 [Schi...	63	2e-08
ref ZP_01852414.1	Putative phosphinothricin N-acetyltransferase...	63	2e-08

ref YP_002794590.1	Phosphinothricin acetyltransferase [Laribact...	63	2e-08
ref YP_001865339.1	GCN5-related N-acetyltransferase [Nostoc pun...	63	2e-08
gb EFU15691.1	acetyltransferase, GNAT family [Enterococcus faec...	63	2e-08
ref YP_686313.1	GNAT family acetyltransferase [uncultured metha...	63	2e-08
ref ZP_04322990.1	GCN5-related N-acetyltransferase [Bacillus ce...	62	3e-08
ref YP_146446.1	phosphinothricin N-acetyltransferase [Geobacill...	62	3e-08
ref ZP_02140906.1	acetyltransferase, putative [Roseobacter lito...	62	3e-08
ref ZP_01446058.1	GCN5-related N-acetyltransferase [Pelagibaca ...	62	3e-08
ref ZP_05475424.1	phosphinothricin N-acetyltransferase [Enteroc...	62	3e-08
ref ZP_00048643.1	COG1247: Sortase and related acyltransferases...	62	3e-08
gb EGC98046.1	GCN5-related N-acetyltransferase [Burkholderia sp...	62	4e-08
ref ZP_06971607.1	transcriptional regulator, ArsR family [Ktedo...	62	4e-08
ref ZP_04946138.1	hypothetical protein BDAG_02064 [Burkholderia...	62	4e-08
ref YP_003996590.1	phosphinothricin acetyltransferase [Leadbett...	62	4e-08
ref ZP_05571308.1	hypothetical protein Faci_07786 [Ferroplasma ...	61	5e-08
ref ZP_06968560.1	GCN5-related N-acetyltransferase [Ktedonobact...	61	6e-08
ref YP_004205490.1	putative phosphinothricin acetyltransferase ...	61	6e-08
ref ZP_08000132.1	hypothetical protein HMPREF1012_01166 [Bacill...	61	6e-08
ref YP_079109.1	GCN5-related N-acetyltransferase [Bacillus lich...	61	6e-08
ref YP_001636579.1	GCN5-related N-acetyltransferase [Chloroflex...	61	6e-08
ref YP_001126960.1	phosphinothricin N-acetyltransferase [Geobac...	61	7e-08
ref YP_353862.1	GNAT family acetyltransferase [Rhodobacter spha...	61	7e-08
ref ZP_03149547.1	GCN5-related N-acetyltransferase [Geobacillus...	61	8e-08
ref ZP_05076285.1	phosphinothricin N-acetyltransferase [Rhodoba...	61	8e-08
ref ZP_03593460.1	hypothetical protein Bsubsl_19761 [Bacillus s...	61	8e-08
ref YP_004091673.1	GCN5-related N-acetyltransferase [Ethanolige...	61	8e-08
ref NP_391537.1	phosphinothricin acetyltransferase [Bacillus su...	61	8e-08
ref ZP_01129948.1	phosphinothricin acetyltransferase protein [m...	60	9e-08
ref XP_003034027.1	hypothetical protein SCHCODRAFT_52412 [Schiz...	60	9e-08
ref YP_003729814.1	acyltransferase [Pantoea vagans C9-1] >gi 29...	60	1e-07
ref ZP_04292465.1	GCN5-related N-acetyltransferase [Bacillus ce...	60	1e-07
ref YP_333836.1	phosphinothricin acetyltransferase [Burkholderi...	60	1e-07
gb EFS50244.1	acetyltransferase, GNAT family [Propionibacterium...	60	1e-07
ref ZP_06427550.1	acetyltransferase, GNAT family [Propionibacte...	60	1e-07
ref YP_108060.1	putative acetyltransferase [Burkholderia pseudo...	60	1e-07
ref ZP_06308276.1	GCN5-related N-acetyltransferase [Cylindrospe...	60	1e-07
ref ZP_04386509.1	transcriptional regulator, ArsR family [Rhodo...	60	1e-07
ref ZP_01078874.1	Phosphinothricin N-acetyltransferase, putativ...	60	1e-07
ref YP_001059314.1	acetyltransferase [Burkholderia pseudomallei...	60	1e-07
ref ZP_03918120.1	Phosphinothricin acetyltransferase [Corynebac...	60	1e-07
ref ZP_06263749.1	acetyltransferase, GNAT family [Propionibacte...	60	1e-07
gb AAV70501.1	unknown [Bacillus sp. MB24]	60	1e-07
ref YP_001812670.1	GCN5-related N-acetyltransferase [Exiguobact...	60	1e-07
ref YP_574837.1	GCN5-related N-acetyltransferase [Chromohalobac...	60	1e-07
ref YP_002776597.1	putative ArsR family transcriptional regulat...	60	2e-07
ref ZP_07468658.1	phosphinothricin acetyltransferase [Corynebac...	60	2e-07
ref YP_002766834.1	ArsR family transcriptional regulator [Rhodo...	60	2e-07
ref YP_001137970.1	hypothetical protein cgr_1092 [Corynebacteri...	60	2e-07
ref YP_003086321.1	GCN5-related N-acetyltransferase [Dyadobacte...	59	2e-07
ref ZP_06735037.1	putative phosphinothricin N-acetyltransferase...	59	2e-07
ref YP_002526507.1	GCN5-related N-acetyltransferase [Rhodobacte...	59	2e-07
ref YP_001271389.1	GCN5-related N-acetyltransferase [Lactobacil...	59	2e-07
dbj BAI87305.1	hypothetical protein BSNT_05581 [Bacillus subtil...	59	2e-07
ref YP_003832435.1	GNAT family acetyltransferase [Butyrivibrio ...	59	3e-07
gb EFS74684.1	acetyltransferase, GNAT family [Propionibacterium...	59	3e-07
ref YP_001044314.1	GCN5-related N-acetyltransferase [Rhodobacte...	59	3e-07
ref YP_001029322.1	phosphinothricin acetyltransferase [Burkhold...	59	3e-07
ref ZP_03931541.1	Phosphinothricin acetyltransferase [Corynebac...	59	3e-07
ref ZP_04231266.1	GCN5-related N-acetyltransferase [Bacillus ce...	59	3e-07
ref ZP_02186123.1	phosphinothricin N-acetyltransferase [Carnoba...	59	3e-07
ref YP_002897089.1	phosphinothricin acetyltransferase [Burkhold...	59	3e-07
ref YP_002464793.1	GCN5-related N-acetyltransferase [Chloroflex...	59	3e-07
ref YP_055338.1	N-acetyltransferase [Propionibacterium acnes KP...	59	3e-07

ref ZP_01038277.1	phosphinothricin N-acetyltransferase, putativ...	59	3e-07
ref YP_003314238.1	sortase-like acyltransferase [Sanguibacter k...	59	3e-07
ref YP_103078.1	phosphinothricin acetyltransferase [Burkholderi...	59	3e-07
pdb 1VHS A Chain A, Crystal Structure Of A Putative Phosphinothr...		59	4e-07
ref ZP_03495248.1	GCN5-related N-acetyltransferase [Alicyclobac...	59	4e-07
ref ZP_05394037.1	GCN5-related N-acetyltransferase [Clostridium...	59	4e-07
ref ZP_04433180.1	GCN5-related N-acetyltransferase [Bacillus co...	59	4e-07
ref ZP_02489505.1	phosphinothricin acetyltransferase [Burkholde...	59	4e-07
ref YP_002005514.1	acetyltransferase; phosphinothricin acetyltr...	59	4e-07
ref ZP_03509327.1	putative phosphinothricin N-acetyltransferase...	59	4e-07
ref ZP_01879208.1	phosphinothricin N-acetyltransferase, putativ...	59	4e-07
ref ZP_03146870.1	GCN5-related N-acetyltransferase [Geobacillus...	58	4e-07
ref YP_003085328.1	GCN5-related N-acetyltransferase [Dyadobacte...	58	5e-07
gb EFS03227.1	gnt family acetyltransferase [Listeria seeligeri...	58	5e-07
ref YP_003975090.1	putative phosphinothricin acetyltransferase ...	58	5e-07
ref YP_001404157.1	GCN5-related N-acetyltransferase [Candidatus...	58	5e-07
ref YP_323829.1	GCN5-like N-acetyltransferase [Anabaena variabi...	58	5e-07
ref YP_001341823.1	GCN5-like N-acetyltransferase [Marinomonas s...	58	6e-07
ref ZP_07630836.1	GCN5-related N-acetyltransferase [Clostridium...	58	6e-07
ref YP_003842069.1	GCN5-related N-acetyltransferase [Clostridiu...	58	6e-07
gb EFS00154.1	gnt family acetyltransferase [Listeria seeligeri...	58	6e-07
ref YP_591201.1	GCN5-related N-acetyltransferase [Candidatus Ko...	58	6e-07
ref YP_687122.1	GNAT family acetyltransferase [uncultured metha...	58	7e-07
ref YP_644434.1	GCN5-related N-acetyltransferase [Rubrobacter x...	58	7e-07
ref ZP_05391837.1	GCN5-related N-acetyltransferase [Clostridium...	57	7e-07
ref YP_003183978.1	GCN5-like N-acetyltransferase [Alicyclobacil...	57	8e-07
ref ZP_04217151.1	GCN5-related N-acetyltransferase [Bacillus ce...	57	8e-07
ref YP_002130283.1	phosphinothricin N-acetyltransferase [Phenyl...	57	8e-07
ref ZP_07873781.1	gnt family acetyltransferase [Listeria ivano...	57	8e-07
ref ZP_03073935.1	GCN5-related N-acetyltransferase [Lactobacill...	57	8e-07
ref YP_684987.1	GNAT family acetyltransferase [uncultured metha...	57	9e-07
ref ZP_08006391.1	hypothetical protein HMPREF1013_03004 [Bacill...	57	9e-07
ref XP_001261229.1	GNAT family acetyltransferase, putative [Neo...	57	9e-07
ref ZP_01886255.1	phosphinothricin N-acetyltransferase [Pedobac...	57	9e-07
ref YP_003356173.1	GCN5-related N-acetyltransferase family prot...	57	9e-07
ref YP_003245194.1	GCN5-like N-acetyltransferase [Paenibacillus...	57	9e-07
ref ZP_05067648.1	phosphinothricin acetyltransferase [Octadecab...	57	1e-06
gb AAA26766.2	ORF X product (put.); putative [Streptomyces coel...	57	1e-06
ref ZP_07992477.1	acetyltransferase [Neisseria mucosa C102] >gi...	57	1e-06
ref ZP_01750878.1	putative acetyltransferase, GNAT family prote...	57	1e-06
ref YP_825858.1	GCN5-related N-acetyltransferase [Candidatus So...	57	1e-06
ref YP_002777200.1	ArsR family transcriptional regulator [Rhodo...	57	1e-06
ref YP_003095172.1	phosphinothricin N-acetyltransferase [Flavob...	57	1e-06
gb EFS49061.1	acetyltransferase, GNAT family [Propionibacterium...	57	1e-06
ref YP_003841929.1	GCN5-related N-acetyltransferase [Clostridiu...	57	1e-06
ref YP_001467661.1	acetyltransferase [Campylobacter concisus 13...	57	1e-06
ref ZP_06873759.1	putative phosphinothricin acetyltransferase [...	57	1e-06
ref YP_001031090.1	polyprenyl synthetase [Methanocorpusculum la...	57	1e-06
ref YP_001488516.1	acetyltransferase [Bacillus pumilus SAFR-032...	57	1e-06
ref YP_003682387.1	ArsR family transcriptional regulator [Nocar...	57	1e-06
ref ZP_07088258.1	GNAT family acetyltransferase [Chryseobacteri...	57	1e-06
ref ZP_07054844.1	GNAT family acetyltransferase [Listeria grayi...	57	2e-06
gb EFT74943.1	acetyltransferase, GNAT family [Propionibacterium...	56	2e-06
ref ZP_04224647.1	GCN5-related N-acetyltransferase [Bacillus ce...	56	2e-06
ref ZP_07707784.1	GCN5-related N-acetyltransferase family prote...	56	2e-06
gb ADI18697.1	sortase and related acyltransferases [uncultured ...	56	2e-06
ref NP_600226.1	sortase or related acyltransferase [Corynebacte...	56	2e-06
ref NP_488508.1	hypothetical protein alr4468 [Nostoc sp. PCC 71...	56	2e-06
ref YP_442677.1	phosphinothricin acetyltransferase [Burkholderi...	56	2e-06
ref YP_003464554.1	acetyltransferase, GNAT family [Listeria see...	56	2e-06
ref YP_003357066.1	GCN5-related N-acetyltransferase family prot...	56	2e-06
ref YP_003869679.1	Sortase [Paenibacillus polymyxa E681] >gi 30...	56	2e-06
ref YP_001537972.1	GCN5-related N-acetyltransferase [Salinispor...	56	2e-06

ref	ZP_04306448.1	Phosphinothricin N-acetyltransferase [Bacillu...	56	2e-06
ref	YP_001659372.1	GCN5-related N-acetyltransferase [Microcysti...	56	2e-06
ref	YP_003254040.1	GCN5-related N-acetyltransferase [Geobacillu...	56	2e-06
ref	YP_846122.1	GCN5-related N-acetyltransferase [Syntrophobact...	56	3e-06
ref	YP_374818.1	acetyltransferase [Chlorobium luteolum DSM 273]...	56	3e-06
ref	YP_511330.1	GCN5-related N-acetyltransferase [Jannaschia sp...	56	3e-06
ref	ZP_03054807.1	YwnH [Bacillus pumilus ATCC 7061] >gi 1940116...	55	3e-06
ref	YP_148773.1	phosphinothricin N-acetyltransferase [Geobacill...	55	3e-06
ref	ZP_02463190.1	phosphinothricin acetyltransferase [Burkholde...	55	3e-06
ref	YP_003186386.1	GCN5-related N-acetyltransferase [Alicycloba...	55	3e-06
ref	ZP_04157106.1	Phosphinothricin N-acetyltransferase [Bacillu...	55	4e-06
ref	ZP_06595853.1	acetyltransferase, GNAT family [Bifidobacteri...	55	4e-06
ref	YP_004042043.1	gcn5-related N-acetyltransferase [Paludibact...	55	4e-06
ref	YP_003596647.1	GNAT family acetyltransferase [Bacillus mega...	55	5e-06
ref	YP_756942.1	GCN5-related N-acetyltransferase [Maricaulis ma...	55	5e-06
ref	ZP_05745074.1	phosphinothricin N-acetyltransferase [Lactoba...	55	5e-06
ref	YP_003945614.1	phosphinothricin n-acetyltransferase, putati...	55	5e-06
ref	YP_003670212.1	Phosphinothricin acetyltransferase [Geobacil...	55	5e-06
ref	YP_002950799.1	GCN5-related N-acetyltransferase [Geobacillu...	55	5e-06
dbj	BAJ27042.1	putative acetyltransferase [Kitasatospora setae ...	55	6e-06
ref	YP_004100431.1	GCN5-related N-acetyltransferase [Intraspora...	54	6e-06
emb	CA089677.1	unnamed protein product [Microcystis aeruginosa ...	54	6e-06
ref	YP_003511953.1	GCN5-related N-acetyltransferase [Stackebran...	54	7e-06
ref	ZP_07729425.1	acetyltransferase, GNAT family [Lactobacillus...	54	7e-06
ref	YP_003593537.1	GCN5-related N-acetyltransferase [Caulobacte...	54	7e-06
ref	ZP_03970056.1	acetyltransferase [Sphingobacterium spiritivo...	54	7e-06
ref	ZP_07729782.1	acetyltransferase, GNAT family [Lactobacillus...	54	7e-06
ref	NP_241299.1	phosphinothricin N-acetyltransferase [Bacillus ...	54	8e-06
ref	ZP_06567725.1	hypothetical protein SeryN2_35005 [Saccharopo...	54	8e-06
ref	ZP_08206806.1	N-acetyltransferase [Gordonia neofelifaecis N...	54	8e-06
ref	ZP_00955324.1	phosphinothricin N-acetyltransferase, putativ...	54	9e-06
ref	ZP_01049506.2	acetyltransferase (GNAT) family protein [Dokd...	54	9e-06
ref	ZP_03973496.1	acetyltransferase [Lactobacillus reuteri CF48...	54	9e-06
ref	ZP_01629051.1	GCN5-related N-acetyltransferase [Nodularia s...	54	9e-06
ref	ZP_03211253.1	Sortase related acyltransferase [Lactobacillu...	54	9e-06
ref	YP_001107169.1	hypothetical protein SACE_4980 [Saccharopoly...	54	1e-05
ref	YP_001166607.1	GCN5-related N-acetyltransferase [Rhodobacte...	54	1e-05
ref	ZP_02962821.1	possible N-acetyl transferase [Bifidobacteriu...	54	1e-05
ref	YP_001353673.1	acetyltransferase [Janthinobacterium sp. Mar...	54	1e-05
ref	ZP_05744891.1	phosphinothricin N-acetyltransferase [Lactoba...	54	1e-05
ref	YP_949323.1	putative phosphinothricin N-acetyltransferase [...	54	1e-05
ref	ZP_05025230.1	acetyltransferase, GNAT family [Microcoleus c...	54	1e-05
ref	YP_003838423.1	GCN5-related N-acetyltransferase [Micromonos...	54	1e-05
ref	YP_003961511.1	GCN5-related N-acetyltransferase [Eubacteriu...	54	1e-05
ref	ZP_06500009.1	GCN5-related N-acetyltransferase [Pseudomonas...	54	1e-05
ref	ZP_05915841.1	putative phosphinothricin N-acetyltransferase...	54	1e-05
ref	YP_002469889.1	N-acetyl transferase [Bifidobacterium animal...	54	1e-05
ref	YP_340976.1	acetyltransferase [Pseudoalteromonas haloplankt...	54	1e-05
ref	ZP_04758433.1	acetyltransferase [Neisseria flavescens SK114...	54	1e-05
ref	ZP_04440177.1	acetyltransferase [Lactobacillus rhamnosus LM...	53	1e-05
ref	YP_003123028.1	GCN5-related N-acetyltransferase [Chitinopha...	53	1e-05
ref	ZP_01614149.1	putative acetyltransferase [Alteromonadales b...	53	2e-05
ref	ZP_07717069.1	GNAT family acetyltransferase [Aeromicrobium ...	53	2e-05
ref	ZP_05984327.1	phosphinothricin N-acetyltransferase [Neisser...	53	2e-05
ref	ZP_07082756.1	phosphinothricin N-acetyltransferase [Sphingo...	53	2e-05
gb	ADC86037.1	Phosphinothricin N-acetyltransferase [Bifidobacte...	53	2e-05
ref	ZP_03945194.1	phosphinothricin N-acetyltransferase [Lactoba...	53	2e-05
ref	YP_001843725.1	phosphinothricin N-acetyltransferase [Lactob...	53	2e-05
ref	YP_004096812.1	GCN5-related N-acetyltransferase [Bacillus c...	53	2e-05
ref	YP_001104201.1	hypothetical protein SACE_1966 [Saccharopoly...	53	2e-05
ref	YP_004082619.1	gcn5-related n-acetyltransferase [Micromonos...	53	2e-05
ref	ZP_05868293.1	LOW QUALITY PROTEIN: conserved hypothetical p...	53	2e-05
ref	XP_002486528.1	GNAT family N-acetyltransferase, putative [T...	53	2e-05

ref ZP_02148288.1	phosphinothricin N-acetyltransferase, putativ...	53	2e-05
ref YP_003489765.1	N-acetyltransferase [Streptomyces scabiei 87...	52	3e-05
ref YP_003136446.1	GCN5-related N-acetyltransferase [Cyanothece...	52	3e-05
ref YP_726072.1	sortase or related acyltransferase [Ralstonia e...	52	3e-05
ref ZP_06753129.1	phosphinothricin N-acetyltransferase [Simonsi...	52	3e-05
ref YP_001224775.1	fused glutathione synthetase/acetyltransfera...	52	3e-05
ref ZP_05054348.1	acetyltransferase, GNAT family [Octadecabacte...	52	3e-05
ref ZP_01076405.1	GCN5-related N-acetyltransferase [Marinomonas...	52	4e-05
ref ZP_06381746.1	GCN5-related N-acetyltransferase [Arthrospira...	52	4e-05
ref YP_003561921.1	GNAT family acetyltransferase [Bacillus mega...	52	4e-05
ref YP_003356174.1	GCN5-related N-acetyltransferase family prot...	52	4e-05
ref ZP_00962754.1	phosphinothricin N-acetyltransferase, putativ...	52	4e-05
gb EEH06992.1	conserved hypothetical protein [Ajellomyces capsu...	52	4e-05
ref YP_002323294.1	GCN5-related N-acetyltransferase [Bifidobact...	52	4e-05
ref ZP_05614148.1	acetyltransferase, GNAT family [Faecalibacter...	52	5e-05
ref ZP_03718257.1	hypothetical protein NEIFLAOT_00057 [Neisseri...	52	5e-05
ref ZP_04665228.1	phosphinothricin N-acetyltransferase [Bifidob...	52	5e-05
ref ZP_05101405.1	phosphinothricin acetyltransferase [Roseobact...	52	5e-05
ref YP_001319533.1	GCN5-related N-acetyltransferase [Alkaliphil...	52	5e-05
ref ZP_07921530.1	phosphinothricin N-acetyltransferase [Pseudor...	51	5e-05
gb EFR93939.1	gnat family acetyltransferase [Listeria innocua F...	51	5e-05
ref ZP_04601883.1	hypothetical protein GCWU000324_01357 [Kingel...	51	5e-05
ref YP_002370892.1	GCN5-like N-acetyltransferase [Cyanothece sp...	51	5e-05
ref ZP_03612047.1	hypothetical protein AM202_0459 [Actinobacill...	51	6e-05
ref ZP_04151343.1	Phosphinothricin N-acetyltransferase [Bacillu...	51	6e-05
ref ZP_03236003.1	acetyltransferase, gnat family protein [Bacil...	51	7e-05
ref YP_003488051.1	acetyltransferase [Streptomyces scabiei 87.2...	51	7e-05
ref ZP_05258358.1	acetyltransferase, gnat family protein [Liste...	51	7e-05
ref ZP_03960042.1	acetyltransferase [Lactobacillus vaginalis AT...	51	7e-05
ref YP_003212786.1	hypothetical protein Ctu_3p00420 [Cronobacte...	51	7e-05
ref ZP_03959265.1	acetyltransferase [Lactobacillus vaginalis AT...	51	8e-05
ref ZP_04268014.1	Phosphinothricin N-acetyltransferase [Bacillu...	51	8e-05
ref ZP_03272313.1	GCN5-related N-acetyltransferase [Arthrospira...	51	9e-05
ref YP_002378285.1	GCN5-related N-acetyltransferase [Cyanothece...	51	9e-05
ref NP_470773.1	hypothetical protein lin1437 [Listeria innocua ...	51	9e-05
ref YP_003605073.1	GCN5-related N-acetyltransferase [Burkholder...	50	9e-05
ref ZP_05822107.1	conserved hypothetical protein [Brucella abor...	50	1e-04
ref YP_003172350.1	phosphinothricin N-acetyltransferase [Lactob...	50	1e-04
ref ZP_07902166.1	GCN5-related N-acetyltransferase [Paenibacill...	50	1e-04
ref YP_562118.1	GCN5-related N-acetyltransferase [Shewanella de...	50	1e-04
ref ZP_00120498.1	COG1247: Sortase and related acyltransferases...	50	1e-04
ref YP_002350131.1	acetyltransferase, gnat family [Listeria mon...	50	1e-04
ref ZP_04242914.1	Acetyltransferase, GNAT [Bacillus cereus Rock...	50	1e-04
ref NP_982169.1	acetyltransferase, GNAT family protein [Bacillu...	50	1e-04
ref ZP_06557427.1	acetyltransferase [Listeria monocytogenes FSL...	50	1e-04
ref ZP_06981307.1	phosphinothricin N-acetyltransferase [Neisser...	50	1e-04
emb CBK99284.1	Sortase and related acyltransferases [Faecalibac...	50	1e-04
ref YP_001099698.1	putative acetyltransferase [Herminiimonas ar...	50	1e-04
ref YP_002758108.1	N-acetyltransferase [Listeria monocytogenes ...	50	2e-04
ref ZP_04253227.1	GCN5-related N-acetyltransferase [Bacillus ce...	50	2e-04
ref YP_001820434.1	GCN5-related N-acetyltransferase [Opitutus t...	50	2e-04
ref ZP_05620974.1	phosphinothricin N-acetyltransferase [Enhydro...	50	2e-04
ref YP_004067627.1	acetyltransferase [Pseudoalteromonas sp. SM9...	50	2e-04
ref YP_014017.1	acetyltransferase [Listeria monocytogenes str. ...	50	2e-04
ref YP_003014556.1	GCN5-related N-acetyltransferase [Paenibacil...	50	2e-04
ref ZP_00232961.1	acetyltransferase, GNAT family [Listeria mono...	50	2e-04
ref ZP_01743299.1	putative acetyltransferase, GNAT family prote...	50	2e-04
ref ZP_04384226.1	transcriptional regulator, ArsR family [Rhodo...	49	2e-04
ref YP_004214188.1	GCN5-related N-acetyltransferase [Rahnella s...	49	2e-04
ref YP_003192986.1	GCN5-related N-acetyltransferase [Desulfotom...	49	2e-04
ref ZP_06303809.1	GCN5-related N-acetyltransferase [Raphidiopsi...	49	2e-04
ref YP_001801960.1	putative GCN5-related N-acetyltransferase [C...	49	2e-04
ref ZP_02355372.1	phosphinothricin acetyltransferase [Burkholde...	49	2e-04

ref ZP_07149324.1	putative acetyltransferase [Corynebacterium r...	49	2e-04
emb CAK50857.1	putative phosphinothricin N-acetyltransferase [S...	49	3e-04
ref ZP_08124242.1	hypothetical protein PsePl_30385 [Pseudonocar...	49	3e-04
ref YP_849613.1	GNAT family acetyltransferase [Listeria welshim...	49	3e-04
ref YP_001812925.1	GCN5-related N-acetyltransferase [Exiguobact...	49	3e-04
ref ZP_02144841.1	phosphinothricin N-acetyltransferase, putativ...	49	3e-04
ref YP_003116235.1	GCN5-related N-acetyltransferase [Catenulisp...	49	3e-04
ref ZP_05109686.1	conserved hypothetical protein [Legionella dr...	49	3e-04
ref YP_002766969.1	ArsR family transcriptional regulator [Rhodo...	49	3e-04
ref ZP_03398367.1	sortase/acyltransferase [Pseudomonas syringae...	49	3e-04
ref ZP_05316934.1	putative phosphinothricin N-acetyltransferase...	49	3e-04
ref YP_003583021.1	GNAT family acetyltransferase [Zunongwangia ...	49	3e-04
ref ZP_06811307.1	GCN5-related N-acetyltransferase [Geobacillus...	49	3e-04
ref ZP_07089105.1	phosphinothricin acetyltransferase [Chryseoba...	49	4e-04
ref ZP_04860080.1	polyprenyl synthetase [Fusobacterium varium A...	49	4e-04
ref ZP_04851039.1	phosphinothricin acetyltransferase [Paenibaci...	49	4e-04
ref YP_003861768.1	phosphinothricin N-acetyltransferase [Mariba...	49	4e-04
ref YP_003988012.1	Phosphinothricin acetyltransferase [Geobacil...	49	4e-04
ref YP_345546.1	ArsR family transcriptional regulator [Rhodococ...	49	4e-04
ref ZP_06882616.1	GCN5-related N-acetyltransferase [Clostridium...	49	4e-04
ref NP_696198.1	N-acetyl transferase [Bifidobacterium longum NC...	48	5e-04
ref YP_003885733.1	GCN5-like N-acetyltransferase [Cyanotheca sp...	48	5e-04
gb ADI17869.1	sortase and related acyltransferases [uncultured ...	48	5e-04
ref NP_464925.1	hypothetical protein lmo1400 [Listeria monocyto...	48	6e-04
ref NP_691376.1	phosphinothricin N-acetyltransferase [Oceanobac...	48	6e-04
ref YP_003660980.1	GCN5-like N-acetyltransferase [Bifidobacteri...	48	6e-04
ref YP_003486909.1	acetyltransferase [Streptomyces scabiei 87.2...	48	7e-04
ref YP_003428574.1	GCN5-related N-acetyltransferase [Bacillus p...	48	7e-04
ref YP_721385.1	GCN5-related N-acetyltransferase [Trichodesmium...	48	7e-04
gb EFW18117.1	GNAT family N-acetyltransferase [Coccidioides pos...	48	7e-04
ref ZP_03058612.1	phosphinothricin acetyltransferase [Escherich...	48	7e-04
ref ZP_03963018.1	acetyltransferase [Lactobacillus paracasei su...	48	7e-04
ref XP_001218368.1	predicted protein [Aspergillus terreus NIH26...	48	7e-04
ref YP_306013.1	putative acetyltransferase [Methanosarcina bark...	47	8e-04
gb ADZ78327.1	Phosphinothricin acetyltransferase [Sphingobacter...	47	8e-04
ref ZP_00134886.2	COG1247: Sortase and related acyltransferases...	47	8e-04
ref ZP_03742864.1	hypothetical protein BIFPSEUDO_03442 [Bifidob...	47	8e-04
ref ZP_02212214.1	hypothetical protein CLOBAR_01831 [Clostridiu...	47	8e-04
ref ZP_05265944.2	acetyltransferase [Listeria monocytogenes HPB...	47	8e-04
ref YP_177262.1	phosphinothricin N-acetyltransferase [Bacillus ...	47	8e-04
ref ZP_07544750.1	Predicted sortase and acyltransferase [Actino...	47	8e-04
ref ZP_05978211.1	putative phosphinothricin N-acetyltransferase...	47	8e-04
ref ZP_04673483.1	phosphinothricin N-acetyltransferase [Lactoba...	47	8e-04
ref ZP_02883607.1	GCN5-related N-acetyltransferase [Burkholderi...	47	8e-04
ref YP_807782.1	sortase related acyltransferase [Lactobacillus ...	47	9e-04
ref ZP_03265871.1	GCN5-related N-acetyltransferase [Burkholderi...	47	0.001
ref YP_001651515.1	sortase and related acyltransferase [Actinob...	47	0.001
ref ZP_07714682.1	phosphinothricin acetyltransferase [Corynebac...	47	0.001
ref ZP_03324286.1	hypothetical protein BIFCAT_01074 [Bifidobact...	47	0.001
ref YP_796138.1	sortase related acyltransferase [Lactobacillus ...	47	0.001
ref YP_004228168.1	phosphinothricin acetyltransferase [Burkhold...	47	0.001
ref ZP_05704697.1	GNAT family toxin-antitoxin system, toxin com...	47	0.001
ref YP_002549278.1	acetyltransferase [Agrobacterium vitis S4] >...	47	0.001
ref ZP_01135619.1	putative acetyltransferase [Pseudoalteromonas...	47	0.001
ref ZP_08067122.1	phosphinothricin N-acetyltransferase [Actinob...	47	0.001
ref ZP_03073379.1	GCN5-related N-acetyltransferase [Lactobacill...	47	0.001
ref XP_002563497.1	Pc20g10030 [Penicillium chrysogenum Wisconsi...	47	0.001
gb ABX10632.1	phosphinothricin N-acetyltransferase [uncultured ...	47	0.001
ref ZP_07801142.1	acetyltransferase, GNAT family [Faecalibacter...	47	0.001
ref ZP_05232348.2	acetyltransferase [Listeria monocytogenes FSL...	47	0.002
ref ZP_01724099.1	phosphinothricin N-acetyltransferase [Bacillu...	47	0.002
ref YP_001968334.1	predicted sortase--related acyltransferase [...	47	0.002
ref YP_002834382.1	putative N-acetyltransferase [Corynebacteriu...	47	0.002

ref YP_001272503.1	GCN5-related N-acetyltransferase [Lactobacil...	46	0.002
ref ZP_05366550.1	acetyltransferase, gnat family [Corynebacteri...	46	0.002
ref ZP_07542630.1	Predicted sortase and acyltransferase [Actino...	46	0.002
ref YP_003321282.1	GCN5-like N-acetyltransferase [Sphaerobacter...	46	0.002
ref ZP_07296419.1	GNAT family acetyltransferase [Streptomyces h...	46	0.002
emb CBL03028.1	Sortase and related acyltransferases [Faecalibac...	46	0.002
ref ZP_06500010.1	GCN5-related N-acetyltransferase [Pseudomonas...	46	0.002
ref ZP_03463681.1	hypothetical protein BACPEC_02780 [Bacteroides...	46	0.002
ref YP_581302.1	GCN5-related N-acetyltransferase [Psychrobacter...	46	0.002
ref YP_001125715.1	phosphinothricin N-acetyltransferase [Geobac...	46	0.003
ref YP_003783135.1	hypothetical protein cpfr_00734 [Corynebact...	46	0.003
ref ZP_03973757.1	acetyltransferase [Lactobacillus reuteri CF48...	46	0.003
ref ZP_04609105.1	GCN5 N-acetyltransferase [Micromonospora sp. ...	46	0.003
ref YP_518100.1	hypothetical protein DSY1867 [Desulfitobacteriu...	46	0.003
ref YP_004095829.1	GCN5-related N-acetyltransferase [Bacillus c...	46	0.003
ref ZP_08042081.1	GNAT family acetyltransferase [Streptococcus ...	45	0.003
gb EEH23616.1	conserved hypothetical protein [Paracoccidioides ...	45	0.003
ref ZP_07870722.1	gnat family acetyltransferase [Listeria marth...	45	0.003
ref ZP_04753113.1	sortase and related acyltransferase [Actinoba...	45	0.003
ref NP_104417.1	hypothetical protein mlr3271 [Mesorhizobium lot...	45	0.004
ref YP_561875.1	GCN5-related N-acetyltransferase [Shewanella de...	45	0.005
ref YP_002138059.1	GNAT family acetyltransferase [Geobacter bem...	45	0.005
ref YP_004044624.1	acetyltransferase [Halogeometricum borinquen...	45	0.005
ref ZP_03931540.1	possible Phosphinothricin acetyltransferase [...	45	0.005
ref YP_089481.1	hypothetical protein SPBc2p012 [Mannheimia succini...	45	0.005
ref YP_004260817.1	GCN5-like N-acetyltransferase [Cellulophaga ...	45	0.005
ref ZP_02092539.1	hypothetical protein FAEPRAM212_02833 [Faecal...	45	0.005
ref YP_233975.1	GCN5-related N-acetyltransferase [Pseudomonas s...	45	0.005
ref YP_002941961.1	GCN5-related N-acetyltransferase [Variovorax...	45	0.005
ref YP_003936999.1	GNAT family acetyltransferase [Clostridium s...	45	0.006
ref NP_939298.1	putative phosphinothricin N-acetyltransferase [...	45	0.006
ref NP_046564.1	hypothetical protein SPBc2p012 [Bacillus phage ...	44	0.007
dbj BAI85559.1	hypothetical protein BSNT_03093 [Bacillus subtil...	44	0.007
ref ZP_07990096.1	putative acetyltransferase [Corynebacterium v...	44	0.008
ref ZP_07468657.1	phosphinothricin acetyltransferase [Corynebact...	44	0.008
ref ZP_04588131.1	acetyltransferase [Pseudomonas syringae pv. o...	44	0.008
ref ZP_01059497.1	N-acetyltransferase [Leeuwenhoekiella blanden...	44	0.008
ref YP_804838.1	sortase related acyltransferase [Pediococcus pe...	44	0.009
ref NP_828437.1	acetyltransferase [Streptomyces avermitilis MA...	44	0.009
ref YP_265042.1	phosphinothricin acetyltransferase [Psychrobact...	44	0.009
ref XP_002538119.1	conserved hypothetical protein [Ricinus comm...	44	0.009
ref YP_703758.1	phosphinothricin N-acetyltransferase [Rhodococc...	44	0.010
ref ZP_01727450.1	GCN5-related N-acetyltransferase [Cyanotheca ...	44	0.010
gb EER38620.1	GNAT family N-acetyltransferase [Ajellomyces caps...	44	0.010
ref YP_684288.1	acetyltransferase, putative [Roseobacter denitr...	44	0.010
ref ZP_05635004.1	GCN5-related N-acetyltransferase [Fusobacteri...	44	0.011
ref ZP_01862614.1	putative acetyltransferase [Erythrobacter sp....	44	0.011
ref YP_003973202.1	putative acetyltransferase; phage SPbeta [Ba...	44	0.011
ref ZP_03931617.1	phosphinothricin N-acetyltransferase [Coryneb...	44	0.011
ref XP_002623155.1	GNAT family N-acetyltransferase [Ajellomyces...	44	0.011
ref NP_440374.1	hypothetical protein sl11647 [Synechocystis sp....	44	0.012
ref ZP_02919047.1	hypothetical protein BIFDEN_02369 [Bifidobact...	44	0.014
ref YP_001343476.1	GCN5-related N-acetyltransferase [Actinobaci...	43	0.015
ref YP_003736550.1	GCN5-related N-acetyltransferase [Halalkalic...	43	0.015
ref YP_001800003.1	putative acetyltransferase [Corynebacterium ...	43	0.015
ref ZP_03393715.1	acetyltransferase, gnat family [Corynebacteri...	43	0.015
ref ZP_01667257.1	ribosomal-protein-alanine acetyltransferase [...	43	0.016
ref YP_002834468.1	putative acetyltransferase [Corynebacterium ...	43	0.017
ref YP_003264892.1	GCN5-related N-acetyltransferase [Haliangium...	43	0.017
ref ZP_05117902.1	acetyltransferase, gnat family [Vibrio paraha...	43	0.018
ref ZP_07263169.1	GCN5-related N-acetyltransferase [Pseudomonas...	43	0.018
ref YP_002828185.1	putative acyl-CoA N-acyltransferase, GNAT fa...	43	0.018
ref ZP_04977988.1	acyltransferase [Mannheimia haemolytica PHL21...	43	0.019

emb CBL03517.1	Sortase and related acyltransferases [Gordonibac...	43	0.019
gb ADZ92302.1	GCN5-related N-acetyltransferase [Marinomonas med...	43	0.019
ref YP_003640603.1	GCN5-related N-acetyltransferase [Thermincol...	43	0.020
ref ZP_05989200.1	acyltransferase [Mannheimia haemolytica serot...	43	0.022
ref YP_003411640.1	GCN5-related N-acetyltransferase [Geodermato...	43	0.024
ref YP_002507954.1	SSU ribosomal protein S18P alanine acetyltra...	42	0.024
ref YP_002016217.1	GCN5-related N-acetyltransferase [Prosthecoc...	42	0.024
ref XP_002540679.1	predicted protein [Uncinocarpus reesii 1704]...	42	0.026
ref YP_003327372.1	GCN5-related N-acetyltransferase [Xylanimona...	42	0.027
ref ZP_07714579.1	probable phosphinothricin N-acetyltransferase...	42	0.027
ref ZP_05362847.1	phosphinothricin N-acetyltransferase [Campylo...	42	0.028
ref YP_004171066.1	GCN5-like N-acetyltransferase [Deinococcus m...	42	0.030
ref YP_003479445.1	GCN5-related N-acetyltransferase [Natrialba ...	42	0.030
ref YP_002550145.1	acetyltransferase protein [Agrobacterium vit...	42	0.032
ref YP_909505.1	N-acetyl transferase [Bifidobacterium adolescen...	42	0.033
ref ZP_04850775.1	conserved hypothetical protein [Paenibacillus...	42	0.034
ref YP_003410975.1	GCN5-related N-acetyltransferase [Geodermato...	42	0.034
ref ZP_07953439.1	ribosomal-protein-alanine acetyltransferase [...	42	0.034
ref YP_003404965.1	GCN5-related N-acetyltransferase [Haloterrig...	42	0.037
dbj BAI77988.1	phosphinothricin N-acetyltransferase [Pseudomona...	42	0.037
ref YP_003476587.1	GCN5-related N-acetyltransferase [Thermoanae...	42	0.040
dbj BAI77987.1	phosphinothricin N-acetyltransferase [Pseudomona...	42	0.040
ref YP_003194023.1	N-acetyltransferase [Robiginitalea biformata...	42	0.041
ref YP_863525.1	GNAT family acetyltransferase [Gramella forseti...	42	0.043
ref ZP_02028574.1	hypothetical protein BIFADO_01007 [Bifidobact...	42	0.043
ref YP_003859178.1	(SSU ribosomal protein S18P)-alanine acetyl t...	42	0.045
ref YP_002544534.1	N-acetyltransferase protein [Agrobacterium r...	42	0.048
ref YP_004152368.1	gcn5-related N-acetyltransferase [Variovorax...	42	0.050
ref YP_038811.1	acetyltransferase [Bacillus thuringiensis serov...	42	0.050
ref ZP_06499389.1	GCN5-related N-acetyltransferase [Pseudomonas...	42	0.050
ref ZP_05365511.1	phosphinothricin N-acetyltransferase [Coryneb...	42	0.051
ref ZP_00518247.1	GCN5-related N-acetyltransferase [Crocospheae...	42	0.052
ref ZP_01040135.1	YnaD [Erythrobacter sp. NAP1] >gi 85690603 gb...	41	0.054
ref YP_001525754.1	acetyltransferase [Azorhizobium caulinodans ...	41	0.054
ref ZP_05629105.1	sortase and related acyltransferase [Actinoba...	41	0.055
ref ZP_05784948.1	putative phosphinothricin N-acetyltransferase...	41	0.057
ref ZP_07326841.1	GCN5-related N-acetyltransferase [Acetivibrio...	41	0.057
ref YP_786135.1	acetyltransferase [Bordetella avium 197N] >gi 1...	41	0.058
ref ZP_04148126.1	hypothetical protein bthur0001_46870 [Bacillu...	41	0.060
ref ZP_05075392.1	acetyltransferase, gnat family [Rhodobacterial...	41	0.060
emb CBG92007.1	phosphinothricin acetyltransferase [Streptomyces...	41	0.061
ref ZP_01154999.1	acetyltransferase, GNAT family protein [Ocean...	41	0.062
gb ADZ81183.1	GCN5-related N-acetyltransferase [Sphingobacteriu...	41	0.064
ref YP_003388727.1	GCN5-related N-acetyltransferase [Spirosoma ...	41	0.066
gb EFW82027.1	acetyltransferase [Pseudomonas syringae pv. glyci...	41	0.067
ref ZP_04776977.1	ribosomal-protein-alanine acetyltransferase [...	41	0.073
ref YP_076248.1	putative acetyltransferase [Symbiobacterium the...	41	0.075
ref ZP_03754730.1	hypothetical protein ROSEINA2194_03159 [Roseb...	41	0.077
ref YP_002905889.1	putative acetyltransferase [Corynebacterium ...	41	0.077
ref ZP_04783922.1	phosphinothricin N-acetyltransferase [Weissel...	41	0.079
ref ZP_04241767.1	hypothetical protein bcere0018_44690 [Bacillu...	41	0.079
ref ZP_02613950.1	acetyltransferase [Clostridium botulinum NCTC...	41	0.082
ref YP_001895573.1	GCN5-related N-acetyltransferase [Burkholder...	41	0.083
ref ZP_08132925.1	phosphinothricin N-acetyltransferase [Kingell...	41	0.083
emb CBG92010.1	pat [Streptomyces viridochromogenes]	41	0.085
ref ZP_06604042.1	ribosomal-protein-alanine acetyltransferase [...	41	0.085
ref ZP_04448201.1	hypothetical protein BIFANG_03206 [Bifidobact...	41	0.086
ref ZP_040281143.1	hypothetical protein bcere0011_44930 [Bacillu...	41	0.087
ref ZP_06860143.1	acetyltransferase, gnat family protein [Citro...	41	0.088
ref ZP_01622046.1	hypothetical protein L8106_22596 [Lyngbya sp....	41	0.088
ref NP_834464.1	acetyltransferase [Bacillus cereus ATCC 14579] ...	41	0.088
ref ZP_04194030.1	hypothetical protein bcere0027_44300 [Bacillu...	41	0.090
ref YP_001815262.1	ribosomal-protein-alanine acetyltransferase ...	40	0.090

ref YP_002967100.1	putative acetyltransferase [Methylobacterium...	40	0.093
ref YP_079508.1	putative N-acetyltransferase [Bacillus lichenif...	40	0.094
ref YP_001445734.1	hypothetical protein VIBHAR_02546 [Vibrio ha...	40	0.094
ref ZP_04122658.1	hypothetical protein bthur0005_44820 [Bacillu...	40	0.098
ref ZP_04308421.1	hypothetical protein bcere0005_44320 [Bacillu...	40	0.11
ref ZP_04320007.1	hypothetical protein bcere0002_47020 [Bacillu...	40	0.11
ref ZP_03230810.1	acetyltransferase, gnat family [Bacillus cere...	40	0.11
gb ABA47270.1	phosphinothricin N-acetyltransferase [Pseudomonas...	40	0.11
ref YP_645273.1	CoA-binding protein [Rubrobacter xylanophilus D...	40	0.11
ref ZP_04205474.1	hypothetical protein bcere0025_44320 [Bacillu...	40	0.11
ref ZP_04117060.1	hypothetical protein bthur0006_44090 [Bacillu...	40	0.11
ref ZP_05492640.1	GCN5-related N-acetyltransferase [Thermoanaer...	40	0.11
ref XP_001246318.1	hypothetical protein CIMG_00089 [Coccidioides...	40	0.11
ref YP_003901482.1	ribosomal-protein-alanine acetyltransferase ...	40	0.12
ref ZP_04214509.1	hypothetical protein bcere0023_46470 [Bacillu...	40	0.12
gb EGC44325.1	conserved hypothetical protein [Ajellomyces capsu...	40	0.12
ref YP_002940564.1	GCN5-related N-acetyltransferase [Kosmotoga ...	40	0.12
ref YP_928642.1	GCN5-related N-acetyltransferase [Shewanella am...	40	0.12
ref ZP_08168265.1	acetyltransferase, GNAT family [Turicibacter ...	40	0.12
gb EEH09853.1	conserved hypothetical protein [Ajellomyces capsu...	40	0.12
ref ZP_07665673.1	ribosomal-protein-alanine acetyltransferase [...	40	0.12
ref YP_002940792.1	GCN5-related N-acetyltransferase [Kosmotoga ...	40	0.12
ref YP_003676537.1	GCN5-related N-acetyltransferase [Thermoanaer...	40	0.12
ref ZP_06622285.1	acetyltransferase, GNAT family [Turicibacter ...	40	0.13
ref ZP_03702661.1	GCN5-related N-acetyltransferase [Flavobacter...	40	0.13
ref YP_003405120.1	ribosomal-protein-alanine acetyltransferase ...	40	0.13
dbj BAG24087.1	phosphinothricin N-acetyltransferase [Pseudomona...	40	0.13
ref ZP_07290419.1	phosphinothricin N-acetyltransferase [Strepto...	40	0.13
ref NP_981206.1	acetyltransferase [Bacillus cereus ATCC 10987] ...	40	0.13
ref XP_002844551.1	conserved hypothetical protein [Arthroderma ...	40	0.14
ref YP_317104.1	GCN5-related N-acetyltransferase [Nitrobacter w...	40	0.14
ref YP_251248.1	putative acetyltransferase [Corynebacterium jei...	40	0.14
ref NP_354328.2	acetyltransferase [Agrobacterium tumefaciens st...	40	0.15
ref ZP_06964844.1	GCN5-related N-acetyltransferase [Ktedonobact...	40	0.15
ref ZP_03942033.1	acetyltransferase [Lactobacillus buchneri ATC...	40	0.15
ref YP_001972175.1	hypothetical protein Smlt2386 [Stenotrophomo...	40	0.15
ref ZP_03939126.1	acetyltransferase [Lactobacillus brevis subsp...	40	0.15
ref YP_283420.1	GCN5-related N-acetyltransferase [Dechloromonas...	40	0.16
ref ZP_03955019.1	acetyltransferase [Lactobacillus hilgardii AT...	40	0.16
ref ZP_08098391.1	putative acetyltransferase [Vibrio brasiliens...	40	0.17
ref ZP_06177647.1	conserved hypothetical protein [Vibrio harvey...	40	0.17
ref YP_003958986.1	ribosomal-protein-alanine acetyltransferase ...	40	0.17
ref YP_002805376.1	acetyltransferase [Clostridium botulinum A2 ...	40	0.18
ref YP_004114156.1	GCN5-like N-acetyltransferase [Pantoea sp. A...	40	0.18
ref YP_001267788.1	GCN5-related N-acetyltransferase [Pseudomona...	40	0.19
ref ZP_06190054.1	GCN5-related N-acetyltransferase [Serratia od...	40	0.19
ref ZP_04599568.1	hypothetical protein VEIDISOL_01005 [Veillone...	40	0.20
dbj BAI77986.1	phosphinothricin N-acetyltransferase [Pseudomona...	40	0.20
ref ZP_05296504.1	hypothetical protein LmonocyFSL_15566 [Lister...	39	0.20
ref YP_001547447.1	GCN5-related N-acetyltransferase [Herpetosip...	39	0.20
ref YP_003647086.1	glycoside hydrolase family 38 [Tsukamurella ...	39	0.22
ref YP_002479907.1	GCN5-related N-acetyltransferase [Desulfovib...	39	0.22
ref NP_745432.1	acetyltransferase [Pseudomonas putida KT2440] >...	39	0.22
ref YP_001833465.1	GCN5-related N-acetyltransferase [Beijerinck...	39	0.22
ref YP_003750846.1	hypothetical protein, acyl-CoA N-acyltransf...	39	0.23
ref ZP_08212291.1	GCN5-related N-acetyltransferase [Thermoanaer...	39	0.24
ref ZP_01740397.1	GCN5-related N-acetyltransferase [Rhodobacter...	39	0.25
ref YP_273193.1	acetyltransferase [Pseudomonas syringae pv. pha...	39	0.25
ref YP_001030055.1	hypothetical protein Mlab_0614 [Methanocorpu...	39	0.26
gb AAU82639.1	probable acetyltransferase [uncultured archaeon G...	39	0.27
ref ZP_05845618.1	acetyltransferase [Corynebacterium jeikeium A...	39	0.27
ref ZP_06976320.1	acetyltransferase [Gardnerella vaginalis 5-1]...	39	0.28
ref ZP_01616171.1	hypothetical protein GP2143_04500 [marine gam...	39	0.29

ref YP_001435167.1	ribosomal-protein-alanine acetyltransferase ...	39	0.29
ref ZP_07469914.1	acetyltransferase [Corynebacterium accolens A...	39	0.29
ref YP_004093376.1	ribosomal-protein-alanine acetyltransferase ...	39	0.29
ref NP_558835.1	N-acyltransferase [Pyrobaculum aerophilum str. ...	39	0.29
ref YP_001191493.1	GCN5-related N-acetyltransferase [Metallosph...	39	0.30
ref YP_003938802.1	ribosomal-protein-alanine N-acetyltransferas...	39	0.30
ref XP_001542255.1	predicted protein [Ajellomyces capsulatus NA...	39	0.31
ref YP_003119106.1	GCN5-related N-acetyltransferase [Catenulisp...	39	0.31
gb EGC23553.1	acetyltransferase [Streptococcus sanguinis SK353]	39	0.31
ref YP_001578082.1	GCN5-related N-acetyltransferase [Lactobacil...	39	0.32
ref ZP_04559314.1	conserved hypothetical protein [Citrobacter s...	39	0.32
ref ZP_03932074.1	histone acetyltransferase HPA2 family protein...	39	0.33
ref YP_575960.1	GCN5-related N-acetyltransferase [Nitrobacter h...	39	0.33
gb EGC25902.1	acetyltransferase [Streptococcus sanguinis SK405]...	39	0.33
ref ZP_00788288.1	acetyltransferase, GNAT family [Streptococcus...	39	0.33
ref ZP_02182565.1	GCN5-related N-acetyltransferase [Flavobacter...	39	0.35
ref XP_001374182.1	PREDICTED: hypothetical protein [Monodelphis...	39	0.37
ref ZP_00208304.1	COG1670: Acetyltransferases, including N-acet...	39	0.37
ref ZP_01364096.1	hypothetical protein PaerPA_01001200 [Pseudom...	39	0.38
ref YP_002935498.1	acetyltransferase [Eubacterium eligens ATCC ...	39	0.38
ref YP_003382392.1	GCN5-related N-acetyltransferase [Kribbella ...	39	0.39
ref YP_136761.1	acetyltransferase [Haloarcula marismortui ATCC ...	39	0.39
ref YP_001538076.1	thioester reductase domain-containing protei...	39	0.40
ref YP_003683239.1	GCN5-related N-acetyltransferase [Nocardiops...	39	0.41
ref ZP_05663843.1	conserved hypothetical protein [Enterococcus ...	39	0.42
ref YP_003680354.1	GCN5-related N-acetyltransferase [Nocardiops...	39	0.43
ref YP_001863614.1	aminotransferase class-III [Burkholderia phy...	39	0.44
ref YP_003297965.1	GCN5-related N-acetyltransferase [Thermomono...	39	0.45
ref YP_002882859.1	GCN5-related protein N-acetyltransferase [Be...	38	0.45
ref ZP_05752266.1	phosphinothricin N-acetyltransferase [Lactoba...	38	0.46
gb EEQ90903.1	GNAT family N-acetyltransferase [Ajellomyces derm...	38	0.46
ref YP_001013176.1	acetyltransferase [Hyperthermus butylicus DS...	38	0.46
ref YP_001645660.1	GCN5-related N-acetyltransferase [Bacillus w...	38	0.46
ref YP_558760.1	putative phosphinothricin N-acetyltransferase [...]	38	0.47
ref YP_001152298.1	ribosomal-protein-alanine acetyltransferase ...	38	0.48
ref YP_004170058.1	GCN5-like N-acetyltransferase [Deinococcus m...	38	0.48
ref YP_079920.1	GCN5-related N-acetyltransferase [Bacillus lich...	38	0.48
ref YP_004288199.1	acetyltransferase [Streptococcus gallolyticu...	38	0.49
ref YP_003430715.1	acetyltransferase, GNAT family [Streptococcu...	38	0.50
ref YP_171992.1	putative acetyltransferase [Synechococcus elong...	38	0.52
ref YP_920983.1	GCN5-related N-acetyltransferase [Thermofilum p...	38	0.52
ref ZP_03646501.1	ribosomal-protein-alanine N-acetyltransferase...	38	0.54
ref ZP_01984676.1	hypothetical acetyltransferase YafP [Vibrio h...	38	0.54
ref YP_330531.1	acetyltransferase [Streptococcus agalactiae A90...	38	0.54
ref ZP_07835149.1	GCN5-related N-acetyltransferase [Thermaeroba...	38	0.55
ref NP_386563.2	hypothetical protein SMC01824 [Sinorhizobium me...	38	0.55
ref ZP_04932411.1	hypothetical protein PACG_05270 [Pseudomonas ...	38	0.55
ref ZP_02445001.1	hypothetical protein ANACOL_04336 [Anaerotrunc...	38	0.57
ref ZP_03743073.1	hypothetical protein BIFPSEUDO_03658 [Bifidob...	38	0.59
ref ZP_05913840.1	N-acetyltransferase [Brevibacterium linens BL2]	38	0.60
ref ZP_08017910.1	ribosomal-protein-alanine acetyltransferase [...]	38	0.61
emb CBJ28808.1	ribosomal-protein-alanine acetyltransferase-like...	38	0.63
ref YP_003971182.1	ribosomal-protein-S18-alanine acetyltransfer...	38	0.64
ref ZP_02929682.1	hypothetical protein VspiD_23575 [Verrucomicr...	38	0.64
ref YP_003868969.1	Histone acetyltransferase HPA2-like protein ...	38	0.68
ref ZP_05784651.1	acetyltransferase, gnat family [Silicibacter ...	38	0.69
ref ZP_02194079.1	putative acetyltransferase [Vibrio sp. AND4] ...	38	0.69
ref NP_688964.1	acetyltransferase [Streptococcus agalactiae 260...	38	0.69
ref YP_347744.1	hypothetical protein Pfl01_2012 [Pseudomonas fl...	38	0.69
ref ZP_07464734.1	GNAT family acetyltransferase [Streptococcus ...	38	0.75
ref YP_384797.1	SSU ribosomal protein S18P alanine acetyltransf...	37	0.77
ref XP_001356126.2	GA16428 [Drosophila pseudoobscura pseudoobsc...	37	0.79
ref YP_003906914.1	phosphinothricin acetyltransferase [Burkhold...	37	0.81

ref ZP_06700579.1	phosphinothricin N-acetyltransferase [Enteroc...	37	0.82
ref ZP_06474333.1	mycothiol biosynthesis acetyltransferase [Fra...	37	0.82
ref ZP_05965160.1	putative phosphinothricin N-acetyltransferase...	37	0.82
ref XP_002021961.1	GL14242 [Drosophila persimilis] >gi 19410385...	37	0.83
ref ZP_03978230.1	phosphinothricin N-acetyltransferase [Coryneb...	37	0.84
ref XP_001355453.2	GA10986 [Drosophila pseudoobscura pseudoobsc...	37	0.86
ref ZP_01066033.1	Histone acetyltransferase HPA2 and related ac...	37	0.87
ref YP_658242.1	protein N-acetyltransferase-like protein [Haloq...	37	0.88
ref ZP_00785850.1	acetyltransferase, GNAT family [Streptococcus...	37	0.92
ref ZP_05666635.1	phosphinothricin N-acetyltransferase [Enteroc...	37	0.93
ref ZP_05749879.1	probable phosphinothricin acetyltransferase p...	37	0.94
ref YP_003176066.1	GCN5-related N-acetyltransferase [Halomicrob...	37	0.95
ref XP_001374166.1	PREDICTED: similar to putative N-acetyltrans...	37	0.95
ref YP_002633376.1	putative N-acetyltransferase [Staphylococcus...	37	0.98
ref ZP_07721400.1	acetyltransferase, GNAT family [Algoriphagus ...	37	0.98
gb EFR90833.1	gnat family acetyltransferase [Listeria innocua F...	37	0.98
dbj BAJ27343.1	putative acetyltransferase [Kitasatospora setae ...	37	0.98
ref YP_001084545.1	putative antibiotic resistance [Acinetobacte...	37	0.99

```
>ref|ZP_07302142.1| phosphinothricin-N-acetyltransferase [Streptomyces
    viridochromogenes DSM 40736]
sp|Q57146.1|PAT_STRVR RecName: Full=Phosphinothricin N-acetyltransferase; Short=PPT
    N-acetyltransferase; AltName:
    Full=Phosphinothricin-resistance protein
gb|AAA72709.1| phosphinothricin-N-acetyltransferase [Streptomyces
    viridochromogenes]
emb|CAA46314.1| phosphinothricin acetyl transferase [Streptomyces
    viridochromogenes]
gb|AAS78932.1| PAT [Binary Vector pORE_E1]
gb|AAS78938.1| PAT [Binary Vector pORE_E3]
gb|AAS78950.1| PAT [Binary Vector pORE_O1]
gb|AAS78956.1| PAT [Binary Vector pORE_O3]
gb|AAS78962.1| PAT [Binary Vector pORE_O5]
gb|AAS78982.1| PAT [Binary Vector pORE_R5]
gb|AAU00088.1| phosphinothricin N-acetyltransferase [Streptomyces
    viridochromogenes]
gb|ABA55627.1| phosphinothricin acetyltransferase [synthetic construct]
gb|ACL35314.1| phosphinothricin acetyltransferase [Binary vector pWY109]
gb|EFL30511.1| phosphinothricin-N-acetyltransferase [Streptomyces
    viridochromogenes DSM 40736]
    Length = 183
```

Score = 378 bits (971), Expect = e-103, Method: Compositional matrix adjust.
Identities = 183/183 (100%), Positives = 183/183 (100%)

```
Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
    MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL
Sbjct: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
    VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK
Sbjct: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
    SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV
Sbjct: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180

Query: 181 TQI 183
    TQI
Sbjct: 181 TQI 183
```

>gb|AAF15587.1|AF187951_1 promotes resistance to glutamine synthetase inhibitors

[Activation-tagging vector pSKI015]
gb|ABF81836.1| phosphinothricin acetyltransferase [Activation-tagging vector
pEnLox]
Length = 183

Score = 301 bits (770), Expect = 4e-80, Method: Compositional matrix adjust.
Identities = 144/168 (85%), Positives = 151/168 (89%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
MSPERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
Sbjct: 1 MSPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLDVRLRERYPWL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
VAEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGF
Sbjct: 61 VAEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGF 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
SVVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 121 SVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 168

>sp|P16426.1|PAT_STRHY RecName: Full=Phosphinothricin N-acetyltransferase; Short=PPT
N-acetyltransferase; AltName:
Full=Phosphinothricin-resistance protein

gb|AAF62892.1|AF218816_2 basta resistance protein [Cloning vector pEGAD]
gb|AAL30502.1|AF404854_1 phosphinothricin acetyltransferase [Binary vector pJawohl3-
RNAi]

emb|CAA35093.1| unnamed protein product [Streptomyces hygroscopicus]
emb|CAA29262.1| unnamed protein product [Streptomyces hygroscopicus]
gb|AAB81249.1| phosphinothricin acetyl transferase [synthetic construct]
emb|CAA77216.1| phosmothricin acetyl transferase [Cloning vector pSLJ8313]
gb|AAM19766.1| phosphinothricin N-acetyltransferase [Cloning Vector pBANF-bar]
gb|AAP78910.1| phosphinothricin acetyl transferase [Binary vector pFGC5941]
gb|AAR14725.1| Basta resistance protein [Binary vector pAMPAT-MCS]
gb|AAS13537.1| pat [Plant binary vector pXCS-HAStrep]
gb|AAS16457.1| phosphinothricine acetyltransferase [synthetic construct]
gb|AAS75426.1| BAR [Cloning vector pAGRIKOLA]
gb|AAS79014.1| phosphinothricin acetyl transferase [Cloning vector pMCG161]
gb|AAV97914.1| bar [Phosphinothricin resistance plant expression vector pSAT6-bar]
gb|AAW52572.1| phosphinothricin acetyltransferase [Cloning vector p713-905]
gb|AAW52576.1| phosphinothricin acetyltransferase [Cloning vector p713-947]
gb|AAW52580.1| phosphinothricin acetyltransferase [Cloning vector p713-1511]
gb|AAX18425.1| basta resistance protein [T-DNA vector pDs-Lox]
gb|AAX97760.1| phosphinothricin acetyl transferase [Binary vector pPZP 35S
hRluc-attR]
gb|AAX97765.1| phosphinothricin acetyl transferase [Binary vector pPZP 35S
attR-hRluc]

gb|AAY25358.1| Bar [Cloning vector pSAT1A-ocsAocsP-bar-ocsT]
gb|AAY25387.1| Bar [Cloning vector pRCS2-ocs-bar]
gb|AAY66999.1| phosphinothricin acetyltransferase [Cloning vector p713-1160]
gb|AAY79158.1| BASTA resistance protein [Cloning vector pRGK335]
gb|AAY79160.1| BASTA resistance protein [Cloning vector pRGK336]
gb|AAY82474.1| phosphinothricin acetyltransferase [Cloning vector pRD29A-GFP]
gb|AAY82478.1| phosphinothricin acetyltransferase [Cloning vector pRD29A-GUS]
gb|ABB17281.1| phosphinothricin acetyl transferase [Gateway vector pFSPGW]
gb|ABB17284.1| phosphinothricin acetyl transferase [Gateway vector pFGCGW]
gb|ABB59951.1| phosphinothricin acetyltransferase [Gene trapping Ds/T-DNA vector
pUR224NA]
gb|ABB59957.1| phosphinothricin acetyltransferase [Gene trapping Ds/T-DNA vector
pUR224NB]
gb|ABB59963.1| phosphinothricin acetyltransferase [Gene trapping Ds/T-DNA vector
pNU393A1]
gb|ABB59969.1| phosphinothricin acetyltransferase [Gene trapping Ds/T-DNA vector

pNU393B2]

gb|ABB59975.1| phosphinothricin acetyltransferase [Gene trapping Ds/T-DNA vector pNU435]

gb|ABD16409.1| Phosphinothricin acetyltransferase [Gateway adapted binary vector pFYTAG]

gb|ABD16425.1| phosphinothricin acetyltransferase [Binary vector pFYFPBT]

dbj|BAE93936.1| phosphinothricin acetyltransferase [Cloning vector pBARST]

gb|ABG75720.1| BASTA resistance protein [Cloning vector pRGK 366]

gb|ABG75723.1| BASTA resistance protein [Cloning vector pRGK 367]

emb|CAL26911.1| phosphinothricin N-acetyltransferase [Cloning vector pGWLuc]

gb|ABI30074.1| BAR [Binary vector pMOA36]

gb|ABI64009.1| phosphinothricin acetyltransferase [Gene trapping Ds/T-DNA vector pDsG8]

gb|ABO10008.1| phosphinothricin acetyl transferase [Binary gene-trap vector piGL]

gb|ABQ10904.1| phosphinothricin acetyl transferase [Expression vector p7NBT]

gb|ABR28048.1| bar [Transformation vector pYW100b]

gb|ABR28050.1| bar [Transformation vector pYW200]

gb|ABR28052.1| bar [Transformation vector pYW210]

gb|ABR28054.1| bar [Transformation vector pYW220]

gb|ABR28056.1| bar [Transformation vector pYW230]

gb|ABR28058.1| bar [Transformation vector pYW300]

gb|ABR28060.1| bar [Transformation vector pYW301]

gb|ABR28062.1| bar [Transformation vector pYW310]

gb|ABY41251.1| phosphinothricin acetyl transferase [Transformation vector pC23LB]

gb|ACO48268.1| basta resistance protein [Cloning vector pNIGEL07]

gb|ACO48277.1| basta resistance protein [Cloning vector pNIGEL09]

gb|ACO48279.1| basta resistance protein [Cloning vector pNIGEL11]

gb|ACO48281.1| basta resistance protein [Cloning vector pNIGEL13]

gb|ACO48284.1| basta resistance protein [Cloning vector pNIGEL15]

gb|ACO48287.1| basta resistance protein [Cloning vector pNIGEL16]

gb|ACO56767.1| phosphinothricin acetyltransferase [Vector miniTn7-bar]

gb|ACX31714.1| bialaphos resistance protein [Vector pWFRT-PCS12-bar]

dbj|BAI67366.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB601]

dbj|BAI67369.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB602]

dbj|BAI67372.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB602omega]

dbj|BAI67376.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB604]

dbj|BAI67380.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB605]

dbj|BAI67383.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB606]

dbj|BAI67386.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB607]

dbj|BAI67389.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB608]

dbj|BAI67392.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB609]

dbj|BAI67395.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB610]

dbj|BAI67398.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB611]

dbj|BAI67401.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB612]

dbj|BAI67404.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB613]

dbj|BAI67407.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB614]

dbj|BAI67410.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB615]

dbj|BAI67413.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB616]

dbj|BAI67416.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB617]

dbj|BAI67419.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB618]

dbj|BAI67422.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB619]

dbj|BAI67425.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB620]

dbj|BAI67428.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB621]

dbj|BAI67431.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB622]

dbj|BAI67434.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB623]

dbj|BAI67437.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB624]

dbj|BAI67440.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB625]

dbj|BAI67443.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB626]

dbj|BAI67446.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB627]

dbj|BAI67449.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB628]

dbj|BAI67452.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB629]

dbj|BAI67456.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB633]

dbj|BAI67460.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB635]
 dbj|BAI67463.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB640]
 dbj|BAI67466.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB641]
 dbj|BAI67469.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB642]
 dbj|BAI67472.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB643]
 dbj|BAI67475.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB644]
 dbj|BAI67478.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB645]
 dbj|BAI67482.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB650]
 dbj|BAI67486.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB651]
 dbj|BAI67489.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB652]
 dbj|BAI67493.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB653]
 dbj|BAI67497.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB654]
 dbj|BAI67500.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB655]
 dbj|BAI67504.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB659]
 dbj|BAI67508.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB660]
 dbj|BAI67511.1| phosphinothricin acetyltransferase [Gateway binary vector pGWB661]
 dbj|BAI67514.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB601]
 dbj|BAI67518.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB604]
 dbj|BAI67521.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB607]
 dbj|BAI67524.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB610]
 dbj|BAI67527.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB613]
 dbj|BAI67530.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB616]
 dbj|BAI67533.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB619]
 dbj|BAI67536.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB622]
 dbj|BAI67539.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB625]
 dbj|BAI67542.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB628]
 dbj|BAI67546.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB633]
 dbj|BAI67550.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB635]
 dbj|BAI67553.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB640]
 dbj|BAI67556.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB643]
 dbj|BAI67560.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB650]
 dbj|BAI67564.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB653]
 dbj|BAI67568.1| phosphinothricin acetyltransferase [Gateway binary vector
 R4pGWB659]
 gb|ADM88584.1| phosphinothricin N-acetyltransferase [Plant binary vector
 pXNS1pat-Strep]
 gb|ADM88586.1| phosphinothricin N-acetyltransferase [Plant binary vector
 pXNS2pat-Strep]
 gb|ADM88588.1| phosphinothricin N-acetyltransferase [Plant binary vector
 pXS1pat-Strep]
 gb|ADM88590.1| phosphinothricin N-acetyltransferase [Plant binary vector
 pXS2pat-Strep]
 gb|ADR00304.1| glufosinate tolerance (bar) protein [Cloning vector pSIM1]
 gb|ADR00309.1| glufosinate tolerance (bar) protein [Cloning vector pSIM3]
 emb|CBX26422.1| phosphinothricin acetyltransferase [Binary vector pAMARENA]
 gb|ADW78953.1| phosphinothricin acetyltransferase [Cloning vector pVC4-bar]

Length = 183

Score = 300 bits (769), Expect = 4e-80, Method: Compositional matrix adjust.
Identities = 144/168 (85%), Positives = 151/168 (89%)

```
Query: 1  MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
          MSPERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
Sbjct: 1  MSPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLVLRLRERYPWL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
          VAEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGF
Sbjct: 61 VAEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGF 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          SVVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 121 SVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFQWQLDF 168
```

```
>gb|ABU39932.1| bialaphos/phosphinothricin resistance protein [Cloning vector
pGreenII 0229]
gb|ABU39934.1| bialaphos/phosphinothricin resistance protein [Cloning vector
pGreenII 0229 62-SK]
emb|CAQ68376.1| bialaphos/phosphinothricin resistance protein [Cloning vector
pDEX00]
emb|CAQ68377.1| bialaphos/phosphinothricin resistance protein [Cloning vector
pG001]
emb|CAQ68382.1| bialaphos/phosphinothricin resistance protein [Cloning vector
pG002]
emb|CAQ68387.1| bialaphos/phosphinothricin resistance protein [Cloning vector
pG004]
emb|CAZ61330.1| PAT protein [Cloning vector pG003]
          Length = 183
```

Score = 299 bits (766), Expect = 8e-80, Method: Compositional matrix adjust.
Identities = 143/168 (85%), Positives = 151/168 (89%)

```
Query: 1  MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
          MSPERRP +IR AT ADM AVC IVNHYI+TSTVNFRTPEQ PQEW DDL RL++RYPWL
Sbjct: 1  MSPERRPADIRRATEADMPAVCTIVNHYIQTSTVNFRTPEQPQEWTDLVLRLRERYPWL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
          VAEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGF
Sbjct: 61 VAEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGF 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          SVVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 121 SVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFQWQLDF 168
```

```
>gb|ADN51987.1| phosphinothricin acetyltransferase [Binary vector pBI121-ELEMENTS]
          Length = 183
```

Score = 299 bits (766), Expect = 9e-80, Method: Compositional matrix adjust.
Identities = 143/168 (85%), Positives = 151/168 (89%)

```
Query: 1  MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
          M+PERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
Sbjct: 1  MNPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLVLRLRERYPWL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
          VAEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGF
Sbjct: 61 VAEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGF 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
```

SVVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
 Sbjct: 121 SVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 168

>gb|ABB52512.1| editing-dependent chimeric phosphinothricin acetyltransferase
 [synthetic construct]
 Length = 187

Score = 299 bits (765), Expect = 1e-79, Method: Compositional matrix adjust.
 Identities = 143/167 (85%), Positives = 150/167 (89%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
 SPERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
 Sbjct: 6 SPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLVLRLRERYPWL 65

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 121
 AEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGF 121
 Sbjct: 66 AEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGF 125

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
 VVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
 Sbjct: 126 VVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 172

>gb|ABB52513.1| phosphinothricin acetyltransferase [synthetic construct]
 Length = 197

Score = 299 bits (765), Expect = 1e-79, Method: Compositional matrix adjust.
 Identities = 143/167 (85%), Positives = 150/167 (89%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
 SPERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
 Sbjct: 16 SPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLVLRLRERYPWL 75

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 121
 AEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGF 121
 Sbjct: 76 AEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGF 135

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
 VVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
 Sbjct: 136 VVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 182

>gb|ADF81054.1| phosphinothricin acetyltransferase [Tobacco plastid transformation
 vector pSS33]
 gb|ADF81056.1| phosphinothricin acetyltransferase [Tobacco plastid transformation
 vector pSS42]
 Length = 188

Score = 299 bits (765), Expect = 1e-79, Method: Compositional matrix adjust.
 Identities = 143/167 (85%), Positives = 150/167 (89%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
 SPERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
 Sbjct: 7 SPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLVLRLRERYPWL 66

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 121
 AEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGF 121
 Sbjct: 67 AEVDGEVAGIAYAGPWKARNAYDWTAESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGF 126

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
 VVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
 Sbjct: 127 VVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 173

>gb|AAR86773.1| phosphinothricin acetyl transferase [synthetic construct]
Length = 183

Score = 299 bits (765), Expect = 1e-79, Method: Compositional matrix adjust.
Identities = 143/168 (85%), Positives = 150/168 (89%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
M PERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
Sbjct: 1 MDPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLDLRLRERYPWL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
VAEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGFK
Sbjct: 61 VAEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGFK 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
SVVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 121 SVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 168

>gb|AA085360.1| phosphinothricin acetyl transferase [Binary vector pLH7000]
gb|AA085365.1| phosphinothricin acetyl transferase [Binary vector pLH7500]
Length = 183

Score = 298 bits (764), Expect = 2e-79, Method: Compositional matrix adjust.
Identities = 143/168 (85%), Positives = 150/168 (89%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
M PERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
Sbjct: 1 MGPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLDLRLRERYPWL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
VAEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGFK
Sbjct: 61 VAEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGFK 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
SVVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 121 SVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 168

>gb|AAK21981.1| phosphinothricin acetyltransferase [synthetic construct]
Length = 184

Score = 298 bits (763), Expect = 2e-79, Method: Compositional matrix adjust.
Identities = 143/167 (85%), Positives = 150/167 (89%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
SPERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWL
Sbjct: 3 SPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQPQEWTDLDLRLRERYPWL 62

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
AEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGFKS
Sbjct: 63 AEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGFKS 122

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
VVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 123 VVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFWQLDF 169

>prf||1311256A gene bar,herbicide resistance
Length = 181

Score = 296 bits (758), Expect = 7e-79, Method: Compositional matrix adjust.
Identities = 142/166 (85%), Positives = 149/166 (89%)

```
Query: 3   PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA 62
          PERRP +IR AT ADM AVC IVNHYIETSTVNFRTPEQ PQEW DDL RL++RYPWLVA
Sbjct: 1   PERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTPEQEPQEWTDLVLRLRERYPWLVA 60

Query: 63  EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
          EV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGFKSV
Sbjct: 61  EVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGFKSV 120

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          VAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 121 VAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFQWQLDF 166
```

```
>gb|ABK32772.1| BastaR [Silencing vector pFE12860S]
gb|ABK32773.1| BastaR [Silencing vector pSE12860S]
gb|ABK32774.1| BastaR [Silencing vector p3UTR12850S]
gb|ABK41842.1| BastaR [Overexpression vector pFE12860OE]
gb|ABK41844.1| BastaR [Overexpression vector pLE12860OE]
gb|ABK41846.1| BastaR [Overexpression vector pFC12850OE]
gb|ABK41848.1| BastaR [Overexpression vector pFC12860OE]
          Length = 182
```

Score = 287 bits (735), Expect = 4e-76, Method: Compositional matrix adjust.
Identities = 140/168 (83%), Positives = 148/168 (88%), Gaps = 1/168 (0%)

```
Query: 1   MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
          MSPERRP +IR AT ADM AVC IVNHYIETSTVNFRT + QEW DDL RL++RYPWL
Sbjct: 1   MSPERRPADIRRATEADMPAVCTIVNHYIETSTVNFRTS-RRKQEWTDLVLRLRERYPWL 59

Query: 61  VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
          VAEV+G VAGIAYAGPWKARNAYDWT ESTVYVS RHQR GLGSTLYTHLLKS+EAQGFK
Sbjct: 60  VAEVDGEVAGIAYAGPWKARNAYDWTAEESTVYVSPRHQRTGLGSTLYTHLLKSLEAQGFK 119

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          SVVAVIGLPNDPSVR+HEALGY RG LRAAG+KHG WHDVGFWQ DF
Sbjct: 120 SVVAVIGLPNDPSVRMHEALGYAPRGMLRAAGFKHGNWHDVGFQWQLDF 167
```

```
>gb|ABA55625.1| phosphinothricin acetyltransferase [synthetic construct]
          Length = 109
```

Score = 228 bits (580), Expect = 3e-58, Method: Compositional matrix adjust.
Identities = 109/109 (100%), Positives = 109/109 (100%)

```
Query: 75  GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 134
          GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV
Sbjct: 1   GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 60

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQI 183
          RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQI
Sbjct: 61  RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQI 109
```

```
>ref|YP_001156945.1| GCN5-related N-acetyltransferase [Salinispora tropica CNB-440]
gb|ABP52567.1| GCN5-related N-acetyltransferase [Salinispora tropica CNB-440]
          Length = 192
```

Score = 190 bits (482), Expect = 9e-47, Method: Compositional matrix adjust.
Identities = 95/178 (53%), Positives = 117/178 (65%), Gaps = 1/178 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 PV +R ATAAD AV DIVNHYI T+T+N TE +T Q+W D R ++RYPWLVA +
 Sbjct: 4 PVTVREATAADWPAVTDIVNHYIATTTLLNLHTEARTLQDWTADWTRYRERYPWLVAATDDD 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G+AYAGPWKARNAYDW E T YVS + +G LY LL ++AQGF+S +AVI
 Sbjct: 64 RVVGVAAYAGPWKARNAYDWCAEVTGYVSTDMRGRVGHALYRSLAVLDAQGFRSQIAVI 123

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183
 GLPNDPSPS HE+ G+ GTL G+K+G W DVGFWQR + P P+ P +
 Sbjct: 124 GLPNDPSSAGFHESFGFRHVGTLAGVGFKNGTWLDVGFWQRSAGDTSQAPDPLLPACADV 181

>ref|YP_234588.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae B728a]
 gb|AA36550.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae B728a]
 Length = 184

Score = 149 bits (376), Expect = 2e-34, Method: Compositional matrix adjust.
 Identities = 74/174 (42%), Positives = 102/174 (58%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +R A+ D AA+ I +E + ++F EP T +E +E +YP+LVAE EG V
 Sbjct: 7 VRSASPTDAAAIQGIYAPMVERTAISFELEPPTVEEMAHRIESTLSKYPYLVAEREGQVV 66

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + R AY W+V+ TVYV+ + R G+ LY L+ +E QGF + A I LP
 Sbjct: 67 GYAYASQHRTREAYQWSVDVTYVYVAPQAHRSGIARVLYARLIPILERQGFHTAYAGIALP 126

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQI 183
 N SV LHEALG+ GT G+KHG WHDVG+W++ PP P+ P +Q+
 Sbjct: 127 NAGSVGLHEALGFHEHLGTYTEVGFKHGKWHDVGWYWRKRLNSATPPGPIVPFSQL 180

>ref|YP_003776508.1| phosphinothricin N-acetyltransferase [Herbaspirillum seropedicae SmR1]
 gb|ADJ64600.1| phosphinothricin N-acetyltransferase (sortase) protein
 [Herbaspirillum seropedicae SmR1]
 Length = 167

Score = 144 bits (364), Expect = 4e-33, Method: Compositional matrix adjust.
 Identities = 70/160 (43%), Positives = 94/160 (58%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRPATAAD A+C I NHY+ T+ ++F TEP + + + + +Q ++PWLVE EG V
 Sbjct: 5 IRPATAADAPALCGIYNHYVATTAISFETEPVSEESMVARIAEVQAKFPWLVEEEGQVL 64

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA WK R AY +VES+VY+ H G+G LY L ++ G V+ I P
 Sbjct: 65 GYAYATQWKPRAYRQSVESVYLRHDAGRGIGKRLYRQLFAELKPLGIHLVIGGIAQP 124

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N SV LHE+LG+ G GYK G W D+G+WQ +
 Sbjct: 125 NAASVALHESLGFVKCGVFNEVGKMGWIDMGYWLKLQ 164

>ref|YP_327183.1| N-acetyltransferase [Natronomonas pharaonis DSM 2160]
 emb|CAI49626.1| probable N-acetyltransferase [Natronomonas pharaonis DSM 2160]
 Length = 206

Score = 143 bits (360), Expect = 1e-32, Method: Compositional matrix adjust.
 Identities = 76/173 (43%), Positives = 99/173 (57%), Gaps = 3/173 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V +R AT D AA+ DI YIE++ FR EP P + D+++ + YPW VAE +G
 Sbjct: 18 VSLRVATTRDAAAIAIDYRPIESTAAATFREEPLEPSDVADEID--EPTYPFVFAERDGR 75

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G A+AG + R AY W E TVY+ G+GS LY LL+++ QGF S V+
 Sbjct: 76 VIGYAHAGELRKRAAYRWATELTVYLRESAHGAGVGSALYRLLLRTLARQGFVSAYGVVT 135

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
 LPN SV LHE+LG+ T A GYK GGWHDV +++R PP P P
 Sbjct: 136 LPNQSSVALHESLGFERNATFFPAVGKLGWHDVAWYERQLR-ERPPEPSEPT 187

>ref|ZP_08023172.1| phosphinothricin acetyltransferase, putative [Dietzia cinnamea P4]
 gb|EFV92319.1| phosphinothricin acetyltransferase, putative [Dietzia cinnamea P4]
 Length = 190

Score = 142 bits (357), Expect = 3e-32, Method: Compositional matrix adjust.
 Identities = 77/171 (45%), Positives = 98/171 (57%), Gaps = 1/171 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRPAT D A D+ Y+ +TV F E T E+ + R DRY WLVAE++G +A
 Sbjct: 2 IRPATIGDAAGCRDVYAPYVRETTVTFEDEVPTVDEFAARISRALDRYDWLVAELDGR 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYAGP K R AY W+ E +VYV + GLG Y L +E GF+ ++A+I LP
 Sbjct: 62 GYAYAGPVKERAAYAWSCEVSVYVDPDARGNGLGRAFYRELFTRLEGLGFRMLAIITLP 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRP 179
 N+PSV +H ALG+ G L G+KHG W DV + Q D PA P RP
 Sbjct: 122 NEPSVGMHRALGFREAGRLERIGFKHGRWLDVTWMQADLGPDPASPPTARP 172

>ref|NP_925472.1| phosphinothricin N-acetyltransferase [Gloeobacter violaceus PCC
 7421]
 dbj|BAC90467.1| phosphinothricin N-acetyltransferase [Gloeobacter violaceus PCC
 7421]
 Length = 212

Score = 137 bits (346), Expect = 5e-31, Method: Compositional matrix adjust.
 Identities = 74/170 (43%), Positives = 94/170 (55%), Gaps = 2/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR A D AV DI ++ S V F +P + E + +RYPWL V
 Sbjct: 19 IRLADGTDAQAVLDIYTPFVSGSPVTFEVQPPSAAEMQRRIGSTIERYPWLVCASANRVL 78

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA +AR AY W+V+ +VY+ H R G+ LYT L + QGF +V A I LP
 Sbjct: 79 GYAYASEHRARAAYGWSVDCSVYIDPHHSRRGMARGLYTSLFALLRLQGFFNVFAGITLP 138

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA--PPRPV 177
 N SV LHEA+G+ A GT RA G+K G WHDVG+WQ + P PP P+
 Sbjct: 139 NAASVGLHEAMGFEAVGTYRAVGHKLGAWHDVGWWQLPLQAPLCPDPPSPI 188

>ref|YP_003130042.1| GCN5-related N-acetyltransferase [Halorhabdus utahensis DSM
 12940]
 gb|ACV11309.1| GCN5-related N-acetyltransferase [Halorhabdus utahensis DSM 12940]
 Length = 200

Score = 136 bits (343), Expect = 1e-30, Method: Compositional matrix adjust.
 Identities = 74/174 (42%), Positives = 101/174 (58%), Gaps = 4/174 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE--GV 67
 +R AT AD A+ I Y+E++ + F TE T +E D +E+ + +PW+V E E GV
 Sbjct: 5 LRIATPADGPAIRSIYAPYVESTAITFETEVPTTEEMTDQIEQTHEAFPWIVCETENEGV 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 V G A A +++ AY W VE TVYV Q+ G+G+ LYT LL+++ QG+ A +
 Sbjct: 65 V-GYATASSLSKAAYAWAVELTVYVDDDIQQSGVGTALYTSLLETREQGYVDDAYAAVT 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-ELPAPPRPVRPV 180
 LPN SV LHE + GT AAG+K G WHDV +W R E PA P P P+
 Sbjct: 124 LPNSASVSLHENFAFEPVGTFFPAAGHKQGSWHDVQWWHRQLGEHPADPEPPTPM 177

>ref|ZP_06174053.1| hypothetical protein VME_04370 [Vibrio harveyi 1DA3]
 gb|EEZ89675.1| hypothetical protein VME_04370 [Vibrio harveyi 1DA3]
 Length = 164

Score = 135 bits (340), Expect = 2e-30, Method: Compositional matrix adjust.
 Identities = 68/166 (40%), Positives = 103/166 (62%), Gaps = 5/166 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEV 64
 +EIR D+A + +I N+Y+E+++++F EP + Q+ I+++ L PWLVAEV
 Sbjct: 1 MEIREVKDITDLAQIVEIYNYVESTSISFEEEPISVEVMQQRIEEV--LSLGLPWLVAEV 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +G V G AYA WK R+AY +TVE ++YV G+GSTLY++LL ++ + K+V+
 Sbjct: 59 DGQVLGYAYANRWKPRSAYRFTVEPSIYVKLGITSKGIGSTLYSYLLDNLREKQIKNVIG 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFEL 170
 VI LPN+ S+RLHE LG+ G G K G VG+WQ + +
 Sbjct: 119 VITLPNESSIRLHERLGFKKVGEFPNIGLKFGKKSVGYWQLELNV 164

>ref|YP_001546382.1| GCN5-related N-acetyltransferase [Herpetosiphon aurantiacus ATCC 23779]
 gb|ABX06254.1| GCN5-related N-acetyltransferase [Herpetosiphon aurantiacus ATCC 23779]
 Length = 198

Score = 133 bits (334), Expect = 1e-29, Method: Compositional matrix adjust.
 Identities = 74/176 (42%), Positives = 99/176 (56%), Gaps = 5/176 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 EIR AT AD A+ I +E + ++F E + E + + + YPWLV + + V
 Sbjct: 15 EIRVATVADAVAIQAIYAPIVEQTVISFEIETPSVAEMGQRIGKTLESYPWLWVCDEQAV 74

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 V G AYA + R AY W+V++TVYV++ QR G+G LY LL + G+ S A I
 Sbjct: 75 VQGYAYASQHRTRAAYQWSVDTTVYVANTAQRQGVGRALYQQLAILRGLGYYSAYAGIT 134

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFEL----PAPPRPVRP 179
 LPN SV LHEALG+T G R AG+KH WHDVG+WQ ++ P PR P
 Sbjct: 135 LPNVKSVGLHEALGFTPVGVYRQAGFKHERWHDVGWQCQLQVGDQAPVAPRKFD 190

>ref|ZP_07277001.1| phosphinothricin N-acetyltransferase [Streptomyces sp. AA4]
 gb|EFL05370.1| phosphinothricin N-acetyltransferase [Streptomyces sp. AA4]
 Length = 179

Score = 131 bits (329), Expect = 4e-29, Method: Compositional matrix adjust.
 Identities = 68/171 (39%), Positives = 94/171 (54%), Gaps = 5/171 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR A D A I Y+ +T++F TEP TP E + + Y WL V E++G V
 Sbjct: 9 IRAAEERDAEACAAIYAPYVRDTTISFETEPPTPTEMAARIAKATKSYAWLVLEMDGSVV 68

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AY P+K R AY W+ E +VY++ +R G G LY L + +GF+ VA + P
 Sbjct: 69 GYAYGSPYKERAAYRWSCEVSVYLAQDRRRAGGGKALYEALFARLAERGFRMAVAGMTQP 128

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDF-----ELPAPPR 175
 N+PSV LH+A+G+ GT R G+KHG W DV + QR+ + P PR
 Sbjct: 129 NEPSVGLHKAMGFELIGTWRRIGWKHGAWRDVTWMQRELVPASDDTPEEPR 179

>ref|ZP_01235017.1| Phosphinothricin N-acetyltransferase, putative [Vibrio angustum
 S14]
 gb|EAS65221.1| Phosphinothricin N-acetyltransferase, putative [Vibrio angustum
 S14]
 Length = 166

Score = 130 bits (327), Expect = 7e-29, Method: Compositional matrix adjust.
 Identities = 63/163 (38%), Positives = 96/163 (58%), Gaps = 1/163 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVAEVEG 66
 ++IR D A+ I N+Y+ + + F T + + + ++QD YPWL V E +G
 Sbjct: 1 MDIRTVNKDDAGAIKINYYVNETIITFEETELTEDQMRERISKIQDTSYPWLVLKEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AYA PW ++AY +T EST+Y+S+++ G G LY LL ++A G K+V+A+I
 Sbjct: 61 DIIGFAYASPWHTKSAYRYTAESTIYISNQNIGGGYGRALYQALLTQLKAIGIKNVMAI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDFE 169
 LPND SV L+EALG+ G G+K + VG WQ +F+
 Sbjct: 121 ALPNDAVLLNEALGFNLVGEYNNVGFKFDRFISVGCWQLEFK 163

>ref|YP_675890.1| GCN5-related N-acetyltransferase [Mesorhizobium sp. BNC1]
 gb|ABG64725.1| GCN5-related N-acetyltransferase [Chelativorans sp. BNC1]
 Length = 186

Score = 129 bits (324), Expect = 2e-28, Method: Compositional matrix adjust.
 Identities = 68/164 (41%), Positives = 97/164 (59%), Gaps = 3/164 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + IR A AD+ + I H ++T T ++ EP + +E +E L+ + YP+LVAE E
 Sbjct: 2 ISIRSAIPADLPFITSIYAHAVKTGTSSYELEPPSLEEMTSRMEALRSKEYPYLVAEER 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G AYAGP++ R AY + VE ++Y++ Q G+G L T L++ GF+ +VAVI
 Sbjct: 62 RVLGYAYAGPFRPRRAYRFMVEDSIYIAPDAQGRGMGRLLTSLIEECRRLGFRQIVAVI 121

Query: 127 --GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDF 168
 G P SV+LHEALG+ G L A+GYKHG W D F Q +
 Sbjct: 122 GDGSPQSASVKLHEALGFRHAGVLEASGYKHGRWLDTVFMQLEL 165

>ref|YP_003479949.1| Phosphinothricin acetyltransferase [Natrialba magadii ATCC 43099]
 gb|ADD05387.1| Phosphinothricin acetyltransferase [Natrialba magadii ATCC 43099]
 Length = 198

Score = 128 bits (321), Expect = 4e-28, Method: Compositional matrix adjust.
 Identities = 67/163 (41%), Positives = 89/163 (54%), Gaps = 2/163 (1%)

Query: 23 DIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE-VEGVVAGIAYAGPWKARN 81

DI + +S V F P T E D +E ++YPWLVAE +G V G AYAGP + R
 Sbjct: 18 DIYAPFCSSSAVTFEETPPTADEMADRIESTLEQYPWLVAESADGTVLGYAYAGPLRKQR 77

Query: 82 AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPSVRLHEALG 141

AY W VE +VYV+ ++ G+G LY L +E QGF AV LPN +VR HE LG
 Sbjct: 78 AYQWVVELSVYVAADARQSGVGRALYESLFAILERQGFYDAYAVTTLPNPATVRFHERLG 137

Query: 142 YTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183

+ GY G WHDV +W+R+ + P P P+ P + +
 Sbjct: 138 FERFADFPRVGYTQGEWHDVRRWRREIADKPENPEPITPFSTV 180

>ref|ZP_07864612.1| acetyltransferase, GNAT family [Streptococcus anginosus F0211]
 gb|EFU22135.1| acetyltransferase, GNAT family [Streptococcus anginosus F0211]
 Length = 180

Score = 128 bits (321), Expect = 4e-28, Method: Compositional matrix adjust.
 Identities = 64/171 (37%), Positives = 96/171 (56%), Gaps = 2/171 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IR A D A+ I Y+E + + F + + +E+ D +E+ +RYP+LVAE +G
 Sbjct: 1 MNIRLANKNATALVAIYAPYVEKTAITFEYDIPSVEEFSRIEKTLERYPYLVAEEDGA 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127

+ G AYA + R AY+W VE +VYV+ ++ G+G LY L + +E QGF +A I
 Sbjct: 61 ILGYAYASTYYGREAYNWAVELSVYVADENRGRGIGKQLYDKLEEILEQQGFVHFLACIA 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178

LPND S+ H+ GY GYK G WHD + Q+ + PA RP++
 Sbjct: 121 LPNDASISFHKRGYQQVAHF PKIGYFGCWHD TVWLQKSLDKPA--RPIK 169

>ref|ZP_00994644.1| GCN5-related N-acetyltransferase [Janibacter sp. HTCC2649]
 gb|EAQ00898.1| GCN5-related N-acetyltransferase [Janibacter sp. HTCC2649]
 Length = 164

Score = 128 bits (321), Expect = 4e-28, Method: Compositional matrix adjust.
 Identities = 64/159 (40%), Positives = 88/159 (55%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGP 76

D A I HY+E ST F + +E + Q+R+ W+VAE G + G AY GP
 Sbjct: 5 DAAGCAAIIYGHVEQSTATFEEAAPSAAEMAARIASAQERHAWIVAERG GTIVGYAYGGP 64

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPSVRL 136

+KAR AY ++ E +VY+ + GLG TLY LL ME+ G + + +PND SV L
 Sbjct: 65 FKARAAYRYSCEVSVYLDAPARGGGLGR TLYAALLDRMESLGLRMACGGVTMPNDASVAL 124

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175

H A+G+ GT R G+KHG W DV ++Q+ PPR
 Sbjct: 125 HLAGMFEEVGTYRQIGWKHGAWRDVTWFQKPLGGDGPPR 163

>ref|YP_003536939.1| Phosphinothricin N-acetyltransferase [Haloferax volcanii DS2]
 gb|ADE04346.1| Phosphinothricin N-acetyltransferase [Haloferax volcanii DS2]
 Length = 199

Score = 127 bits (320), Expect = 4e-28, Method: Compositional matrix adjust.
 Identities = 66/158 (41%), Positives = 93/158 (58%), Gaps = 1/158 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

V +R AT +D+ A+ +I ++E + ++F +P + + LE+ D YPWL V E++G
 Sbjct: 3 VRLRAATPSDLPAIREIYAPFVENTAISFAYDPPSVADLET KLEQKTD-YPWLVCELDGE 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 VAG AYAG + R AY W VE+++YV QR G+ LYT LL +E QG+ S VAVI
 Sbjct: 62 VAGYAYAGAIRERIAIRWAVETSIIYVRPEFQRRGVARGLYTALLDLLERQGYVSAVAVIT 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 PN S+ HE+ G+ G GYK WHDV +W
 Sbjct: 122 TPNPASIAFHESFGFERVGRFERYVGYKGDWHDVWWS 159

>ref|ZP_08119923.1| phosphinothricin acetyltransferase [Pseudonocardia sp. P1]
 Length = 173

Score = 127 bits (320), Expect = 4e-28, Method: Compositional matrix adjust.
 Identities = 72/170 (42%), Positives = 94/170 (55%), Gaps = 1/170 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-G 66
 ++IR ATA D A I Y+ + V+F +EP P E + Q+RY WLVA + G
 Sbjct: 1 MQIRDATAEDADACAVIYAPYVRDTAVSFESPEPPGPVEMAGRIAAQERYVWLVAVTTDDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126
 V G AY P+K R AY WT E +VY+ + G G LY LL + A G VAV+
 Sbjct: 61 DVLGYAYGAPFKPREAYRWTCEVSVYLHPEARGRTGRALYEALLARLTACGLVAVAVL 120

Query: 127 GLPNDSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 LPN+ SV LH ALG+T G R G+K G W DV ++RD P+P P
 Sbjct: 121 TLPNEASVALHRALGFTVGVFRGVGKLGAWRDVVWYRRDLADPSPQGP 170

>ref|ZP_01869333.1| Phosphinothricin N-acetyltransferase, putative [Vibrio shilonii
 AK1]
 gb|EDL52078.1| Phosphinothricin N-acetyltransferase, putative [Vibrio shilonii
 AK1]
 Length = 162

Score = 127 bits (320), Expect = 5e-28, Method: Compositional matrix adjust.
 Identities = 65/158 (41%), Positives = 89/158 (56%), Gaps = 1/158 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR D A+ I NHYI ST F P T + + + + D PWLV E +G V
 Sbjct: 2 IRNVQETDSIAIARIYNHYIAHSTCTFEEHPVTDADMAERIRVVDSALPWLVEHQGVV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 G YA W AR+AY +TVES+VYV H G+GS LY L ++ +G K++++VI L
 Sbjct: 62 VGYCYAKRWNARSAYRFTVESSVYVDHETPIKGVGSRLYDALFNDLQTRGVKNIMSVITL 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
 PND SV+ H+ +G G + G+K W DVG+WQ+
 Sbjct: 122 PNDASVKFHDKMGMQVGHFKQIGFKFEQWLDVGYWQK 159

>ref|YP_001198067.1| sortase and related acyltransferase [Streptococcus suis 05ZYH33]
 ref|YP_001200261.1| sortase and related acyltransferase [Streptococcus suis 98HAH33]
 ref|YP_003024648.1| putative acetyltransferase [Streptococcus suis SC84]
 ref|YP_003026549.1| acetyltransferase [Streptococcus suis P1/7]
 ref|YP_003028903.1| acetyltransferase [Streptococcus suis BM407]
 gb|ABP89667.1| Sortase and related acyltransferase [Streptococcus suis 05ZYH33]
 gb|ABP91861.1| Sortase and related acyltransferase [Streptococcus suis 98HAH33]
 emb|CAZ51402.1| putative acetyltransferase [Streptococcus suis SC84]
 emb|CAZ56031.1| putative acetyltransferase [Streptococcus suis BM407]
 emb|CAR45419.1| putative acetyltransferase [Streptococcus suis P1/7]
 gb|ADE31149.1| GCN5-related N-acetyltransferase [Streptococcus suis GZ1]
 gb|ADV69875.1| sortase and related acyltransferase [Streptococcus suis JS14]
 Length = 169

Score = 127 bits (320), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 63/161 (39%), Positives = 92/161 (57%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++IR A D A + I Y+E + + F TE T + + +E+ +++P+LVA EG
Sbjct: 2 IDIRSARIEDAADLVAIYAPYVEKTAITFETEVPTEAFASRIEKTLEKFPYLVAVEEGK 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIG 127
V G AYA + AR AYDWTVE +VY+ + G+G+ LY L K + A+GFK+ +A I
Sbjct: 62 VVGAYASTYYARAAYDWTVELSVYIKQEARGKGIGTLLYNALEKDLTARGFKNFLACIA 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
LPN S+ LHE GY + GYK WHD+ + Q+
Sbjct: 122 LPNAASIALHEKRGYEQVAHFKKVGYKFDTWHDIVWLQKSL 162

>ref|ZP_08069452.1| phosphinothricin acetyltransferase [Streptococcus vestibularis ATCC 49124]
gb|EFX96344.1| phosphinothricin acetyltransferase [Streptococcus vestibularis ATCC 49124]
Length = 177

Score = 127 bits (320), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 63/170 (37%), Positives = 97/170 (57%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL 61
S E+ + IRPA+ +D A+ I Y+E + F E + QE+ + + ++YP+LV
Sbjct: 3 SKEKMMLTIRPASLSDAQIAIYTPYVEKTAFTFEYEVPSVQEFKRICKTLEKYPYL 62

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
AE G V G AYA + AR AYDWT E ++YV+ + G+GS LYT L + ++A+G+
Sbjct: 63 AEENGQVLGYAYASTYYARTAYDWTTELSIYVAKEARGQGIGSALYTALEEELQARGYL 122

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELP 171
+A I +PN+ S+ +HE GY GYK WHD+ + Q+ + P
Sbjct: 123 FLACIAVPNEASISMHEKRGYVQVAHFPPKIGYKFNKWHDIVWMQKTIDGP 172

>ref|YP_001261029.1| GCN5-like N-acetyltransferase [Sphingomonas wittichii RW1]
gb|ABQ66891.1| GCN5-related N-acetyltransferase [Sphingomonas wittichii RW1]
Length = 182

Score = 127 bits (320), Expect = 5e-28, Method: Compositional matrix adjust.
Identities = 70/162 (43%), Positives = 97/162 (59%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
P+ IR A AD A+ I +Y+ T + F +P + E + + +P+LVAE++G
Sbjct: 4 PLRIRAARPADAEIAAIYAYVLTGPITFEVDPPSAEMARRMTDILPHHPYLVAELDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVI 126
+AG AYA R AY W VE+TVYV+ R G+G+ LY L+ S+ QGF++V+ I
Sbjct: 64 GIAGYAYATRLYERAAYRWAVEATVYVAPGSHRQGIGAALYRALIASLGEQGFRTVIGKI 123

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
LPN SVRLHE+LG+ G L G+K GGWHDVG +Q D
Sbjct: 124 TLPNPASVRLHESLGFVCAGVLAKIGFKQGGWHDVGIYQLDL 165

>ref|YP_820655.1| phosphinothricin acetyltransferase, putative [Streptococcus thermophilus LMD-9]
gb|ABJ66459.1| Sortase or related acyltransferase [Streptococcus thermophilus

LMD-9]
Length = 170

Score = 127 bits (319), Expect = 6e-28, Method: Compositional matrix adjust.
Identities = 66/171 (38%), Positives = 96/171 (56%), Gaps = 2/171 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEVEGV 67
+ IRPA AD A+ I Y+E + + F E + QE+ + +RYP+LVAE +G
Sbjct: 2 ITIRPANLADAQAIQAIYAPYVEKTAITFEYEVPSVQEFKISRNTIERYPYLVAEEDGQ 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
V G AYA P+ AR AYDWT E ++Y++ + GLGS LY L + +E +GF +A I
Sbjct: 62 VLGAYAYSPYYARTAYDWTTELSIYLNEDARGRGLGSQLYGALEEELEKRGFLRFLACIA 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
+PN+ S+ +HE GY GYK WHD+ + Q+ + P R +R
Sbjct: 122 VPNEASIAMHEKRGYIQVAHF PKVGYKFEQWHDIVWMQKTID--GPVRKIR 170

>ref|YP_141658.1| phosphinothricin acetyltransferase [Streptococcus thermophilus
CNRZ1066]
gb|AAV62843.1| phosphinothricin acetyltransferase, putative [Streptococcus
thermophilus CNRZ1066]
Length = 193

Score = 126 bits (316), Expect = 2e-27, Method: Compositional matrix adjust.
Identities = 66/177 (37%), Positives = 98/177 (55%), Gaps = 2/177 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
S E+ + IRPA AD A+ I Y+E + + F E + QE+ + +RYP+LV
Sbjct: 19 SKEKLMITIRPANLADAQAIQAIYAPYVEKTAITFEYEVPSVQEFKISRNTIERYPYL 78

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
AE +G V G AYA + AR AYDWT E ++Y++ + GLGS LY L + +E +GF
Sbjct: 79 AEEDGQVLGYAYASTYYARTAYDWTTELSIYLNEDARGRGLGSQLYGALEEELEKRGFLR 138

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
+A I +PN+ S+ +HE GY GYK W+D+ + Q+ + P R +R
Sbjct: 139 FLACIAVPNEASIAMHEKRGYIQVAHF PKVGYKFEQWYDIVWMQKTID--GPVRKIR 193

>ref|ZP_07832184.1| putative phosphinothricin N-acetyltransferase [Clostridium sp.
HGF2]
gb|EFR38166.1| putative phosphinothricin N-acetyltransferase [Clostridium sp.
HGF2]
Length = 207

Score = 125 bits (313), Expect = 3e-27, Method: Compositional matrix adjust.
Identities = 63/165 (38%), Positives = 97/165 (58%), Gaps = 1/165 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEVEGVVA 69
IR A +D A+ I HY+E S + F + + +E+ + ++Q YP+LV E++ +
Sbjct: 16 IRFAQLSDAPALLSIYAHYVENSIVITFEYDVPSLEEFEGRMKIQREYPYLVCELDQNI 75

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
G AYA R AY W VE ++Y+ + QR +G+ LYT LL+ ++ QG ++ ++ I LP
Sbjct: 76 GYAYAHRHMERAAAYQWNVEVSIYLLPQVQRRQIGTALYTALLEILKLQGLQTAISCITLP 135

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAP 173
ND S+ LH++ G+T G LR AGYK W DV + Q+ E P P
Sbjct: 136 NDASLALHKSFGFTEIGVLRNAGYKFDWARDVWLQKALHEHPVP 180

>ref|YP_003401819.1| GCN5-related N-acetyltransferase [Haloterrigena turkmenica DSM 5511]
 gb|ADB59146.1| GCN5-related N-acetyltransferase [Haloterrigena turkmenica DSM 5511]
 Length = 203

Score = 124 bits (312), Expect = 4e-27, Method: Compositional matrix adjust.
 Identities = 69/172 (40%), Positives = 93/172 (54%), Gaps = 1/172 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT D AAV DI + E++ V F P T E + + + YPWL V E++G VA
 Sbjct: 7 IRVATPDDAAAVRDIYAPFCESTAVTFEETPPTAEVANRIASTLETYPWLVC EIDGAVA 66

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + R AY WTVE +VYV+ ++ G+G LY L +E QG + AV +P
 Sbjct: 67 GYAYASRLRERRAYQWTVELSVYVADDARQSGVGRALYESLFAVLERQGV RDGYAVTTVP 126

Query: 130 NDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQ RDF-ELPAPPRPVRPV 180
 N + R HE LG+ A G+ G W DV +W+R E A P P+ P+
 Sbjct: 127 NPETERFHERLGFERCVDFFPAIGHSEGEWRDVAWRRSIGEKTADPEPITPL 178

>gb|ADQ63288.1| Sortase acyltransferase-like protein [Streptococcus thermophilus ND03]
 Length = 170

Score = 124 bits (312), Expect = 4e-27, Method: Compositional matrix adjust.
 Identities = 65/171 (38%), Positives = 95/171 (55%), Gaps = 2/171 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IRPA AD A+ I Y+E + + F E + QE+ + +RYP+LVAE +G
 Sbjct: 2 ITIRPANLADAQAIQAIYAPYEKTAITFEYEVPSVQEF EKISRNTIERYPYLVAEEDGQ 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G AYA + AR AYDWT E ++Y++ + GLGS LY L + +E +GF +A I
 Sbjct: 62 VLG YAYASTYYARTAYDWTTELSIYL NEDARGRGLGSQLYGALEEELEKRGFLRFLACIA 121

Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQ RDFELPAPPRPVR 178
 +PN+ S+ +HE GY GYK WHD+ + Q+ + P R +R
 Sbjct: 122 VPNEASIAMHEKRGYIQVAHF PKVGYKFEQWHDIVWMQKT--IDGPVRKIR 170

>ref|ZP_08021317.1| phosphinothricin acetyltransferase [Streptococcus australis ATCC 700641]
 gb|EFV99390.1| phosphinothricin acetyltransferase [Streptococcus australis ATCC 700641]
 Length = 170

Score = 124 bits (312), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 64/167 (38%), Positives = 91/167 (54%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IRP T D + I Y+E + + F + T +E+ +E++ R+P+LVAE +G
 Sbjct: 2 LKIRPVT LKDAPELVRIYAPYEKTAITFEYQIPTIEEFEGRIEKILQRFPYLVAEEDGQ 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V AY + R+AYDW VE +VYV H+ GLGS LY L +EA+G+ +A I
 Sbjct: 62 VLAYAYGSTYYDRSAYDWAVEVSVYVDQDHRGQGLGSRLYEAL EMELEARGYLRFLACIA 121

Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQ RDFELPAPP 174
 LPN S+ LHE GY GYK WHD+ + Q+ E P P
 Sbjct: 122 LPNPASIALHEKRGYVKVAHF PKIGYKFDQWHDIVWMQKTIEGPVKP 168

>ref|ZP_04062352.1| phosphinothricin N-acetyltransferase [Streptococcus salivarius SK126]
 ref|ZP_07723731.1| putative phosphinothricin N-acetyltransferase [Streptococcus vestibularis F0396]
 gb|EEK09823.1| phosphinothricin N-acetyltransferase [Streptococcus salivarius SK126]
 gb|EFQ59234.1| putative phosphinothricin N-acetyltransferase [Streptococcus vestibularis F0396]
 Length = 170

Score = 124 bits (312), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 61/162 (37%), Positives = 93/162 (57%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRPA+ +D A+ I Y+E + F E + QE+ + + ++YP+LVAE G V
 Sbjct: 4 IRPASLSDAQAIQAIYTPYVEKTAFTFEYEVPSVQFEKRICKTLEKYPYLVAEENGQVL 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + AR AYDWT E ++YV+ + G+GS LYT L + ++A+G+ +A I +P
 Sbjct: 64 GYAYASTYYARTAYDWTTELSIYVAKEARGQGIGSALYTALEEELQARGYLRLFLACIAVP 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELP 171
 N+ S+ +HE GY GYK WHD+ + Q+ + P
 Sbjct: 124 NEASISMHEKRGYVQVAHFPGKIGYKFNKWHDIVWMQKTIDGP 165

>ref|ZP_08098012.1| phosphinothricin N-acetyltransferase, putative [Vibrio brasiliensis LMG 20546]
 gb|EGA66063.1| phosphinothricin N-acetyltransferase, putative [Vibrio brasiliensis LMG 20546]
 Length = 164

Score = 124 bits (311), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 62/162 (38%), Positives = 93/162 (57%), Gaps = 1/162 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + R +D A+ DI N ++ STV F + T ++ +E++ D +PW+V E +G
 Sbjct: 1 MNFRTVNLSDSQAIADIYNPFVTDSTVTFFEEKAVTAEQISQRIEKVLDSGFPWIVLEQDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AYAGPW R+AY +T EST+Y+S G G LY LL ++ QG K+V+ V+
 Sbjct: 61 EILGYAYAGPWHTRSAYRFTAESTIYLSPDAGGKGYGHKLYRELLARLKEQGIKNVMGVV 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168
 LPN PSV+LH++LG+T G + G K V +WQ +
 Sbjct: 121 ALPNPPSVKLHQSLGFTKVGEFKNIGVKFERQISVSYWQLEL 162

>ref|YP_003409278.1| phosphinothricin acetyltransferase [Geodermatophilus obscurus DSM 43160]
 gb|ADB74907.1| Phosphinothricin acetyltransferase [Geodermatophilus obscurus DSM 43160]
 Length = 198

Score = 124 bits (311), Expect = 5e-27, Method: Compositional matrix adjust.
 Identities = 70/168 (41%), Positives = 91/168 (54%), Gaps = 3/168 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +R AT D AA I Y+ + V+F EP T E + R+ WL V E +G V
 Sbjct: 11 VRDATGDDAAACARIYEPYVRD TVVSFELEPPTAAEVAGRIAAALAHAWLVLEDDGRVV 70

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIGLP 129
 G AY + AR AYDWT +VY +R G G LYT LL + A+G+++ +A I LP
 Sbjct: 71 GYAYGSTFNARAAYDWTTSVSVYTEPGRRRRTGAGRALYTALLDRLAARGYRTALAGIALP 130

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELP---APP 174
 ND SV LH A+G+ GT R G+K G W+DV +QR P APP
 Sbjct: 131 NDASVGLHTAMGFELVGYRRVGVKLGWWDVARYQRPLGEPTDDAPP 178

>gb|ADZ90538.1| Phosphinothricin acetyltransferase [Marinomonas mediterranea MMB-1]
 Length = 163

Score = 124 bits (311), Expect = 6e-27, Method: Compositional matrix adjust.
 Identities = 61/157 (38%), Positives = 93/157 (59%), Gaps = 1/157 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR AT D A + I NHYI +++ F EP + + ++ ++++Q + PWLVAEV+G +
 Sbjct: 2 IRNATPQDAAKIAAIYNHYIVKTSITFEEEPVSIIDIVERVQKVQKDLPLWVAEVDGEI 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIGL 128
 AG AYA W R+AY ++VE++VY+S + GLG+ LY L +++ +V+ + L
 Sbjct: 62 AGYAYAAHWHNRSAYRFSVEASVYLSPCYSGKGLGTALYQALFDALKKTDVHTVIGCLAL 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 PN+ SV LH G G+K G W DVG+WQ
 Sbjct: 122 PNEASVALHNKFDMMKIGHFEQVGFKFGQWWDVGYWQ 158

>ref|YP_139746.1| phosphinothricin acetyltransferase, putative [Streptococcus
 thermophilus LMG 18311]
 gb|AAV60931.1| phosphinothricin acetyltransferase, putative [Streptococcus
 thermophilus LMG 18311]
 Length = 193

Score = 124 bits (311), Expect = 6e-27, Method: Compositional matrix adjust.
 Identities = 65/177 (36%), Positives = 97/177 (54%), Gaps = 2/177 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
 S E+ + IRPA AD A+ I Y+E + + F E + +E+ + +RYP+LV
 Sbjct: 19 SKEKLMITIRPANLADAQAIQAIYAPYVEKTAITFEYEVPSIKEFEKRISNTIERYPYL 78

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 AE +G V G AYA + R AYDWT E ++Y++ + GLGS LY L + +E +GF
 Sbjct: 79 AEEDGQVLGYAYASTYYDRAYDWTTELSIYLNEDARGRLGSQLYGALIEEELEKRGFLR 138

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 +A I +PN+ S+ +HE GY GYK WHD+ + Q+ + P R +R
 Sbjct: 139 FLACIAPNEASIAMHEKRGYIQVAHFPPKVGKFEQWHDIVWMQKTID--GPVRKIR 193

>ref|ZP_03399908.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato T1]
 ref|ZP_07230949.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas
 syringae pv. tomato Max13]
 ref|ZP_07253783.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas
 syringae pv. tomato K40]
 gb|EEB57012.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato T1]
 Length = 185

Score = 123 bits (309), Expect = 1e-26, Method: Compositional matrix adjust.
 Identities = 66/167 (39%), Positives = 92/167 (55%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
      ++IR A AD A+ I + + ++F P + +E + YP+LVAE G
Sbjct: 3  LKIRTAVTADAEAIQRIYAPIVSNTAISFEETPPSVEEIAQRIATTLQTYPYLVAEEGGE 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVIG 127
      + G AYA +AR AY W V+ TVYV+ +R G+G LY LL +E Q F++ A I
Sbjct: 63 IKGYAYASQHRARAAYQWAVDVTYVVAESARRQGVGRELYETLLPILEKQRFRAAYAGIA 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
      PN+ SV LHE+LG+T GT G+K G WHDVG+W+ PP
Sbjct: 123 RPNEGSVGLHESLGFTHIGTYPEVGFKLKGWHDVGYWRLGLCQATPP 169

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>ref|ZP_06060563.1| acyltransferase [Streptococcus sp. 2_1_36FAA]
gb|EEY79747.1| acyltransferase [Streptococcus sp. 2_1_36FAA]
      Length = 189

```

Score = 123 bits (309), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 66/175 (37%), Positives = 98/175 (56%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
      +EIR AT +D AA+ I Y+E + + F E T +++ + + + ++YP+LVAE +GV
Sbjct: 12 MEIRLATPSDAAALLAIYAPYVENTAITFEYEVPTIEDFTNRIAKTLEKYPYLVAEEDGV 71

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVIG 127
      V G AYA + AR AYDW VE +VYVS + G+GS LY L ++ G+ +A I
Sbjct: 72 VLGAYASTYYARAAYDWAVELSVYVSLDSRGQGVGSKLYDALEYLLDQMGYVHFLACIS 131

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQ 182
      LPN+ S+ LH GY GYK WHD+ + Q+ + A P + V +
Sbjct: 132 LPNEASLALHRKRGYQQVAYFPKIGYKFERWHDIVWLQKSLDKEAGPIKLLKVKE 186

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```

>ref|ZP_05877484.1| phosphinothricin N-acetyltransferase putative [Vibrio furnissii
CIP
      102972]
gb|EEX41765.1| phosphinothricin N-acetyltransferase putative [Vibrio furnissii CIP
      102972]
      Length = 165

```

Score = 123 bits (309), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 63/166 (37%), Positives = 95/166 (57%), Gaps = 3/166 (1%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
      +EIR D+ + +I N YIE +T+ F +P + + + + + ++ PWLV EG
Sbjct: 1  MEIRDIQDVIVTITEIYNRYIEQTTITFEEDPISVSDMGERVNKKIRAAGLPWLVAHEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVI 126
      V G AYAG W R+AY +TVE ++Y+S + + G G +Y LL ++ G ++V+ VI
Sbjct: 61 TVVGYAYAGQWNTRSAYRFTVEPSIYLSQAKGQGWGRAIYQMLLSKLKDLGIRNVLGVI 120

Query: 127 GLPNDSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA 172
      LPN S+ LHE+LG+ G GYK W VG+WQ E+PA
Sbjct: 121 ALPNGASIGLHESLGFRKVGFEFSQVGKFERWLSVGYWQ--LEIPA 164

```

```

>ref|ZP_07837484.1| Phosphinothricin acetyltransferase [Eubacterium cellulosolvens 6]
gb|EFR66575.1| Phosphinothricin acetyltransferase [Eubacterium cellulosolvens 6]
      Length = 183

```

Score = 123 bits (308), Expect = 1e-26, Method: Compositional matrix adjust.
Identities = 58/159 (36%), Positives = 91/159 (57%), Gaps = 7/159 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR A+ AD + +I ++Y+ + + F E + +E+ +E++ RYP+LVAE +G +
 Sbjct: 4 IRDASVADAKRLLEIYDYVRKTAITFEYETPSIEEFTARMEKIMKRYPYLVAERDQGIV 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G +YAG +K R AYDW+ E+T+Y+ H ++ GLG LY L + ++A G ++ A IG P
 Sbjct: 64 GYSYAGVFKDRAAYDWCETTTIYIDHNERKSGLGRLLYEALKEELKAIGIMNLYACIGYP 123

Query: 130 -----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 S H LGYT G GYK+G W+D+
 Sbjct: 124 IEEDEYLTKNSAEFHAHLGYTKVGEFHKCGYKYGRWYDM 162

>ref|ZP_07726783.1| putative phosphinothricin N-acetyltransferase [Streptococcus
 parasanguinis F0405]
 gb|EFQ56096.1| putative phosphinothricin N-acetyltransferase [Streptococcus
 parasanguinis F0405]
 Length = 169

Score = 122 bits (307), Expect = 2e-26, Method: Compositional matrix adjust.
 Identities = 60/162 (37%), Positives = 92/162 (56%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP +D AA+ I Y+ + + F + T QE+ + + ++P+LVAEV+G V
 Sbjct: 3 IRPVQLSDAAAIRAIYQPYVTETAITFEVDVPTVQEFESRIAKTLTQFPYLVAEVDGKVV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + AR AYDWT E ++YV+ + G+G LYT L + ++A+G+ +A I +P
 Sbjct: 63 GYAYASTYYARAAYDWTTELSIYVAKEARGQGIGLALYTALEELQARGYLRFACIAPV 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELP 171
 N+ S+ +HE GY GYK WHD+ + Q+ E P
 Sbjct: 123 NEASISMHEKRGYVQVAHFPGKIGYKFNKWHDIVWMQKTIEGP 164

>ref|YP_003074738.1| phosphinothricin N-acetyltransferase [Teredinibacter turnerae
 T7901]
 gb|ACR11359.1| phosphinothricin N-acetyltransferase [Teredinibacter turnerae
 T7901]
 Length = 204

Score = 122 bits (307), Expect = 2e-26, Method: Compositional matrix adjust.
 Identities = 61/169 (36%), Positives = 92/169 (54%), Gaps = 4/169 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 + IR AD A+ +I N+YI + ++F P + + + + ++ YPWLVAE G
 Sbjct: 36 SIMIRACRPADAGAI AEIYNYINETVISFEQTPLESEAQMAERIAKISANYPWLVAEENG 95

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AY W+ R AY ++ +TVY++ H GLG LY L +++ + + +VA I
 Sbjct: 96 EILGFAYVALWQERVAYRHSLVTTVYLNRNHTGRGLGKALYEALFEALTSVDCRVLVAGI 155

Query: 127 GLPNDSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ----DFELP 171
 LPN SV LHE +G+ + G KHG W DVG+WQ+ D E P
 Sbjct: 156 ALPNAASVALHEKVGFEKVAHFKDVGRKHGQWVDVGYWQKTINTDREFP 204

>ref|ZP_03624439.1| GCN5-related N-acetyltransferase [Streptococcus suis 89/1591]
 gb|EEF65250.1| GCN5-related N-acetyltransferase [Streptococcus suis 89/1591]
 Length = 169

Score = 122 bits (307), Expect = 2e-26, Method: Compositional matrix adjust.

Identities = 60/161 (37%), Positives = 93/161 (57%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
          ++IR A   D A +   I   Y+E + + F TE T + +   +E+   +++P+LV+ EG
Sbjct: 2   IDIRSARIEDAADLVAIYAPYVEKTAITFETEVPTVEAFASRIEKTLEKFPYLVSVVEGK 61

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
          V G AYA + AR AYDWTVE +VY+   +   G+GS LY + + ++A+GFK+ +A I
Sbjct: 62  VVGAYASTYYARAAYDWTVELSVYIKQEARGKGIGSLLYDAIEEDLKARGFKNFLACIA 121

Query: 128  LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          LPN S+ LH+ GY   +   GYK   WHD+ + Q+
Sbjct: 122  LPNPASLSLHKRGYEQVAHFKNVGYKFDTWHDIVWLQKSL 162
```

```
>ref|YP_001354135.1| phosphinothricin N-acetyltransferase [Janthinobacterium sp.
Marseille]
gb|ABR90070.1| phosphinothricin N-acetyltransferase [Janthinobacterium sp.
Marseille]
Length = 173
```

Score = 122 bits (307), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 63/156 (40%), Positives = 84/156 (53%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR AT D AA+C I NHY+ + ++F E + E   +E   ++PWLV E +G +
Sbjct: 5   IRLATVNDAAAICHIYNHYVLNTVISFEMEAVSADEMALRIEETLQQFPWLVEADGRIL 64

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
          G AYA WK R AY +VE +VY+   GLG+ LY L+ + Q   +V+ I LP
Sbjct: 65  GYAYASKWKVRKAYQHSVEGSVYLGQDSGGKGLGTLLYKALIAELAKQSVHAVLGGIVLP 124

Query: 130  NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
          N SV LHE LG+   L   G K   W DVG+WQ
Sbjct: 125  NPGSVALHEKLGFKVAHLPGIGKKFDQWLDVGYWQ 160
```

```
>ref|ZP_05645407.1| conserved hypothetical protein [Enterococcus casseliflavus EC30]
ref|ZP_05651742.1| conserved hypothetical protein [Enterococcus casseliflavus EC10]
gb|EEV28740.1| conserved hypothetical protein [Enterococcus casseliflavus EC30]
gb|EEV35075.1| conserved hypothetical protein [Enterococcus casseliflavus EC10]
Length = 177
```

Score = 122 bits (306), Expect = 2e-26, Method: Compositional matrix adjust.
Identities = 64/160 (40%), Positives = 90/160 (56%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR AT AD A+ I   +Y+E + + F TE + QE+ + + +   RYP+LVAE G +
Sbjct: 3   IRSATIADAQALTAIYAYVENTPITFETEVPSVQEFAERIAKTLKRYPYLVAEEAGEIV 62

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
          G AYA +K R AYDWTVE TVY++   +   GLG+ LY L + ++AQ   ++ A I
Sbjct: 63  GYAYASAYKERAAYDWTVEVTVYLAPDAKAKGLGTALYQALEEKLKAQN NVNLTACITGG 122

Query: 130  NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
          N S   HE LGY   GYK   WHDV + Q++ +
Sbjct: 123  NQQSEAFHEKLG YRKVADFAQVGYKFNQWHDVIWMQKELQ 162
```

```
>ref|ZP_05655037.1| conserved hypothetical protein [Enterococcus casseliflavus EC20]
gb|EEV38370.1| conserved hypothetical protein [Enterococcus casseliflavus EC20]
Length = 177
```


Score = 122 bits (305), Expect = 3e-26, Method: Compositional matrix adjust.
Identities = 64/160 (40%), Positives = 90/160 (56%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR AT AD A+ I +Y+E + + F TE + QE+ + + + RYP+LVAE G +
Sbjct: 3 IRSATIADAQALTAIYAYVENTPITFETEVPVQFEFAERIAKTLKRYPYLVAAEEAGEIV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G AYA +K R AYDWTVE TVY++ + GLG+ LY L + ++AQ ++ A I
Sbjct: 63 GYAYASAYKERAAYDWTVEVTVYLAPDAKAKGLGTALYQALEEKLKAQNVVNLTAITGG 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
N S HE LGY GYK WHDV + Q++ +
Sbjct: 123 NQQSEAFHEKLG YRKVADFAHVG YKFNQWHDVIWMQKELQ 162

>ref|YP_927219.1| phosphinothricin N-acetyltransferase [Shewanella amazonensis SB2B]
gb|ABL99549.1| phosphinothricin N-acetyltransferase, putative [Shewanella
amazonensis SB2B]
Length = 171

Score = 121 bits (303), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 64/161 (39%), Positives = 89/161 (55%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR A D +AV DI NHYIE++ + F P E ++ +Q PVLVA +
Sbjct: 2 IRHAALHDASAVADIYNHYIESTAITFEETPLQAAEIAARIQHVQAAGLPWLVALEGNAL 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G AYA WK R+AY +TVE+TVYV+ G+G+ LY L++ ++ SV+ I L
Sbjct: 62 TGYAYATKWKERSAYRFTVETTVYVAPNGHGKGVGTALYQALIERLKILKVNNSVIGGITL 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
PN S+ LHE +G + GYK G W DVG+WQ + +
Sbjct: 122 PNPASIALHEKMGMKVAHFQNI GYKFGQWQDVG YWQLNLQ 162

>ref|YP_001758117.1| GCN5-related N-acetyltransferase [Methylobacterium radiotolerans
JCM 2831]
gb|ACB27434.1| GCN5-related N-acetyltransferase [Methylobacterium radiotolerans
JCM 2831]
Length = 176

Score = 121 bits (303), Expect = 4e-26, Method: Compositional matrix adjust.
Identities = 68/161 (42%), Positives = 94/161 (58%), Gaps = 2/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IRPAT AD+ A+ I + TST +F TEP T E E L+ +P+LVA+ +G V
Sbjct: 5 IRPATQADLPAIATIYGDAVTTSTASFETEPPTLAEMTRRFEVL RAGGFPYLVADRDTGTV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
AG AYAGP+ R AY T+E ++YV+ + G+G L T L+ + E +++VA+I
Sbjct: 65 AGYAYAGPYHQRAAYRSTLED SIYVARTARGGGVGRLLLTALIAASEQIDCRTLVAIIAD 124

Query: 129 PNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
P S+ LH +LG+T GTL G+KHG W DV QR
Sbjct: 125 SGSPASIALHASLGFTPVGTLAGVGHKHGRWLDVTLMQRSL 165

>ref|YP_001893235.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12J]
ref|YP_002983578.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12D]
gb|ACD29808.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12J]
gb|ACS64906.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12D]

Length = 182

Score = 120 bits (302), Expect = 6e-26, Method: Compositional matrix adjust.
Identities = 67/170 (39%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWL 60
+P + +++RPAT AD+ A+ I H++ T T +F T+P E + LQD P++
Sbjct: 13 APGTQTIDVRPATLADLPAIVAIYAHHVRTGTASFETDPPDLAEMTRRFQALQDAGMPYV 72

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
VAE +G + G AYAGP +AR AY TVE ++Y+ Q G+G+ L L++ EA+GFK
Sbjct: 73 VAEADGTLGLYAYAGPHRARPAYRNTVEDSIYLDTAQAQGRGVGTLLQLALIRDCEARGFK 132

Query: 121 SVVAVI--GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
+VAV+ G N S RLH G+ G L GYK W D QR
Sbjct: 133 QMVAVVGGGHQNPQSARLHARCGFREVGVLEHVGYKFDRWLDCLLMQRSL 182

>ref|YP_001601101.1| putative phosphinothricin N-acetyltransferase [Gluconacetobacter
diazotrophicus PAL 5]
emb|CAP54763.1| putative phosphinothricin N-acetyltransferase [Gluconacetobacter
diazotrophicus PAL 5]
Length = 222

Score = 120 bits (301), Expect = 7e-26, Method: Compositional matrix adjust.
Identities = 67/163 (41%), Positives = 97/163 (59%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEG 66
V IR A A D+ + I H++ T +F TEP + ++ + L+ +P+LVAE G
Sbjct: 48 VTIRSARAEDVPGIAAIYAHVHLHGTSASFETEPSPAEDMARRMAALRAGDFPYLVAEEGG 107

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVI 126
V G AYAG + R AY TVE++VY++H G+GS L LL + A+GF+ ++A++
Sbjct: 108 AVIGYAYAGLYHLRAAYRDTVENSIVLAHDAAGRGVGSMLLDALLAACVARGFRQMIALV 167

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
G N S+RLHE LG+ GTL++ GYKHG W DV QR+
Sbjct: 168 GDSANIASIRLHERLGFRTVGTLSVGYKHGRWLDVVLQREL 210

>gb|ADI12131.1| Phosphinothricin acetyltransferase [Streptomyces bingchengensis
BCW-1]
Length = 185

Score = 120 bits (301), Expect = 7e-26, Method: Compositional matrix adjust.
Identities = 71/174 (40%), Positives = 92/174 (52%), Gaps = 5/174 (2%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWL 60
SPE IRPA AD+ AV DI HY+ + F P++ EW L+ L R P+L
Sbjct: 3 SPE---ATIRPAVHADLKAVADIYAHVYRHTVTTFDETSPSAAEWEQRLDELGTGRDLPL 59

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
VAE+ G VAG AYAGPW+ + AY TVE T+Y++ GLG+ L L+ G +
Sbjct: 60 VAELSGAVAGFAYAGPWRPKPAYQHTVEDTIYLAAPDATGRGLGTALLGPLIAEATRAGR 119

Query: 121 SVVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAP 173
++AVI +D S LH G+T G L A G+KHG W D QR P
Sbjct: 120 QMIAVIADTGSDASAALHRRFGFTDAGRLLTAVGHKHGRWIDTLLMQRPLSGQGP 173

>gb|EGC23067.1| phosphinothricin acetyltransferase [Streptococcus sanguinis SK353]
Length = 207

Score = 120 bits (300), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 62/167 (37%), Positives = 93/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR AT +D + I Y+E + + F E T +++ +E+ +RYP+LVAE +G+
Sbjct: 31 MNIRFATPSDATLLAIYAPYVENTAITFEYEVPTIEDFATRIEKTLEERYPYLVAEEDGL 90

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA + AR AYDW VE +VYVS + G+GS LY L ++ G+ +A I
Sbjct: 91 ILGYAYASTYYARAAYDWAVELSVYVSQDARGKGVGSKLYDELEDLLDQMGYMHFLACIS 150

Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGVFWQDFELPAPP 174
LPN+ S+ LH+ GY GYK WHD+ + Q+ + A P
Sbjct: 151 LPNEASLALHQKRGYQQVAHFPGYKFERWHDIVWLQKSLDKQAGP 197

>ref|ZP_04747260.1| GCN5-related N-acetyltransferase [Mycobacterium kansasii ATCC
12478]
Length = 178

Score = 120 bits (300), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 73/177 (41%), Positives = 96/177 (54%), Gaps = 4/177 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
P +R A AAD AA + Y+ + + F TE T +E + + + WLV EV G
Sbjct: 2 PEHVRSAIAADAAACLAAYRYPVLDTVITFETEVPTEEMAARIVAARVMHEWLVLEVAG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VAG AYA + R AY W+VE++VY++ R G G LY LL + A+GF+ A I
Sbjct: 62 DVAGYAYAQQFNPRAYRWSVETSVMARDRVRTGGGRKLYAELLSRLAARGFRRAFAAI 121

Query: 127 GLPNDSVRLHEALGYTARGLRAAGYKHGGWHDVGVFWQDF----ELPAPPRPVRP 179
PND S LHEA G+ G LR G+KHG WHDV +WQ D + PPR + P
Sbjct: 122 AQPNDASNALHEAFGFQAGRLRRVGVKHWGAWHDVQWWQLDLVACEDEVDPREIAP 178

>ref|YP_002275595.1| GCN5-like N-acetyltransferase [Gluconacetobacter diazotrophicus
PAL
5]
gb|ACI50980.1| GCN5-related N-acetyltransferase [Gluconacetobacter diazotrophicus
PAL 5]
Length = 184

Score = 120 bits (300), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 67/163 (41%), Positives = 97/163 (59%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEG 66
V IR A A D+ + I H++ T +F TEP + ++ + L+ +P+LVAE G
Sbjct: 10 VTIRSARAEVPGIAAIYAHVHLHGTSASFETEPSPAEDMARRMAALRAGDFPYLVAEEGG 69

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G AYAG + R AY TVE++VY++H G+GS L LL + A+GF+ ++A++
Sbjct: 70 AVIGYAYAGLYHLRAAYRDTVENSIVLAHDAAGRGVGSMLLDALLAACVARGFRQMIALV 129

Query: 127 G-LPNDSVRLHEALGYTARGLRAAGYKHGGWHDVGVFWQDF 168
G N S+RLHE LG+ GTL++ GYKHG W DV QR+
Sbjct: 130 GDSANIASIRLHERLGFRTVGTLSVGYKHGRWLDVLLQREL 172

>ref|ZP_08145758.1| phosphinothricin acetyltransferase [Enterococcus casseliflavus
ATCC
12755]
gb|EGC69432.1| phosphinothricin acetyltransferase [Enterococcus casseliflavus ATCC

12755]
Length = 177

Score = 119 bits (299), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 63/160 (39%), Positives = 90/160 (56%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR AT AD A+ I +Y+E + + F TE + QE+ + + + RYP+LVAE G +
Sbjct: 3 IRSATIADAQALTAIYAYVENTPITFETEVPSPVQFEFAERIAKTLKRYPYLVAEEAGEIV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G AYA +K R AYDWTVE TVY++ + GLG+ LY L + ++A+ ++ A I
Sbjct: 63 GYAYASAYKERAAYDWTVEVTVYLAPDAKAKGLGTALYQGLEEKLKAKNVVNLACITGG 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFE 169
N S HE LGY GYK WHDV + Q++ +
Sbjct: 123 NQQSEAFHEKLG YRKVADFAHVGYKFNQWHDVIWMQKELQ 162

>gb|EGD36393.1| phosphinothricin acetyltransferase [Streptococcus sanguinis SK150]
Length = 185

Score = 119 bits (299), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 62/167 (37%), Positives = 93/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR A +D A + I Y+E + + F E T +++ +E+ +RYP+LVAE +G+
Sbjct: 9 MNIRLARPSDAATLLAIYAPYVENTAITFEYEVPTIEDFATRIEKTLEKYPYLVAEEDGL 68

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA + AR AYDW VE +VYVS + G+GS LY L ++ G+ +A I
Sbjct: 69 ILGYAYASTYYARAAYDWAVELSVYVSQDARGKGVGSKLYDELEDLLDQMGYMHFLACIS 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFELPAPP 174
LPN+ S+ LH+ GY GYK WHD+ + Q+ + A P
Sbjct: 129 LPNEASLALHQKRGYQQVAHF PKIGYKFERWHDIVWLQKSLDKQAGP 175

>gb|EGC26393.1| phosphinothricin acetyltransferase [Streptococcus sanguinis SK678]
Length = 215

Score = 119 bits (299), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 61/167 (36%), Positives = 93/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR AT +D A + I Y+E + + F E T +++ +E+ ++YP+LVAE +G+
Sbjct: 39 MNIRFATPSDAATLLAIYAPYVENTAITFEYEVPTIEDFANRIEKTLEKYPYLVAEEDGL 98

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA + AR +YDW VE +VYVS + G+GS LY L ++ G+ +A I
Sbjct: 99 ILGYAYASTYYARASYDWAVELSVYVSQDARGKGVGSKLYDELEDLLDQMGYMHFLACIS 158

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFELPAPP 174
LPN S+ LH GY GYK WHD+ + Q+ + A P
Sbjct: 159 LPNKASLALHRKRGYQQVAHF PKIGYKFECWHDIVWLQKSLDKQAGP 205

>gb|EGC24800.1| phosphinothricin acetyltransferase [Streptococcus sanguinis SK405]
Length = 215

Score = 119 bits (299), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 63/167 (37%), Positives = 92/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR AT +D A + I Y+E + + F E T +++ + + + +YP+LVAE +GV
 Sbjct: 39 MNIRFATPSDAATLLAIYAPYVENTAITFEYEVPTIEDFTNRIAKTLGKYPYLVAEEDGV 98

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G AYA + AR AYDW VE +VYVS + G+GS LY L ++ G+ +A I
 Sbjct: 99 VVGAYASTYYARAAYDWAVELSVYVSQDARGKGVGSKLYDKLEDLLDQMGYMHFLACIS 158

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 LPN+ S+ LH GY GYK WHD+ + Q+ + A P
 Sbjct: 159 LPNEASLALHRKRGYQQVAHFPMGYKFERWHDIVWLQKSLDKQAGP 205

>ref|YP_001450496.1| acyltransferase [Streptococcus gordonii str. Challis substr. CH1]
 gb|ABV10255.1| acyltransferase [Streptococcus gordonii str. Challis substr. CH1]
 Length = 178

Score = 119 bits (298), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 63/173 (36%), Positives = 97/173 (56%), Gaps = 5/173 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +EIR A +D ++ DI Y+E + + F E T +++ + +E+ ++YP+LVAE +GV
 Sbjct: 1 MEIRLAKPSDARSLLDIYAPYEKTAITFEYEVPTVEDFANRVEKTLKYPYLVAEEDGV 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G AYA + AR AYDW VE ++ VS + G+G+ LY L ++ G+ +A I
 Sbjct: 61 VVGAYASTYYARAAYDWAVELSICVSLDSRGQGVGKLYDALEYLLDQMGYIHFLACIS 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
 LPN+ S+ LH GY GYK WHD+ + Q+ E + VRP+
 Sbjct: 121 LPNEASLALHRKRGYQQVAHFPMGYKFNWHDIVWLQKSLE----KEVRPI 168

>gb|EGD29501.1| phosphinothricin acetyltransferase [Streptococcus sanguinis SK72]
 Length = 207

Score = 119 bits (298), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 62/167 (37%), Positives = 92/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A +D A + I Y+E + + F E T +++ +E+ ++YP+LVAE +G+
 Sbjct: 31 MNIRLARPSDAATLLAIYAPYVENTAITFEYEVPTIEDFATRIEKTLEKYPYLVAEEDGL 90

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA + AR AYDW VE +VYVS + G+GS LY L +E G+ +A I
 Sbjct: 91 ILGYAYASTYYARAAYDWAVELSVYVSQDARGKGVGSKLYDKLEDLLEQMGYMHFLACIS 150

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 LPN+ S+ LH GY GYK WHD+ + Q+ + A P
 Sbjct: 151 LPNEASLALHRKRGYQQVAHFPMGYKFEHWHDIVWLQKSLDKQAGP 197

>ref|YP_004016335.1| phosphinothricin acetyltransferase [Frankia sp. Eu11c]
 gb|ADP80465.1| Phosphinothricin acetyltransferase [Frankia sp. Eu11c]
 Length = 180

Score = 119 bits (298), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 73/175 (41%), Positives = 99/175 (56%), Gaps = 4/175 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 P +IRPATAAD A I Y+ + + F TE + +E ++R +R+ WLW EV+G
 Sbjct: 5 PWQIRPATAADAPACAAIYADYVTDTAITFETEVPISIEEMAGRIQRSNERHAWLVLEVDG 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G AY + AR AY W+ E++VY+ +R G G LY LL + +G++ V+A I
 Sbjct: 65 TVVGAYAGREYHARAAYGWSCEASVYLRMGRRRTGAGRALYQALLPRLAERGYRRVIAGI 124

Query: 127 GLPNDPVSRVRLHEALGYTARGLRAAGYKHGGWHDVGVFWQRDF---ELPA-PPRPV 177
 PND S LH A G+T G + G+KHG WHDV + Q D E P PP PV
 Sbjct: 125 TQPNDASNGLHYAFGFTDVGVMYKIGWKHGVWHDVAWLQLDLTPDEDPVKPPDPV 179

>ref|ZP_08087207.1| phosphinothricin acetyltransferase [Streptococcus sanguinis VMC66]
 gb|EFX93765.1| phosphinothricin acetyltransferase [Streptococcus sanguinis VMC66]
 Length = 207

Score = 119 bits (297), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 62/167 (37%), Positives = 92/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A +D A + I Y+E + + F E T +++ +E+ ++YP+LVAE +G+
 Sbjct: 31 MNIRFARPSDAATLLAIYAPYVENTAITFEYEVPTIEDFATRIEKTLEKYPYLVAEEDGL 90

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA + AR AYDW VE +VYVS + G+GS LY L +E G+ +A I
 Sbjct: 91 ILGYAYASTYYARAAYDWAVELSVYVSQDARGKGVGSKLYDKLEDLLEQMGYMHFLACIA 150

Query: 128 LPNDPVSRLHEALGYTARGLRAAGYKHGGWHDVGVFWQRDFELPAPP 174
 LPN+ S+ LH GY GYK WHD+ + Q+ + A P
 Sbjct: 151 LPNEASMALHRKRGYQQVAHFPGKIGYKFECWHDIVWLQKSLDKQAGP 197

>gb|EGD38415.1| phosphinothricin acetyltransferase [Streptococcus sanguinis SK160]
 Length = 185

Score = 119 bits (297), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 62/167 (37%), Positives = 93/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A +D A++ I Y+E + + F E T +++ + +E+ ++YP+LVAE +G+
 Sbjct: 9 MNIRLANPSDAASLLAIYAPYVENTAITFEYEVPTIEDFGNRIEKTLEKYPYLVAEEDGL 68

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G AYA + AR AYDW VE +VYVS + G+GS LY L ++ G+ +A I
 Sbjct: 69 VLGAYASTYYARAAYDWAVELSVYVSQDARGKGVGSKLYDELEDLLDQMGYMHFLACIS 128

Query: 128 LPNDPVSRLHEALGYTARGLRAAGYKHGGWHDVGVFWQRDFELPAPP 174
 LPN S+ LH GY GYK WHD+ + Q+ + A P
 Sbjct: 129 LPNKASLALHRKRGYQQVAHFPGKIGYKFECWHDIVWLQKSLDKQAGP 175

>ref|YP_004140179.1| phosphinothricin acetyltransferase [Mesorhizobium ciceri biovar
 biserrulae WSM1271]
 gb|ADV10129.1| Phosphinothricin acetyltransferase [Mesorhizobium ciceri biovar
 biserrulae WSM1271]
 Length = 190

Score = 119 bits (297), Expect = 2e-25, Method: Compositional matrix adjust.
 Identities = 69/176 (39%), Positives = 98/176 (55%), Gaps = 9/176 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEW---IDDLERLQDRYPWLVAEV 64
 + IRPATAAD+ ++ I + T ++ EP + E D L + +P+LVAE
 Sbjct: 4 ITIRPATAADLDSITGIYADAVAKGTASYELEPPSRAEMGVRFDSL--MAGGFYPYLVAEK 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +G V G AYAG ++ R AY + VE +VYV+ + G+G L L++++ GF+ ++A

Sbjct: 62 DGAVLGYAYAGAFRPRPAYRFIVEDSVYVAPEAKGQGVGLKLMQSLIEAVTTAGFRQIIA 121

Query: 125 VI--GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA--PPRP 176

VI G P+ SVRLHE LG+ G L +GYKHG W D F Q A PP P

Sbjct: 122 VIGDGRPDSASVRLHEKLGFRHSGRLEGSGYKHGRWLDTVFMQLSLNGGASTPPDP 177

>ref|YP_001035153.1| phosphinothricin acetyltransferase, putative [Streptococcus sanguinis SK36]

gb|ABN44603.1| Phosphinothricin acetyltransferase, putative [Streptococcus sanguinis SK36]

Length = 215

Score = 119 bits (297), Expect = 2e-25, Method: Compositional matrix adjust.
Identities = 62/167 (37%), Positives = 92/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IR AT +D A + I Y+E + + F E T +++ + + + ++YP+LVAE +GV

Sbjct: 39 MNIRFATPSDAATLLAIYAPYVENTAITFEYEVPTIEDFTNRIAKTLEKYPYLVAEEDGV 98

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

V G AYA + AR AYDW E +VYVS + G+GS LY L ++ G+ +A I

Sbjct: 99 VVGAYASTYYARAAYDWAELSVMYVVSQDARGKGVGSKLYDELEDLLDQMGYMHFLACIS 158

Query: 128 LPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174

LPN+ S+ LH GY GYK WHD+ + Q+ + A P

Sbjct: 159 LPNEASLALHRKRGYQQVAHFPMGYKFERWHDIVWLQKSLDKQAGP 205

>ref|ZP_06895655.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC 49957]

gb|EFH12643.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC 49957]

Length = 183

Score = 119 bits (297), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 71/177 (40%), Positives = 97/177 (54%), Gaps = 16/177 (9%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY--- 57

MS + +RPA AD+ A+ I H++ +F T P DL+ ++ R+

Sbjct: 1 MSSTAPSLTLRPAEADLPAIAAIYGHVHVAHGRASFETAPP-----DLDEMRRRHAAI 53

Query: 58 -----PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112

P+LVAE EG V G AYA ++ R AY TVE+++YV GLG L L+

Sbjct: 54 TGAGMPYLVAAEAGEVLGYAYASAYRPRAAYGNTVENSIIYVRADAVGRGLGRQLLAALIS 113

Query: 113 SMEAQGFKSVAVIGLPND-PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168

+ EA GF+ ++AVIG N+ S+RLHEA G+T GTLR+ G KHG W DV QR

Sbjct: 114 ACEALGFRQMIAVIGDSNNMASIRLHEAAGFTPVGTLSVGRKHGEWLDVVLQRAL 170

>ref|YP_463756.1| GCN5-related N-acetyltransferase [Anaeromyxobacter dehalogenans 2CP-C]

gb|ABC80319.1| GCN5-related N-acetyltransferase [Anaeromyxobacter dehalogenans 2CP-C]

Length = 197

Score = 118 bits (296), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 74/175 (42%), Positives = 95/175 (54%), Gaps = 1/175 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR AT D V +I + + ++F EP P+E +E + PWLV E +G V

Sbjct: 4 IRMATLEDAGDVAEIIYGAVVTGTPISFELEPPGPEEMARRMEAVLALAPWLVEEDGRVD 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 G YA R AY W+V+ TVYV +R GLG LYT LL+ + AQGF + A I LP
 Sbjct: 64 GYVYASRHHERAAYRWSVDVTYVVRDGRRRGGLGRALYTALLELLRAQGFHAAHAGITLP 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183
 N SV LHEALG+ G G+K G WHDVG+WQ + E P P+ PV +
 Sbjct: 124 NAGSVGLHEALGFRPIGVYPRVGWKMGAWHDVGYWQLELRERTGAPGPILPVEAL 178

>ref|ZP_08047697.1| phosphinothricin N-acetyltransferase [Streptococcus sp. C150]
 gb|EFX55272.1| phosphinothricin N-acetyltransferase [Streptococcus sp. C150]
 Length = 172

Score = 118 bits (296), Expect = 3e-25, Method: Compositional matrix adjust.
 Identities = 61/168 (36%), Positives = 91/168 (54%), Gaps = 2/168 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP +D A+ I Y+E + + F E + QE+ + + + + YP+LVAE G V
 Sbjct: 5 IRPVKLSDAKAIQSIYAPYVEKTAITFEYEVPSVQEFENRINKTLENYPYLVAEENGQVL 64

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 G AYA + AR AY+WT E ++Y+ + GLGS LY L K ++ +GF +A I +P
 Sbjct: 65 GYAYASTYYARTAYNWTTELSIYLHEDARGRGLGSQLYDALEKELKKRGLRFLACIAPV 124

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N+ S+ +HE GY GYK WHD+ + Q+ L P R +
 Sbjct: 125 NEASIAMHEKRGYVQVAHFPGVGYKFEQWHDIVWMQKT--LNGPVRKI 170

>ref|ZP_05648693.1| phosphinothricin N-acetyltransferase [Enterococcus gallinarum EG2]
 gb|EEV32026.1| phosphinothricin N-acetyltransferase [Enterococcus gallinarum EG2]
 Length = 178

Score = 118 bits (296), Expect = 3e-25, Method: Compositional matrix adjust.
 Identities = 58/162 (35%), Positives = 87/162 (53%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A AD ++ I Y++ + + F TE T +E+ + + YP+L+AE GV
 Sbjct: 1 MNIRKAAVADTKSLLKIYAPYVDHTAITFETEIPTEEEFAHRITQTLQHYPYLIAEENG 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G AYA +K R AYDWT E TVY+ + G+G+ LY HL ++ Q ++ A I
 Sbjct: 61 ILGYAYATAYKTRAAYDWTAEVTVYIDREVKAKGIGTMLYHHLESELKKQNIVNLTACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N+ SVR H+ GY GYK WHDV + Q++ +
 Sbjct: 121 AGNESSVRFHQKFGYKEVAYFPQIGYKFEQWHDVLWMQKELQ 162

>ref|ZP_01131943.1| phosphinothricin N-acetyltransferase [Pseudoalteromonas tunicata
 D2]
 gb|EAR30309.1| phosphinothricin N-acetyltransferase [Pseudoalteromonas tunicata
 D2]
 Length = 164

Score = 118 bits (295), Expect = 4e-25, Method: Compositional matrix adjust.
 Identities = 61/158 (38%), Positives = 90/158 (56%), Gaps = 2/158 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAE-VEGV 67
 IR A + D ++ +I NHYI + V F TE + ++ ++ + ++Q D PWL+AE G
 Sbjct: 2 IRNAVSKDATSIAEIIYNHYSISDVTVTFTFEMISAEDILNRISKVQSDDLPWLIAEDSSGA 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA W+ R AY ++VE TVY+S + G+GS LY L ++++ SV+ I
 Sbjct: 62 LIGYAYATKWRRERFAYRFSVEVTVYLSPKCIGNGVGSQLYDALFSELKSRSIHSVIGGIT 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 LPN SV LHE G + G+K W DVG+WQ
 Sbjct: 122 LPNPASVALHEKFGLEKVAHFQVGFKEQWKDVGWYQ 159

>gb|EGD31687.1| phosphinothricin acetyltransferase [Streptococcus sanguinis SK115]
 Length = 207

Score = 118 bits (295), Expect = 4e-25, Method: Compositional matrix adjust.
 Identities = 60/167 (35%), Positives = 93/167 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A +D A + DI ++E + + F E T +++ +E+ ++YP+LVAE +G+
 Sbjct: 31 MNIRFARPSDAATLLDIYAPFVENTAITFEYEVPTIEDFATRIEKTLEKYPYLVAEEDGL 90

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA + AR AYDW E +VYVS + G+GS LY L ++ G+ +A I
 Sbjct: 91 ILGYAYASTYYARAAYDWAAELSVYVSQDARGKGVGSRLYDELEDLLDQMGYMHFLACIS 150

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 LPN+ S+ LH+ GY GYK WHD+ + Q+ + A P
 Sbjct: 151 LPNEASLALHQKRGYQQVAHFQKIGYKFERWHDIVWLQKSLDKQAGP 197

>ref|YP_155176.1| phosphinothricin N-acetyltransferase, putative [Idiomarina
 loihiensis L2TR]
 gb|AAV81627.1| Phosphinothricin N-acetyltransferase, putative [Idiomarina
 loihiensis L2TR]
 Length = 166

Score = 117 bits (294), Expect = 5e-25, Method: Compositional matrix adjust.
 Identities = 59/157 (37%), Positives = 85/157 (54%), Gaps = 1/157 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQD-RYPWLVAEVEGVV 68
 IR A D A+ DI N+YIE +++ F P + +E +Q+ PWLV ++
 Sbjct: 2 IRDANKGSDAIADIYNYIENTSITFEETPVLGSQMQRRIEDVQECSLPWLVLVDNEII 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G AYA WK R+AY ++VE TVY++++ + GLG LY L ++ G +V+ I L
 Sbjct: 62 VGYAYATKWKDRSAYRFSVEVTVYLANQMRGRGLGKKLYEALFLRLKEHGIHTVIGGIAL 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 PN SV LHE +G G+K W DVG+WQ
 Sbjct: 122 PNPSSVALHEKMGKKVAHFQVGFKEFNEWRDVGWYQ 158

>ref|ZP_06900531.1| phosphinothricin acetyltransferase [Streptococcus parasanguinis
 ATCC 15912]
 gb|EFH18269.1| phosphinothricin acetyltransferase [Streptococcus parasanguinis
 ATCC 15912]
 Length = 174

Score = 117 bits (293), Expect = 6e-25, Method: Compositional matrix adjust.
 Identities = 56/160 (35%), Positives = 90/160 (56%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP +D A + I Y+ + + F + T QE+ + + ++P+LVAEV+G V
 Sbjct: 3 IRPVQISDAATIRAIYQPYVTETAITFEVDVPTVQEFERRITKTLPKFPYLVAEVDGKVV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + AR AYDWT E ++Y++ + G+GS LYT L + ++ +G+ +A I +P
 Sbjct: 63 GYAYASTYYARAAYDWTTELSIYIAKEARGQGIGSALYTALEELQTRGYLRFLACIAVP 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N+ S+ +H+ GY GYK WHD+ + Q+ E
 Sbjct: 123 NEASISMHKKRGYIQVAHFPGYKFNQWHDIVWMQKTIE 162

>ref|ZP_05813493.1| GCN5-related N-acetyltransferase [Mesorhizobium opportunistum
 WSM2075]
 gb|EEW30225.1| GCN5-related N-acetyltransferase [Mesorhizobium opportunistum
 WSM2075]
 Length = 191

Score = 117 bits (293), Expect = 6e-25, Method: Compositional matrix adjust.
 Identities = 64/161 (39%), Positives = 93/161 (57%), Gaps = 3/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEG 66
 + IRPAT+AD+ + +I + T ++ EP E + L +P+LVAE +G
 Sbjct: 4 IAIRPATSADLDTITEIYADAVTNGTASYELEPPGRAEMGKRFDALTAGGFYPYLVAERDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G AYAG ++ R AY + VE +VYV+ + G+G L L+ ++EA GF+ ++AVI
 Sbjct: 64 AVLGYAYAGAFRPRPAYRFVVEDSVYVAPDAKGQGVGLRLMQSLIAAVEAAGFRQIIAVI 123

Query: 127 --GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
 G P+ SV+LHE LG+ G L +GYKHG W D F Q
 Sbjct: 124 GDGRPDASVKLHERLGFRHSGRLEGSGYKHGRWLDTVFMQ 164

>ref|YP_550242.1| GCN5-related N-acetyltransferase [Polaromonas sp. JS666]
 gb|ABE45344.1| GCN5-related N-acetyltransferase [Polaromonas sp. JS666]
 Length = 226

Score = 117 bits (292), Expect = 8e-25, Method: Compositional matrix adjust.
 Identities = 64/161 (39%), Positives = 95/161 (59%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDL-ERLQDRYPWLVAEVEG 66
 + I P +D+ A+ I HY+ T+ F EP T ++ + + L+ YP+LVA +G
 Sbjct: 25 LSIHPCAESDIEAIQAIYAHYVATNLATFELEPPTVRQMLSRRGDILRGGYPYLVARRDG 84

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AYAG +++R AY TVE ++YV+ ++ G+GS L L++ E +GF+ +VAV+
 Sbjct: 85 ELVGAYAGAYRSRPAYRHTVEDSIYVAPGMRQAGVGSALLRELIRQCEQRGFRQMVAVV 144

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G N S+R HEALG+T GTL GYK G W D QR
 Sbjct: 145 GNSANTGSLRAHEALGFTRVGTLCIGYKFGQWVDTVLMQR 185

>ref|ZP_01898379.1| Phosphinothricin N-acetyltransferase, putative [Moritella sp.
 PE36]
 gb|EDM67196.1| Phosphinothricin N-acetyltransferase, putative [Moritella sp. PE36]
 Length = 162

Score = 117 bits (292), Expect = 8e-25, Method: Compositional matrix adjust.
 Identities = 61/158 (38%), Positives = 85/158 (53%), Gaps = 1/158 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR AT D A+ I NHYI + + F + T + ++ Q PWLVAE V
 Sbjct: 2 IRTATELDABEAIISHIYNHYIANTVITFEEKLVTSDDIASRIKATQAAGLPWLVAEDNNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G AYA PWK+R+AY ++VE++VY++ + G GS LY L ++ ++V+ I L
 Sbjct: 62 LGYAYASPWKSR SAYQFSVETS VYLAPDASKKGWGSQLYQALFIQLKTTKVRTVIGGIAL 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 PN S+ LHE LG GYK W DVG+WQ+
 Sbjct: 122 PNPASIALHEKLG MQSAHFSEVGYKFNQWVDVGYWQK 159

>ref|YP_003914549.1| phosphinothricin acetyltransferase [Ferrimonas balearica DSM 9799]
 gb|ADN77475.1| Phosphinothricin acetyltransferase [Ferrimonas balearica DSM 9799]
 Length = 165

Score = 116 bits (291), Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 62/159 (38%), Positives = 85/159 (53%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP D+ A+ I NHY+E F + + + L + YP LV E +G
 Sbjct: 2 IRPYQPGDIPAITAIYNHYVEHEIATFEEVALSDAQMTERLTAIAATYPVLVLEE QGRVCV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AY +K R+AY + E+TVY++ G GS LY LL ++ AQG + V+ V+ P
 Sbjct: 62 GYAYGNHFKPR SAYRYCAETTVYLAPDCIGGGRSRLYRALLDALAAQGIREVLGVLTQP 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDF 168
 N S LH+ LGY +GTL A G+K G W DV FWQ+
 Sbjct: 122 NPASAALHQKLGYRHQGTLTAVGFKFGRWLDVAFWQKSL 160

>ref|ZP_05981641.1| phosphinothricin N-acetyltransferase [Subdoligranulum variabile DSM 15176]
 gb|EFB74715.1| phosphinothricin N-acetyltransferase [Subdoligranulum variabile DSM 15176]
 Length = 299

Score = 116 bits (291), Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 68/176 (38%), Positives = 97/176 (55%), Gaps = 2/176 (1%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-E 63
 R + +R AT D A V + N Y+ T F+ E T E+ ++ + ++ P+LVA
 Sbjct: 106 RSRLTVMATPDDAADVVALYNWYVTHGTQTQFYELSTEAEYRQNI AEVLEKAPFLVAYT 165

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 +G +AG A A PW R A+ W VE+TVY + G G LYT LL+ + QG+ +
 Sbjct: 166 ADGRLAGYACAH PWHTTRAFADVDVETTVYCAPDVLGQGTGRRLYTALLELLRRQGYHNAF 225

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPA-PPRPVR 178
 A+I PN S H+ALG+T G + +GYK G W D+G+W + PA PP PVR
 Sbjct: 226 ALITRPNPQSDAFHKALGFTRYGVEKN SGYKFGRWLDLGYWAYELNPPADPPAPVR 281

>ref|YP_004104996.1| phosphinothricin acetyltransferase [Ruminococcus albus 7]
 gb|ADU22362.1| Phosphinothricin acetyltransferase [Ruminococcus albus 7]
 Length = 191

Score = 116 bits (291), Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 60/188 (31%), Positives = 99/188 (52%), Gaps = 9/188 (4%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV 64
 + + IRP T +D + DI ++Y+E + + F + T E+ + + +YP++ A
 Sbjct: 2 KNNITIRPVTESDAKQLLDIYSYVENTAITFEYDVPTIPEFQERIRHTLKKYPYIAAVK 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +G++ G AYAG +K R AYD++VE TVY H + G+G LYT L +++ G ++ A
 Sbjct: 62 DGIILGYAYAGVFKDRAAYDYSVEVTVYTHRSHHKEGIGKLLYTELEAILKSMGITNLYA 121

Query: 125 VIGLPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-ELPAPPR 175
 IG+P D S+ H +GYT G GYK G W+D+ + ++ E A
 Sbjct: 122 CIGIPADEDEYLDHNSMDFHTHIGYTMAGRFHKCGYKFGRWYDMVWLEKMAEHDAIDH 181

Query: 176 PVRPVTQI 183
 + P + I
 Sbjct: 182 SIIPASSI 189

>emb|CAM78141.1| phosphinothricin acetyltransferase [Magnetospirillum
 gryphiswaldense MSR-1]
 Length = 176

Score = 116 bits (291), Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 67/165 (40%), Positives = 92/165 (55%), Gaps = 2/165 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV 64
 R + IR +T AD+AA I H++ T T +F P + +E L D+ PWLVAE
 Sbjct: 2 RGMIIIRASTPADIAAAQAIYAHVLTGTASFELAPPSLEEMARRRSALTDKGLPWLVAEQ 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +G + G AYAGP++ R AYDWTVE ++Y+ G+G L T L+ A G++ +VA
 Sbjct: 62 DGRMLGYAYAGPYRTRPAYDWTVEDSIYIHPDSHGQIGKALLTRLIDECTALGYRQMV 121

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 VIG N SV LH + G+ G L+A G+K G W D QR
 Sbjct: 122 VIGDSANAGSVGLHRSCGFHDAGILKAVGWKFGRWIDSVLQMQRSL 166

>ref|ZP_07453833.1| phosphinothricin acetyltransferase [Eubacterium yurii subsp.
 margaretiae ATCC 43715]
 gb|EFM39737.1| phosphinothricin acetyltransferase [Eubacterium yurii subsp.
 margaretiae ATCC 43715]
 Length = 365

Score = 116 bits (290), Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 52/168 (30%), Positives = 96/168 (57%), Gaps = 7/168 (4%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
 + + +R A+ D+ + +I ++Y+E + + F E + +E +D +E+ +YP+LV E +
 Sbjct: 178 KRISVRRASLQDVKILEIYSYYVENTAITFEYETPSREEMDRMEKFSSKYPFLVIECD 237

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 V G +YA +K+R AY+WT E ++Y+S+ ++ GLG LY + K++++ G ++ A
 Sbjct: 238 KKVCGYSYANVFKSRPAYNWTCEMSIYISNDMRKYGLGRKLYEEME KALKSMGIIVTLYAC 297

Query: 126 I-GLPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166
 + + D SV+ HE LGY G GYK W+D+ F ++
 Sbjct: 298 VTSIEKDDEYLTKNVSKFHEHLGYRLIGKFEKCGYKFDRWYDMIFMEK 345

>ref|YP_002132943.1| GCN5-related N-acetyltransferase [Anaeromyxobacter sp. K]
 gb|ACG71814.1| GCN5-related N-acetyltransferase [Anaeromyxobacter sp. K]
 Length = 197

Score = 116 bits (290), Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 73/175 (41%), Positives = 94/175 (53%), Gaps = 1/175 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT D V +I + + ++F EP P E + + + PWLV E +G V
 Sbjct: 4 IRMATLDDAGDVAEIYGAVVAGTPISFELEPPGPGEMARRMAAVLELAPWLVICEEDGRVD 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G YA R AY W+V+ TVYV +R GLG LYT LL+ + AQGF + A I LP
 Sbjct: 64 GYVYASRHHERAAYRWSVDVTYVYVREGRRRGGLGRALYTALLELLRAQGFHAAHAGITLP 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQF-ELPAPPRPVRPVTQI 183
 N SV LHEALG+ G G+K G WHDVG+WQ + E P P+ PV +
 Sbjct: 124 NAGSVGLHEALGFRPIGVYPRVGWKMGAWHVDVGYWQLELRERTGAPGPILPVDAL 178

>ref|ZP_07296464.1| GNAT family toxin-antitoxin system, toxin component [Streptomyces
 hygroscopicus ATCC 53653]
 gb|EFL24833.1| GNAT family toxin-antitoxin system, toxin component [Streptomyces
 hygroscopicus ATCC 53653]
 Length = 193

Score = 116 bits (290), Expect = 1e-24, Method: Compositional matrix adjust.
 Identities = 69/183 (37%), Positives = 91/183 (49%), Gaps = 17/183 (9%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IRPA AD+ AV DI HY+ S + F P++ +W L L R P+LVAE+ G V
 Sbjct: 8 IRPAGHADLKAVADIYTHYVRHSVITFDETPRSAADWEQLGLDLTARGLPFLVAELSGEV 67

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI-- 126
 G AYA PW+ + AY +TVE T+Y++ GLGS L L+ G ++++AVI
 Sbjct: 68 VGFAYAAPWRPKPAYRYTVEDTIYLPDATGQGLGSALLGRLIAEAGRAGKRTMIAVIAD 127

Query: 127 -----GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFELPA 172
 G +D S LH G+T G L A G+KHG W D QR
 Sbjct: 128 TGGDDTGSAGTGSAGTGSASTALHRRFGFTDAGRLTAVGHKHGRWVDTALLQRPLSAQE 187

Query: 173 PPR 175
 P R
 Sbjct: 188 PAR 190

>ref|YP_269286.1| phosphinothricin N-acetyltransferase [Colwellia psychrerythraea
 34H]
 gb|AAZ28061.1| phosphinothricin N-acetyltransferase [Colwellia psychrerythraea
 34H]
 Length = 169

Score = 115 bits (289), Expect = 2e-24, Method: Compositional matrix adjust.
 Identities = 59/161 (36%), Positives = 86/161 (53%), Gaps = 2/161 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVE 65
 V IR D++++C I NH+IE + V F E T + + + ++ D PW VAE E
 Sbjct: 6 KVMIRAVKEQDVSSICTIYNHFIENTVVTFEDEVVTASDILKRITKITADDLPWFVAEDE 65

Query: 66 -GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G + G AYA W+ R +Y ++VE TVY+S H GLG+ LY L + ++ S +
 Sbjct: 66 SGNIMGYAYATKWRDRFSYRFSVEVTYVLSPEHTSKGLGTKLYQVLFEEELKRIKIHAIG 125

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQ 165
 I +PN+ S+ LHE G + G K W DVG+WQ
 Sbjct: 126 GITIPNEASIALHEKFGMVKAHFKEVGLKFDRWLDVGYWQ 166

>ref|YP_003679970.1| phosphinothricin acetyltransferase [Nocardiosis dassonvillei
 subsp. dassonvillei DSM 43111]

gb|ADH67464.1| Phosphinothricin acetyltransferase [Nocardiosis dassonvillei
subsp. dassonvillei DSM 43111]
Length = 175

Score = 115 bits (289), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 57/158 (36%), Positives = 88/158 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ +R AT AD A I + Y+ + + F EP T ++ + + Q R+ W+V E
Sbjct: 10 LTVRDATPADAPACAAIYSPYVTDITFEYEPPTAEQMAERIAAAQRRHAWIVLEADG 69

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
V G AY GP++ R+AY W+ E +VY++ +R G G LY LL + +G ++ VA +
Sbjct: 70 VVGAYAGGPFRTDAYRWSCEVSVYLAMGRRRTGAGRALYRELLPRLAERGMRTAVACMT 129

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
LPN+ S+ LH +LG+ G +R G K WHDV + Q
Sbjct: 130 LPNEASLGLHRSGLGFEDVGMRRVGRKFDWHDVAVAWQ 167

>ref|YP_003484882.1| putative acetyltransferase [Streptococcus mutans NN2025]
dbj|BAH87990.1| putative acetyltransferase [Streptococcus mutans NN2025]
Length = 163

Score = 115 bits (289), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 52/159 (32%), Positives = 92/159 (57%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++IR A D + I Y+E + + F + + +E+ + +E+ + ++P+LVAE EG+
Sbjct: 1 MKIRNACKEDAKQLIAIYAPYVEKTAITFEYQVPSLEEFEEERIEKTKQKFPYLVAEEEG 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G AYA + R AYDWTVE ++Y+ + + +GS LY L ++++ GF +++ I
Sbjct: 61 LQGYAYASAYNRAAYDWTVELSIYIREKARGKHIGSQLYASLERNLQETGFVNLLVCIA 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
LPN+ S+ H+ GY + GYK WHD+ + Q+
Sbjct: 121 LPNNASLTFHKKHGYEQVAHFKKVGYKFDKWHDIVWMQK 159

>ref|YP_003749344.1| phosphinothricin n-acetyltransferase (ppt n-acetyltransferase)
(phosphinothricin-resistance protein) [Ralstonia
solanacearum PSI07]
emb|CBJ34703.1| Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
(Phosphinothricin-resistance protein) [Ralstonia
solanacearum PSI07]
Length = 183

Score = 115 bits (288), Expect = 2e-24, Method: Compositional matrix adjust.
Identities = 65/164 (39%), Positives = 92/164 (56%), Gaps = 3/164 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
+ +RPA AD+ AV I H++ T T +F +P E + LQD P+LVAE +G
Sbjct: 20 IVVRPARLADLPAAVAIYAAHVRTGTASFELDPDLAEMTRRFQALQDTGMPYLVAEADG 79

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
+ G AYAGP +AR AY TVE ++Y+ Q G+G+ L L++ A+GF+ +VAV+
Sbjct: 80 NLLGYAYAGPHRARPAYRHTVEDSIYLDTAAQGRGVGTLLDRTLRECTARGFRQMVAVV 139

Query: 127 --GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 168
G N S+RLH G+ G L GYK G W D+ QR+
Sbjct: 140 GGGQENLGSMLRHARCGFREVGVLAKEVGYKFGRWLDIVLMQREL 183

>ref|YP_002551041.1| acetyltransferase [Agrobacterium vitis S4]

gb|ACM38029.1| acetyltransferase [Agrobacterium vitis S4]

Length = 209

Score = 115 bits (287), Expect = 3e-24, Method: Compositional matrix adjust.

Identities = 61/162 (37%), Positives = 92/162 (56%), Gaps = 2/162 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVE 65
 PV+IR AT AD+ + +I H I T ++ P E +E + + YP++VAE +
 Sbjct: 26 PVQIRAATPADIPHITEIYRHAILTGKASYEITPPDEAEMAHRMETITSQFYYPYIVAEDD 85

Query: 66 -GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 G + G AYA ++ R AY W VE ++Y++ Q G+G L T L+ A GF+ ++A
 Sbjct: 86 DGSLLGYAYASAFRTRPAYRWLVEDSIYLAEEAQQKGIGKALLTDLVAQCTALGFRQMIA 145

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 VIG N S+ +H +LG+T G + +G+KHG W D F QR
 Sbjct: 146 VIGGANPASIGVHRS LGFTHAGGINGSGFKHGTWLDTVFMQR 187

>ref|ZP_08044113.1| GCN5-related N-acetyltransferase [Haladaptatus paucihalophilus DX253]

gb|EFW92929.1| GCN5-related N-acetyltransferase [Haladaptatus paucihalophilus DX253]

Length = 196

Score = 115 bits (287), Expect = 4e-24, Method: Compositional matrix adjust.

Identities = 57/138 (41%), Positives = 79/138 (57%)

Query: 29 IETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVE 88
 + +T++F T P E D ++ YPW+V E + + G AYAG ++R AY W+ +
 Sbjct: 23 VRETTISFETTPPDEDEMADRIQTTLPTYPWVCEHDELLGYAYAGSHRSREAYQWSAD 82

Query: 89 STVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA VIGLPNDPSVRLHEALGYTARGTL 148
 +VYV H+R G+G+ LY L +E QGF + A I LPN SV LHE+LG+ GT
 Sbjct: 83 VSVYVHRDHRRSGVGNGLYESLFSLLERQGFYNAYAGIALPNPASVGLHESLGFEHVGTY 142

Query: 149 RAAGYKHGGWHDVGFQWR 166
 A GYK W VG+W R
 Sbjct: 143 EAVGYKDDAWRSVGWWHR 160

>ref|ZP_07343113.1| phosphinothricin N-acetyltransferase [Burkholderiales bacterium 1_1_47]

gb|EFL83667.1| phosphinothricin N-acetyltransferase [Burkholderiales bacterium 1_1_47]

Length = 176

Score = 114 bits (286), Expect = 4e-24, Method: Compositional matrix adjust.

Identities = 60/165 (36%), Positives = 93/165 (56%), Gaps = 2/165 (1%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVA 62
 E+ V IR A AD+ + I + T +F P + +E + ++ ++ YP+LVA
 Sbjct: 2 EKLFVNIRKAEPADIGGIASIEQAVLLGTASFVTPPSEEEMLSRMQTIEAGHPYPLVA 61

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 122
 E+E + G AYAG ++ R AY +TVE ++YV +RLG+G+ L T L+ + +GF+ +
 Sbjct: 62 ELEHQILGFAYAGQYRPRKAYRYTVEDSIYVHPECRR LGVGTQLLTSLIAECDLRGFREM 121

Query: 123 VAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 +AVIG N S++LHE G+ G L+ GYK W D QR
 Sbjct: 122 IAVIGDSENTASIKLHEHCGRHVGV LKNVGYKFDRWLD SVLMQR 166

>ref|ZP_03755566.1| hypothetical protein ROSEINA2194_04006 [Roseburia inulinivorans DSM

16841]

gb|EEG92136.1| hypothetical protein ROSEINA2194_04006 [Roseburia inulinivorans DSM

16841]

Length = 189

Score = 114 bits (286), Expect = 4e-24, Method: Compositional matrix adjust.

Identities = 62/166 (37%), Positives = 86/166 (51%), Gaps = 8/166 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR AT AD + I YIE + + F + +E+ + +R+P+L AE +G +A

Sbjct: 4 IRVATEADAEIILAIYAKYIEQTAITFEYVVPSEIEFRGRIRHTLERFPYLAAEKDGKIA 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129

G AY P+K R AYDW+VE+++YV +R G+G LY L ++ QG +V A I P

Sbjct: 64 GYAYVSPFKERAAYDWSVETSIYVDMEQKRSGIGRRLYELENILKQQGILNVNACIAYP 123

Query: 130 N-----DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168

SV HE LGYT GT GYK W+D+ W F

Sbjct: 124 QAEDEYLTKDSVLFHEKLGTYTMVGTTFHQCGYKFHRWYDM-VWMEKF 168

>ref|ZP_08196974.1| phosphinothricin N-acetyltransferase [Nocardioideaceae bacterium Broad-1]

gb|EGD43547.1| phosphinothricin N-acetyltransferase [Nocardioideaceae bacterium Broad-1]

Length = 170

Score = 114 bits (285), Expect = 5e-24, Method: Compositional matrix adjust.

Identities = 59/159 (37%), Positives = 85/159 (53%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR AT D AA I Y+ + ++F TEP T +E D ++ Q + WL V E + V

Sbjct: 12 IRDATPDDAAACAAIYEPYVRDVTISFETEPPTTEEMADRIKAAQAEHAWLVLEADDRVV 71

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129

G AYA + R AY W + ++Y+ +R G G LY LL + +G++ +A I LP

Sbjct: 72 GYAYATSHRTRAAYRWACDVSIYLETGRRRSAGALKALYAALLPILRERGERALAGIALP 131

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168

N+ S+ LH + G+T G R G+K WHDV + Q D

Sbjct: 132 NEASIGLHRSFGFTDVGVRIGWKLDWHDVAVWMQLDL 170

>ref|YP_003766886.1| acetyltransferase [Amycolatopsis mediterranei U32]

gb|ADJ46484.1| acetyltransferase [Amycolatopsis mediterranei U32]

Length = 171

Score = 114 bits (284), Expect = 7e-24, Method: Compositional matrix adjust.

Identities = 63/159 (39%), Positives = 84/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR AT D AA + Y+ + V+F TEP E R+ + WL V E G VA

Sbjct: 2 IRHATTEDAAACATLYAPYVTDTVVSFETEPDPTAEMA---RRIAGAHAWLVLEDHGRVA 58

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129

G AYA + AR AY W+ E+++Y+ +R G G LY LL+ + +G A + LP

Sbjct: 59 GYAYATRFAARAAYRWSCETSIYLEQRRRTGAGRALYEALLERLRERGLCRAFAGMTLP 118

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168

ND S LH ALG+ G R G+KHG W DV + Q+D
 Sbjct: 119 NDASAGLHRALGFEPAGVYRRVGVKHWGAWRDVAWVQKDL 157

>ref|ZP_03797973.1| hypothetical protein COPCOM_00226 [Coprococcus comes ATCC 27758]
 gb|EEG91531.1| hypothetical protein COPCOM_00226 [Coprococcus comes ATCC 27758]
 Length = 189

Score = 114 bits (284), Expect = 7e-24, Method: Compositional matrix adjust.
 Identities = 62/184 (33%), Positives = 99/184 (53%), Gaps = 8/184 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IRPAT AD A + +I YI + + F + T +E+ + ++YP+LVA +
 Sbjct: 6 IKIRPATEADAAEILNIYAPYITDTAITFEYDVPTLEEF TGRIRHTLEKYPYLVAVRDSE 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYAG + R AYDW+ E+T+YV + +G+G LY L +++AQ ++ A IG
 Sbjct: 66 IIGYAYAGAFYGRAAYDWSAETTIYVKKGRHIGVGKLLYQALETALKAQNIINLYACIG 125

Query: 128 LPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRP 179
 P + S + HE LGY G R GYK G W+ + + ++ E P P V+
 Sbjct: 126 YPEEDDEYLTKNKQFHEHLGYRLIGEFRKCGYKFGRWYHVMWMEKMIGEHPEKPEQVKR 185

Query: 180 VTQI 183
 ++I
 Sbjct: 186 FSEI 189

>ref|ZP_02434166.1| hypothetical protein BACSTE_00385 [Bacteroides stercoris ATCC 43183]
 gb|EDS16710.1| hypothetical protein BACSTE_00385 [Bacteroides stercoris ATCC 43183]
 Length = 161

Score = 113 bits (283), Expect = 8e-24, Method: Compositional matrix adjust.
 Identities = 60/161 (37%), Positives = 82/161 (50%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP D+ + DI N YI ST F TEP + E + + +P+ V E + V
 Sbjct: 2 IRPVQPQDVKYITDIYNEYILNSTYTFETEP ISEDEMRLRIAEIFPHFPFFVCETDHKVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G YA PWK R AY +T+E+TVY+S RH+ GLG L L++ + +++A I
 Sbjct: 62 GYCYAHPWKQRTAYRYTLETTVYLSARHRGKGLGKLLMQVLIEECRQHNYHTLIACITAC 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170
 N S LH LG+T + G K G W DV D+EL
 Sbjct: 122 NTASCSLHSLGFTQVSHFKEVGMKFGEWLDVA---DYEL 158

>ref|YP_003392558.1| GCN5-related N-acetyltransferase [Conexibacter woesei DSM 14684]
 gb|ADB49183.1| GCN5-related N-acetyltransferase [Conexibacter woesei DSM 14684]
 Length = 176

Score = 113 bits (283), Expect = 9e-24, Method: Compositional matrix adjust.
 Identities = 65/154 (42%), Positives = 82/154 (53%), Gaps = 6/154 (3%)

Query: 28 YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTV 87
 Y+ S +F P E +E+L + +LV E +G VAG AYAGP + R AY W
 Sbjct: 21 YVVDASAASFEETPPGAAELARRIEQLSHTHAFLVDERDGRVAGYAYAGPHRTRAAYRWAA 80

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGT 147
 + +VYV QR G+G LY LL + +GF+ A I LPN SV LHEA G+ G

Sbjct: 81 DVSUYVDAAAFQRRGVGRALYEPDLLALLRERGFRIACAGITLPNAGSVGLHEAFGFEQVGI 140

Query: 148 LRAAGYKHGGWHDVGFQWQ-----RDFELPAPPR 175

RA G+K G W DVG+WQ D P PPR

Sbjct: 141 YRAIGWKAGAWRDVGWWQLQLAPREDGAQPEPPR 174

>ref|YP_001913381.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae

PX099A]

gb|ACD58849.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae PX099A]

Length = 170

Score = 113 bits (283), Expect = 9e-24, Method: Compositional matrix adjust.
Identities = 61/156 (39%), Positives = 83/156 (53%), Gaps = 3/156 (1%)

Query: 21 VCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVAEVEGVVAGIAYAGPWKA 79

+ DI N+YI + + F +P T E + +Q PWLVA V G AYA W+A

Sbjct: 14 LADIYNYIIANTRITFEMDPVTSVEMAKRIADVQSIGLPWLVALEGDQVVGAYATQWRA 73

Query: 80 RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEA 139

R AY +VESTVY++ H+ GLG+ LY L++ + +++ + PND S RLHEA

Sbjct: 74 RKAYQSSVESTVYLADGHRGRGLGTALYGKLEELRGLLEHAIIGGVAQPNDAARLHEA 133

Query: 140 LGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175

LG+ GYK G W DV +WQ LP R

Sbjct: 134 LGFKKVAHFQVGYKLGQWVDVAYWQ--LLLVPSSR 167

>ref|YP_003388108.1| GCN5-related N-acetyltransferase [Spirosoma linguale DSM 74]

gb|ADB39309.1| GCN5-related N-acetyltransferase [Spirosoma linguale DSM 74]

Length = 185

Score = 113 bits (283), Expect = 9e-24, Method: Compositional matrix adjust.
Identities = 65/173 (37%), Positives = 92/173 (53%), Gaps = 1/173 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IR A AD +A+ + YI ST+ F E E+ + +Q ++P+LVAE EG

Sbjct: 1 MTIRFAQPADASAILAVYAPYITGSTITFEYEVPPIAEFAGRIRAIQQQFPYLVAEEEGS 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G AYA + R AY W+VE++VYV R G+ LYT L + QG+ + A I

Sbjct: 61 LLGYAYASRRDRPAYQWSVETSIVYVHPAGHRRGIARQLYTRLFDLLVQQGYNAYAGIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180

PN S H ++G+ GT GYK G WHDV ++QR + P PV P+

Sbjct: 121 SPNPQSESFHRSMGFDYIGTYAKIGYKMGAWHDVSWFQRTLQ-PHQINPVIPM 172

>ref|ZP_05034621.1| acetyltransferase, GNAT family [Brevundimonas sp. BAL3]

gb|EDX82050.1| acetyltransferase, GNAT family [Brevundimonas sp. BAL3]

Length = 189

Score = 113 bits (283), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 66/166 (39%), Positives = 89/166 (53%), Gaps = 2/166 (1%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAE 63

R V+IR AT ADMAA+ I + F EP E +Q P LVAE

Sbjct: 2 RSEVQIREATPADMAAITAIYAESVANGRGTFELEPPDEIEMTARFAAVQALGLPRLVAE 61

Query: 64 VEGVAVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123

++G V G AYAGP++ R AY + VE ++YV+ + G+ L L+ + EA G + +V

Sbjct: 62 IDGAVVGAYAGPFRTRQAYRYMVEDSIYVAPEARGRGVAGALLDALIVACEALGLRQMV 121

Query: 124 AVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168

AVIG N S+ LH A G+ G +AAG+KH W DV F QR+

Sbjct: 122 AVIGDSDNAGSIALHRARGFADAGVFKAAAGWKHDDWRDVVFMQREL 167

>ref|YP_003268792.1| phosphinothricin acetyltransferase [Haliangium ochraceum DSM 14365]

gb|ACY16899.1| Phosphinothricin acetyltransferase [Haliangium ochraceum DSM 14365]

Length = 190

Score = 113 bits (283), Expect = 1e-23, Method: Compositional matrix adjust.

Identities = 66/153 (43%), Positives = 87/153 (56%), Gaps = 3/153 (1%)

Query: 29 IETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVE 88

+ + ++F EP E + L +Q RYPWLVE G +AG AYA ++ R AY WT E

Sbjct: 32 VRDTAISFELEPPDEAEMVRRLLAAVQGRYPWLVLERAGALAGYAYASSFRERPAYRWTAE 91

Query: 89 STVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPSVRLHEALGYTARGTL 148

+VYV H+R G+ LY LL + AQG ++ VAVI LP+ S +HE LG+ G +

Sbjct: 92 VSVYVHAEHRRRGVARALYGELLARLRAQGLRTAVAVITLPDAGSATMHERLGFAPAGRI 151

Query: 149 RAAGYKHGGWHDVGFWRDF---ELPAPPRPVR 178

AGYK W+D+GFWQ PA PRP R

Sbjct: 152 ARAGYKFDRWYDIGFWQLALGGDGAPASPRPPR 184

>ref|ZP_02041092.1| hypothetical protein RUMGNA_01858 [Ruminococcus gnavus ATCC 29149]

gb|EDN77703.1| hypothetical protein RUMGNA_01858 [Ruminococcus gnavus ATCC 29149]

Length = 183

Score = 113 bits (283), Expect = 1e-23, Method: Compositional matrix adjust.

Identities = 63/175 (36%), Positives = 94/175 (53%), Gaps = 2/175 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR AT D A+ I +YI+T + F E T E+ + + YP+L+ E G +

Sbjct: 2 IRFATEEDAQALLAIYAYIDTE-ITFEYELPTEAEFRKRIRTVLEEYPYLIYEDAGNIL 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129

G AYA R AY W VE TVY+ G+G LY LL+ + QG + ++I P

Sbjct: 61 GYAYAHRHLERAAYQWNVELTVYLHPDAVSRGIGRRLYEELLRLILTEQGICNAYSLITRP 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFE-LPAPPRPVRPVTQI 183

N+ S +LHEA+G+T G L+ GYK+G W DV ++++ P P P R + ++

Sbjct: 121 NEKSEKLHEAMGFTLMGVLKNTGYKNGKWRDVSWEKQLNPYPEHPVPFRKIDEL 175

>ref|ZP_08157709.1| putative phosphinothricin N-acetyltransferase [Ruminococcus albus 8]

gb|EGC04391.1| putative phosphinothricin N-acetyltransferase [Ruminococcus albus 8]

Length = 188

Score = 113 bits (283), Expect = 1e-23, Method: Compositional matrix adjust.

Identities = 61/180 (33%), Positives = 93/180 (51%), Gaps = 8/180 (4%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV 64

+ + IR A D A + DI +Y+E + + F + + E+ + + + RYP++VAE

Sbjct: 2 KSEITIRTAVPDDAAELLDIYAYVEKTAITFEYDVPSLAEFKERISQTLMRYPYIVAEEK 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124

GV+AG AYAG +K R AYD++VE TVY + GLG LYT L ++ G ++ A

Sbjct: 62 NGVIAGYAYAGVFKDRAAYDYSVEVTYVYTHRSCHKQGLGRLLYTELEAMLKQMGITNLYA 121

Query: 125 VIGLPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176

IG+P D S+ H +GY G GYK G W+D+ + ++ A P

Sbjct: 122 CIGVPADSADEYLDNNSMDFHTHMGYVLGRFHKCGYKFGRWYDMVWLEKLSQHAENMP 181

>ref|YP_003178172.1| GCN5-related N-acetyltransferase [Halomicrobium mukohataei DSM 12286]

gb|ACV48465.1| GCN5-related N-acetyltransferase [Halomicrobium mukohataei DSM 12286]

Length = 196

Score = 113 bits (282), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 61/156 (39%), Positives = 78/156 (50%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR A D A DI Y+ S V+F P E D L + YPWL V E E V

Sbjct: 4 IRRARPDDATAACADIYAPYVRDSAVSFETTPPASGEMRDRLRATLETYPWLV CEREDRVV 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129

G AYA + R AY W+VE ++YV H+R G+ + LY L + QGF + A + LP

Sbjct: 64 GFAYASDHRDRTAYQWSVELSIYVDGDHRRAGIATALYESLFAVLGEQGFYNGYAGVTLP 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165

N SV H +G+ GT GY G W DV +W+

Sbjct: 124 NRASVEFHREMGFEPVGYENVGYTAGEWQDVQWWR 159

>ref|ZP_07669863.1| phosphinothricin N-acetyltransferase [Erysipelotrichaceae bacterium

3_1_53]

gb|EFP63119.1| phosphinothricin N-acetyltransferase [Erysipelotrichaceae bacterium

3_1_53]

Length = 195

Score = 113 bits (282), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 57/165 (34%), Positives = 89/165 (53%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR A +D A+ I +Y+ S + F E T +E+ + +Q YP+LV E++ +

Sbjct: 4 IRFAQLSDAPALLSIYAYVGNVITFEYEAPTLEEFEGRMHIIQQEYPYLVC EIDQKIV 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129

G AYA R AY W VE +VY+ + Q +G LYT LL+ ++ Q ++ ++ I LP

Sbjct: 64 GYAYAHRHMERAAAYQWNVELSVYLQPQAQHRQIGKALYTALLEILKLQRLQTAISCITLP 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174

N S+ LH++ G+ G L AGYK W DV + Q++ + P

Sbjct: 124 NTASLALHKSFGFKEMGILHNAGYKFDARWDVIWLQKELQKHTVP 168

>ref|YP_002490995.1| GCN5-related N-acetyltransferase [Anaeromyxobacter dehalogenans 2CP-1]

gb|ACL63929.1| GCN5-related N-acetyltransferase [Anaeromyxobacter dehalogenans 2CP-1]

Length = 197

Score = 112 bits (281), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 72/176 (40%), Positives = 94/176 (53%), Gaps = 1/176 (0%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVV 68

+IR AT D V +I + + ++F EP P E + + + PVLV E +G V

Sbjct: 3 QIRMATLDDAGDVAEIIYGAVVAGTPISFELEPPGPGEMARRMAAVLELAPWLVCEEDGRV 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128

G YA R AY W+V+ TVYV +R GLG LYT LL+ + A QGF + A I L

Sbjct: 63 DGYVYASRHHDRAAAYRWSVDVTYVVRDGRRRGGLGRALYTALLELLRAQGFHAAHAGITL 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQWQDF-ELPAPPRPVRPVTQI 183

PN SV LHEALG+ G G+K G WHDVG+WQ + E P P+ V +

Sbjct: 123 PNAGSVGLHEALGFRPIGVYPRVGWKMGAWHDVGYWQLELRERTRAPGPILAVDAL 178

>ref|YP_001523874.1| GCN5-related N-acetyltransferase [Azorhizobium caulinodans ORS 571]

dbj|BAF86956.1| GCN5-related N-acetyltransferase [Azorhizobium caulinodans ORS 571]
Length = 174

Score = 112 bits (281), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 63/162 (38%), Positives = 95/162 (58%), Gaps = 3/162 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVA-EVEGV 67

+RPAT AD+ A+ DI + + T T +F +P E + L YP+LVA + +

Sbjct: 3 LRPATLADVPAIADIYDDAVRTGTASFELDPGPGVEMTRFRFDALMAGDYPLYLVAVDTDDET 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G AYAG ++ R AY +TVE+++YV+ QR G+G L T L++ EA+GF+ +VAVIG

Sbjct: 63 LLGYAYAGAFRPRIAYRFTVENSIVAPGAQRRGVGKALLTALVRECEARGFRQMVAVIG 122

Query: 128 -LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQWQDF 168

N S+ +H A G+ G ++++G K G W D QRD

Sbjct: 123 DSANAGSIGVHRACGFRDVGIIKSSGLKFGRWLDTVLMQRDL 164

>ref|YP_001363663.1| GCN5-related N-acetyltransferase [Kineococcus radiotolerans SRS30216]

gb|ABS05399.1| GCN5-related N-acetyltransferase [Kineococcus radiotolerans SRS30216]
Length = 176

Score = 112 bits (281), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 62/152 (40%), Positives = 85/152 (55%), Gaps = 3/152 (1%)

Query: 28 YIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTV 87

Y+ + ++F EP E +E R+ WL V E G VAG AYA P+ AR AYDW+

Sbjct: 24 YVRDTAISFELEPPDAAEVARRIEASGQRHAWLVLEDAGR VAGYAYASPFAARPAYDWSC 83

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGT 147

E +VY++ +R G G LYT L +E +GF+++VA + +PN+ S+ LH A G+ GT

Sbjct: 84 EVSVYLAPGLRRSGAGRALYTELFARLEQRGFRTL VAGVTVPN EASLGLHRATGFEVVG 143

Query: 148 LRAAGYKHGGWHDVGFQWQWQDFELPAPPRPVRP 179

R G+K G W DV QR P R V P

Sbjct: 144 FRDIGFKLGRWWDVTRLQRPL---GPGRDVAP 172

>ref|ZP_08014935.1| hypothetical protein HMPREF9464_00154 [Sutterella wadsworthensis 3_1_45B]

gb|EFW02716.1| hypothetical protein HMPREF9464_00154 [Sutterella wadsworthensis 3_1_45B]
Length = 192

Score = 112 bits (281), Expect = 2e-23, Method: Compositional matrix adjust.
Identities = 63/176 (35%), Positives = 94/176 (53%), Gaps = 5/176 (2%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAG 70
 R A D A+ I + YI ST+ F T +E+ + + + YP++VAE +G G
 Sbjct: 4 RLAVPEDAPALLQIYSEYIH-STITFEYTLPTTEEFAERIRTIAGFYPIVAEEDGRCMG 62

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130
 AYA R AY W E +VY++ GLG LY+ L+ ++AQG SV + PN
 Sbjct: 63 YAYAHRHMERAAAYQWNAELSVYLAKSAVGCGLGGGLYSRLMTLLKAQGVLSVFGCVTSPN 122

Query: 131 DPSVRLHEALGYTARCTLRAAGYKHGGWHDVGFWR----DFELPAPPRPVRPVTQ 182
 PS RLH+ +G+ GT AG+K+G WHDV ++Q+ + P PP P+ + +
 Sbjct: 123 PPSDRHLKRMGFKLVGTYLQAGFKNGAWHDVNWYQKMLGDHLDDPKPPVPLSALEK 178

>ref|YP_003383991.1| phosphinothricin acetyltransferase [Kribbella flavida DSM 17836]
 gb|ADB35192.1| Phosphinothricin acetyltransferase [Kribbella flavida DSM 17836]
 Length = 178

Score = 112 bits (281), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 59/139 (42%), Positives = 81/139 (58%)

Query: 28 YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTV 87
 Y+ + ++F EP TP E + + Q + WL V E G V G AY GP KAR AY W+
 Sbjct: 27 YVRETAISFELEPPTPAEMAERITAAQSTHAWLVLEDAGR VVG YAYGGPMKARAAYRWSC 86

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARCT 147
 E +VY+ +R G G LY L + + +G+++ +A + LPND SV LH ALG+ GT
 Sbjct: 87 EVSVYLESGRRRTGGRLLYEALFERLAERGYRTAAGMTLPNDASVGLHRALGFEPITG 146

Query: 148 LRAAGYKHGGWHDVGFWR 166
 R G+KH WHDV + QR
 Sbjct: 147 YRRIGWKHNAWHDVAWAQR 165

>ref|YP_002720780.1| Sortase related acyltransferase [Brachyspira hyodysenteriae WA1]
 gb|ACN83076.1| Sortase related acyltransferase [Brachyspira hyodysenteriae WA1]
 Length = 190

Score = 112 bits (280), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 54/180 (30%), Positives = 101/180 (56%), Gaps = 6/180 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG- 66
 ++IR A D + + I + YI+TS + F + T +E+ + +E + +YP+LV E E
 Sbjct: 1 MKIRLANIEDASQILSIYSQYIDTS-ITFEYKLP TLEEFKNRIENI IKYPYLVCEDENN 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G YA + R AY+W+ E ++Y+ + G+G L + +++ ++ QG K++ + I
 Sbjct: 60 KIIGYCYANKFLEREAYNWSSELSIYLDKNNINRGIGKKLCSIIIEILKYQGIKNIYSKI 119

Query: 127 GLPNDPSVRLHEALGYTARCTLRAAGYKHGGWHDVGFWR----DFELPAPPRPVRPVTQ 182
 +PN S +LH +LG+ GT GYK+G WH V +++ D++ P P++ + +
 Sbjct: 120 TVPNTKSEKLHHS LGFNLI GTYNNIGYKNGKWSVRLFEKELIFDYDNP KAIPIKEIDK 179

>ref|YP_567667.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris BisB5]
 gb|ABE37766.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris BisB5]
 Length = 181

Score = 112 bits (280), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 65/159 (40%), Positives = 87/159 (54%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IRPAT D+ AV I + + T T F P E E L +P+LV ++G V
 Sbjct: 6 IRPATDDLPAVTAIYDEAVRTGTATFELTPDLAEMTRRFETLTGGGFPYLVGLLDGRV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 AG AYAGP++ R AY +TVE++VY+ R GLG+ L L+ EA+GF+ ++AVIG
 Sbjct: 66 AGYAYAGPYRPRPAYRFTVENSIVLDPATHRRGLGTALMRELIAQCEARGFRQMIIVIGD 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N SV +H G+ GT R G+K G W D QR
 Sbjct: 126 SANSGLSVGVHRKTGFDMIGTHRVNFGFKGRWLDTVMMQR 164

>emb|CBK80336.1| Sortase and related acyltransferases [Coproccoccus catus GD/7]
 Length = 197

Score = 112 bits (280), Expect = 2e-23, Method: Compositional matrix adjust.
 Identities = 60/162 (37%), Positives = 87/162 (53%), Gaps = 9/162 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V IR AT D A + I HY+ + ++F E + +E+ + +E RYP++VAE EG
 Sbjct: 5 VMIRLATPKDAAEMLKIYAHYVNTAISFEYEVPSSEEFREIERESTLKRYPIYIAEQEGH 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AY + R AYDW VE+++YV ++R G G LY L K ++ Q ++ A I
 Sbjct: 65 IIGYAYVSIFHERKAYDWAVETSIYVDKDYKRSGCGKLLYQALEKILKKQHISNLYACIA 124

Query: 128 -----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 L ND S+ HE LGY GT + GYK W+D+
 Sbjct: 125 YTEQEDEHLTND-SMHFHEHLGYELVGTFKQCGYKFNKWYDM 165

>ref|NP_347494.1| phosphinothricin acetyltransferase [Clostridium acetobutylicum ATCC
 824]
 gb|AAK78834.1|AE007601_5 Phosphinothricin acetyltransferase [Clostridium
 acetobutylicum ATCC
 824]
 gb|ADZ19909.1| Phosphinothricin acetyltransferase [Clostridium acetobutylicum EA
 2018]
 Length = 196

Score = 112 bits (279), Expect = 3e-23, Method: Compositional matrix adjust.
 Identities = 51/175 (29%), Positives = 95/175 (54%), Gaps = 1/175 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR D + +I +I+ + + F + + Q++ + + + ++Y +LV E++ VA
 Sbjct: 4 IRLVKKEDESEILNIYKPFIQNTAITFDYDIPSIQKFTEKVSNISNKYAYLVCEIDEKVA 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + R AYDW V+ ++YV ++Q G+G LY L++++ QG+ ++ A++
 Sbjct: 64 GYAYASSFNRAAYDWAVDLISYVDDKYQGKGIGKALYYTLIETLKIQGYCNMYALVTSS 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAP-PRPVRPVTQI 183
 N S HE + GT ++GYK WHDV +++ E A P + + +I
 Sbjct: 124 NTRSKNFHEYFDFKLSGTYHSSGYKFEKWHDVDVFEKIIEDNAKNPHEIIAINKI 178

>ref|ZP_07458488.1| phosphinothricin acetyltransferase [Streptococcus sp. oral taxon
 071 str. 73H25AP]
 gb|EFM35556.1| phosphinothricin acetyltransferase [Streptococcus sp. oral taxon
 071 str. 73H25AP]
 Length = 170

Score = 112 bits (279), Expect = 3e-23, Method: Compositional matrix adjust.
 Identities = 58/170 (34%), Positives = 91/170 (53%), Gaps = 3/170 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
 +IR +D+ + I Y+ + + F E + +E+ +++ +YP+LV E EG +
 Sbjct: 3 KIRTVRESIDPDLLAIYAPYVLNTAITFEYEVPSVEEFQRRIQKTLTKYPYLVLEEEGKI 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G AYA + R AYDW+VE ++Y+ + GLGS LY L + +E++G+ +A I L
 Sbjct: 63 LGYAYASTYYDRRAYDWSVEVSIYHLHQEAEGRLGLSLLYDCLEEELESRGYLRFLACIAL 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 PND S+ LH GY GYK G WHD+ + Q+ PP +R
 Sbjct: 123 PNDRSILLHRKRGYEQVAHFPEIGYKFGKWHDIVWMQKSL---TPPDMMR 169

>ref|ZP_04115199.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
 serovar kurstaki str. T03a001]
 ref|ZP_04203535.1| Phosphinothricin N-acetyltransferase [Bacillus cereus F65185]
 ref|ZP_04212527.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock4-2]
 ref|ZP_04279228.1| Phosphinothricin N-acetyltransferase [Bacillus cereus m1550]
 gb|EEK89195.1| Phosphinothricin N-acetyltransferase [Bacillus cereus m1550]
 gb|EEL55830.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock4-2]
 gb|EEL64774.1| Phosphinothricin N-acetyltransferase [Bacillus cereus F65185]
 gb|EEM53115.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
 serovar kurstaki str. T03a001]
 Length = 170

Score = 111 bits (278), Expect = 3e-23, Method: Compositional matrix adjust.
 Identities = 60/170 (35%), Positives = 98/170 (57%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + + YP +V E++ V
 Sbjct: 2 IREATKKDLAYILDYNDAILYTTAVYAYKPVTLNLRIDWYEQKKAEEYPIIVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY ++VE +VYV +++ G+GS+L L+K + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKAYRKNGIGSSLMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELNGPENPIE 169

>ref|YP_001033220.1| phosphinothricin N-acetyltransferase [Lactococcus lactis subsp.
 cremoris MG1363]
 emb|CAL98527.1| phosphinothricin N-acetyltransferase [Lactococcus lactis subsp.
 cremoris MG1363]
 gb|ADJ60933.1| phosphinothricin N-acetyltransferase [Lactococcus lactis subsp.
 cremoris NZ9000]
 Length = 186

Score = 111 bits (277), Expect = 5e-23, Method: Compositional matrix adjust.
 Identities = 53/154 (34%), Positives = 85/154 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +E R A AD + +I Y+E + + F E T +E+ + +E++ ++P+L+A G
 Sbjct: 1 MEFRLLAKKADAQRLLEIYRPYVEKTAITFEYEVPTLEEFENRIEKIGSQFPYLLAIENGK 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYAG ++ R AYDW VE ++Y+ + ++ G GS LY LL ++ A ++ A I
 Sbjct: 61 IIGYAYAGAYRERAAVDWVVELSIYLDKERQHAGSALYQKLLTALAALNYQRAYACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 PN SV HE G+ G AGYK W+ +
 Sbjct: 121 YPNPASVAFHEKFGFQQIGLFPKAGYKFEQWYGI 154

>ref|ZP_04186528.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH1271]
 gb|EEL81776.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH1271]
 Length = 179

Score = 111 bits (277), Expect = 5e-23, Method: Compositional matrix adjust.
 Identities = 60/174 (34%), Positives = 99/174 (56%), Gaps = 3/174 (1%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVA 62
 ER+ V IR A D+ + DI N I +T + +P T + ID E+ + + YP LV
 Sbjct: 5 ERKKVMIREARKQDVTYILDIYNDAILYTTAVYTYKPVTLENRIDWYEQKKAESYPILVY 64

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 E++ V G A GP++A +AY +++E +VYV +++ G+G++L L+ + + + ++
 Sbjct: 65 ELDNKVVGFFATFGPFRAWSAYKYSIEHSVYVHKEYRKNGIGTSLMKALITVAKEREYMTL 124

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 +A I N S+ LHE G+ GT++ AGYK W D+ F+Q EL P +P
 Sbjct: 125 IAGIDAENKKSIALHENYGFVHAGTIKKAGYKFNRWLDLAFYQ--LELNGPKKP 176

>ref|YP_779246.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris
 BisA53]
 gb|ABJ04266.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris
 BisA53]
 Length = 179

Score = 110 bits (276), Expect = 6e-23, Method: Compositional matrix adjust.
 Identities = 66/176 (37%), Positives = 95/176 (53%), Gaps = 7/176 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + IRPATAAD A+ I + T F P + +E + L +P+LVA+++G
 Sbjct: 4 ILIRPATAADFPAITAIYREAVLHGTATFELTPPSLEEMTRRFDSLTTGGGFYPYLVAADLDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AYAGP++ R AY +TVE++VY+S R G+G L L+ EA+G++ ++AVI
 Sbjct: 64 ELVGYAYAGPYRPRPAYRFTVENSIVLSPAVHRRGIGGLLLRRLIADSEARGYRQMIAMI 123

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-----ELPAPPRP 176
 G N S+ LH +LG+ GT A G K G W D QR +P P P
 Sbjct: 124 GDAANAGSIGLHRSGLGFALIGTHPAVGLKFGRWLDTVMMQRALGQGGETVPTTPEP 179

>ref|YP_001557413.1| GCN5-related N-acetyltransferase [Clostridium phytofermentans
 ISDg]
 gb|ABX40674.1| GCN5-related N-acetyltransferase [Clostridium phytofermentans ISDg]
 Length = 184

Score = 110 bits (276), Expect = 6e-23, Method: Compositional matrix adjust.
 Identities = 58/175 (33%), Positives = 91/175 (52%), Gaps = 1/175 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT D + +I Y+ + + F T QE+ + ++ RYP+LVAE EG +
 Sbjct: 7 IRMATILDAPKLLEIYAPYVRETAITFEYTVPTVQEFESRIAKILTRYPYLVAEKEGEIL 66

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AY +K R AYDW VE+T+Y++ + G+G LY L + ++ Q ++ A I P
 Sbjct: 67 GYAYVSSFKERAAAYDWAETTTIYINQNQRGSGVGKRLYLKLEEIVKRQNIINMNACIAYP 126

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL-PAPPRPVRPVTQI 183
 N S+ HE LGY GYK W+D+ + ++ E P P+ P+ ++
 Sbjct: 127 NPGSIAFHEHLGYKTVAHF TKCGYKLDWYDMIWMEKILEEHPEKPKKEFIPINKL 181

>ref|ZP_02027156.1| hypothetical protein EUBVEN_02425 [Eubacterium ventriosum ATCC 27560]
 gb|EDM50473.1| hypothetical protein EUBVEN_02425 [Eubacterium ventriosum ATCC 27560]
 Length = 192

Score = 110 bits (276), Expect = 6e-23, Method: Compositional matrix adjust.
 Identities = 58/162 (35%), Positives = 87/162 (53%), Gaps = 7/162 (4%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 V IR AT D + I ++Y+E + + F + E+ + ++ YP+LV+EV+G
 Sbjct: 2 EVMIRFATEEDAEELLRIYSYVENTAITFEYDTPALDEFKYRIRTIKAMYPLYVSEVDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 + G AYA +K R AYDW VE+T+Y+ + G G LY L K+++AQ ++ A I
 Sbjct: 62 KIVGYAYANTFKDRAAYDWAVETTIYLDKDARGKGYGKELYEAELEKALKAQNITNLYACI 121

Query: 127 GLP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 G P SV+ HE LGY GT + GYK W+D+
 Sbjct: 122 GYPEVEDQYLTKNSVQYHEHLGYRFIGTFKKCGYKFNRWYDM 163

>ref|ZP_03110621.1| acetyltransferase, GNAT family [Bacillus cereus 03BB108]
 gb|EDX64361.1| acetyltransferase, GNAT family [Bacillus cereus 03BB108]
 Length = 170

Score = 110 bits (276), Expect = 6e-23, Method: Compositional matrix adjust.
 Identities = 59/170 (34%), Positives = 96/170 (56%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
 Sbjct: 2 IREATEKDVIYILDYINDAILNTTAVYTYKPVTLNLRIDWYEQQKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++AVI
 Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRKCGIGTSLMRALITIAKEREYMTLIAVIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELCGPKNPLE 169

>ref|NP_721464.1| putative acetyltransferase [Streptococcus mutans UA159]
 gb|AAN58770.1|AE014945_7 putative acetyltransferase [Streptococcus mutans UA159]
 Length = 163

Score = 110 bits (276), Expect = 7e-23, Method: Compositional matrix adjust.
 Identities = 50/159 (31%), Positives = 90/159 (56%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR A D + I Y+E + + F + + +E+ + +E+ + ++P+LVAE EG+
 Sbjct: 1 MKIRNACKEDAQQLIAIYASYVEKTAITFEYQVPSLEEFEERIEKTKQKFPYLVAEEEGI 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
 + G AYA + AYDWTVE ++Y+ + +GS LY L +++ GF +++ I
 Sbjct: 61 LQGYAYASVYNNHAAAYDWTVELSIYIKEEARGKHIGSQLYASLERNLQEAGFVNLLVCIA 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 LPN+ S+ H+ GY + GYK W+D+ + Q+
 Sbjct: 121 LPNNASLTFFHKHGYEQVAHFKKVGYKFDKWDIVWMQK 159

>ref|NP_105235.1| phosphinotricin acetyltransferase [Mesorhizobium loti MAFF303099]
 dbj|BAB51021.1| phosphinotricin acetyltransferase [Mesorhizobium loti MAFF303099]
 Length = 194

Score = 110 bits (276), Expect = 7e-23, Method: Compositional matrix adjust.
 Identities = 64/161 (39%), Positives = 90/161 (55%), Gaps = 3/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEG 66
 + IR A+AAD+ + +I + T ++ EP + E L +P+LVAE +G
 Sbjct: 4 IVIRAASAADLDTITEIYADAVTHGTASYELEPPSRAEMGTRFATLTAGGFPYLVAEKDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G AYAG ++ R AY + VE +VYV+ + G+G L L+ + EA GF+ +VAVI
 Sbjct: 64 AVLGYAYAGAFRPRPAYRFIVEDSVYVAPDAKGQGIGLKLMSRLITAAEAAGFRQIVAVI 123

Query: 127 --GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 G + SVRLHE LG+ G L +GYKHG W D F Q
 Sbjct: 124 GDGHADSASVRLHEKLGFRHSGRLEGSYKHGRWLDTVFMQ 164

>ref|YP_002559467.1| acetyltransferase family protein [Macrococcus caseolyticus
 JCSC5402]
 dbj|BAH16771.1| acetyltransferase family protein [Macrococcus caseolyticus
 JCSC5402]
 Length = 162

Score = 110 bits (276), Expect = 7e-23, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 91/159 (57%), Gaps = 5/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP--QEWDLLERLQDRYPWLVAEVEG 66
 IR AT D+ + DI NH I +T + E + ++W+ +E+ + YP + E++G
 Sbjct: 2 IRHATQNDLPKILDIYNHAILNTTAIYTYEKTSLLEKQWL--MEKEKQGYPVFIFEIDG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VAG A GP++ AY +TVE +VYVS + +G+G L +H++ S +G+K++VA I
 Sbjct: 60 RVAGFATYGPFRNFPAYQFTVEHSVYVSPYFRHMGIGEKLLSHIIDSARKEGYKTMVAGI 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N S+ LH+ + GTL+ GYK W D+ F+Q
 Sbjct: 120 DSENKGSIIYLHKKFNFKYTGTLDVGYKFNKWLDFYQ 158

>ref|ZP_04084797.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
 serovar huazhongensis BGSC 4BD1]
 gb|EEM83565.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
 serovar huazhongensis BGSC 4BD1]
 Length = 170

Score = 110 bits (275), Expect = 7e-23, Method: Compositional matrix adjust.
 Identities = 60/170 (35%), Positives = 97/170 (57%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + + YP V E++ V
 Sbjct: 2 IREATKKDLAYILDYNDAILYTTAVYAYKPVTLNLRIDWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY ++VE +VYV +++ G+GS+L L+K + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKAYRKSGIGSSLMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDAFYQ--LELNGPENPIE 169

>ref|ZP_04671490.1| phosphinothricin N-acetyltransferase [Clostridiales bacterium
1_7_47_FAA]
gb|EEQ58471.1| phosphinothricin N-acetyltransferase [Clostridiales bacterium
1_7_47FAA]
Length = 189

Score = 110 bits (275), Expect = 8e-23, Method: Compositional matrix adjust.
Identities = 57/155 (36%), Positives = 82/155 (52%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
P+ IR A+ +D A+ I Y+E + + F T +++ + R RYP+LVAE G
Sbjct: 5 PITIRTASVSDAPALLSIYAPYVERTAITFEYTVPTLEDFRSRISRTLARYPYLVAECSE 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+ G AYA + R AYDW+ E ++YVS + G+G+ LY L ++ Q +V A I
Sbjct: 65 IAMGYAYASAFHPRAAYDWSAEVSIYVSEDARGTGIGTRLYGALEDILKQONIINVNACI 124

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDV 161
PN S+ HE LGY G GYK G W D+
Sbjct: 125 AYPNPGSISFHEKLGVRTVGHFTKCGYKLGKWWDM 159

>ref|ZP_02188752.1| GCN5-related N-acetyltransferase [alpha proteobacterium BAL199]
gb|EDP64580.1| GCN5-related N-acetyltransferase [alpha proteobacterium BAL199]
Length = 180

Score = 110 bits (275), Expect = 8e-23, Method: Compositional matrix adjust.
Identities = 68/178 (38%), Positives = 97/178 (54%), Gaps = 2/178 (1%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPW 59
M+ V +RP+T D+AA+ I H++ +F P E + + +R P
Sbjct: 1 MTD RDASVHVRPSTTDDLAIIHAIYAHVHTNGLGSFEEVPPGIDEMAERRLAIVERGM 60

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
LVAE G + G AY GP++ R AY +TVE++VYV+ RLG+G L L++ EA +
Sbjct: 61 LVAEANGRLGAYVGPYRPRPAYRYTVENS VYVAPEATRLGVGRALLGT LIEICEAGRW 120

Query: 120 KSVVAVIG-LPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
+ +VAVIG N S+ LH ALG+ G L+A G+KHG W DV QR + RP
Sbjct: 121 RQM VAVIGDRGNTASIALHAALGFHEAGHLKAVGFKHGRWVDVIMQRALGVGDDEP 178

>ref|ZP_03234565.1| acetyltransferase, GNAT family [Bacillus cereus H3081.97]
gb|EDZ59192.1| acetyltransferase, GNAT family [Bacillus cereus H3081.97]
Length = 170

Score = 110 bits (275), Expect = 9e-23, Method: Compositional matrix adjust.
Identities = 59/170 (34%), Positives = 96/170 (56%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATEKDVIYILDYNDAILNTTAVYTYKPVTLNRI DWYEQKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A IG
Sbjct: 62 VGFATFGPFRAPAYKYSIEHSVYVDKEYRKCIGTSLMRALITIAKEREYMTLIAGIGA 121

Query: 129 PNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELCGPKNP 169

>ref|YP_713648.1| putative N-acetyltransferase [Frankia alni ACN14a]
 emb|CAJ62083.1| putative N-acetyltransferase [Frankia alni ACN14a]
 Length = 184

Score = 110 bits (274), Expect = 9e-23, Method: Compositional matrix adjust.
 Identities = 66/174 (37%), Positives = 90/174 (51%), Gaps = 3/174 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V IR A +D A + I Y+ S F E TP + + R PWLVAE G
 Sbjct: 2 VTIRAAHPSDAAGIRAIYAPYVAGSPSTFEEELPTPAD-LQARMLASPRRPWLVAEAGGE 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G AYA + R +Y W+V+++VY++ H R GLG LY L+ + G+ ++ A I
 Sbjct: 61 IVGYAYASAHRTASYSRVSVDTSVYLAAGHHRRGLGRRLYDELIAQVRTLGYNLYACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF--ELPAPPRPVRP 179
 LPN SV LH ++G+ G GYK G WHDVG++ E PA P RP
 Sbjct: 121 LPNAASVALHTSVGFRPIGVFTDVGYKLGAWHDVGFGLTLVDEHPAEPAEPRP 174

>ref|YP_003340665.1| phosphinothricin acetyltransferase [Streptosporangium roseum DSM
 43021]
 gb|ACZ87922.1| Phosphinothricin acetyltransferase [Streptosporangium roseum DSM
 43021]
 Length = 170

Score = 110 bits (274), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 66/163 (40%), Positives = 87/163 (53%), Gaps = 3/163 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV 64
 RP IR A D+ AV +I HY+ S F P+ +W LE L +R P+LVA++
 Sbjct: 5 RPT-IRAAAPEDLKAVAEINAHYVTNSVATFDETPRAFDDWRPWLEELAERGLPFLVADL 63

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 G VAG AYAGPW+ + AY TVE T+Y++ H GLG+ L L+ G + ++A
 Sbjct: 64 SGEVAGYAYAGPWRPKPAYRHTVEDTIYIAPGHLGRGLGTALLGTLVAESAQAGMRHMIA 123

Query: 125 VIGLPND-PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 VI D S LH G+T G L G+KHG W D QR
 Sbjct: 124 VIADTGDGASALHRRSGFTEAGRLTGVGFKHGRWIDTLLMQR 166

>ref|NP_744077.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas putida
 KT2440]
 gb|AAN67541.1|AE016383_3 phosphinothricin N-acetyltransferase, putative [Pseudomonas
 putida
 KT2440]
 Length = 186

Score = 110 bits (274), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 65/178 (36%), Positives = 95/178 (53%), Gaps = 2/178 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR A D + I + + ++F + ++ + + YP+LVA EG
 Sbjct: 5 IDIRVARPEDAEIQQIYAPIVLNTAISFEEAVPSVEQMRERISTTLQTYPYLVAVREGR 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 V G AYA +AR AY W V+ TVYV+ +R G+ LY LL ++ G++S A I
 Sbjct: 65 VVGAYAYASQHRARAAYRWAVDVTVYVAEGQRRSGIARQLYDVLLPVLKRLGYRSAYAGIA 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF--ELPAPPRPVRPVTQI 183
 LPN+ SV LHE LG+ GT G+K WHDVG+W+ DF E P P+ ++QI

Sbjct: 125 LPNEGSVGLHERLGFQHIGTFPQVGFKLDAWHVDVGWYRFDGDEGLHPEAPLGFLSQI 182

>ref|ZP_04174994.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH1273]
 ref|ZP_04180759.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH1272]
 gb|EEL87532.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH1272]
 gb|EEL93335.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH1273]
 Length = 170

Score = 110 bits (274), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 59/170 (34%), Positives = 94/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR A D+ + DI N I ST + P T + ID E+ + D YP LV E++ V
 Sbjct: 2 IREAMKKDVTFILDIYNDAILNSTAVYAYNPVTLENRIDWYEQKKADGYPILVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G A GP++A AY ++ E +VYV +++ G+GS+L L+ + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSAEHSVYVDREYRKNIGSSLMELITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N+ S+ +H+ G+ GT++ AGYK GW D+ F+Q EL P P+
 Sbjct: 122 ENEKSIAMHKNFGFVYSGTIKKAGYKFNGLDLAFYQ--LELNGPGNPIE 169

>ref|YP_003738151.1| phosphinothricin N-acetyltransferase [Halalkalicoccus jeotgali B3]
 gb|ADJ16359.1| phosphinothricin N-acetyltransferase [Halalkalicoccus jeotgali B3]
 Length = 196

Score = 109 bits (273), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 61/157 (38%), Positives = 85/157 (54%), Gaps = 1/157 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +RPATA D A+ I ++E S V+F T P T E + +R+PWLV +G V
 Sbjct: 5 LRPATADDAPAIRRIYAPFVEESAVSFETRPTATEVGTTRIATTTERHPWLVC-TDGDVI 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G AYA + R AY W+++ +VYV + R G+ LY L QGF + A I LP
 Sbjct: 64 GYAYATSHREREAYRWSIDSVYVDPAYHRRGIARALYGALFALAGEQGFLNAYAGISLP 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S HE++G+ GT G+K G WHDV +++R
 Sbjct: 124 NPASTAFHESMGFEPVGTYHDVGHKDGEGWHDVVRWYER 160

>ref|ZP_05136289.1| phosphinothricin N-acetyltransferase [Stenotrophomonas sp. SKA14]
 gb|EED40350.1| phosphinothricin N-acetyltransferase [Stenotrophomonas sp. SKA14]
 Length = 176

Score = 109 bits (273), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 65/172 (37%), Positives = 92/172 (53%), Gaps = 2/172 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVE 65
 V IR A AD+ A+ I + + + E + + + DR +P+LVAE++
 Sbjct: 2 AVLIRDAGLADIDAITAIYAVEVTDVFNTYEYDIPDASEMLRRMRDIIDRGFPYLVAEID 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
 G VAG AYA ++ R AY WTVE++VYV R Q G+G+ L L+ + A+G++ +VAV
 Sbjct: 62 GQVAGYAYANTYRTRVAYQWTVENSVMYVDARFQKGVTGLLQALIDACVARGYRQMVAV 121

Query: 126 IGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 IG P N S++LHE G+ G R G KHG W D QR A P

Sbjct: 122 IGEPTNTASIKLHERFGFELVGVFRGLGRKHGRWLDTVQMQRALGDGADTAP 173

>ref|ZP_06897931.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC 49957]
 gb|EFH10302.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC 49957]
 Length = 190

Score = 109 bits (273), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 66/161 (40%), Positives = 92/161 (57%), Gaps = 3/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAE-VE 65
 V IRPA ADM AV I H++ T F TE T ++ + +R P+LVAE +
 Sbjct: 16 VTIRPAREADMDAVATIYRHHVLHGTATFETEAPTAEDMRQRRIAITERGLPYLVAEDTD 75

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
 V G AYAG ++ R AY T+E++VY+S + G+G L L++ A G++ +VAV
 Sbjct: 76 CRVLGYAYAGAYRPRPAYRNTLENSVYIIEEARGRGIGRRLLEALIQECAALGYRQMVAV 135

Query: 126 IG-LPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 IG N+ S+RLH+A G+ GTLR+ G KHG W D Q
 Sbjct: 136 IGDSANEASIRLHKAFGFQPIGTLSRVGRKHGRWLDTVLMQ 176

>ref|ZP_04120739.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis serovar pakistani str. T13001]
 ref|ZP_04239831.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock1-15]
 gb|EEL28513.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock1-15]
 gb|EEM47615.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis serovar pakistani str. T13001]
 Length = 170

Score = 109 bits (273), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 60/169 (35%), Positives = 97/169 (57%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + + YP V E++ V
 Sbjct: 2 IREATKRDLAYILDYNDAILYTTAVYAYKPVTLNRIWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G A GP++A AY ++VE +VYV +++ G+GS+L L+K + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKAYRKNGIGSSLMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFIHAGTIKKAGYKFNKWLDAFYQ--LELNGPENPI 168

>ref|YP_811544.1| sortase related acyltransferase [Lactococcus lactis subsp. cremoris SK11]
 gb|ABJ73431.1| Sortase related acyltransferase [Lactococcus lactis subsp. cremoris SK11]
 Length = 186

Score = 109 bits (273), Expect = 1e-22, Method: Compositional matrix adjust.
 Identities = 53/154 (34%), Positives = 84/154 (54%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +E R A AD + +I Y+E + F E T +E+ + +E++ ++P+L+A G
 Sbjct: 1 MEFRLLAKKADAQRLLEIYRPYVEKIAITFEYEVPTLEEFENRIEKIGSQFPYLLAIENGK 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127

+ G AYAG ++ R AYDW VE ++Y+ + ++ G GS LY LL ++ A ++ A I
 Sbjct: 61 IIGYAYAGAYRERAAAYDWVVELSIYLDEKERQHGAGSVLYQKLLTALAALNYQRAYACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

PN SV HE G+ G AGYK W+ +

Sbjct: 121 YPNPASVAFHEKFGFQQIGLFPKAGYKFEQWYGI 154

>ref|ZP_04169245.1| Phosphinothricin N-acetyltransferase [Bacillus mycoides DSM 2048]

gb|EEL99000.1| Phosphinothricin N-acetyltransferase [Bacillus mycoides DSM 2048]

Length = 170

Score = 109 bits (273), Expect = 1e-22, Method: Compositional matrix adjust.

Identities = 59/170 (34%), Positives = 96/170 (56%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68

IR AT D+A + DI N I +T + +P T + ID E+ + D YP V E++ V

Sbjct: 2 IREATKKDLACILDIYNDIAVYTTAVYAYKPVTLLENRIDWYEQKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128

G A GP++A AY +++E +VYV +++ G+GS+L L+ + + + +++A I

Sbjct: 62 VGFATFGPFRAPWAPYKYSIEHSVYVDKEYRKNGIGSSLMEELITFAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178

N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+

Sbjct: 122 ENEKSIALHQNYGFVHAGTIQKAGYKFNRWLDLAFYQ--LELNGPENPIE 169

>ref|NP_959023.1| hypothetical protein MAP0089 [Mycobacterium avium subsp.
 paratuberculosis K-10]

gb|AAS02406.1| hypothetical protein MAP_0089 [Mycobacterium avium subsp.
 paratuberculosis K-10]

Length = 192

Score = 109 bits (273), Expect = 1e-22, Method: Compositional matrix adjust.

Identities = 66/177 (37%), Positives = 92/177 (51%), Gaps = 1/177 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 67

+ +R AT+ D A V + Y+ + ++F T+ + +E L PWLV

Sbjct: 1 MTLRMATSDDAAGVAAYVLPYVRDTAISFETQQPSVEEMRSRLTTTTLATLPWLVTIDGPR 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127

V G AYA P +AR AY W+V+ ++Y+ R G G LYT LL + AQG+ + A I

Sbjct: 61 VKGYAYASPHRAREAYRWSVDVSLYLDASIHROGQGRRLYTALLNLLGAQGYINAYAAIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183

LPN SV LHEAL + G G+K W DVG+W R + PA P RP T++

Sbjct: 121 LPNAASVGLHEALAFRRVGVFPRVGFQQRWWDVGWWHRLADPPAVPEEPRPWTRL 177

>ref|YP_002367523.1| acetyltransferase, GNAT family [Bacillus cereus B4264]

gb|ACK58907.1| acetyltransferase, GNAT family [Bacillus cereus B4264]

Length = 170

Score = 109 bits (272), Expect = 2e-22, Method: Compositional matrix adjust.

Identities = 59/169 (34%), Positives = 96/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68

IR AT D+A + DI N I +T + +P T + ID E+ + + YP V E++ V

Sbjct: 2 IREATKRDLAYILDYNDAILYTTAVYAYKPVTLLENRIDWYEQKKAEGYPIFVCELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128

G A GP++A AY ++ E +VYV +++ G+GS+L L+K + + + +++A I

Sbjct: 62 VGFATFGPFRAPAYKYSFEHSVYVDKAYRKNIGSSLMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177

N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+

Sbjct: 122 ENEKSIALHQKYGFVHAGTIKQAGYKFNKWLDLAFYQ--LELNGPENPI 168

>ref|ZP_05130852.1| phosphinothricin acetyltransferase [Clostridium sp. 7_2_43FAA]

gb|EEH97746.1| phosphinothricin acetyltransferase [Clostridium sp. 7_2_43FAA]

Length = 197

Score = 109 bits (272), Expect = 2e-22, Method: Compositional matrix adjust.

Identities = 53/177 (29%), Positives = 91/177 (51%), Gaps = 1/177 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

++IR A+ D + I Y++ + + F E T E+ + ++ YP+LV ++

Sbjct: 3 IKIRMASENDAEEILRIYAPYVKNTIITFEYEVPTVDEFKKRIRKISKDYPYLVCTLDDK 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

+ G AY+ K R AY W VE +VY+ + + R GLG YT L++ + Q K++ V+

Sbjct: 63 IIGYAYSYRHKERAAYQWNVLSVYIDNAYLRYGLGKAFYTALIEISKLNQNIYGVVT 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183

N +LHE G+ G GYK G WHDV ++++ E P+P++ + +

Sbjct: 123 SNNMNIEKLHEYFGFKLGIYHNTGYKFGKWHDVTWFEKSINEEYCEPKPLKSIKDV 179

>ref|ZP_05346405.1| phosphinothricin N-acetyltransferase [Bryantella formatexigens DSM

14469]

gb|EET60728.1| phosphinothricin N-acetyltransferase [Bryantella formatexigens DSM

14469]

Length = 199

Score = 109 bits (272), Expect = 2e-22, Method: Compositional matrix adjust.

Identities = 59/180 (32%), Positives = 95/180 (52%), Gaps = 10/180 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IRP T AD + DI Y+E + ++F + +P+ + + + RYP++ AE G

Sbjct: 8 IRIRPVTADARQLLDIYAPYVEKTAISFEYDVPSPEAFEKIRKTLQRYPIAAERNGE 67

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

+ G AY P+ R AYDW VE+++Y+ +++G+G LY + + AQ S+ A IG

Sbjct: 68 LLGYAYTSPFVGRAAYDWAVETSIYLRDCRKMIGKMLYAKIEEISRAQNILSLNACIG 127

Query: 128 LP-NDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPV 177

P ND S++ H LG+ G GYK G W+++ + ++ E PA P PV

Sbjct: 128 CPENDAADAHLDRNSMQFHAHLGFRLVGEFYKCGYKFGTWYNMVWMEKIIGEHPAVPAPV 187

>ref|YP_004267013.1| Phosphinothricin acetyltransferase [Syntrophobotulus glycolicus DSM

8271]

gb|ADY57012.1| Phosphinothricin acetyltransferase [Syntrophobotulus glycolicus DSM

8271]

Length = 190

Score = 109 bits (272), Expect = 2e-22, Method: Compositional matrix adjust.

Identities = 55/156 (35%), Positives = 83/156 (53%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR A+ D + I + Y+E + ++F T + E + ++ D++ WLVE EG +

Sbjct: 5 IRLASTKDAEQIRQIYSPYVENTVISFETAGPSAAEMEMRIRQVMDKHLWLVEQEGEIL 64

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA R+AY W V+ ++YV G+G +LY+ K ++ QGF + A+I LP
 Sbjct: 65 GYAYASSHHERSAYSWAVDVSIYVKADRVGRGIGKSLYSPFFKLLKLQFCNAYAIIALP 124

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N S LHE G+ G GYK G W DV +W+
 Sbjct: 125 NQASTALHEYFGFKPIGISSKVGKFGKWIDVQWWE 160

>ref|ZP_04126827.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
 serovar sotto str. T04001]
 gb|EEM41473.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
 serovar sotto str. T04001]
 Length = 170

Score = 108 bits (271), Expect = 2e-22, Method: Compositional matrix adjust.
 Identities = 59/169 (34%), Positives = 95/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + + YP + E++ V
 Sbjct: 2 IREATKRDLAYILDYNDAILYTTAVYAYKPVTLNENRIDWYEQKKAEGYPIFIYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY ++VE +VYV +++ G+GS L+K E + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKTYRKNIGSLFMKELIKIAEEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELNGPENPI 168

>emb|CAM74335.1| GCN5-related N-acetyltransferase [Magnetospirillum gryphiswaldense
 MSR-1]
 Length = 195

Score = 108 bits (271), Expect = 2e-22, Method: Compositional matrix adjust.
 Identities = 70/181 (38%), Positives = 94/181 (51%), Gaps = 11/181 (6%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTE-PQTPQEWIDDLERLQDRYPWLVAEVE 65
 PV +RPAT ADM V I +Y+ S +F E P + + + P+LVAE +
 Sbjct: 10 PVLVRPATPADMDQVQAIYAYVTRSAASFEEVEVPSVAEMRRRRDDVVDRLNLPYLVAEDD 69

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G YAGPW+ R+AY +TVE ++YV+ Q G+G L L+ G++ ++AV
 Sbjct: 70 GEVLGYTYAGPWRPRSAYRYTVEDSIYVAPFVQGRGIGKALLGALIDRCTELGYRRMIAV 129

Query: 126 IG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ-----DFELP----APPR 175
 IG N S+ LH +LG+ G LR G K G W DV R D LP APP
 Sbjct: 130 IGDSANQGSIGLHRSGLGRQEGVLRGVGLKFGRWVDVIMHRVLGDDDRPLPDGGSAPPL 189

Query: 176 P 176
 P
 Sbjct: 190 P 190

>ref|NP_832560.1| phosphinothricin N-acetyltransferase [Bacillus cereus ATCC 14579]
 ref|ZP_04257129.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-Cer4]
 gb|AAP09761.1| Phosphinothricin N-acetyltransferase [Bacillus cereus ATCC 14579]
 gb|EEL11278.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-Cer4]
 Length = 170

Score = 108 bits (271), Expect = 2e-22, Method: Compositional matrix adjust.

Identities = 60/169 (35%), Positives = 96/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + + YP V E++ V
 Sbjct: 2 IREATKRDLAFILDIYNDAILYTTAVYAYKPVTLNLRIDWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G A GP++A AY ++VE +VYV +++ G+GS L L+K + + + +++A I
 Sbjct: 62 VGFATFGPFRAPWAPYKYSVEHSVYVDKAYRKNIGSALMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFIHAGTIKKAGYKFNKWLDAFYQ--LELNGPENPI 168

>emb|CBK99483.1| Sortase and related acyltransferases [Faecalibacterium prausnitzii
 L2-6]
 Length = 186

Score = 108 bits (271), Expect = 2e-22, Method: Compositional matrix adjust.
 Identities = 57/161 (35%), Positives = 86/161 (53%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR AT AD + +I +Y+E + + F ++ + E+ + + +YP+LV E +G
 Sbjct: 4 ITIRNATLADAPRILEIYAYVEHTVITFESDVPSLAEFKGRMRDIMKKYPYLVIERDGR 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
 + G AYA + R AYDW E T+Y+ H +R GLG LY L ++A G ++ A IG
 Sbjct: 64 IEGYAYAHAFVGRAAYDWAAELTIYLDHDARRGGLGRVLYEALADRLKAMGVNLNLYARIG 123

Query: 128 LPN-----DPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 P S + HE LG+T GT GYK G W+D+
 Sbjct: 124 YPQVEDEYLTKNSAQFHEHLGFTFAGTFHNCGYKFGRWYDM 164

>ref|YP_003354349.1| GNAT family acetyltransferase [Lactococcus lactis subsp. lactis
 KF147]
 gb|ADA65524.1| Acetyltransferase, GNAT family [Lactococcus lactis subsp. lactis
 KF147]
 Length = 187

Score = 108 bits (271), Expect = 2e-22, Method: Compositional matrix adjust.
 Identities = 54/176 (30%), Positives = 91/176 (51%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +E R A +D + +I Y+E + + F E T E+ +E++ RYP++VA
 Sbjct: 1 MEFRLLAKKSDAKRLLEIYKPYVEKTAITFEYEVPTIAEFKRIEKIGSRYPYIVAIENDK 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
 + G AYAG ++ R AYDW VE ++Y+ ++ G GS LY LL ++ A ++ A I
 Sbjct: 61 IIGYAYAGAYRERVAYDWVVELSIYLDENERQHAGSALYQKLLTALSALNYQRAYACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQI 183
 PN SV H+ +G+ G AGYK W+ + + +R + ++ +T +
 Sbjct: 121 YPNPASVAFHKKIGFEQIGLFPKAGYKFEQWYGIVWLESLQTDDKVTAIKLLTDL 176

>ref|YP_004106813.1| phosphinothricin acetyltransferase [Rhodopseudomonas palustris
 DX-1]
 gb|ADU42080.1| Phosphinothricin acetyltransferase [Rhodopseudomonas palustris
 DX-1]
 Length = 176

Score = 108 bits (271), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 62/161 (38%), Positives = 86/161 (53%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
V IRPAT+AD+ AV I + T F P E L +P+LVA +G
Sbjct: 4 VLIRPATSADLPAVTAIYEQAVRFGTATFELTPDLAEMTRRFEALTGAGFPYLVASADG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+AG AYAGP++ R AY +TVE+++Y+ R G+GS L L+ ++GF+ ++AVI
Sbjct: 64 AIAGYAYAGPYRPRPAYRFTVENSIIYLDPAAHRRGIGSALLDDLVAICTSRGFRQMIAVI 123

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
G N S+ LH G+ GT G+K G W D QR
Sbjct: 124 GDSANAASIALHRKAGFVPIGTHTDVGFKFGRWLDSVLMQR 164

>ref|ZP_03232858.1| acetyltransferase, GNAT family [Bacillus cereus AH1134]
gb|EDZ50467.1| acetyltransferase, GNAT family [Bacillus cereus AH1134]
Length = 170

Score = 108 bits (271), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 59/170 (34%), Positives = 96/170 (56%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+A + DI N I +T + +P T + ID E+ + + YP V E++ V
Sbjct: 2 IREATKKDLAYILDYNDAILYTTAVYAYKPVTLNRI DWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++ AY ++VE +VYV +++ G+GS+L L+K + + + +++A I
Sbjct: 62 VGFATFGPFRTWPAYKYSVEHSVYVDKAYRKNGIGSSLMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQDRDFELPAPPRPVR 178
N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELNGPENPIE 169

>ref|ZP_02075451.1| hypothetical protein CLOL250_02227 [Clostridium sp. L2-50]
gb|EDO57041.1| hypothetical protein CLOL250_02227 [Clostridium sp. L2-50]
Length = 182

Score = 108 bits (271), Expect = 3e-22, Method: Compositional matrix adjust.
Identities = 54/161 (33%), Positives = 91/161 (56%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++I + AD + I Y+E + ++F E + E+ + +E++ +YP++ A V+G
Sbjct: 1 MKIEKVSTADAEELLAIYAPYVEETAISFEYEVPSVDEFNRNIEQISAKYPYIKAVVDGK 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+AG AYA +K R AYDW+VE+T+Y+ ++LGLG LY +L K ++ G ++ A I
Sbjct: 61 IAGYAYAAGFKDRKAYDWSVETIYIRKDCRQLGLGKALYENLEKLLKEMGILNMNACIA 120

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
P D S R H+ +G+T G +GYK W+D+
Sbjct: 121 SPAAESGHLTDDSYRFHKKMGFTLVGRFHNSGYKFCEWYDM 161

>ref|ZP_04146050.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar tochiensis BGSC 4Y1]
gb|EEM22249.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar tochiensis BGSC 4Y1]
Length = 170

Score = 108 bits (270), Expect = 3e-22, Method: Compositional matrix adjust.

Identities = 58/170 (34%), Positives = 94/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVEGVV 68
 IR AT D+ + DI N I +T + +P T + ID E+ D YP V E++ V
 Sbjct: 2 IREATEKDVICILDIYNDAILNTTAVYTYKPVTLLENRIDWYEEKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
 Sbjct: 62 VGFATFGPFRAPWAPYKYSIEHSVYVDKEYRKCIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELCGPKNPLE 169

>ref|YP_002028028.1| GCN5-related N-acetyltransferase [Stenotrophomonas maltophilia
 R551-3]
 gb|ACF51345.1| GCN5-related N-acetyltransferase [Stenotrophomonas maltophilia
 R551-3]
 Length = 176

Score = 108 bits (270), Expect = 3e-22, Method: Compositional matrix adjust.
 Identities = 65/171 (38%), Positives = 92/171 (53%), Gaps = 2/171 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 V IR A AD+ A+ I + + + E + + + DR +P+LVAE++G
 Sbjct: 3 VLIRDAGPADIDAITAIYAVEVTDFVNTYEDIPDTSEMLRRMRDIIDRGFPYLVAEIDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VAG AYA ++ R AY WTVE++VYV R Q G+G+ L L+ + A+G++ +VAVI
 Sbjct: 63 QVAGYAYANTYRTRIAYQWTVENSIVYDARFQGGQVGTGLLQALIDACVARGYRQMVAVI 122

Query: 127 GLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 G P N S++LHE G+ G R G KHG W D QR A P
 Sbjct: 123 GEPTNAASIKLHERFGFELVGVFRGLGRKHGRWLDTVQMQRALGDGADTAP 173

>ref|ZP_03011953.1| hypothetical protein BACCOP_03879 [Bacteroides coprocola DSM
 17136]
 gb|EDU99131.1| hypothetical protein BACCOP_03879 [Bacteroides coprocola DSM 17136]
 Length = 160

Score = 108 bits (270), Expect = 3e-22, Method: Compositional matrix adjust.
 Identities = 58/156 (37%), Positives = 77/156 (49%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR T D +A+ I N YI ST F EP + +E + + RYP+ V E +G +
 Sbjct: 2 IRAVTLQDTSAITAIYNEYIAHSTSTFDIEPVSEEMQKRRISEISARYPYFVYETDGEIV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G YA PWK R AY+ T+E+TVY+S H GLG L L +G ++A I
 Sbjct: 62 GYCYAHPWKEREAYNRTLETTVYLSAHTGKGLGRLLMQRLTDECRRRGIHVLIACITSE 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N S HEALG+ + G K G W V +Q
 Sbjct: 122 NTASCAFHEALGFRKASSFEEVGMKFGRWLGVTDYQ 157

>ref|YP_001971847.1| putative acetyltransferase [Stenotrophomonas maltophilia K279a]
 emb|CAQ45545.1| putative acetyltransferase [Stenotrophomonas maltophilia K279a]
 Length = 176

Score = 108 bits (270), Expect = 3e-22, Method: Compositional matrix adjust.

Identities = 65/171 (38%), Positives = 92/171 (53%), Gaps = 2/171 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 V IR A AD+AA+ I + + + E + + + DR +P+LVAE++G
 Sbjct: 3 VLIRDAGPADIAAITAIYAVEVTDVFNTEYEDIPDASEMLRRMRDIIDRGFPYLVAEIDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VAG AYA ++ R AY WTVE++VYV Q G+G+ L L+ + A+G++ +VAVI
 Sbjct: 63 QVAGYAYANTYRTRVAYQWTVENSVYVDAAFQGGKGVGTGLLQALIDACVARGYRQMVAVI 122

Query: 127 GLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 G P N S++LHE G+ G R G KHG W D QR A P
 Sbjct: 123 GEPTNTASIKLHERFGFELVGVFRLGRKHGRWLDTVQMQRALGDGADTAP 173

>ref|ZP_08127907.1| phosphinothricin N-acetyltransferase [Clostridium sp. D5]
 gb|EGB93900.1| phosphinothricin N-acetyltransferase [Clostridium sp. D5]
 Length = 190

Score = 108 bits (269), Expect = 4e-22, Method: Compositional matrix adjust.
 Identities = 58/181 (32%), Positives = 92/181 (50%), Gaps = 1/181 (0%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 E+ +R A D + DI Y++ + + F EP + +E+ + R ++YPWL A
 Sbjct: 2 EKEKFVVRMADIRDAQEMLDIYVPYVKETAITFEYEPSPVEEFSARIVRTLEKYPWLAAV 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
 G + G Y +K R AYDW+VE+TVY+ + G+G LY L + ++ Q ++
 Sbjct: 62 DNGRIVGYCYVSQFKEREAYDWSVETTVYIRPEDKGRGIGRLLYEKLEELKVQHILNLN 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQ 182
 A I P+ S+ HE +GY GYK G W+D+ + ++ E P P V PV +
 Sbjct: 122 ACIAYPHPEsIAFHEKMGYKTVAHFHKCGYKLGWYDMVWMEKMLGEHPDRPLSVIPVGE 181

Query: 183 I 183
 I
 Sbjct: 182 I 182

>gb|EFV98070.1| phosphinothricin acetyltransferase [Streptococcus agalactiae ATCC
 13813]
 Length = 163

Score = 108 bits (269), Expect = 4e-22, Method: Compositional matrix adjust.
 Identities = 52/157 (33%), Positives = 85/157 (54%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP +D + I Y+ +T+ F + + E+ + ++ + +P+LVAE G V
 Sbjct: 3 IRPVLPSDAKELLAIYAPYVTDTTITFEYDIPSISEFTNRIKNISKSFPYLVAEENGKV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 G AYA + AR AYDWT E ++Y+ + +GS LY L K + +QG+ +++A I LP
 Sbjct: 63 GYAYASTYYARAAYDWTCELSIYLDKDARSKKIGSQLYDTLEKELVSQGYVNLLACISLP 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 ND S+ H+ G+ G+K WHD+ + Q+
 Sbjct: 123 NDISIAFHKKRGFNQVAHFPKIGFKFEQWHDIVWLQK 159

>ref|YP_001591522.1| hypothetical protein SPAB_05416 [Salmonella enterica subsp.
 enterica serovar Paratyphi B str. SPB7]
 gb|ABX70689.1| hypothetical protein SPAB_05416 [Salmonella enterica subsp.
 enterica serovar Paratyphi B str. SPB7]

Length = 171

Score = 108 bits (269), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 54/163 (33%), Positives = 94/163 (57%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
++I A + A+CDI H++ T +F TEP E + L+++++ PW+VA E
Sbjct: 1 MKIVNAEEKHIPAICDIYAHHVHGTASFETEPDPDTHEMLARLKKIRNQALPWVVALEEE 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G Y ++ R AY T+E ++Y+ QR G G L H++ E G++ ++A++
Sbjct: 61 KVIGYCYLTRYRERYAYRHTLEDSIYIHPDSQRQGTGKALLRHVIAWAETHGYRQMIAIV 120

Query: 127 GLPNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
G N+ S+++H+ +G+T +GTL+ G+KHG W D QR+
Sbjct: 121 GDSNNEGSLKVHQVGVFTEKGTLDIGFKHGRWLDTVLLQRNL 163

>ref|ZP_04102502.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar berliner ATCC 10792]
ref|ZP_04133415.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar thuringiensis str. T01001]
ref|ZP_04139734.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
Bt407]
gb|EEM28565.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis Bt407]
gb|EEM34884.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar thuringiensis str. T01001]
gb|EEM65904.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar berliner ATCC 10792]
Length = 170

Score = 108 bits (269), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 59/169 (34%), Positives = 96/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+A + DI N I +T + +P + ID E+ + + YP V E++ V
Sbjct: 2 IREATKRDLAYILDYNDAILYTTAVYAYKPVNLENRIDWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++A AY ++VE +VYV +++ G+GS+L L+K + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKAYRKNGIGSSLMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRPV 177
N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDAFYQ--LELNGPENPI 168

>ref|YP_003399412.1| GCN5-related N-acetyltransferase [Acidaminococcus fermentans DSM
20731]
gb|ADB48097.1| GCN5-related N-acetyltransferase [Acidaminococcus fermentans DSM
20731]
Length = 191

Score = 108 bits (269), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 60/182 (32%), Positives = 95/182 (52%), Gaps = 8/182 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR AT D AA+ + Y+E++ + F + + +E+ + ++RYP+ VAE +G V
Sbjct: 6 IREATVEDAAAIRSVYAPYVESTVITFEYQVPSVEEFRRRIAHTRERYPYFVAEEDGRVL 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G AYAG + R AYDW+ E ++YV ++ GLG LY LL++++ G V A IG P
Sbjct: 66 GYAYAGSFVGRPAYDWSAELSIYVDRHLRKKGLGKKLYGALLEALKKMGILDVYACIGYP 125

Query: 130 NDP-----SVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVT 181
P S + H LG+ G + GYK W+ + + ++ E PVRP
Sbjct: 126 EQPDEYLDNFSAQGFHAHLGFEPVGIFKNCYKFNRYWHMIWMGKNLGEHGKNQPPVRPYP 185

Query: 182 QI 183
++
Sbjct: 186 EV 187

>ref|ZP_02213075.1| acetyltransferase, GNAT family [Bacillus anthracis str. A0488]
ref|ZP_02390648.1| acetyltransferase, GNAT family [Bacillus anthracis str. A0442]
ref|ZP_02876521.1| acetyltransferase, GNAT family [Bacillus anthracis str. A0465]
ref|YP_002814387.1| acetyltransferase, GNAT family [Bacillus anthracis str. CDC 684]
ref|ZP_05149233.1| acetyltransferase, GNAT family protein [Bacillus anthracis str.
CNEVA-9066]
ref|ZP_05200683.1| acetyltransferase, GNAT family protein [Bacillus anthracis str.
Kruger B]
ref|ZP_05204180.1| acetyltransferase, GNAT family protein [Bacillus anthracis str.
Vollum]
gb|EDR20658.1| acetyltransferase, GNAT family [Bacillus anthracis str. A0488]
gb|EDR95255.1| acetyltransferase, GNAT family [Bacillus anthracis str. A0442]
gb|EDT21396.1| acetyltransferase, GNAT family [Bacillus anthracis str. A0465]
gb|ACP16794.1| acetyltransferase, GNAT family [Bacillus anthracis str. CDC 684]
Length = 170

Score = 108 bits (269), Expect = 4e-22, Method: Compositional matrix adjust.
Identities = 58/170 (34%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID E+ +D YP V E++ V
Sbjct: 2 IREATEKDVIYILDYNDAILNTTAVYTYKPVTLNENRIDWYEQKDDGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRKCIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELCGPKNP 169

>ref|ZP_04301002.1| Phosphinothricin N-acetyltransferase [Bacillus cereus MM3]
gb|EEK67430.1| Phosphinothricin N-acetyltransferase [Bacillus cereus MM3]
Length = 182

Score = 108 bits (269), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 58/174 (33%), Positives = 98/174 (56%), Gaps = 3/174 (1%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVA 62
ER+ IR A D+ + DI N I +T + +P T + ID E+ + + YP LV
Sbjct: 8 ERKNAMIREARKQDVTYMLDIYNDAILNTTAVYTYKPVTLNENRIDWYEQKKANGYPILVC 67

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 122
E++ + G A GP++A AY +++E +VYV +++ G+G++L L+ + + + ++
Sbjct: 68 ELDNKIVGFATFGPFRAWPAYKYSIEHSVYVHKEYRKNIGTSLMKALITVAKEREYMTL 127

Query: 123 VAVIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
+A I N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 128 IAGIDAENEKSIALHENYGFVHAGTIKKAGYKFNRLDLAFYQ--LELNGPKKP 179

>ref|ZP_04262522.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-ST196]

gb|EEL05740.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-ST196]
Length = 170

Score = 108 bits (269), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 57/169 (33%), Positives = 95/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR A D+ + DI N I ST + +P T + ID E+ + D YP LV E++ V
Sbjct: 2 IREAMKEDVTFILDIYNDAIFNSTAVYAYKPVTLNRIWYEQKKADGYPILVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A GP++A +AY +++E ++YV +++ G+G +L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWSAYKYSIEHSIYVDKEYRKNIGKSLMKELIAIAQKREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQWQDFELPAPPRPV 177
N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNRLDLAFYQ--LELNGPGNPI 168

>ref|ZP_04223012.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock3-42]
gb|EEL45297.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock3-42]
Length = 170

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 58/170 (34%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATEKDVIYILDIYNDAILNTTAVYMYKPVTLNRIWYEQKKADGYPFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRKCIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQWQDFELPAPPRPVR 178
N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELCGPKNPLE 169

>emb|CBL02997.1| Sortase and related acyltransferases [Faecalibacterium prausnitzii
SL3/3]
Length = 184

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 54/161 (33%), Positives = 80/161 (49%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ +R A D + DI +Y+E + + F T ++ +E RYP+LV E +G
Sbjct: 3 ILVRDAKLEDAERILDIYAYVENTAITFEYVVPVPTLMDFQKRMEMTMKRYPYLVIEKDGA 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
+ G AYAG + R AYDW+ E TVY+ H Q+ GLG +Y L + G ++ A IG
Sbjct: 63 IQGYAYAGAFVGRAAYDWSCELTVYLDHTAQKCGLGKRIYEALENRLSEMILNLYACIG 122

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
P N S H LG++ G GYK G W+++
Sbjct: 123 YPRVEDEYLSNSAEFHAHLGFSKVGFEFYKCGYKFGRWYNM 163

>ref|ZP_04273770.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-ST24]
ref|YP_003665045.1| phosphinothricin N-acetyltransferase [Bacillus thuringiensis
BMB171]
gb|EEK94661.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-ST24]

gb|ADH07325.1| phosphinothricin N-acetyltransferase [Bacillus thuringiensis
BMB171]
Length = 170

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 58/169 (34%), Positives = 97/169 (57%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+A + DI N I +T + +P T + +D E+ + + YP V E++ V
Sbjct: 2 IREATKRDLAYILDIYNDAILYTTAVYAYKPVTLNVRVDWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++A AY ++VE +VYV +++ G+GS+L L++ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKAYRKNGIGSSLMKELIRIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDAFYQ--LELNGPENPI 168

>ref|ZP_04323719.1| Phosphinothricin N-acetyltransferase [Bacillus cereus m1293]
gb|EEK44614.1| Phosphinothricin N-acetyltransferase [Bacillus cereus m1293]
Length = 170

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 58/170 (34%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATEKDVIYILDIYNDAILNTTAVYTYKPVTLNVRIDWYEQKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRKCGIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELNGPKNPLE 169

>ref|ZP_04197844.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH603]
gb|EEL70485.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH603]
Length = 170

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 59/169 (34%), Positives = 96/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+A + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATKRDVAYILDIYNDAILYTTAVYAYKPVTLNVRIDWYEQKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++A AY +++E +VYV +++ G+GS+L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRKNGIGSSLMEELITFAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHQNYGFVHAGTIQKAGYKFNKWLDAFYQ--LELNGPENPI 168

>ref|YP_001645441.1| GCN5-related N-acetyltransferase [Bacillus weihenstephanensis
KBAB4]
gb|ABY43813.1| GCN5-related N-acetyltransferase [Bacillus weihenstephanensis

KBAB4]
Length = 170

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 60/170 (35%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR A D+ + DI N I ST + +P T + ID E+ + D YP LV E++ V
Sbjct: 2 IREAMKKDVTFILDIYNDAILNSTAVYAYKPVTLNLRIDWYEQKKADGYPILVYELDKNV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A GP++A AY ++VE +VYV +++ G+GS+L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKEYRKNVGSSLIEELITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFELPAPPRPVR 178
N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNRLDLAFYQ--LELNGPGNPIE 169

>ref|YP_003550782.1| GCN5-like N-acetyltransferase [Candidatus Puniceispirillum
marinum

IMCC1322]
gb|ADE38698.1| GCN5-related N-acetyltransferase [Candidatus Puniceispirillum
marinum IMCC1322]
Length = 182

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 62/163 (38%), Positives = 90/163 (55%), Gaps = 3/163 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQD-RYPWLVA-EVEGV 67
IR T D+ A I H++ET T +F T + ++ L++ YP LVA + +
Sbjct: 17 IRALTDDDDIVAATAIYAHVETGTGTSFETVAPSVKDMAARFAELRNAHYPTLVAVNADEL 76

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI- 126
V G AYAGP+K R AY TVE ++Y+ H +G+G L ++ QG+K ++AVI
Sbjct: 77 VMGFAYAGPYKPRAAYKHTVEDSIYIHPDHMGMGIGRALLISIIDQARLQGYKQMMAVIG 136

Query: 127 GLPNPDSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFE 169
G N S++LH +LG+T GT + G+K DV F QRD E
Sbjct: 137 GSDNHGSIKLHASLGFTLIGTAQNIGFKFNDMVDVVMQRDLE 179

>ref|YP_895314.1| phosphinothricin N-acetyltransferase acetyltransferase [Bacillus
thuringiensis str. Al Hakam]
ref|ZP_03099863.1| acetyltransferase, GNAT family [Bacillus cereus W]
ref|ZP_03109013.1| acetyltransferase, GNAT family [Bacillus cereus NVH0597-99]
ref|YP_002338807.1| acetyltransferase, GNAT family [Bacillus cereus AH187]
ref|YP_002451767.1| acetyltransferase, GNAT family [Bacillus cereus AH820]
ref|YP_002530364.1| phosphinothricin N-acetyltransferase [Bacillus cereus Q1]
ref|YP_002750161.1| acetyltransferase, GNAT family [Bacillus cereus 03BB102]
ref|ZP_04090908.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar pondicheriensis BGSC 4BA1]
ref|ZP_04108742.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar monterrey BGSC 4AJ1]
ref|ZP_04251572.1| Phosphinothricin N-acetyltransferase [Bacillus cereus 95/8201]
ref|ZP_04284481.1| Phosphinothricin N-acetyltransferase [Bacillus cereus ATCC 4342]
ref|ZP_04312215.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BGSC 6E1]
gb|ABK85807.1| phosphinothricin N-acetyltransferase, acetyltransferase, GNAT
family [Bacillus thuringiensis str. Al Hakam]
gb|EDX59154.1| acetyltransferase, GNAT family [Bacillus cereus W]
gb|EDX66107.1| acetyltransferase, GNAT family [Bacillus cereus NVH0597-99]
gb|ACJ78537.1| acetyltransferase, GNAT family [Bacillus cereus AH187]
gb|ACK90482.1| acetyltransferase, GNAT family [Bacillus cereus AH820]

gb|ACM13075.1| possible phosphinothricin N-acetyltransferase [Bacillus cereus Q1]
gb|ACO26316.1| acetyltransferase, GNAT family [Bacillus cereus 03BB102]
gb|EEK56130.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BGSC 6E1]
gb|EEK83797.1| Phosphinothricin N-acetyltransferase [Bacillus cereus ATCC 4342]
gb|EEL16833.1| Phosphinothricin N-acetyltransferase [Bacillus cereus 95/8201]
gb|EEM59584.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar monterrey BGSC 4AJ1]
gb|EEM77512.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar pondicheriensis BGSC 4BA1]
gb|ADY22036.1| acetyltransferase, GNAT family protein [Bacillus thuringiensis
serovar finitimus YBT-020]
Length = 170

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 58/170 (34%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATEKDVIYILDYNDAILNTTAVYTYKPVTLNLRIDWYEQKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRCKGIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQWQDFELPAPPRPVR 178
N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELCGPKNPLE 169

>ref|YP_001202590.1| phosphinothricin acetyltransferase (PPT N-acetyltransferase)
[Bradyrhizobium sp. ORS278]
emb|CAL74344.1| phosphinothricin acetyltransferase (PPT N-acetyltransferase)
[Bradyrhizobium sp. ORS278]
Length = 175

Score = 107 bits (268), Expect = 5e-22, Method: Compositional matrix adjust.
Identities = 59/160 (36%), Positives = 87/160 (54%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVAEVEG 66
++IRP T AD++A+ I + T F +P E L D +P+ A ++G
Sbjct: 4 IDIRPTTEADLSAITAIYQAVREGTATFELDPDPAEMTRRFRALTDGDFPYFAAVLDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
V G AYAGP++ R AY +TVE+++Y++ QR G+G L L+ + E +GF+ ++AVI
Sbjct: 64 QVVGAYAGPYRPRPAYRFTVENSIIYLAPASQRRGIGMRLMRQLIAACEEKGFQMIAMI 123

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVWQ 165
G N SV LH A G+ GT + G K G W D Q
Sbjct: 124 GDSANAGSVGLHTACGFQMIGTHPSVGLKFGRWLDVTMMQ 163

>ref|YP_421541.1| phosphinothricin N-acetyltransferase [Magnetospirillum magneticum
AMB-1]
dbj|BAE50982.1| Phosphinothricin N-acetyltransferase [Magnetospirillum magneticum
AMB-1]
Length = 197

Score = 107 bits (268), Expect = 6e-22, Method: Compositional matrix adjust.
Identities = 64/161 (39%), Positives = 88/161 (54%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
V+IR AT DMAAV I Y+ S +F E + +E + R P+LVA EG
Sbjct: 10 VQIRDATDDDMAAVQSIYAFYVSRSAASFEEVPSVEEMKARRAAITGRGLPFLVAVEEG 69

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G YAGP++ R+AY +TVE ++YV+ R G+G TL L+ A G++ ++AVI
 Sbjct: 70 EVLGYTYAGPFRQRSAYRYTVEDSIYVAPFVARRGIGRTLLAALIDRCTLALGYRQMIAMI 129

Query: 127 G-LPNDPSSLRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G N S+ +H A+G+ G LR G K G W DV R
 Sbjct: 130 GDSANQGSIGVHRAMGFGQEGVLRGVGLKFGRWVDVIMHR 170

>ref|YP_818802.1| sortase related acyltransferase [Leuconostoc mesenteroides subsp.
 mesenteroides ATCC 8293]
 gb|ABJ62429.1| Sortase related acyltransferase [Leuconostoc mesenteroides subsp.
 mesenteroides ATCC 8293]
 Length = 177

Score = 107 bits (268), Expect = 6e-22, Method: Compositional matrix adjust.
 Identities = 54/177 (30%), Positives = 90/177 (50%), Gaps = 2/177 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + +R AD + +I Y+E +T F T Q++ D + ++YP++V E +
 Sbjct: 2 MNVRTVKLADAPTLLNIYPYVERTTSTFEYNVPTIQDFEDRIANTLEKYPYIVIEEDNT 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA + +R AY WTVE +VYVS + G+G LY+ + ++ Q ++A I
 Sbjct: 62 ILGYAYAHEFNSRGAYKWTVEISVYVSQEARSRGIGKMLYSEIENILKKQNVVHIIACIT 121

Query: 128 LPNDPSSLRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA-PPRPVRPVTQI 183
 N+ S + HE +GY G + G+K G W D FW + P+ P+ P + +
 Sbjct: 122 EENETSKKFHERMGYENVGLFKKIGFKSGKWLD-NFWMQKTLCPSDQPKEFVPFSSL 177

>ref|ZP_04072392.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis IBL
 200]
 gb|EEM95919.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis IBL
 200]
 Length = 170

Score = 107 bits (267), Expect = 6e-22, Method: Compositional matrix adjust.
 Identities = 57/169 (33%), Positives = 96/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + +D E+ + + YP + E++ V
 Sbjct: 2 IREATKRDLAYILDYNDAILYTTAVYAYKPVTLNVRVDWYEQKKAEGYPIFIYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY ++VE +VYV +++ G+GS+ L+K + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKTYRKNGIGSSFMKELIKIAKEREYMTLIAGIDA 121

Query: 129 PNDPSSLRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPRPV 177
 N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELNGPENPI 168

>ref|ZP_02948867.1| phosphinothricin N-acetyltransferase [Clostridium butyricum 5521]
 ref|ZP_04525470.1| acetyltransferase, GNAT family [Clostridium butyricum E4 str.
 BoNT
 E BL5262]
 gb|EDT76236.1| phosphinothricin N-acetyltransferase [Clostridium butyricum 5521]
 gb|EEP55981.1| acetyltransferase, GNAT family [Clostridium butyricum E4 str. BoNT
 E BL5262]
 Length = 179

Score = 107 bits (267), Expect = 6e-22, Method: Compositional matrix adjust.
Identities = 54/178 (30%), Positives = 91/178 (51%), Gaps = 3/178 (1%)

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Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
          +++R A + D + +I Y+E + + F E T +E+ +++ +YP++V E + +
Sbjct: 1   MKLRVAKSEDAKQLVEIYKFYVEKTDITFEYEVPTVEEFAQRIKKTLLVKYPYIVLEKDDI 60

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
          + G AYA +K R AYDW+VE+++YV + G+G+ LY L + + Q +V A I
Sbjct: 61  ILGYAYASAFKERKAYDWSVETSIYVKDGERGGGIGTLLYNELERYLIKQNIINVNACIT 120

Query: 128  LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQWQDF--ELPAPPRPVRPVTQI 183
          PN S HE GY GYK G W D+ W F E P+ + +++
Sbjct: 121  HPNKKSELFHEKFGYKKVAHFTKCGYKFGVWKDM-IWMEKFIGEHKDKPKEIIEFSKL 177
```

>ref|ZP_01962684.1| hypothetical protein RUMOB_E00397 [Ruminococcus obeum ATCC 29174]
gb|EDM89274.1| hypothetical protein RUMOB_E00397 [Ruminococcus obeum ATCC 29174]
Length = 190

Score = 107 bits (267), Expect = 6e-22, Method: Compositional matrix adjust.
Identities = 54/174 (31%), Positives = 91/174 (52%), Gaps = 5/174 (2%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
          ++IR A D + DI ++Y++ + V F E + +E+ + + + YP+L+AE EG
Sbjct: 3   IKIRTAKVEDAEKLLDIYSYVVKTAFTFEYEVPSVEEFQERIRHISHPYLIIEEEGE 62

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
          + G +YA + R A+ W VE T+Y+ +R GLG +YT + + QG + V++I
Sbjct: 63  IIGYSYADRLRPRAAFWDVEMTIYKQDIRRNLGRHMYTLMEDILREQGVVNAVSLIT 122

Query: 128  LPNDP-----SVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQWQDFELPAPPRP 176
          P D SV+ HE +GY G L+ GYK W+ + + + +P P
Sbjct: 123  KPTDEYSDFNSVQFHEKMGYKHAGELKDCGYKFNRWYALLYMDKQIGIPQEEMP 176
```

>ref|ZP_00743946.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis serovar israelensis ATCC 35646]
ref|YP_002446242.1| acetyltransferase, GNAT family [Bacillus cereus G9842]
ref|ZP_04065539.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis IBL 4222]
gb|EA051781.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis serovar israelensis ATCC 35646]
gb|ACK94161.1| acetyltransferase, GNAT family [Bacillus cereus G9842]
gb|EEN02739.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis IBL 4222]
Length = 170

Score = 107 bits (267), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 58/169 (34%), Positives = 95/169 (56%), Gaps = 3/169 (1%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
          IR AT D+A + DI N I +T + +P T + ID E+ + + YP + E++ V
Sbjct: 2   IREATKRDLAYILDYNDAILYTTAVYAYKPVTLNLRIDWYEQKKAEGYPIFIYELDNKV 61

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
          G A GP++A AY ++VE +VYV +++ G+GS L+K + + + +++A I
Sbjct: 62  VGFATFGPFRAWPAYKYSVEHSVYVDKTYRKNGIGSLFMKELIKIAKEREYMTLIAGIDA 121

Query: 129  PNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQWQDFELPAPPRPV 177
          N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122  ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDAFYQ--LELNGPENPI 168
```

>ref|YP_001477588.1| GCN5-related N-acetyltransferase [Serratia proteamaculans 568]
gb|ABV40460.1| GCN5-related N-acetyltransferase [Serratia proteamaculans 568]
Length = 181

Score = 107 bits (267), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 60/165 (36%), Positives = 92/165 (55%), Gaps = 3/165 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVE 65
P+ + ATA DMAAV I H++ +F P T +E L ++Q+ PWLVA+
Sbjct: 6 PLMLTDATADDMAAVQQIYTHHVLYGAASFEETPPTLEEMQQRLSKVQEAGLPWLVAQA 65

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
+V G YA P++ R AY +TVE++VY++ Q G+G L + L+ E ++ ++A
Sbjct: 66 DLVVGICYATPYRPRPAYRFTVENSIVYIAEQQQGKIGKALLSALIARFELGPWRQMLAT 125

Query: 126 IG--LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
+G N S+ LH+ LG+++ GTL A G+K G W D QR
Sbjct: 126 VGNAKENQGSALHKKLGFSSVGTLSAVGFKLGEWRDTHIMQRTL 170

>ref|NP_267934.1| acyltransferase [Lactococcus lactis subsp. lactis Il1403]
gb|AAK05875.1|AE006407_11 acyltransferase [Lactococcus lactis subsp. lactis Il1403]
gb|ADZ64335.1| phosphinothricin acetyltransferase [Lactococcus lactis subsp.
lactis CV56]
Length = 187

Score = 107 bits (267), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 53/176 (30%), Positives = 89/176 (50%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E R A +D + +I Y+E + + F E T E+ +E++ RYP++VA
Sbjct: 1 MEFRLLAKKSDAKRLLEIYKPYVEKTAITFEYEVPTIAEFKRIEKIGSRYPYIVAIENDK 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYAG ++ R AYDW VE ++Y+ ++ G GS LY LL ++ ++ A I
Sbjct: 61 IIGYAYAGAYRERAAAYDWVVELSIYLDENERQHAGSALYQKLLTALSVLNYQRAYACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRVPRVPTQI 183
PN SV H+ G+ G AGYK W+ + + +R + ++ +T +
Sbjct: 121 YPNPASVAFHKKFGFEQIGLFPKAGYKFEQWYGIVWLESLQTTDKVTAIKLLTDL 176

>ref|YP_003211166.1| phosphinothricin N-acetyltransferase [Cronobacter turicensis
z3032]
emb|CBA32211.1| Phosphinothricin N-acetyltransferase [Cronobacter turicensis z3032]
Length = 181

Score = 107 bits (267), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 62/170 (36%), Positives = 91/170 (53%), Gaps = 8/170 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVAEVEGVV 68
IR T D+ A+C I ++E +F P T E + + Q PWLVAE++ +V
Sbjct: 11 IRDVTPEIDIEAICAIYGWHVEHGRASFEETPPTLDEMSARVNAVTTQDLPWLVAEIDIV 70

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI-- 126
G +YA PW+ R AY +T+E ++Y+ G+GS L L++ E ++ ++AVI
Sbjct: 71 VGYSYASPRPRPAYRYTLEESIYIDASMVGRGIGSRLLQALIERCEQGPWRQLMAVIGD 130

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ----DFELP 171
G N S RLH LG+ G+LR+ G+K GGW D QR D+ LP
Sbjct: 131 GENNRGSTRLLHRLLGFEVVGSLRSVGFKFGGWRDTLIMQPLNQGDWTLF 180

>ref|ZP_03913843.1| possible Phosphinothricin acetyltransferase [Leuconostoc
mesenteroides subsp. cremoris ATCC 19254]
gb|EEJ42698.1| possible Phosphinothricin acetyltransferase [Leuconostoc
mesenteroides subsp. cremoris ATCC 19254]
Length = 177

Score = 107 bits (267), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 54/177 (30%), Positives = 90/177 (50%), Gaps = 2/177 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ +R AD + +I Y+E +T F T Q++ D + ++YP++V E +
Sbjct: 2 MNVRTVKLADAPTLNIIKPYVERTTSTFEYNVPTIQDFEDRIANTLEKYPYIVIEEDNT 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
+ G AYA + +R AY WTVE +VYVS + G+G LY+ + ++ Q ++A I
Sbjct: 62 ILGYAYAHEFNSRGAYKWTVEISVYVSQEARSHGIGKMLYSEIENILKKQNVVHIIACIT 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA-PPRPVVRPVTQI 183
N+ S + HE +GY G + G+K G W D FW + P+ P+ P + +
Sbjct: 122 EENETSKKFHERMGYENVGLFKKIGFKSGKWLD-NFWMQKTLCPSPQKEFPVFPSSSL 177

>ref|NP_945552.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris
CGA009]
ref|YP_001989232.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris
TIE-1]
emb|CAE25643.1| putative phosphinothricin acetyltransferase [Rhodopseudomonas
palustris CGA009]
gb|ACE98756.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris TIE-1]
Length = 176

Score = 107 bits (267), Expect = 7e-22, Method: Compositional matrix adjust.
Identities = 59/159 (37%), Positives = 84/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IRPAT+AD+ A+ I + T F P E L + +P+L AE +G +
Sbjct: 6 IRPATSADLPAITAIYEQAVRFGTATFELTPPDLAEMTQRFATLTEAGFPYLAAEADGAI 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
AG AYAGP++ R AY +TVE+++Y+ R G+GS L L+ +GF+ ++AVIG
Sbjct: 66 AGYAYAGPYRPRPAYRFTVENSIIYLDPAAHRRGIGSALLRDLIAGCTERGFQMIAVIGD 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+ LH G+ GT G+K G W D QR
Sbjct: 126 SANAASIALHRKAGFAPIGTHADVGFKFGRWLDSVLMQR 164

>ref|ZP_07674254.1| toxin-antitoxin system, toxin component, GNAT family [Ralstonia
sp.
5_7_47FAA]
gb|EFP67370.1| toxin-antitoxin system, toxin component, GNAT family [Ralstonia sp.
5_7_47FAA]
Length = 178

Score = 107 bits (267), Expect = 8e-22, Method: Compositional matrix adjust.
Identities = 63/166 (37%), Positives = 87/166 (52%), Gaps = 3/166 (1%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA 62
E V IRPA AD+ + I H++ T T +F + E LQ+ P++VA
Sbjct: 11 ESGAVAIRPAIEADLPTIVGIYAHHVRTGTASFEIDAPDLAEMTRRFHALQEAGMPYVVA 70

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVM 122

E G + G AYAGP +AR AY TVE ++Y+ Q G+G+ L L++ +A+ FK +
 Sbjct: 71 EAGGALLGYAYAGPHRARPAYRHTVEDSIYLDATAAQGRGVGTLLEALIRECQARDFKQM 130

Query: 123 VAVI--GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 VAV+ G N S +LH G+ G L A GYK G W D QR

Sbjct: 131 VAVVGGGRENPGSAKLHARCGFREVGVLEAVGYKFGRWLDCLLMQR 176

>ref|YP_002235706.1| putative phosphinothricin N-acetyltransferase [Klebsiella
 pneumoniae 342]
 gb|ACI12185.1| putative phosphinothricin N-acetyltransferase [Klebsiella
 pneumoniae 342]
 Length = 178

Score = 107 bits (266), Expect = 8e-22, Method: Compositional matrix adjust.
 Identities = 60/160 (37%), Positives = 90/160 (56%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + I A + A+ +I H++ T +F TEP QE ++ L +Q R +PW VA

Sbjct: 1 MHIINAEQHQHITAIRNIYAAHVHLHGTGSFETEPDPTQEMLNRLRSIQSRGFPWYVALHGD 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G Y ++ R+AY +TVE+++Y+ +QR G+G L H LK E+QG++ ++AV+

Sbjct: 61 TVIGYCYISRYRERHAYRFTVENSIIYIDPTYQRQGVGKALLNHALKWAESQGYRQMIQAVV 120

Query: 127 G-LPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
 G N SV LH G+T GTL+ G+KHG W D Q

Sbjct: 121 GDSANVASVALHIRTGFTEIGTLKDIGFKHGRWLDTVLLQ 160

>ref|YP_003602596.1| putative phosphinothricin N-acetyltransferase [Enterobacter
 cloacae
 subsp. cloacae ATCC 13047]
 gb|ADF64788.1| putative phosphinothricin N-acetyltransferase [Enterobacter cloacae
 subsp. cloacae ATCC 13047]
 Length = 178

Score = 107 bits (266), Expect = 8e-22, Method: Compositional matrix adjust.
 Identities = 60/160 (37%), Positives = 90/160 (56%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + I A + A+ +I H++ T +F TEP QE ++ L +Q R +PW VA

Sbjct: 1 MHIINAEQHQHITAIRNIYAAHVHLHGTGSFETEPDPTQEMLNRLRSIQSRGFPWYVALHGD 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G Y ++ R+AY +TVE+++Y+ +QR G+G L H LK E+QG++ ++AV+

Sbjct: 61 TVIGYCYISRYRERHAYRFTVENSIIYIDPTYQRQGVGKALLNHALKWAESQGYRQMIQAVV 120

Query: 127 G-LPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
 G N SV LH G+T GTL+ G+KHG W D Q

Sbjct: 121 GDSANVASVALHIRTGFTEIGTLKDIGFKHGRWLDTVLLQ 160

>ref|ZP_04454120.1| hypothetical protein GCWU000342_00100 [Shuttleworthia satelles
 DSM
 14600]
 gb|EEP28759.1| hypothetical protein GCWU000342_00100 [Shuttleworthia satelles DSM
 14600]
 Length = 195

Score = 107 bits (266), Expect = 9e-22, Method: Compositional matrix adjust.
 Identities = 59/161 (36%), Positives = 84/161 (52%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +E+RPAT AD + +I Y+E + ++F TP ++ D + + DRYP+ VAE G
 Sbjct: 7 IELRPATPADAPRLLEIYRPYVEKTAISFELALPTPADFCDRIRAIMDRYPYVAAEEAGE 66

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA + R AYD +VE ++Y+ GLG LY L + + A G + A I
 Sbjct: 67 ILGYAYASAFIHREAYDHSVEMSIYLDQAACQGLGRALYERLERELAAMGVNTNANACIA 126

Query: 128 LP--NDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 P DP SV H+ LGY G GYK G W+D+
 Sbjct: 127 YPVGEDPYLTLNSVDFHKHLGYRMVGRFHKCGYKFRWYDM 167

>ref|ZP_05851266.1| phosphinothricin N-acetyltransferase [Granulicatella elegans ATCC 700633]
 gb|EEW93212.1| phosphinothricin N-acetyltransferase [Granulicatella elegans ATCC 700633]
 Length = 192

Score = 107 bits (266), Expect = 9e-22, Method: Compositional matrix adjust.
 Identities = 50/159 (31%), Positives = 87/159 (54%), Gaps = 7/159 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT D AA+ +I +Y+E + + F + + +E+ ++ ++YP+ V E EG V
 Sbjct: 3 IRVATIEDAAALVEIYRYVEETAITFEYDVPSIEEFERRIQTTLKYPYVIEEEGEVL 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AY+GP+ +R A+ W+ E ++Y+ QR G G LY + ++ G++++ A I P
 Sbjct: 63 GYAYSGPFASRKAFSWSAEISYILKQNNQQRKGYGKKLYQLMEAKLQELGYQNIYACIATP 122

Query: 130 N-----DPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 + SV+ HE +GY+ G + GYK W+ +
 Sbjct: 123 EVEDEYLTNNSVQYHEYMGYSLVGEFKRCGYKFDRWYHI 161

>ref|ZP_04079000.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1]
 gb|EEM89408.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis serovar pulsiensis BGSC 4CC1]
 Length = 170

Score = 107 bits (266), Expect = 9e-22, Method: Compositional matrix adjust.
 Identities = 57/170 (33%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 +R AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
 Sbjct: 2 VREATEKDVIYILDINDAILNTTAVYTYKPVTLNTRIDWYEQKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRCKGIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELNGPKNP 169

>ref|NP_521958.1| phosphinothricin acetyltransferase protein [Ralstonia solanacearum GMI1000]
 emb|CAD17548.1| probable phosphinothricin acetyltransferase protein [Ralstonia solanacearum GMI1000]
 Length = 183

Score = 107 bits (266), Expect = 9e-22, Method: Compositional matrix adjust.
 Identities = 62/164 (37%), Positives = 88/164 (53%), Gaps = 3/164 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 V +RPA AD+ A+ I H++ T T +F +P E + LQD P+LVA+
 Sbjct: 20 VVVRPARLADLPAIAAIYAHVVRTGTASFEIDPPDLAEMTRRFQTLQDTGMPYLVAQTGR 79

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AYAGP +AR AY TVE ++Y+ + G+G+ L L++ A+GF+ +VAV+
 Sbjct: 80 KLLGFAYAGPHRRARPAYRHTVEDSIYLDAAARGRGVGTLLLEALVRECVARGFRQIVAVV 139

Query: 127 --GLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 G N S+RLH G+ G L GYK W DV QR
 Sbjct: 140 GGGQENLGSMRLHARCGFREVGVLAGVGYKFDRLDVLVLMQRTL 183

>ref|YP_003792542.1| putative phosphinothricin N-acetyltransferase [Bacillus anthracis

CI]

gb|ADK05404.1| possible phosphinothricin N-acetyltransferase [Bacillus cereus biovar anthracis str. CI]
 Length = 170

Score = 107 bits (266), Expect = 9e-22, Method: Compositional matrix adjust.
 Identities = 57/170 (33%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 +R AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
 Sbjct: 2 VREATEKDVIIYILDYINDAILNTTAVYTYKPVTLNDRIDWYEQKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRKCGIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELCGPKNPLE 169

>ref|ZP_02234915.1| hypothetical protein DORFOR_01789 [Dorea formicigenerans ATCC 27755]

gb|EDR46566.1| hypothetical protein DORFOR_01789 [Dorea formicigenerans ATCC 27755]
 Length = 195

Score = 107 bits (266), Expect = 9e-22, Method: Compositional matrix adjust.
 Identities = 53/168 (31%), Positives = 89/168 (52%), Gaps = 7/168 (4%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 MS ++ + IR A D + +I Y+ + + F E +P+E+ + + ++YP+L
 Sbjct: 1 MSTLKKEIVIRVAALDAEELLEIYAPYVRETAITFEYEVPSPEEFRERIAHTLEKYPYL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 VAE +G + G AY P+K R AY W VE+++YV +R+G+G L++ L ++ G
 Sbjct: 61 VAEHDGKIVGYAYVSPFKERAAYAWAVETSIYVDQNCNRMGIGKKLHSALEHCLKEMGIL 120

Query: 121 SVVAVIGLPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 ++ A IG P + S + HE LGY G GYK W+++
 Sbjct: 121 NMEACIGYPEEDEYLTKNSAQFHEHLGYRMIGFEFEKCGYKFHRWYNM 168

>ref|YP_760389.1| acetyltransferase [Hyphomonas neptunium ATCC 15444]

gb|ABI76675.1| acetyltransferase, GNAT family [Hyphomonas neptunium ATCC 15444]

Length = 190

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 62/159 (38%), Positives = 87/159 (54%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR-TEPQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
IR A ADM AV I H++ TS F P P+ + L P+LVAE +G+V
Sbjct: 20 IRDADDADMEAVQAIYAHFVLTSPATFEEVPPSLPEMKMRRAGVLASSLPFLVAEADGLV 79

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G YA P+++R AY TVE ++YVS G+GS L L+ EA ++ ++AV+G
Sbjct: 80 VGFCYASPYRSRAAYRHTVEDSIYVSEAFGGRGVGSALLGQLIARCEAGPWRQMLAVMGT 139

Query: 129 P-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
N+ + LH +LG++ GTL+A G K G W D QR
Sbjct: 140 GRNEACIALHRSLSGFSNVGTLKAVGLKFGQWEDTVMMQR 178

>ref|YP_003101109.1| GCN5-related N-acetyltransferase [Actinosynnema mirum DSM 43827]
gb|ACU37263.1| GCN5-related N-acetyltransferase [Actinosynnema mirum DSM 43827]
Length = 168

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 59/160 (36%), Positives = 83/160 (51%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
V IRP D+AAV I HY+E F + ++W + R P+LVAE++G
Sbjct: 6 VTIRPCAGDDLAAVAIAHYVEHGVATFDEVAPSEEDWAGKRADIAARGLPFLVAELDG 65

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VV+G AYA PW+ + AY T E T+Y++ GLG L ++++ G + ++AVI
Sbjct: 66 VVSGFAYAAPWRWKRAYRHTAEDTIYLAPGATGHGLGKALLGSVVEAAREAGIRQLIAVI 125

Query: 127 GLPND-PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 165
D S LH G+ G LR G+KHG W D WQ
Sbjct: 126 ADSGDGSSAALHRRFGFHEAGVLRVGVGHKGRWIDTALWQ 165

>ref|YP_001633138.1| acetyltransferase [Bordetella petrii DSM 12804]
emb|CAP44871.1| acetyltransferase [Bordetella petrii]
Length = 183

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 64/167 (38%), Positives = 93/167 (55%), Gaps = 3/167 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWL 60
SP P+ +R + AAD+ A+ I H+++ T +F +P T E E L R P+L
Sbjct: 4 SPSAAPI-VRDSRAADIDAIQAIYGHVQHGTASFELDPPTVDEMRRARREAVLAQRLPYL 62

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
VAE++G + G AY P++ R AY TVE +VYV H G+G L L++ A G++
Sbjct: 63 VAELDGEIVGYAYCTPYRPRPAYRHTVEDSVYVKPGHAGHGIGGRLLAALIERCTAGGWR 122

Query: 121 SVVAVIGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
++AV+G N S+ LH + G+ GTLR+ GYK G W D QR
Sbjct: 123 QMLAVVGDSRNAASLALHASQGFHPAGTLRSVGKFGAWRDTVLMQR 169

>ref|ZP_04579325.1| conserved hypothetical protein [Oxalobacter formigenes OXCC13]
gb|EE030298.1| conserved hypothetical protein [Oxalobacter formigenes OXCC13]
Length = 188

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.

Identities = 62/175 (35%), Positives = 90/175 (51%), Gaps = 2/175 (1%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR A  D A+ +I  YIET + F E T E+ + + YP LV E EG V
Sbjct: 2   IRFARPDSDVAILEIYGAYIETP-ITFECELPTSEFSKRMADISAFYPCLVCEEEGKVI 60

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
          G AYA      R AY W E +VY+      GLG LY  L++ ++ QG ++V  + +P
Sbjct: 61  GFAYAHRHMERQAYQWNAELSVYLDPSFTSKGLGKKLYAILIEMKLQGVRTVYGGVTVP 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE-LPAPPRPVRPVTQI 183
          N+ S  LH+A+G++ GT  AG+K G W DV +++++ + P PV  + I
Sbjct: 121 NEKSESLHKAMGFSVAGTYHHAGFKDGKWRDVTWFKAIAIPYDSYPEPVVSIGSI 175
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>ref|ZP_01168931.1| probable phosphinothricin acetyltransferase (antibiotic
resistance)
      protein [Bacillus sp. NRRL B-14911]
gb|EAR68000.1| probable phosphinothricin acetyltransferase (antibiotic resistance)
      protein [Bacillus sp. NRRL B-14911]
      Length = 163
```

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 56/159 (35%), Positives = 84/159 (52%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR A  D+ + DI N I T T F E Q+ +      E+  RYP  VAE +G +A
Sbjct: 3   IREAVKEDLPDILDIYNEAIRTLTATFDLEEQSLEHRTAWFEKYGGRYPLTVAEEDGQIA 62

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
          G  GP++ + AY+ T E +VY+S R+  G+G L  +L  + + +++++ +
Sbjct: 63  GYCSIGPFRDKQAYEKTAELSVYISSRFRGKGIGKGLVEDMLSRAASLDYHTIISGLTAG 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          N+ SVRLHE LG+  G  +  G+K G W DV F+Q  F
Sbjct: 123 NEASVRLHERLGFHYIGIFKEVGFKFGEWQDVLFYQYFF 161
```

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>ref|NP_688817.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae
2603V/R]
ref|NP_736302.1| hypothetical protein gbs1868 [Streptococcus agalactiae NEM316]
ref|ZP_00780138.1| acyltransferase [Streptococcus agalactiae 18RS21]
ref|ZP_00790430.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae
515]
emb|CAD47527.1| Unknown [Streptococcus agalactiae NEM316]
gb|EAO63273.1| acyltransferase [Streptococcus agalactiae 18RS21]
gb|EAO70837.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae 515]
      Length = 163
```

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 51/157 (32%), Positives = 84/157 (53%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IRP  +D  + I  Y+ +T+ F  + +  E+ + ++ +  +P+LVAE  G +
Sbjct: 3   IRPVLPSDAKELLAIYAPYVADTTITFEYDIPSISEFTNRIKNISKSFPYLVAEENGKIL 62

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
          G AYA + AR AYDWT E ++Y+  +  +GS LY  L K +  QG+ +++A I LP
Sbjct: 63  GYAYASTYYARAAYDWTCELSIYLDKDARSKKIGSGLYDTLEKELVNQGYVNLLACISLP 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
          ND S+  H+  G+      G+K  WHD+ + Q+
Sbjct: 123 NDISIAFHKKRGFNQVAHFPGKGFGEQWHDIVWLQK 159
```

>ref|YP_003163209.1| GCN5-related N-acetyltransferase [Leptotrichia buccalis C-1013-b]
 gb|ACV38218.1| GCN5-related N-acetyltransferase [Leptotrichia buccalis C-1013-b]
 Length = 197

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
 Identities = 52/184 (28%), Positives = 96/184 (52%), Gaps = 1/184 (0%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 M + + R AT D + +I Y+E +T+ F E + +E+ + + ++ + YP++
 Sbjct: 1 MKLKNEIDLIFRFATENDAKEILEIYRPYVENTTITFEYEVPSVKEFKERIMKILEEYPYI 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
 V E + + G AYA +R AY W E ++Y + + G+G LY L++ ++ Q
 Sbjct: 61 VCEYDKKIIGYAYAHVWSRAAYQWDAELSIYTNNYSNGNIGKKLYKMLMEILKLQNVV 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQD-FELPAPPRPVRP 179
 +V + PN+ S +LHE LG+ G + AGYK G W V ++++ E P+P++
 Sbjct: 121 NVYGCVTYPNENSDKLHEYLGFNKVGIFKNAGYKFGKWIGVTWFKAILEHCENPKPLKK 180

Query: 180 VTQI 183
 + +
 Sbjct: 181 ILDV 184

>ref|ZP_08010212.1| phosphinothricin N-acetyltransferase [Coprobacillus sp. 29_1]
 gb|EFW05667.1| phosphinothricin N-acetyltransferase [Coprobacillus sp. 29_1]
 Length = 187

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
 Identities = 53/154 (34%), Positives = 79/154 (51%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR AT+ D ++ I +Y++ + + F + +E + +YP+LVA G
 Sbjct: 1 MKIRIATSKDAKSIQKIYAYVQNTNITFEYDAPNFEEIERINNTLHQYPYLVAIENG 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G AYA + AR A+DW E ++Y+ R G G+ LY LL ++ K+V A I
 Sbjct: 61 VIGYAYASRYSAKAFDWDCELSIYIKDGLSRKGCGRTRYKTLLSLLKKMNKVNKYACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 PN S R HE G+ G + GYK WHDV
 Sbjct: 121 HPNANSERFHEVFGFQVVGIFQNCGYKFKKWHDV 154

>ref|YP_004259793.1| Phosphinothricin acetyltransferase [Bacteroides salanitronis DSM
 18170]
 gb|ADY37320.1| Phosphinothricin acetyltransferase [Bacteroides salanitronis DSM
 18170]
 Length = 160

Score = 106 bits (265), Expect = 1e-21, Method: Compositional matrix adjust.
 Identities = 55/149 (36%), Positives = 76/149 (51%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR D A+ DI NHYI ST F P +E + L +P+ V E EG +A
 Sbjct: 2 IRKVELQDAHALADIYNHYIAHSTATFDIRPIGEEEMRKRIATLSACHPYFVCEEEGKIA 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G YA PWK ++AY T+E+TVY++ +R G+G+ L L+ S++A I
 Sbjct: 62 GYCYAHPWKEKDAYSRITLTTVYLAPGQERKGIGTQLMRQLIDECCRSEVHSLIACITED 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGW 158
 N S HE LG+T + AG+K G W
 Sbjct: 122 NQASCLFHERLGFQVSHFKEAGFKFGKW 150

>ref|ZP_03210120.1| hypothetical protein BACPLE_03811 [Bacteroides plebeius DSM 17135]
 gb|EDY94357.1| hypothetical protein BACPLE_03811 [Bacteroides plebeius DSM 17135]
 Length = 160

Score = 106 bits (264), Expect = 1e-21, Method: Compositional matrix adjust.
 Identities = 54/161 (33%), Positives = 83/161 (51%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR D A+ I NHYI +T+ F EP + +E ++ + ++YP+ V E EG +A
 Sbjct: 2 IRKVRKEDTPAITAIYNHYIAHTTITFELEPVSEEMWTRIQAISEKYPYFVYETEGQIA 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G Y WK + AY+ + E+T+Y++ H G+G L HL++ G +++A I
 Sbjct: 62 GYCYVHGWEKAAYNQSAETTIYLLAPSHTGKGIGKELMLHLIEECRRYGLHALIACITEG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170
 N+ S LHE LG+ R G K G W + D+EL
 Sbjct: 122 NEASYALHEKLGFEKVSFYFREVGRKFGKWLG I---VDYEL 158

>ref|ZP_02868381.1| hypothetical protein CLOSPI_02223 [Clostridium spiroforme DSM 1552]
 gb|EDS73798.1| hypothetical protein CLOSPI_02223 [Clostridium spiroforme DSM 1552]
 Length = 195

Score = 106 bits (264), Expect = 1e-21, Method: Compositional matrix adjust.
 Identities = 50/154 (32%), Positives = 82/154 (53%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++I PA D + DI YI + + F T +E+ +E +YP+LVA+ + +
 Sbjct: 15 IKIEPAKKEDARRLLDIYTPYILNTAITFEYTIPTVEEFQRIENTLIKYPYLVAKKDDL 74

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
 + G AY +K R AYDW VE+++Y+ ++ LG+G LY L K + Q ++ A I
 Sbjct: 75 IVGYAYTSAFKNRAAYDWAUVETSIIYIDMNYRGLGIGKLLYDELEKITKLQNILNMNACIA 134

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 +P++ SV H+ +GY GYK W+D+
 Sbjct: 135 IPDEGSVIFHKKMGYLEVAYFHCQGYKFDKWDYDM 168

>ref|ZP_04947527.1| hypothetical protein BDAG_03502 [Burkholderia dolosa AU0158]
 gb|EAY70698.1| hypothetical protein BDAG_03502 [Burkholderia dolosa AU0158]
 Length = 191

Score = 106 bits (264), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 66/179 (36%), Positives = 93/179 (51%), Gaps = 7/179 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFR-TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 V +R AT AD+AA+ I H++ S +F T P + L+ P+LVAE +G
 Sbjct: 9 VLVRRDATDADLAAIHAIYAHHRHSVASFEETPPDVAELGARRDAVLRHGLPYLVAECDG 68

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 VAG AYA P++ R+AY TVE ++Y+ + G+G L L++ EA ++ ++AVI
 Sbjct: 69 RVAGYAYATPYRTRSAYRHTVEDSIYIDDTQRGRGIGRALLAALIERCEAGPWRQMIAMI 128

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-----ELPAPPRPVRP 179
 S LH A G+ G L+A G+KHG W D QR LPAPP P

Sbjct: 129 ADGGTGGSTSLHRAFGFEPAGVVKAVGFKHGRWIDTALMQRPLGDGARSLPAPPASSAP 187

>ref|ZP_03297278.1| hypothetical protein COLSTE_01172 [Collinsella stercoris DSM 13279]
gb|EEA90598.1| hypothetical protein COLSTE_01172 [Collinsella stercoris DSM 13279]
Length = 203

Score = 106 bits (264), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 63/185 (34%), Positives = 98/185 (52%), Gaps = 9/185 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V IRPAT AD A+ I Y+ + + F EP T + + + YP++VAE++G+
Sbjct: 12 VTIRPATEADAPALAAIYAPYVRDTAITFEYEPPTAEGFAARMRSTLAFYPYVVAELDGL 71

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
G AYA +K R AYDW VE+++YV+ + G+G L+ L ++ AQG ++ A I
Sbjct: 72 PVGYAYASVFKGRPAYDWAVETSIYVARGYAGRGIGRALHDALEHALTAQGVLNMYACIA 131

Query: 128 LPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVR 178
+P+ S + HE LGY G GYK G W+++ + ++ E A PV+
Sbjct: 132 VPHGEDDETILTRNSQQFHEHLGYRLVGEFELCGYKGGRWYNMVWMEKMIGEHRADQPPVK 191

Query: 179 PVTQI 183
P +I
Sbjct: 192 PFLEI 196

>ref|YP_483910.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris HaA2]
gb|ABD04999.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris HaA2]
Length = 205

Score = 106 bits (264), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 64/159 (40%), Positives = 85/159 (53%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IRPA AAD+ A+ I + T T F P E E L +P+LVA + V
Sbjct: 28 IRPAAAADLPAITAIYADAVRTGTATFELTPPDLAEMTRRFETLAGGGFPYLVALLGDRV 87

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
AG AYAGP++ R AY +TVE++VY+ R GLG+ L L+ EA+GF+ ++AVIG
Sbjct: 88 AGYAYAGPYRPRPAYRFTVENSIVLDPLAHRRLGTALLHELIAQCEARGFRQMIAVIGD 147

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N SV +H G+ G R G+K G W D QR
Sbjct: 148 STNAGSVAVHRKSGFDLIGVHRNVGFKFGRWLDTVMMQR 186

>ref|ZP_04289658.1| Phosphinothricin N-acetyltransferase [Bacillus cereus R309803]
gb|EEK78769.1| Phosphinothricin N-acetyltransferase [Bacillus cereus R309803]
Length = 170

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.
Identities = 57/170 (33%), Positives = 96/170 (56%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+A + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATIKDLAFILDIYNDAILYTTAVYAYKPVTLNRIWDYEQKKADGYPFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A GP++A AY +++E +VYV +++ G+G++L L++ + + + +++A I
Sbjct: 62 VGFATFGPFRAPWPAKYKSYIEHSVYVDKEYRKNGIGTSLMKTLEIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 178
 N+ S+ LH+ G+ G ++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFVPAGI IKKAGYKFDKWLDLAFYQ--LELNGPVNPIE 169

>ref|ZP_04192159.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH676]
 gb|EEL76168.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH676]
 Length = 170

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 57/169 (33%), Positives = 97/169 (57%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + + YP V E++ V
 Sbjct: 2 IREATKRDLAYILDYNDAILYTTAVYAYKPVTLNENRIDWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 G A GP++A AY +++E +VYV +++ G+G++L L++ + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKDYRKNIGTSLMKTLEIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFHAGTIKKAGYKFNKWLDLAFYQ--LELNGPENPI 168

>ref|YP_775946.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria AMMD]
 gb|ABI89612.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria AMMD]
 Length = 207

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 64/179 (35%), Positives = 96/179 (53%), Gaps = 15/179 (8%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT +D+AA+ I H++ S +F +TP + +D+L +D P+LVAE
 Sbjct: 30 VRDATESDLAAIHAIYAHHRHSVASFE---ETPPD-VDELRRRDAVLRHGLPYLVAEC 85

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +G +AG AYA P++ R+AY T+E ++Y+ + G+G L L+ E ++ ++A
 Sbjct: 86 DGRIAGYAYATPYRTRSAYRHTIEDSIYIDDAQRGRGIGRALLAALIARCETGPWRQMIA 145

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-----ELPAPPRPV 177
 VI S LH A G+ A G L+A G+KHG W D QR LPA P PV
 Sbjct: 146 VIADGGTGGSTSLHRAFGEAAGVLKAVGFKHGRWIDTALMQRALGDGARTLPASPEPV 204

>ref|ZP_04228286.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock3-29]
 ref|ZP_04245710.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock1-3]
 gb|EEL22604.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock1-3]
 gb|EEL40051.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock3-29]
 Length = 170

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 58/169 (34%), Positives = 96/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + D YP V E++ V
 Sbjct: 2 IREATKRDVAYILDYNDAILYTTAVYAYKPVTLNENRIDWYEQKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 G A G ++A AY +++E +VYV +++ G+GS+L L+ + + + + +++A I
 Sbjct: 62 VGFATFGSFRAWPAYKYSIEHSVYVDKEYRKNIGSSLMKLIATAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177

N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHQNYGFVHAGTIQKAGYKFNRWLDLAFYQ--LELNGPENPI 168

>ref|ZP_03682824.1| hypothetical protein CATMIT_01460 [Catenibacterium mitsuokai DSM 15897]
 gb|EEF93932.1| hypothetical protein CATMIT_01460 [Catenibacterium mitsuokai DSM 15897]
 Length = 177

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 54/167 (32%), Positives = 81/167 (48%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR AT D ++ I Y+ +T+ F EP T +E D + ++YP+LVA EG
 Sbjct: 3 ITIRIATVEDAESIQKIYAPYVLNTTITFELEPPTVKEMADRIRHTLEKYPYLVAVEEGE 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 V G AYAG R AYD + E ++Y+ R + G+G LY L+ + ++ I
 Sbjct: 63 VIGYAYAGTLYDRRAYDHSaelSIYIDDRKRHKGIGHLLYNALIDYLIRMNITNLYGCIT 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPP 174
 PND S+ HE G+ GYK W DV + ++ + P
 Sbjct: 123 YPNDASIAFHEKYGFKEAAHFHECGYKFDQWLDVVYLEKRLDKTTEP 169

>ref|ZP_04889981.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei 1655]
 gb|EDU10965.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei 1655]
 Length = 247

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 61/163 (37%), Positives = 91/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAHHVLGTGVASFEETPPS----VDDLARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +GVVAG AYA P+++R+AY + +E ++YVS + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRSRSAYRYAIEDSIYVSEACRGRGIGRVLLAALIAECEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|ZP_04317895.1| Phosphinothricin N-acetyltransferase [Bacillus cereus ATCC 10876]
 gb|EEK50400.1| Phosphinothricin N-acetyltransferase [Bacillus cereus ATCC 10876]
 Length = 170

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 58/170 (34%), Positives = 95/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR AT D+A + DI N I +T + +P T + ID E+ + + YP V E++ V
 Sbjct: 2 IREATKKDLAYILDYNDAILYTTAVYAYKPVTLLENKIDWYEQKKAEGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 G A G ++ AY ++VE +VYV +++ G+GS+L L+K + + + +++A I
 Sbjct: 62 VGFATFGLFRTWPAYKYSVEHSVYVDKAYRKNGIGSSLMKELIKAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178

N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+

Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELNGPENPIE 169

>ref|YP_003634998.1| GCN5-related N-acetyltransferase [Brachyspira murdochii DSM 12563]

gb|ADG72799.1| GCN5-related N-acetyltransferase [Brachyspira murdochii DSM 12563]

Length = 190

Score = 105 bits (263), Expect = 2e-21, Method: Compositional matrix adjust.

Identities = 49/161 (30%), Positives = 90/161 (55%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-G 66

++IR A D + I + YI+ + F + T +E+ +E + +YP+L+ E E G

Sbjct: 1 MKIRLANVEDTLPIILKIYSQYIDMP-ITFEYKLPTEEEFKRIENITKKYPYLLCEDESG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126

+ G AYA + R AY+W E +VY+ + G+G L ++ ++ QG +++ + +

Sbjct: 60 KIIGYAYANKFMEREAYNWNTLSVYIDNSSTSKGIGKKLCYIIIDILKYQGIRNIYSKV 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRD 167

LPN+ S +LH +LG+ GT GYK+ W++VG +++++

Sbjct: 120 TLPNEKSEKLGHNLIHTYHNHVGYNKNNWYNVGLFEKE 160

>ref|NP_979141.1| acetyltransferase [Bacillus cereus ATCC 10987]

gb|AAS41749.1| acetyltransferase, GNAT family [Bacillus cereus ATCC 10987]

Length = 170

Score = 105 bits (262), Expect = 2e-21, Method: Compositional matrix adjust.

Identities = 57/169 (33%), Positives = 94/169 (55%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68

IR AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V

Sbjct: 2 IRDATEKDVTYILDYINDAILNTTAVYAYKPVTFKNRIDWYEQKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128

G A GP++A AY +++E ++YV+ ++ G+G++L L+ + + +++A I

Sbjct: 62 VGFATFGPFRAPWYKYSIEHSIYVNKEYRNRGIGTSLMKELIAIAREREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177

N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+

Sbjct: 122 ENERSIALHENYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELNGPKNPL 168

>ref|YP_330444.1| phosphinothricin N-acetyltransferase, putative [Streptococcus agalactiae A909]

ref|ZP_00782738.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae H36B]

ref|ZP_00787883.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae CJB111]

gb|ABA45966.1| phosphinothricin N-acetyltransferase, putative [Streptococcus agalactiae A909]

gb|EA073362.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae CJB111]

gb|EA078504.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae H36B]

Length = 163

Score = 105 bits (262), Expect = 2e-21, Method: Compositional matrix adjust.

Identities = 50/157 (31%), Positives = 84/157 (53%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP +D + I Y+ +T+ F + + E+ + ++ + +P+LVAE G +
 Sbjct: 3 IRPVLPSDAKELLAIYAPYVTDTTITFEYDIPSISEFTNRIKNISKSFPYLVAAEENGKIL 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + AR AYDWT E ++Y+ + + S LY L K + +QG+ +++A I LP
 Sbjct: 63 GYAYASTYYARAAYDWTCELSIYLDKDKARSKKISSQLYDTLEKELVSQGYVNLLACISLP 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 ND S+ H+ G+ G+K WHD+ + Q+
 Sbjct: 123 NDISIAFHKKRGFNQVAHFPGKIGKFEQWHDIVWLQK 159

>ref|ZP_03777241.1| hypothetical protein CLOHYLEM_04290 [Clostridium hylemonae DSM 15053]
 gb|EEG75554.1| hypothetical protein CLOHYLEM_04290 [Clostridium hylemonae DSM 15053]
 Length = 193

Score = 105 bits (262), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 60/177 (33%), Positives = 97/177 (54%), Gaps = 1/177 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR A D AA+ + +Y+E + V F + + +E+ + ++++YP+L+AE +G
 Sbjct: 1 MKIRMAEEKDAAALLAVYAYVEQTAVTFEYKVPSTEEFTRMRMSVKEKYPYLMAEEDGE 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G AY +K R AYDW VE+TVYV + + G+G LY L + ++ Q ++ A I
 Sbjct: 61 VCGYAYVSAFKDRAAYDWAVETTYYVDRQKRSFGVGRRLYETLEEILKLQNIINLNACIA 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF-ELPAPPRPVRPVTQI 183
 PN S+ HE +GY G GYK G W+D+ + ++ P P PV +I
 Sbjct: 121 WPNPDSISFHERMGYKTAGHFTKCGYKQGRWYDMVWMEKMLGGHPLKPEPVVRADEI 177

>ref|ZP_03715013.1| hypothetical protein EUBHAL_00046 [Eubacterium hallii DSM 3353]
 gb|EEG38047.1| hypothetical protein EUBHAL_00046 [Eubacterium hallii DSM 3353]
 Length = 178

Score = 105 bits (262), Expect = 2e-21, Method: Compositional matrix adjust.
 Identities = 55/159 (34%), Positives = 86/159 (54%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR AT D A+ +I +Y++ + + F E + +E+ + + + +RYP+LVAE EG
 Sbjct: 1 MNIRIATPEDAFAIQNIYRYVDNTAITFELEVPSVKEFQERITKTLERYPYLVAAEEGE 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V AYAG + R AYDW+ E +VYV G+G+ LY + + ++ Q ++ A I
 Sbjct: 61 VIAYAYAGIFYDRRAYDWSAEMSVYVQRGHKGKGVGTALYEKMEELLKKQNIIVNLFACIT 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 PN S H A GY + GYK G W D+ + Q+
 Sbjct: 121 HPNAESEAFHAARGYEKKAHFEQCGYKLGKWWDIVWMQK 159

>ref|ZP_01438277.1| putative phosphinothricin N-acetyltransferase (antibiotic resistance) protein [Fulvimarina pelagi HTCC2506]
 gb|EAU43274.1| putative phosphinothricin N-acetyltransferase (antibiotic resistance) protein [Fulvimarina pelagi HTCC2506]
 Length = 187

Score = 105 bits (262), Expect = 3e-21, Method: Compositional matrix adjust.
 Identities = 60/162 (37%), Positives = 87/162 (53%), Gaps = 3/162 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV-EGV 67
 IR AT AD+ A+ I + T + P E + L D YP+ VA+ +G
 Sbjct: 7 IRAATEADIPAITAIYQDEVNLGTATYELVPPEAAEMQRRFQTLNDNDYPYTVAQTPDGA 66

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI- 126
 + G AYAGP++ R AY+W VE T+Y++ + GLG+ L L+ EA GF+ ++AVI
 Sbjct: 67 LLGYAYAGPYRPRPAYNWMVEDTIYLAREARGQGLGTLTLLADLIARSEALGFRQMIAVIG 126

Query: 127 GLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 G N+ S+R+H G+ GT++A G K G W D QR
 Sbjct: 127 GADNNGSIRVHARQGFEMIGTMKATGLKFGRWIDTVLMQFSL 168

>ref|YP_001583998.1| GCN5-related N-acetyltransferase [Burkholderia multivorans ATCC 17616]
 ref|YP_001948868.1| acetyltransferase [Burkholderia multivorans ATCC 17616]
 gb|ABX17706.1| GCN5-related N-acetyltransferase [Burkholderia multivorans ATCC 17616]
 dbj|BAG46332.1| acetyltransferase [Burkholderia multivorans ATCC 17616]
 Length = 186

Score = 105 bits (262), Expect = 3e-21, Method: Compositional matrix adjust.
 Identities = 63/172 (36%), Positives = 91/172 (52%), Gaps = 2/172 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
 +R AT AD+AA+ I H++ S +F P E + L+ P+LVAE +G V
 Sbjct: 9 VRDATDADLAAIQAIYAHHRHSVASFEVEFPDVAELAARRDAVLRHGLPYLVAECDGRV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
 AG AYA P++ R+AY +TVE ++Y+ + G+G L L+ EA ++ ++AVI
 Sbjct: 69 AGYAYATPYRPRHAYRYTVEDSIYIDDAQGRGIGRALLAALIARCEAGPWRQMIAVIAD 128

Query: 128 LPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
 S LH A G+ GTL+A G+KHG W D+ QR A P P
 Sbjct: 129 GGTGGSTSLHRAFGFAPAGTLQAVGFKHGRWIDIALLRPLGEGAATLPASP 180

>ref|ZP_02084880.1| hypothetical protein CLOBOL_02410 [Clostridium bolteae ATCC BAA-613]
 gb|EDP17338.1| hypothetical protein CLOBOL_02410 [Clostridium bolteae ATCC BAA-613]
 Length = 182

Score = 105 bits (262), Expect = 3e-21, Method: Compositional matrix adjust.
 Identities = 67/169 (39%), Positives = 87/169 (51%), Gaps = 1/169 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V IR A AD AA+ I Y+E + + F E T QE+ + + RYP+L A +G
 Sbjct: 6 VTIRMAEEADAAALLSIYAPYVEKTAITFEYEVPTVQEFKNRITSTLKRYPYLAAIRDGR 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
 + G AYA +K R+AYDW VE++VYVS +R G GS LY L + Q +V A I
 Sbjct: 66 IIGYAYASQFKERSAYDWAVETSVYVSGDARRTGAGSLLYEALENYLRRQNVINVNACIA 125

Query: 128 LPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 PN S+ HE GY G GYK G W D+ W P P +P
 Sbjct: 126 YPNPGSITFHEKYGYHTVGHFTKCGYKLGQWWDW-VWMEKMLGPHPEQP 173

>ref|ZP_04295105.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH621]
 gb|EEK73016.1| Phosphinothricin N-acetyltransferase [Bacillus cereus AH621]
 Length = 170

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 59/168 (35%), Positives = 95/168 (56%), Gaps = 3/168 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+A + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATKRDVAYILDIYNDAILYTTAVYAYKPVTLNENRIDWYEQKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A GP++A AY ++VE +VYV +++ G+GS+L L+ + + + +++A I
Sbjct: 62 VGFATFGPFRAWPAYKYSVEHSVYVDKEYRKNGVGSSEELITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
N+ S+ LH+ G+ GT++ AGYK W ++ F+Q EL P P
Sbjct: 122 ENEKSIALHQNYGFVHAGTIKKAGYKFNRLNLAFYQ--LELNGPKNP 167

>ref|YP_001772764.1| GCN5-related N-acetyltransferase [Methylobacterium sp. 4-46]
gb|ACA20330.1| GCN5-related N-acetyltransferase [Methylobacterium sp. 4-46]
Length = 180

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 63/159 (39%), Positives = 86/159 (54%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE-QTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+RP D+ AV I H + T +F +P P+ + YP+LVA +
Sbjct: 9 VRPCGPEDIPAVQAIYAHAVRTGRASFELDPPDMPPEMLRRHAGLVGAGYPYLVAVAGDAL 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
G AYAGP++ R AY TVE++VYV G+G L L+++ A+GF+ +VAVIG
Sbjct: 69 LGYAYAGPYRTRPAYRGTVENSVYVDPARLGQIGIRRLGLDLVEAATARGFRQMVAVIGD 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+RLH ALG+ G LRA G+KHG W D QR
Sbjct: 129 SANAASIRLHAALGFAQVGVLRVGVGKHGLWLDTVLMQR 167

>ref|YP_535527.1| phosphinothricin N-acetyltransferase [Lactobacillus salivarius
UCC118]
ref|ZP_04008503.1| phosphinothricin N-acetyltransferase [Lactobacillus salivarius
ATCC
11741]
ref|ZP_07205561.1| acetyltransferase, GNAT family [Lactobacillus salivarius
ACS-116-V-Col5a]
gb|ABD99444.1| Phosphinothricin N-acetyltransferase [Lactobacillus salivarius
UCC118]
gb|EEJ75057.1| phosphinothricin N-acetyltransferase [Lactobacillus salivarius ATCC
11741]
gb|EFK80717.1| acetyltransferase, GNAT family [Lactobacillus salivarius
ACS-116-V-Col5a]
Length = 198

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 57/183 (31%), Positives = 93/183 (50%), Gaps = 8/183 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+IR D + I Y+E + + F T +E+ + + +YP++VAE++G +
Sbjct: 5 KIRLVNLNDAERILQIYRPYVENTAITFEYTVPTLEEFKNRIASIVKKYPYIVAEIDGKI 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G AYA +K R AYDW+VE+++YV + GLG LY L ++ QG +V A I
Sbjct: 65 MGAYAYANTFKNREAYDWSVETSIYVDENSRGKGLGLQLYRALENLLKKQGILNVNACITN 124

Query: 129 PNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQ RDF-ELPAPPRPVRPV 180
 P+ S+ HE LGY GT +GYK W D+ + ++ E P V +
 Sbjct: 125 PSKESKYVTKGSILFHEKLG YRHVGT FHNSGYKFDEWFDSWMEKSLGEHNLKPGKVIEI 184

Query: 181 TQI 183

+++

Sbjct: 185 SKL 187

>ref|YP_036893.1| phosphinothricin N-acetyltransferase [Bacillus thuringiensis
 serovar konkukian str. 97-27]
 gb|AAT60066.1| possible phosphinothricin N-acetyltransferase [Bacillus
 thuringiensis serovar konkukian str. 97-27]
 Length = 170

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.
 Identities = 56/170 (32%), Positives = 94/170 (55%), Gaps = 3/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 +R T D+ + DI N I +T + +P T + ID E+ + D YP V E++ V
 Sbjct: 2 VREETEKDVIYILDYINDAILNTTAVYTYKPVTLNRI DWYEQKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I
 Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRCKGIGTSLMRALITIAKEREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQ RDFELPAPPRPVR 178
 N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
 Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDLAFYQ--LELCGPKNPLE 169

>emb|CBL41830.1| Sortase and related acyltransferases [butyrate-producing bacterium
 SS3/4]
 Length = 189

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.
 Identities = 55/182 (30%), Positives = 92/182 (50%), Gaps = 8/182 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + +R A +D + DI +Y+E + + F + + +E+ + + + +Y+LV E +G
 Sbjct: 5 ITVRNAKLSAPRILDIYTYVENTVITFEYDVPSLEEFENRMIDIMKKYPYLVIERDGR 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G YA + R AYDW E T+Y+ H ++ GLG LY L ++ G ++ A IG
 Sbjct: 65 IEGYTYAHAFVGRAAYDWASELTIYLDHNAKKYGLGRKLYEALADRLKDMGVLNLYACIG 124

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQ RDF-ELPAPPRPVRP 179
 P N S + HE LG+ GT GYK W+D+ + ++ E PV+P
 Sbjct: 125 YPKVEDEYLNKNSAQFHEHLGFRLCGTFENCYKFNRWYDMIWMEKIIGEHTDDQAPVKP 184

Query: 180 VT 181

+

Sbjct: 185 YS 186

>ref|YP_001703771.1| phosphinothricin N-acetyltransferase [Mycobacterium abscessus
 ATCC 19977]
 emb|CAM63117.1| Hypothetical phosphinothricin N-acetyltransferase [Mycobacterium
 abscessus]
 Length = 177

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.

Identities = 52/138 (37%), Positives = 76/138 (55%)

Query: 28 YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTW 87
Y+ + ++F P + + ++ R+ WLVAE G + G AYA PWK+R AY W
Sbjct: 21 YVTDTAISFEEVPPSDAVLAERIQTAAHRHAWLVAEDGGEILGYAYAAPWKSRTAYQWAC 80

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGT 147
E +VYV ++ G G LYT LL + G+++V+AV+ PN S +LH +G+
Sbjct: 81 EVSVYVDGARRQRGTGRQLYTALLGRRLRELGYRTVLAVVVTNAAASEKLHRTMGFEQVAL 140

Query: 148 LRAAGYKHGGWHDVGFQW 165
R GYK G WHDV +Q
Sbjct: 141 YRRIGYKLGSHWDVTHFQ 158

>ref|ZP_00785183.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae COH1]
gb|EA076097.1| phosphinothricin N-acetyltransferase [Streptococcus agalactiae COH1]
Length = 163

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 50/157 (31%), Positives = 84/157 (53%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IRP +D + I Y+ +T+ F + + E+ + ++ + +P+LVAE G +
Sbjct: 3 IRPVLPSDAKELLAIYAPYVTDTTITFEYDIPSISEFTNRIKNISKSFPYLVAEENGKIL 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G AYA + AR +YDWT E ++Y+ + +GS LY L K + QG+ +++A I LP
Sbjct: 63 GYAYASTYYARASYDWTCELSIYLDKDVRSKKIGSQLYDTLEKELVNQGYVNLLACISLP 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
ND S+ H+ G+ G+K WHD+ + Q+
Sbjct: 123 NDISIAFHKKRGFNQVAHFQKIGFQWHDIVWLQK 159

>ref|ZP_04234094.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock3-28]
gb|EEL34103.1| Phosphinothricin N-acetyltransferase [Bacillus cereus Rock3-28]
Length = 170

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.
Identities = 57/169 (33%), Positives = 96/169 (56%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+A + DI N I +T + +P T + ID E+ + D YP V E++ V
Sbjct: 2 IREATKRDVAYILDYNDAILYTTAVYAYKPVTLNRIWYEQKKADGYPIFVYELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A G ++A AY +++E +VYV +++ G+GS+L L+ + + + + +++A +
Sbjct: 62 VGFATFGSFRAWPAYKYSIEHSVYVDKEYRKNGIGSSLMEKLIATAKEREYMTLIAGVDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPRPV 177
N+ S+ LH+ G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHQNYGFVHAGTIQKAGYKFNRLDLAFYQ--LELNGPENPI 168

>ref|YP_001412546.1| GCN5-like N-acetyltransferase [Parvibaculum lavamentivorans DS-1]
gb|ABS62889.1| GCN5-related N-acetyltransferase [Parvibaculum lavamentivorans DS-1]
Length = 197

Score = 105 bits (261), Expect = 3e-21, Method: Compositional matrix adjust.

Identities = 58/152 (38%), Positives = 77/152 (50%), Gaps = 4/152 (2%)

```
Query: 32  STVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTV 91
          + ++F T P   +   + + Q   PWLV E   G V G AYAGP + R AY W+V++ +
Sbjct: 33  TAISFETVPPDEAQMAARIGKNQPVLPWLHESGGSVTGYAYAGPHRERAAAYRWSVDAAI 92

Query: 92  YVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGLTAA 151
          Y+      R G+GS LY  L  ++  QG+      I LPN  SV LHEA G+   G
Sbjct: 93  YLDGSAHRKGIGSALYAVLFAALRLQGYHAYGGITLPNAASVGLHEAQGFRPIGVYPEV 152

Query: 152 GYKHGGWHDVGVFWQRDF----ELPAPPRPVRP 179
          G+K G W DVG+W  D      PA P P  P
Sbjct: 153 GFKFGAWRDVGWWGLDLAPPDHEPAEPLPFTP 184
```

>gb|ADI12551.1| GCN5-related N-acetyltransferase [Streptomyces bingchengensis
BCW-1]
Length = 162

Score = 105 bits (261), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 63/154 (40%), Positives = 81/154 (52%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
          +E+RPA  D A+  I NH IE ST  +  PQ+P E   L   +R   VAEVEG
Sbjct: 1   MEVRPARPGDAEAIRAIRNHAIEHSTALWTQTPQSPAEGAAWLAHLERGSFVVAEVEGE 60

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
          VAG A  GPW+  + Y  TV+ +VYV      LG+GS L T L+ S   G   ++A I
Sbjct: 61  VAGFAVYGPWRKLDGYQHTVDDSVYVREDRHGLGIGSALLTALIASARETGHVMIADIE 120

Query: 128 LPNDPSVRLHEALGYTARGLTAAAGYKHGGWHDV 161
          N  S+RLHE  G+   GT+   G K G W D+
Sbjct: 121 AENSSSIRLHERFGFHHVGTVPVGVSKFGRWLDL 154
```

>ref|ZP_06645478.1| phosphinothricin N-acetyltransferase [Erysipelotrichaceae
bacterium

5_2_54FAA]
gb|EFE46705.1| phosphinothricin N-acetyltransferase [Erysipelotrichaceae bacterium
5_2_54FAA]
Length = 195

Score = 105 bits (261), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 61/171 (35%), Positives = 85/171 (49%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR AT  D A++  I   Y+  +  F  E  +  E+  +E +Q  YP+LV E EG  +
Sbjct: 2   IRLATKQDAASILAIYAEYVLHDSATFEYEVPSLTEFEQRMEVIQVYPYLVYEEEGNIL 61

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
          G AYA  +K R AY W VE +VYV+      G+GS LY  L  ++ Q      A I  P
Sbjct: 62  GYAYAHRYKERAAYQWDVELSVYVNKDVGKIGSMLYEVLFFILLKKQQVHHAYACITSP 121

Query: 130 NDPSVRLHEALGYTARGLTAAAGYKHGGWHDVGVFWQRDFELPAPPRPVRPV 180
          N  S R+HE LG+      GYK  W DV  +  ++  P  P+P+ P+
Sbjct: 122 NPKSERMHERLGFQLVARFPHTGYKFEKWLDVWMDKELLSPDVPQPIVPL 172
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>ref|YP_001437209.1| hypothetical protein ESA_01105 [Cronobacter sakazakii ATCC BAA-
894]
gb|ABU76373.1| hypothetical protein ESA_01105 [Cronobacter sakazakii ATCC BAA-894]
Length = 199

Score = 104 bits (260), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 62/170 (36%), Positives = 91/170 (53%), Gaps = 8/170 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR T D+ A+ I ++E +F P T E + + + PVLVAE++G+V
Sbjct: 29 IRDVTGPDIDAIRAIYGWHVEHGRASFEETPPTLDEMTARVNAVTAQGLPWLVAEMDGIV 88

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI-- 126
G YA PW+AR AY +T+E ++Y+ G+GS L L++ E ++ ++AVI
Sbjct: 89 VGYCYASPWRARPAYRYTLEESIYIDASMVGRGIGSRLLQALIERCEQGPWRQLMAVIGD 148

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ-----DFELP 171
G N S RLH LG+ G+LR+ G+K GGW D QR D+ LP
Sbjct: 149 GENNRGSTRHLRLLGFEVVGSLRSVGFKFGGWRDTLIMQRPLNQGDWTLP 198

>ref|ZP_01992495.1| phosphinothricin N-acetyltransferase [Vibrio parahaemolyticus
AQ3810]
gb|EDM57649.1| phosphinothricin N-acetyltransferase [Vibrio parahaemolyticus
AQ3810]
Length = 169

Score = 104 bits (260), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 58/154 (37%), Positives = 80/154 (51%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAEV 64
+EIR D+A + DI N YIE + F P TP Q+W +Y VA
Sbjct: 1 MEIRTGKLEDVAGITDIFNFYIEHTNARFEEVPFTPENRQKWFSSQFSS-TTKYQLYVATK 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
GV+ G A + ++A +A+D TVE TVY++ + GLGS LYT L S+ A G V++
Sbjct: 60 NGVLLGFACSQYRAISAFDDTVEVTVYLAQEAQKGLGSKLYTQLFSSIRAYGVHRVLS 119

Query: 125 VIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGW 158
+ LPND SV LH+ G+ G KHG +
Sbjct: 120 GVALPNDTSVALHKRFGFREVGVFNEYAKKHGQY 153

>ref|ZP_02886944.1| GCN5-related N-acetyltransferase [Burkholderia graminis C4D1M]
gb|EDT07414.1| GCN5-related N-acetyltransferase [Burkholderia graminis C4D1M]
Length = 193

Score = 104 bits (260), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 61/161 (37%), Positives = 92/161 (57%), Gaps = 2/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AT AD+ A+ I H++ T +F P + E L +++ P++VAE++G V
Sbjct: 21 IRDATEADLPAIQAIYAHHVLTGVASFEVPPSVDELRLASVRNHGLPYMVAEIDGEV 80

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
AG YA P++ R AY T+E ++YVS ++ GLG L L++ EA ++ +VAVI
Sbjct: 81 AGYCYATPYRPRAAYRNTIEDSIYVSDAYRGRGLGRVLLQALIERCEAGPWRQMVAVIAD 140

Query: 128 LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
+ S+ LH+ LG+ GTL+A G+KHG W D QR
Sbjct: 141 GSGGSLSLHQQQLGFELIGTLKAVGFKHGRWLDSTLMQRTL 181

>gb|ADJ78841.1| Phosphinothricin N-acetyltransferase [Lactobacillus salivarius CECT
5713]
Length = 195

Score = 104 bits (260), Expect = 4e-21, Method: Compositional matrix adjust.

Identities = 57/183 (31%), Positives = 93/183 (50%), Gaps = 8/183 (4%)

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Query: 9   EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
          +IR   D   +   I   Y+E + + F   T +E+ + + + +YP++VAE++G +
Sbjct: 5   KIRLVNLNDAERILQIYRPYVENTAITFEYTVPTLEEFKNRIASIVKKYPYIVAIDGKI 64

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
          G AYA +K R AYDW+VE+++YV   + GLG LY L   ++ QG +V A I
Sbjct: 65  MGAYAYANTFKNREAYDWSVETSIYVDENSRGKGLGLQLYRALENLLKKQGVNLVNACITN 124

Query: 129  PNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPV 180
          P+          S+ HE LGY   GT   +GYK   W D+ + ++   E   P V   +
Sbjct: 125  PSKESKYVTKGSILFHEKLGVRHVGTFFHNSGYKFDEWFDMSWMEKSLGEHNLKPGKVIEI 184

Query: 181  TQI 183
          +++
Sbjct: 185  SKL 187

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>gb|EFV81785.1| acetyltransferase [Achromobacter xylosoxidans C54]
Length = 181

Score = 104 bits (260), Expect = 4e-21, Method: Compositional matrix adjust.
Identities = 61/168 (36%), Positives = 91/168 (54%), Gaps = 2/168 (1%)

```

Query: 1   MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPW 59
          M P   P+ IR + AD+ A+ I H+++ T +F +P + QE   L+ P+
Sbjct: 1   MPPSAAPILIRDSVDADLPAIKSIYAHVQHGTASFELDPPSIQEMRQRAAVLEKDMPY 60

Query: 60  LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
          LVAE++G V G AY P++ R AY TVE +VYV   G+G L   L++ A G+
Sbjct: 61  LVAEIDGEVVGAYVTPYRPRPAYRHTVEDSVYVKAGRAGQGIGGRLATLVERCTAAGW 120

Query: 120  KSVVAVIGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
          + ++AV+G N S+ +H G+ GTLR+ G+KHG W D QR
Sbjct: 121  RQMLAVVGDSRNAASLAVHARQGFHPVGTLSVGHKHGEWRD TVLMQR 168

```

>ref|YP_004148646.1| Phosphinothricin N-acetyltransferase [Staphylococcus
pseudintermedius HKU10-03]
gb|ADV05010.1| Phosphinothricin N-acetyltransferase [Staphylococcus
pseudintermedius HKU10-03]
gb|ADX77212.1| phosphinothricin N-acetyltransferase, putative [Staphylococcus
pseudintermedius ED99]
Length = 165

Score = 104 bits (260), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 58/163 (35%), Positives = 93/163 (57%), Gaps = 5/163 (3%)

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Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
          +R AT D+ A+ I NH I + + EP +E W+ + +R D YP V E EG
Sbjct: 5   VRRATLNDLEAIMAIYNHAILHTATVYTYEPHIEERRQWLAEKQR--DGYPVFVYENEG 62

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          V G A GP++ AY +T+E ++YVS +R G+ S L T +++ A G++++VA I
Sbjct: 63  TVLGATYGPFRNWPAYQYTIHESIYVSPDARRQGVASQLLTVVIEDATANGYQTIVAGI 122

Query: 127  GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFE 169
          N+ S++LHE +G+ GTL+ GYK W ++ F+Q+ +
Sbjct: 123  DDSNEGSLKLHEKMGFNYMGTLKKVGYKFERWLNLFVYQKQLK 165

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>ref|YP_002360568.1| GCN5-related N-acetyltransferase [Methylocella silvestris BL2]

gb|ACK49206.1| GCN5-related N-acetyltransferase [Methylocella silvestris BL2]
Length = 193

Score = 104 bits (260), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 56/164 (34%), Positives = 91/164 (55%), Gaps = 9/164 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-----LQDRYPWLVA 62
+ +R +T D+ A+ DI +++++ +++ EP DDL+R L+ R P +VA
Sbjct: 8 IIVRHSTEVDPAMVDIYAHVQNGLDYQPEPLRD-----DDLKRRRKAMLKRRRLPHIVA 63

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
E+ G V G AYA P+ R AY + V+ ++YV H G+G L L+++ A GF+ +
Sbjct: 64 ELGGAVVGAYAVPFLKRPAYRYAVKHSIYVHKDHLNAGVGRMLLPVLIEACAAAGFRQM 123

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQR 166
+ + N PS+RLHE+ G+ G L++ G+K G W D QR
Sbjct: 124 ICYVDSANGPSLRLHESTGFERMGVLKSVGFKFGHWTDTVLLQR 167

>ref|ZP_02406525.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
DM98]
Length = 247

Score = 104 bits (260), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 61/163 (37%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
Sbjct: 72 VRDATEHDLEAIQAIYAHHVLTGVASFEETPPS-----VDDLRRAREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+GVVAG AYA P++ R+AY + +E ++YVS + G+G L L+ EA ++ +A
Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSIYVSEACRGRGIGRVLLAALIRCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQR 166
VI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|ZP_00054060.1| COG1247: Sortase and related acyltransferases [Magnetospirillum
magnetotacticum MS-1]
Length = 197

Score = 104 bits (260), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 62/161 (38%), Positives = 89/161 (55%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEEVG 66
V+IR AT DMAAV I + Y+ S +F + + +E ++ R P+LVA EG
Sbjct: 10 VQIRDATDDDMAAVQAIYSFYVTRSAASFEEDVPSVEEMKARRAAVEARGLPFLVAVEEG 69

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G YAGP++ R+AY +TVE ++YV+ R G+G L L++ G++ ++AVI
Sbjct: 70 EVLGITYAGPFRQRSAYRYTVEDSIYVAPFVVRGIGRVLLAALIERCTESGYRQMIAVI 129

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQR 166
G N S+ +H ALG+ G LR G K G W DV R
Sbjct: 130 GDSANQGSIAVHRALGFGQEGVLRGVGLKFRWVDVIMHR 170

>ref|YP_084124.1| phosphinothricin N-acetyltransferase [Bacillus cereus E33L]
gb|AAU17722.1| phosphinothricin N-acetyltransferase [Bacillus cereus E33L]
Length = 170

Score = 104 bits (260), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 56/169 (33%), Positives = 94/169 (55%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDRYPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID ++ + YP LV E++ +
Sbjct: 2 IREATEKDVIYILDYINDAILNTTAVYTYKPVTLNENRIDWYGQKAEAYPILVYELDNKI 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A GP++A AY +++E +VYV+ ++ G+G++L L+ + + +++A I
Sbjct: 62 VGFATFGPFRAPWAPYKYSIEHSVYVNKEYRNRGIGTSLMKELIAIAREREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELNGPKNPL 168

>ref|YP_004232049.1| phosphinothricin acetyltransferase [Burkholderia sp. CCGE1001]
gb|ADX58989.1| Phosphinothricin acetyltransferase [Burkholderia sp. CCGE1001]
Length = 195

Score = 104 bits (260), Expect = 5e-21, Method: Compositional matrix adjust.
Identities = 62/169 (36%), Positives = 93/169 (55%), Gaps = 2/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AT AD+ A+ I H++ T +F P + + L ++ P++VAE++G V
Sbjct: 20 IRDATEADLPAIQAIYAHHVLTVGASFEEVPPSVDDLRLASVRSGLPYMVAEIDGEV 79

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
AG YA P++ R AY T+E ++YVS ++ GLG L L++ EA ++ +VAVI
Sbjct: 80 AGYCYATPYRPRAAYRHTIEDSIYVSDAYRGRGLGRVLLQALIERCEAGPWRQMVAVIAD 139

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
+ S+ LH LG+ GTL+A G+KHG W D QR + A P
Sbjct: 140 GSGGSLSLHTQLGFELTGTLKAVGFKHGRWLDTTLMQRTLGVGAATAP 188

>ref|YP_001878529.1| GCN5-related N-acetyltransferase [Akkermansia muciniphila ATCC
BAA-835]
gb|ACD05748.1| GCN5-related N-acetyltransferase [Akkermansia muciniphila ATCC
BAA-835]
Length = 199

Score = 104 bits (259), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 62/167 (37%), Positives = 86/167 (51%), Gaps = 9/167 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR AT D A + +I Y+E + V F E E+ ++ + +YP+LVAE G ++
Sbjct: 6 IRIATRRDAAKLEIYAPYVEKTAVTFEYEVPAVTEFEKRIDHVLGKYPYLVAERAGDIS 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G AYAG +K R AY W VE+TVYV +++G G LY L K + Q ++ A I P
Sbjct: 66 GYAYAGVFKDRAAYRWAVETTVYVREDMKMGTTGRELYAALEKILSMQNILNLNACIAYP 125

Query: 130 ---NDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
DP SV+ H+ LGY G GYK G W+ + W F
Sbjct: 126 CEAEDPYLTRDSVQFHKRLGYQFAGKFHRCGYKFGFRWYHM-IWMEKF 171

>ref|ZP_04446277.1| hypothetical protein COLINT_03009 [Collinsella intestinalis DSM
13280]
gb|EEP44194.1| hypothetical protein COLINT_03009 [Collinsella intestinalis DSM
13280]
Length = 198

Score = 104 bits (259), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 58/190 (30%), Positives = 97/190 (51%), Gaps = 14/190 (7%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V +R A D + I Y+ + + F P TP E+ + + + + +P+LVAE++G
Sbjct: 7 VRVRLARIEDAEELAAIYEPYVRETAITFEYVPPTPAEFAERMKTMEFFPYLVAELDGR 66

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYAG +K R AYDW VE+++YV+ H G+G L+ L +++ AQG ++ A I
Sbjct: 67 LVGYAYAGTFKGRPAYDWAVETSIYVAQGHAGEGIGCALHDALERALAAQGVNLNMYACIA 126

Query: 128 LPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-----ELPAP 173
+P+ S HE +GY G G+K G W+++ + ++ + P
Sbjct: 127 VPDGEDDETLTRNSQHFHEHMGYRLVGFEFCRCGFKGGRWYNMVWMEKMLGEHRADQPPVT 186

Query: 174 PRPVRPVTQI 183
P P VT +
Sbjct: 187 PFPETSVTCV 196

>ref|ZP_04096923.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar andalousiensis BGSC 4AW1]
gb|EEM71388.1| Phosphinothricin N-acetyltransferase [Bacillus thuringiensis
serovar andalousiensis BGSC 4AW1]
Length = 170

Score = 104 bits (259), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 56/169 (33%), Positives = 94/169 (55%), Gaps = 3/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDRYPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID ++ + YP LV E++ +
Sbjct: 2 IREATEKDVIYILDYINDAILNTTAVYTYKPVTLNENRIDWYGQKAEAYPILVHELDNKI 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++A AY +++E +VYV+ ++ G+G++L L+ + + +++A I
Sbjct: 62 VGFATFGPPRAWPAYKYSIEHSVYVNKEYRNRGIGTSLMKELIAIAREREYMTLIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRPV 177
N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+
Sbjct: 122 ENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELCGPKNPL 168

>ref|ZP_02384866.1| phosphinothricin N-acetyltransferase [Burkholderia thailandensis
Bt4]
Length = 188

Score = 104 bits (259), Expect = 6e-21, Method: Compositional matrix adjust.
Identities = 62/167 (37%), Positives = 93/167 (55%), Gaps = 3/167 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWL 60
+P P+ +R AT D+ A+ I H++ T +F P + + E L+ P+L
Sbjct: 6 APAHSPI-VRDATEHDLEAIRSIYAHVLTGVASFEETPPSADDLRARREAVLRHGLPYL 64

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
VAE++GUVAG AYA P++ R+AY +T+E ++YV+ + G+G L L+ EA ++
Sbjct: 65 VAELDGVVAGYAYATPYRPRSAYRYTLEESIVNDACRGRGIGRVLLAVLIARCEAGPWR 124

Query: 121 SVVAVIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166
++AVI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 125 QMIAVIADGGGGSTSLHRALGFEPVGTLRGVGFKHGRWIDTALMQR 171

>ref|YP_371912.1| GCN5-related N-acetyltransferase [Burkholderia sp. 383]
 gb|ABB11268.1| GCN5-related N-acetyltransferase [Burkholderia sp. 383]
 Length = 186

Score = 104 bits (259), Expect = 7e-21, Method: Compositional matrix adjust.
 Identities = 62/172 (36%), Positives = 91/172 (52%), Gaps = 2/172 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
 +R AT AD+ A+ I H++ S +F P E + L+ P+LVAE +G V
 Sbjct: 9 VRDATDADLEAIHAIYAHVHHSVASFEETPPDVAELRARRDAVLRQGLPYLVAECDGRV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 AG AYA P++ R+AY +T+E ++Y+ + G+G L L++ EA ++ ++AVI
 Sbjct: 69 AGYAYATPYRTRSAYRFTIEDSIYIDDAQQRGRGIGRALLAALIERCEAGPWRQMIAVIAD 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
 S LH A G+ G L+AAG+KHG W D QR A PV P
 Sbjct: 129 GGTGGSTSLHRAFGFEPAGMLKAAGFKHGRWIDTALLQRPLGEGARTLPVSP 180

>ref|ZP_06074266.1| conserved hypothetical protein [Bacteroides sp. 2_1_33B]
 gb|EEY84235.1| conserved hypothetical protein [Bacteroides sp. 2_1_33B]
 Length = 165

Score = 103 bits (258), Expect = 7e-21, Method: Compositional matrix adjust.
 Identities = 58/165 (35%), Positives = 82/165 (49%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR + D A+ DI N Y+ S F TEP +E + + YP+LV V
 Sbjct: 2 IRNVSLRDAKAIVDIYNEYVNVSVATFETELRVEEMEGRIAGISASYPYLVIYVDHDEVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G YA WK + AY +T+E+TVY+S R++ G+G L L++ A G+ +++A I
 Sbjct: 62 GYCYAHAWKEKAAYKYTLETTVYLSPRYKKGIGRQLMERLIEECRAGGYHALIACITEG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N+ S LHE LG+ G K G W DV D+EL P
 Sbjct: 122 NEASCSLHEKLGFKKVS RFKVLKFGRWLDV---VDYELI IKP 162

>ref|ZP_03569168.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
 (Phosphinothricin-resistance protein) [Burkholderia
 multivorans CGD2M]
 ref|ZP_03575813.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
 (Phosphinothricin-resistance protein) [Burkholderia
 multivorans CGD2]
 ref|ZP_03582796.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
 (Phosphinothricin-resistance protein) [Burkholderia
 multivorans CGD1]
 gb|EEE02969.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
 (Phosphinothricin-resistance protein) [Burkholderia
 multivorans CGD1]
 gb|EEE09156.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
 (Phosphinothricin-resistance protein) [Burkholderia
 multivorans CGD2]
 gb|EEE15075.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
 (Phosphinothricin-resistance protein) [Burkholderia
 multivorans CGD2M]
 Length = 186

Score = 103 bits (258), Expect = 8e-21, Method: Compositional matrix adjust.
 Identities = 62/173 (35%), Positives = 90/173 (52%), Gaps = 2/173 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
+R AT AD+AA+ I H++ S +F P E + L+ P+LVAE +G V
Sbjct: 9 VRDATDADLAAIQAIYAAHVRHSVASFEVPPDVAELAARRDAVLRHGLPYLVAECDGRV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
AG AYA P++ R+AY +TVE ++Y+ + G+G L L+ EA ++ ++A I
Sbjct: 69 AGYAYATPYRPRHAYRYTVEDSIYIDDAQRGRGIGRALLAALIARCEAGPWRQMIAAIAD 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
S LH A G+ GTL+A G+KHG W D+ QR A P P
Sbjct: 129 GGTGGSTSLHRAFGFAPAGTLQAVGFKHGRWIDIALLRPLGEGAATLPASPA 181

>ref|ZP_02370975.1| phosphinothricin N-acetyltransferase [Burkholderia thailandensis
TXDOH]
Length = 188

Score = 103 bits (258), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 62/167 (37%), Positives = 93/167 (55%), Gaps = 3/167 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWL 60
+P P+ +R AT D+ A+ I H++ T +F P + + E L+ P+L
Sbjct: 6 APAHSPI-VRDATEHDLEAIRAIYAAHVLTGVSFEETPPSADDLRARREAVLRHGLPYL 64

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
VAE++GUVAG AYA P++ R+AY +T+E ++YV+ + G+G L L+ EA ++
Sbjct: 65 VAELDGVVAGYAYATPYRPSAYRFTLEDSIYVNDACRGRGIGRVLLAALIARCEAGPWR 124

Query: 121 SVVAVIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
++AVI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 125 QMIAVIADGGGGSTSLHRLGFEPVGTLRGVGFKHGRWIDTALMQR 171

>ref|YP_003781205.1| putative acetyltransferase [Clostridium ljungdahlii DSM 13528]
gb|ADK16103.1| predicted acetyltransferase [Clostridium ljungdahlii DSM 13528]
Length = 194

Score = 103 bits (258), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 56/184 (30%), Positives = 93/184 (50%), Gaps = 8/184 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V +R AT AD + DI Y+ S ++F + + +E+ + + + +YP++VA
Sbjct: 10 VTMRMATKADAKEILDIYEPYVRNSAISFEYDVPSIEFTERINNILKKYPYIVAVDNNQ 69

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G AY +K R AYDW VE+T+Y+S + G+G LY L K ++ Q ++ A I
Sbjct: 70 IIGYAYVSSFKERVAYDWAVETTIYLSQDCRGKGVGKKLYLALEKILKRQNIINLNACIA 129

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRP 179
+ S+ HE LGY GYK G W+D+ + ++ E P+PV P
Sbjct: 130 YTTTDNAYLTNASMYFHENLGYRKVAHFTKCGYKFGNWYDMIWMEKIIGEHSNPKEVIP 189

Query: 180 VTQI 183
++ +
Sbjct: 190 ISDL 193

>ref|ZP_07634831.1| Sortase related acyltransferase [Ruminococcaceae bacterium D16]
Length = 189

Score = 103 bits (258), Expect = 8e-21, Method: Compositional matrix adjust.
Identities = 61/179 (34%), Positives = 91/179 (50%), Gaps = 10/179 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +R AT D A+ I YI T + F E +P+E+ D + + YP+LV E G
 Sbjct: 3 LRLATPMDAPALVGIYGYIHTP-ITFEYELPSREFQDRITHLTLEGYPYLWVEENGTPV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA +K R AY W E +VYV+ H +G LY L++ + QG ++V ++ +P
 Sbjct: 62 GYAYAHRFKERAAYQWGAELSVYVAQGHSTQKVGKLYGALMELLAIQGVRTVYGIPTVP 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR-----DFELPAPPRPVRPVTQI 183
 N+ S LH ++G+ G R GY G W DV +++ D E P P+ P Q+
 Sbjct: 122 NEKSEGLHRSMGFQDAGICRNTGYVDGAWRDVQTFEKAIGPYDLE----PVPITPFPQL 176

>ref|YP_548523.1| GCN5-related N-acetyltransferase [Polaromonas sp. JS666]
 gb|ABE43625.1| GCN5-related N-acetyltransferase [Polaromonas sp. JS666]
 Length = 178

Score = 103 bits (258), Expect = 8e-21, Method: Compositional matrix adjust.
 Identities = 64/175 (36%), Positives = 93/175 (53%), Gaps = 11/175 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 IRP+ D+ A+ I H++ T F TEP + + + L P+LVAE +G +
 Sbjct: 4 IRPSRDEDLPAITAIYGHVHLHGTGTFTETPPSLADMTARRADVLSKGLPYLVAEEDGRI 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 AG AY +K R AY ++VE ++Y++ R GLG L T LL EA G + ++A+IG
 Sbjct: 64 AGFAYGNWFKPRPAYRYSVEDSIYLPDLHRKGLGRALLTALLAHCEAVGIRKMMMAIIGD 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF-----ELPAP 173
 N SV +H ALG+T G + + G+K G W D+ Q+ ELPAP
 Sbjct: 124 SANAGSVGVHLALGFTQVGIVESCGWKFGAWRDIVIMQKTLGVGDTQPPTLPAP 178

>ref|ZP_02415035.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 14]
 Length = 323

Score = 103 bits (257), Expect = 9e-21, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAHVLTGVASFETPPS----VDDLRRAREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|ZP_07966268.1| acetyltransferase [Segniliparus rugosus ATCC BAA-974]
 gb|EFV12512.1| acetyltransferase [Segniliparus rugosus ATCC BAA-974]
 Length = 177

Score = 103 bits (257), Expect = 9e-21, Method: Compositional matrix adjust.
 Identities = 59/152 (38%), Positives = 81/152 (53%), Gaps = 1/152 (0%)

Query: 28 YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWT 87
 Y+ + + F EP T +E + + Q+R+ WL V E EG V G AYAGP+ +R AY W+
 Sbjct: 24 YVLDTAITFEEEPPTAEEMAARIGKAQERHAWLVLEQEGRVVGYAYAGPFASRAAYRWSC 83

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGET 147
 E +VY+ R G G LY LL + +G++ LPN S LH A+G+ G
 Sbjct: 84 EVSVYLEQGSVRRGGKALYAALLARLAERGYRRAFGGYTLPNPASESLHRAMGFRLCGV 143

Query: 148 LRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
 R G+KHG W DV + QRD + P P P
 Sbjct: 144 HREVGFKHGAWRDVAWAQRDLGVDGAP-PCSP 174

>ref|YP_002131561.1| phosphinothricin N-acetyltransferase [Phenylobacterium zucineum
 HLK1]
 gb|ACG79132.1| phosphinothricin N-acetyltransferase [Phenylobacterium zucineum
 HLK1]
 Length = 179

Score = 103 bits (257), Expect = 9e-21, Method: Compositional matrix adjust.
 Identities = 64/159 (40%), Positives = 86/159 (54%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IRPA A D A+ I H++ T F P TP E + DR P++VAE+ V
 Sbjct: 3 IRPAQAGDADALAAIYGHVLTGFGTFEEVPTPAEMERRRAAVADRGLPYVVAELGRKV 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 G AYA P++ R AY +TVE +VYV+ G+G L +L A G + VVAVIG
 Sbjct: 63 LGFAYAAPFRPRAAYRYTVEDSVYVAPDAIGRGVGRALLVRVLDECAALGVRQVAVIGD 122

Query: 128 LPNDPSVRLHEALGYTARGETLRAAGYKHGGWHDVGFQWQR 166
 N S+ LH ALG+ G R+ G+KHG W D+ + Q+
 Sbjct: 123 SGNAASIGLHTALGFEPGSGVGRSLGFKHGRWVDIVWMQK 161

>gb|ACO70893.1| putative acetyltransferase [uncultured Verrucomicrobia bacterium]
 Length = 164

Score = 103 bits (257), Expect = 9e-21, Method: Compositional matrix adjust.
 Identities = 58/152 (38%), Positives = 79/152 (51%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT AD+AA+ I NHY+E ST ++ P++ + R +P VAE G V
 Sbjct: 6 IRLATEADLAAINAIYNHYVEHSTCTYQLAPESEAAARLAWFYRHGAHPVTVAEAAAGEVL 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A + R AY TVE++VY+ H H R GLG + L+ A +++A I
 Sbjct: 66 GWASLNVFNPREAYARTVENSVMYIHHEHHRRGLGRAMLADLIARARALDHHTIIAGISAE 125

Query: 130 NDPSVRLHEALGYTARGETLRAAGYKHGGWHDV 161
 S+RLH G+ G LR G+KHG W DV
 Sbjct: 126 QTASIRLHLGFGFEEIGRLRQVGFKHGQWLDV 157

>ref|YP_001301874.1| phosphinothricin N-acetyltransferase [Parabacteroides distasonis
 ATCC 8503]
 gb|ABR42252.1| phosphinothricin N-acetyltransferase, putative [Parabacteroides
 distasonis ATCC 8503]
 Length = 167

Score = 103 bits (257), Expect = 9e-21, Method: Compositional matrix adjust.
 Identities = 58/165 (35%), Positives = 83/165 (50%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR + D A+ DI N Y+ S F TEP +E + + YP+LV + V
 Sbjct: 4 IRNVSLRDAKAIVDIYNEYVNSVATFETPLRVEEMEGRIGASISYPYLVYVDQDEVV 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 G YA WK + AY +T+E+TVY+S R++ G+G L L++ A G+ +++A I
 Sbjct: 64 GYCYAHTWKEKAAYKYTLETTVYLSPRYKKGIGRQLMERLIEECRAGGYHALIACITEG 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N+ S LHE LG+ G K G W DV D+EL P
 Sbjct: 124 NEASYSLHEKLGFRKVSHEKVGKFGRWLDV---VDYELIIP 164

>ref|ZP_05287381.1| phosphinothricin N-acetyltransferase, putative [Bacteroides sp.
 2_1_7]
 Length = 165

Score = 103 bits (257), Expect = 1e-20, Method: Compositional matrix adjust.
 Identities = 58/165 (35%), Positives = 83/165 (50%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR + D A+ DI N Y+ S F TEP +E + + YP+LV + V
 Sbjct: 2 IRNVSLRDAKAIVDIYNEYVNSVATFETELRVEEMEGRIAGISASYPYLVIYVDQDEVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 G YA WK + AY +T+E+TVY+S R++ G+G L L++ A G+ +++A I
 Sbjct: 62 GYCYAHTWKEKAAYKYTLETTVYLSPRYKKGIGRQLMERLIEECRAGGYHALIACITEG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N+ S LHE LG+ G K G W DV D+EL P
 Sbjct: 122 NEASYSLHEKLGFRKVSHEKVGKFGRWLDV---VDYELIIP 162

>ref|YP_003308709.1| phosphinothricin acetyltransferase [Sebaldella termitidis ATCC
 33386]
 gb|ACZ08778.1| Phosphinothricin acetyltransferase [Sebaldella termitidis ATCC
 33386]
 Length = 165

Score = 103 bits (257), Expect = 1e-20, Method: Compositional matrix adjust.
 Identities = 56/160 (35%), Positives = 91/160 (56%), Gaps = 6/160 (3%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEV 64
 R VEIR A AD+AA I N+YI + + F TE E + +++ L+ YP++V E
 Sbjct: 3 RGVEIRDA--ADIAA---IYNYIIRETIITFETEEIDTAEMENRIKKILEAGYPFIVHEE 57

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 + G AY G ++ R+AY ++E+++Y+ + G+G LY L++ + G ++
 Sbjct: 58 NNKITGYAYVGKFRERSAYSESLETSIYLDINEKGRGIGRKLYKRLIELSQEAGVHVLI 117

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF 164
 V+ PN S RLHE++G+ G ++ AG K G + DV FW
 Sbjct: 118 VVSYPNLASQRLHESVGFEEKAGVIKEAGKKFGKYIDVEFW 157

>ref|YP_001308116.1| GCN5-related N-acetyltransferase [Clostridium beijerinckii NCIMB
 8052]
 gb|ABR33160.1| GCN5-related N-acetyltransferase [Clostridium beijerinckii NCIMB
 8052]
 Length = 170

Score = 103 bits (257), Expect = 1e-20, Method: Compositional matrix adjust.
 Identities = 57/173 (32%), Positives = 88/173 (50%), Gaps = 7/173 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR AT D+A + +I N I +T + +E W D E+ +D P LV E +

Sbjct: 2 IREATEKDLADILEIYNDAILNTTAIYDYTAHNLEERKQWFD--EKKKDGCPLLVFEKDD 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
G A G ++ A+ +T+E +VYV ++ LG+G L L+ + + ++VA I

Sbjct: 60 KAVGFATYGSFRTPAFKYTIEHSVYVHKYRNRLGIGKILLKELIDAANRDEYATMVACI 119

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
ND S+++HE G+ GT+ AGYK G W D+ F+Q D L P P+

Sbjct: 120 DSLNDGSIKIHEKFGFKYSGTVTKAGYKFGKWLDFVYQLD--LTGPKYPIEK 170

>ref|ZP_04521588.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
(Phosphinothricin-resistance protein) [Burkholderia
pseudomallei MSHR346]
gb|EEP50502.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
(Phosphinothricin-resistance protein) [Burkholderia
pseudomallei MSHR346]
Length = 247

Score = 103 bits (257), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+

Sbjct: 72 VRDATEHDLEAIQAIYAHHVLTVGASFEETPPS---VDDLARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A

Sbjct: 128 DGVVAGYAYATPYRPRSAIRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
VI S LH ALG+ GTLR G+KHG W D QR

Sbjct: 188 VIADGGRGGSTSLHRALGFEPIGTLRGVGFKHGRWIDTALMQR 230

>ref|YP_001062349.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
668]
gb|ABN88367.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
668]
Length = 247

Score = 103 bits (257), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+

Sbjct: 72 VRDATEHDLEAIQAIYAHHVLTVGASFEETPPS---VDDLARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A

Sbjct: 128 DGVVAGYAYATPYRPRSAIRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
VI S LH ALG+ GTLR G+KHG W D QR

Sbjct: 188 VIADGGRGGSTSLHRALGFEPIGTLRGVGFKHGRWIDTALMQR 230

>ref|ZP_02501639.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
112]
Length = 247

Score = 103 bits (257), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAAHVLTGVASFETPPS----VDDLRRARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|ZP_02493429.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 NCTC 13177]
 Length = 247

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAAHVLTGVASFETPPS----VDDLRRARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|ZP_02451118.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 91]
 Length = 247

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAAHVLTGVASFETPPS----VDDLRRARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|ZP_04967733.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 406e]
 gb|ED087006.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 406e]
 Length = 247

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAAHVLTGVASFEETPPS----VDDLRRARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|YP_337680.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1710b]
 ref|YP_001075309.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1106a]
 ref|ZP_02474788.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 B7210]
 ref|ZP_02485288.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 7894]
 ref|ZP_02509533.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 BCC215]
 ref|ZP_04810141.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1106b]
 ref|ZP_04896533.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 Pasteur 52237]
 ref|ZP_04899563.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 S13]
 gb|ABA53754.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1710b]
 gb|ABN94562.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1106a]
 gb|EDO93371.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 Pasteur 52237]
 gb|EDS82575.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 S13]
 gb|EES20766.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1106b]
 Length = 247

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAAHVLTGVASFEETPPS----VDDLRRARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|ZP_07894787.1| phosphinothricin acetyltransferase [Enterococcus italicus DSM
 15952]
 gb|EFU75064.1| phosphinothricin acetyltransferase [Enterococcus italicus DSM
 15952]
 Length = 185

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 57/172 (33%), Positives = 88/172 (51%), Gaps = 2/172 (1%)

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Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEV-EGVV 68
          +R A  D+A + I  Y+E ++ F  +  + E+  ++ +Q RYP+LV E  EG +
Sbjct: 8   VRSAELTDVAELLRIYTPYVEKTAITFEYDVPSIDEFTQRVKTIQQRYPYLVCESEGEI 67

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
          G AYA  +K R AYDWTVE+++Y+  + G GS LY  L  + ++ Q  ++A I
Sbjct: 68  VGYAYASTYKGRATAYDWTVETSIYMDQSLKGRGGGSVLYHALEEQLKKQNVYVLLACITA 127

Query: 129  PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFF-LPAPPRPVRP 179
          N  SV  H   Y           GYK+G W DV + Q++ + +  P P  P
Sbjct: 128  GNAESVGFHGKFAYREVAYFPNLGYKNGEWLDVLWMQKELQPIQGSPNPFIP 179
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>ref|ZP_01765750.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
305]
gb|EBA49537.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
305]
Length = 247
```

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVAEV 64
          +R AT  D+ A+  I  H++ T  +F  P  +  +DDL  ++          P+LVAE+
Sbjct: 72  VRDATEHDLEAIQAIYAHHVLTVGASFEETPPS----VDDLRRARREAVRRHGLPYLVAEL 127

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
          +GVVAG AYA P++ R+AY + +E ++YV+  + G+G L  L+  EA  ++ ++A
Sbjct: 128  DGVVAGYAYATPYRPRSAYRYAIEDSIYNEACRGRGIGRVLLAALIRCEAGPWRQMIA 187

Query: 125  VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
          VI          S  LH ALG+  GTLR  G+KHG W D  QR
Sbjct: 188  VIADGGRGGSTSLHRALGFEPVGTILRGVGFKHGRWIDTALMQR 230
```

```
>ref|YP_439663.1| phosphinothricin N-acetyltransferase [Burkholderia thailandensis
E264]
ref|ZP_05591064.1| phosphinothricin N-acetyltransferase [Burkholderia thailandensis
E264]
gb|ABC35766.1| phosphinothricin N-acetyltransferase [Burkholderia thailandensis
E264]
Length = 188
```

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 60/159 (37%), Positives = 89/159 (55%), Gaps = 2/159 (1%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
          +R AT  D+ A+  I  H++ T  +F  P  +  +  E L+  P+LVAE++GVV
Sbjct: 13  VRDATEHDLEAIRSIYAHHVLTVGASFEETPPSADDLRRARREAVLRHGLPYLVAELDGVV 72

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
          AG AYA P++ R+AY +T+E ++YV+  + G+G L  L+  EA  ++ ++AVI
Sbjct: 73  AGYAYATPYRPRSAYRYTLEESIYVNDACRGRGIGRVLLAVLIARCEAGPWRQMIAVIAD 132

Query: 129  PN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
          S  LH ALG+  GTLR  G+KHG W D  QR
Sbjct: 133  GGRGGSTSLHRALGFEPVGTILRGVGFKHGRWIDTALMQR 171
```

```
>ref|YP_001180792.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor
```

saccharolyticus DSM 8903]
gb|ABP67601.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor
saccharolyticus DSM 8903]
Length = 162

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 48/160 (30%), Positives = 86/160 (53%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
IR AT +D+ + I N+ + S+ F T P++ +++ + +YP ++V + +
Sbjct: 3 IRKATISDIPQILSIYNYEVLNSSSTFDTRPKSTEDFLKLFDMHSYKYPIYVVEDGTNSI 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G Y P+ + Y TVE ++Y+ H H+ G+G L L++ +GFK+++A I
Sbjct: 63 IGYGYLSPFSDKEGYSITVEDSIYIHHLHRGKGIGKMLLKFLIQKAREKGFKNIIAKICA 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
N PS+ LH++LG+ G L + GYK + DV Q +
Sbjct: 123 ENQPSLNLHKSLSGFVEVGKLYSVGYKFNRYLDVIILQLNL 162

>ref|ZP_02737400.1| putative acetyltransferase [Gemmata obscuriglobus UQM 2246]
Length = 167

Score = 103 bits (256), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 56/156 (35%), Positives = 78/156 (50%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR ATA D+ A+ I N+Y+E ST ++ EP T E +YP VAE +G V
Sbjct: 6 IRLATAEDLEAIRAIYNYVERSTCTYQVEPDTAAERAAWFRDRSAKYPATVAERDGA VI 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G PWK+R Y W+ E++VY+ H H R GLG L L+ A G +++
Sbjct: 66 GWGALSPWKSRCGYAWSAEASVYIHHEHHRRLGKALLLDLIARGRAAGLHTIIGATSSD 125

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
S+ L ++G+ GT R G K W DV + Q
Sbjct: 126 QTASLALQVSVGFVIGTHREVGRKFDRWLDVITYTQ 161

>ref|YP_003981951.1| GNAT family acetyltransferase 28 [Achromobacter xylosoxidans A8]
gb|ADP19236.1| acetyltransferase, GNAT family protein 28 [Achromobacter
xylosoxidans A8]
Length = 181

Score = 102 bits (255), Expect = 1e-20, Method: Compositional matrix adjust.
Identities = 64/185 (34%), Positives = 95/185 (51%), Gaps = 10/185 (5%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-----LQD 55
MS + IR + AD+ A+ I H+++ +F +P + I D+ + L+
Sbjct: 1 MSSPAPTILIRDSAEADLPAIKTIYAHVQHGAASFELDPPS----IQDMRQRRAAVLEK 56

Query: 56 RYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
P+LVAE+ G V G AY P++ R AY TVE +VYV LG+G L L++
Sbjct: 57 EMPYLVAEINGEVVGAYVTPYRPRPAYRHTVEDSVYVKAGRSGLGIGKLLATLIERCT 116

Query: 116 AQGFKSVMVAVIGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
A G++ ++AV+G N S+ LH + G+ GTLR+ G+KHG W D QR
Sbjct: 117 AAGWRQMLAVVGDSRNAASLALHASQGFHPAGTLRSVGHKHGEWRD TVLMQRALGEGDAT 176

Query: 175 RPVRP 179
P RP
Sbjct: 177 PPQRP 181

>ref|ZP_06987509.1| phosphinothricin N-acetyltransferase [Bacteroides sp. 3_1_19]
 gb|EFI07237.1| phosphinothricin N-acetyltransferase [Bacteroides sp. 3_1_19]
 Length = 167

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 58/165 (35%), Positives = 83/165 (50%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR + D A+ DI N Y+ S F TEP +E + + YP+LV + V
 Sbjct: 4 IRNVSLRDAKAIVDIYNEYVNVSVATFETEPLRVEEVEGRIAGISASYPYLVYVDQDEVV 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G YA WK + AY +T+E+TVY+S R++ G+G L L++ A G+ +++A I
 Sbjct: 64 GYCYAHTWEKAAYKYTLETTVYLSPRYKKGKIGRQLMERLIEECRAGGYHALIACITEG 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N+ S LHE LG+ G K G W DV D+EL P
 Sbjct: 124 NEASYSLHEKLGFRKVSHEFKVGLKFGRWLDV---VDYELIIP 164

>ref|YP_001236578.1| phosphinothricin acetyltransferase (PPT N-acetyltransferase)
 [Bradyrhizobium sp. BTAi1]
 gb|ABQ32672.1| phosphinothricin acetyltransferase (PPT N-acetyltransferase)
 [Bradyrhizobium sp. BTAi1]
 Length = 176

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 58/160 (36%), Positives = 85/160 (53%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 ++IRP AD+ A+ I + T F + E L D +P+ VA ++G
 Sbjct: 4 IDIRPTGEADLPATAIYQAVREGTATFELDAPDLTEMTRRFRALTDGGFPYFVALLDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G AYAGP++ R AY +TVE+++Y++ QR G+G L L+ + E +GF+ ++AVI
 Sbjct: 64 EVVGYAYAGPYRPRPAYRFTVENSIIYLAPASQRRGIGRRLMQRLITACEERGFRQMIAMI 123

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
 G N SV LH A G+ GT + G K G W D Q
 Sbjct: 124 GDSANAGSVGLHRACGFQMIGTHPSVGLKFGRWLDVTMMQ 163

>ref|ZP_02426951.1| hypothetical protein CLORAM_00328 [Clostridium ramosum DSM 1402]
 gb|EDS19453.1| hypothetical protein CLORAM_00328 [Clostridium ramosum DSM 1402]
 Length = 191

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 55/177 (31%), Positives = 92/177 (51%), Gaps = 1/177 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + + ATA D A + +I Y+ T+ + F E T +E+ + ++YP+LVA+++
 Sbjct: 9 IRLAVATADDAARLLEIYRPYVLTAITFEYEVPTLEEFRARIVSTLEKYPYLVAKLDDK 68

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AY +K+R AY W VE+++Y+ ++ G+GS LY L + + Q ++ A I
 Sbjct: 69 IVGYAYTSAPKSRAYQWAVETSIYIDL DYKGGGIGSMLYHKLEITKQQNIINLNACIT 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183
 N S+ HE GY GYK WHD+ + ++ E P P PV P ++
 Sbjct: 129 AGNPESIVFHEHFGYQKVAYFTKCGYKFNQWHDMIWMEKMLGEHPGKPAPVIPFVKL 185

>ref|YP_001414928.1| GCN5-related N-acetyltransferase [Xanthobacter autotrophicus Py2]
 gb|ABS65271.1| GCN5-related N-acetyltransferase [Xanthobacter autotrophicus Py2]
 Length = 180

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 63/159 (39%), Positives = 85/159 (53%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVAEVEGVV 68
 IRPAT AD+ A+ I + + T T +F P E L + +P+LV + GVV
 Sbjct: 3 IRPATPADIPAIAAIYDEAVRTGTASFELAPPGVSEMTRRHAALVEAGFPYLVMEDEGGVV 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G AY G ++ R AY TVE+++YV+ Q G+G L L+ + EA GF+ +VAVIG
 Sbjct: 63 LGYAYVGAFRPRIAIRHTVENSIIYVAPAAQGRGVGRALLEALIAACEAAGFRQMVAVIGD 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N S+ LH A G+ G L A G K G W D QR
 Sbjct: 123 SANAGSIGLHRACGFADIGILPATGLKFGRWIDTVLMQR 161

>ref|ZP_06189127.1| putative N-acetyltransferase [Serratia odorifera 4Rx13]
 gb|EFA17429.1| putative N-acetyltransferase [Serratia odorifera 4Rx13]
 Length = 178

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 62/177 (35%), Positives = 92/177 (51%), Gaps = 3/177 (1%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWL 61
 P P+ I AT D+AAV I +++ +F P T +E ++Q+ PVLV
 Sbjct: 2 PLSAPLIITDATPDDLAAVQQIYAYHVLGAASFETPPTCEEMQQRCSKVQEAGLPWL 61

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 A+ E V G YA P++ R AY +TVE +VY++ Q G+G L L+ E ++
 Sbjct: 62 AKREDRVVGYCYATPYRPRPAYRFTVEDSVYIAEGLQGHGIGKALLAELIARCERGPWRQ 121

Query: 122 VVAVIGLP--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPPRP 176
 ++A++G N S+ LH LG+T+ GTL+A G+K G W D QR RP
 Sbjct: 122 MLAIVGNAENNQGLALHRTLGFSTVGTGLKAVGFKLGEWRDTQIMQRALSGGDGSRP 178

>ref|ZP_02459278.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei 9]
 Length = 210

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 35 VRDATEHDLEAIQAIYAHVLTGVASFETPPS---VDDLRRAREAVRRHGLPYLVAEL 90

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 91 DGVVAGYAYATPYRPRSAIRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 150

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 151 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 193

>ref|ZP_02211453.1| hypothetical protein CLOBAR_01066 [Clostridium bartlettii DSM
 16795]
 gb|EDQ96664.1| hypothetical protein CLOBAR_01066 [Clostridium bartlettii DSM

16795]
Length = 208

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 48/179 (26%), Positives = 91/179 (50%), Gaps = 1/179 (0%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
+ ++ R A +D + DI YI + + F + + +E+ +E + YP++V +
Sbjct: 18 KDIKFRLLADVSDTKEILDYAPYITDTAITFEYDIPSIEEFRGRIEHISLEYPYVVCYK 77

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125
+ G AYA + R A+ W VE ++Y+ ++ LG+G LY +++ ++ Q +++ A
Sbjct: 78 DEIIGYAYAHRYGERAAFQWDVELSIYLDMNYKSLGIGKILYNKVIEILKLQNVQNIYAC 137

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVG-FWQRDFELPAPPRPVRPVTQI 183
I ND S++ HE +G+ G + GYK W+D+ F R + P V+ + I
Sbjct: 138 ITSANDKSIKFHEKMGFEFIGFKDTGYKFDKWDITWFGMRVKDKNENPAKVKNIKDI 196

>ref|NP_767103.1| acetyltransferase [Bradyrhizobium japonicum USDA 110]
dbj|BAC45728.1| acetyltransferase [Bradyrhizobium japonicum USDA 110]
Length = 176

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 61/162 (37%), Positives = 84/162 (51%), Gaps = 2/162 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGV 67
EIRP AD+ A+ I + T F EP E L D YP+ VA ++G
Sbjct: 5 EIRPTLEADLPAITAIYQQAVRVGTATFELEPPDLAEMTRRYRALVDGGYPYFVAILDGR 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
VAG AYAG ++ R AY +TVE+++Y+ R G+GS L L+ EA+GF+ ++AVIG
Sbjct: 65 VAGYAYAGVYRPRPAYRFTVENSIIYLDPSFHRRGVGSLLLERLIAECEARGFRQMIAVIG 124

Query: 128 -LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
N S+ +H G+ GT G K G W D QR+
Sbjct: 125 DSANAGSIGVHTKGGFRMIGTHPNVGLKFGRWLDTVMMQREL 166

>ref|ZP_03450133.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
576]
gb|EEC37945.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
576]
Length = 210

Score = 102 bits (255), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
Sbjct: 35 VRDATEHDLEAIQAIYAHVLTGVASFEEPPS---VDDLARREAVRRHGLPYLVAEL 90

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
Sbjct: 91 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIRCEAGPWRQMIA 150

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
VI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 151 VIADGGRGGSTSLHRALGFEPIGTLRGVGFKHGRWIDTALMQR 193

>ref|YP_001908169.1| Putative N-acetyltransferase [Erwinia tasmaniensis Et1/99]
emb|CAO97291.1| Putative N-acetyltransferase [Erwinia tasmaniensis Et1/99]

Length = 179

Score = 102 bits (254), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 58/160 (36%), Positives = 88/160 (55%), Gaps = 3/160 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVAEVEGVV 68
+R AT DM+A+ + ++ +F P E +++D + PVLVAE++G V
Sbjct: 9 VRDATDDMSAMTSVYAGHVLHGCGSFETPPDLAEMTARYVKVRDLQLPWLVAEMDGEV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI-- 126
AG AYA ++ R AY +TVE +VY++ G+GS L L+ + Q F+ ++A +
Sbjct: 69 AGFAYASLYRPRAAYRFTVEDSVYIAAHLGGRGIGSALLEALIVRCQQSFQQMLANVG D 128

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
G N SV LH+ +G+ G LRA G+KHG W D QR
Sbjct: 129 GYRNTASVSLHKKMGFEVVGHLRAVGFKHGEWRDTLLMQR 168

>ref|ZP_02907912.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MEX-5]
gb|EDT40936.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MEX-5]
Length = 186

Score = 102 bits (254), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 63/179 (35%), Positives = 94/179 (52%), Gaps = 15/179 (8%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+AA+ I H++ S +F +TP + +D+L +D P+LVAE
Sbjct: 9 VRDATDLDLAAIHSIYAHHRHVSASF---ETPPD-VDELRRRDAVLRHGLPYLVAEC 64

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+G +AG AYA P++ R+AY T+E ++Y+ + G+G L L+ E ++ ++A
Sbjct: 65 DGRIAGYAYATPYRPRSA YRHTIEDSIYIDDAQRGRGIGRALLAALIARCETGPWRQMIA 124

Query: 125 VIG-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-----ELPAPPRPV 177
VI S LH A G+ G L+A G+KHG W D QR LPA P PV
Sbjct: 125 VIADGGTGGSTSLHRAFGFEPAGALKAVGFKHGRWDTALMQRALGDGARTLPASPEPV 183

>ref|YP_001811189.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MC40-6]
gb|ACB66973.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MC40-6]
Length = 187

Score = 102 bits (254), Expect = 2e-20, Method: Compositional matrix adjust.
Identities = 64/184 (34%), Positives = 92/184 (50%), Gaps = 7/184 (3%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPW 59
MS IR +T AD+AA+ I H++ S +F P E + L+ P+
Sbjct: 1 MSATPAACVIRDSTDADLAAIHAIYAHHRHVSASFETPPDVGELRGRDAVLRHGLPY 60

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
LVAE +G +AG AYA P++ R+AY T+E ++Y+ + G+G L L+ E +
Sbjct: 61 LVAECDGHIAGYAYATPYRTRSA YRHTIEDSIYIDDAQRGRGIGRALLATLIARCETGPW 120

Query: 120 KSVVAVIG-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-----ELPAP 173
+ ++AVI S LH A G+ G L+A G+KHG W D QR LPA
Sbjct: 121 RQMIAVIADGGTGGSTSLHRAFGFEPAGVLKAVGFKHGRWIDTALMQRALGDGARTLPAS 180

Query: 174 PRPV 177
P PV
Sbjct: 181 PEPV 184

>ref|YP_110939.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei]

K96243]
 ref|ZP_04954575.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1710a]
 emb|CAH38393.1| putative phosphinothricin N-acetyltransferase [Burkholderia
 pseudomallei K96243]
 gb|EET04097.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
 1710a]
 Length = 188

Score = 102 bits (254), Expect = 2e-20, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 13 VRDATEHDLEAIQAIYAHHVLTGVASFEETPPS----VDDLARREAVRRHGLPYLVAEL 68

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
 Sbjct: 69 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 128

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 129 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 171

>ref|YP_989894.1| phosphinothricin N-acetyltransferase [Burkholderia mallei SAVP1]
 ref|YP_001024370.1| phosphinothricin N-acetyltransferase [Burkholderia mallei NCTC
 10229]
 ref|ZP_04881278.1| phosphinothricin N-acetyltransferase [Burkholderia mallei ATCC
 10399]
 ref|ZP_04911086.1| phosphinothricin N-acetyltransferase [Burkholderia mallei JHU]
 gb|ABM47945.1| phosphinothricin N-acetyltransferase [Burkholderia mallei SAVP1]
 gb|ABM99800.1| phosphinothricin N-acetyltransferase [Burkholderia mallei NCTC
 10229]
 gb|EDK61383.1| phosphinothricin N-acetyltransferase [Burkholderia mallei JHU]
 gb|EDP85632.1| phosphinothricin N-acetyltransferase [Burkholderia mallei ATCC
 10399]
 Length = 247

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
 Identities = 60/163 (36%), Positives = 89/163 (54%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVAEV 64
 +R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
 Sbjct: 72 VRDATEHDLEAIQAIYAHHVLTGVASFEETPPS----VDDLARREAVRRHGLPYLVAEL 127

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +GVVAG AYA P++ R+AY + +E + YV+ + G+G L L+ EA ++ ++A
 Sbjct: 128 DGVVAGYAYATPYRPRSAYRYAIEDSTYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 187

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 VI S LH ALG+ GTLR G+KHG W D QR
 Sbjct: 188 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 230

>ref|YP_003285848.1| toxin resistance protein [Vibrio sp. Ex25]
 gb|ACY51383.1| toxin resistance protein [Vibrio sp. Ex25]
 Length = 169

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
 Identities = 58/169 (34%), Positives = 86/169 (50%), Gaps = 4/169 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEV 64

+EIR D+A + DI N YIE + F P T Q+W +Y VA
 Sbjct: 1 MEIRTKGIKDVAGITDIFNFYIEHTNSRFEEVPFTLENRQKWFSSQFSS-TTKYQLYVATE 59
 Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 GV+ G A + ++A +A+D TVE TVY++ + GLGS LYT L S+ A G V++
 Sbjct: 60 NGVLLGFACSQQYRAISAFDDTVEVTVYLAQEAKGKGLGSKLYTQLFSSIRAYGVHRVLS 119
 Query: 125 VIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFWQDFELPAP 173
 + LPND SV LH+ G+ G KHG + +++++ F + +
 Sbjct: 120 GVALPNDASVALHKRFGFREVGVFNEYAKKHGQYISSVWFKAFAFNESA 168

>ref|ZP_03758704.1| hypothetical protein CLOSTASPAR_02725 [Clostridium asparagiforme
 DSM 15981]
 gb|EEG55206.1| hypothetical protein CLOSTASPAR_02725 [Clostridium asparagiforme
 DSM 15981]
 Length = 214

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
 Identities = 56/161 (34%), Positives = 89/161 (55%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V+IRPA AAD AA+ +I Y+ +T+ F E + + +E + YP+LV E++G
 Sbjct: 18 VKIRPAVAADAAALLEIYAPYVRETTITFEYETPGKETFAGRIEAIAAEYPYLVCEIDGR 77
 Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 +A AY R AY W E +VYV R G+G LY +++ ++ Q ++V ++
 Sbjct: 78 IAAAYAGHRHMERAAQWNAELSVYVDRGQLRRGIGRALYQAVMEILKLQNVQTVYGIVT 137
 Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFWQDF 168
 PN+ S RLH A+G+T R GYK W DV +++++
 Sbjct: 138 SPNENSERLHVAMGFTKRALFPQMGYKFDRWLDVAWYEKNL 178

>ref|ZP_07357026.1| phosphinothricin N-acetyltransferase [Desulfovibrio sp. 3_1_syn3]
 gb|EFL87430.1| phosphinothricin N-acetyltransferase [Desulfovibrio sp. 3_1_syn3]
 Length = 189

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
 Identities = 62/177 (35%), Positives = 90/177 (50%), Gaps = 2/177 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + +R A D AA+ I YI+T V F + E+ + + YP+LV E +G
 Sbjct: 1 MNVRWARPDQAALLRIYAQYIDTP-VTFEYTLPSSENEFAARIGAIASAEYPYLVCEEDGE 59
 Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 G AYA R AY W E +VY+ G+G+ LY LL + QG ++ A++
 Sbjct: 60 TLGYAYAHQAEREAYQWNAELSVYLDPASTRGIGARLYRMLLDILLQGVRTAYALVT 119
 Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFWQDFE-LPAPPRPVRPVTQI 183
 LPN S RLH +LG+ R AG+K G WHDV ++ + A P+P+ PV +I
 Sbjct: 120 LPNRKSERLHASLGFQTLTIQRKAGFKGGRWHDVAWYTKALAPHDADPQPILPVDRI 176

>ref|ZP_04565925.1| phosphinothricin N-acetyltransferase [Mollicutes bacterium D7]
 gb|EEO31280.1| phosphinothricin N-acetyltransferase [Coprobaecillus sp. D7]
 Length = 186

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
 Identities = 55/177 (31%), Positives = 92/177 (51%), Gaps = 1/177 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + + ATA D A + +I Y+ T+ + F E T +E+ + ++YP+LVA+++

Sbjct: 4 IRLAVATADDAARLLEIYRPYVLTITAITFEYEVPTLEEFRRARIVSTLEKYPYLVAKLDDK 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AY +K+R AY W VE+++Y+ ++ G+GS LY L + + Q ++ A I

Sbjct: 64 IVGYAYTSAPFKSRAAYQWAVETSIYIDLDYKGGGIGSMLYHKLEEITKQQNIINLNACIT 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183
N S+ HE GY GYK WHD+ + ++ E P P PV P ++

Sbjct: 124 AGNPESIVFHEHFGYQKVAYFTKCGYKFNQWHDMIWMEKMLGEHPGKPAVIPFGKL 180

>ref|ZP_03643045.1| hypothetical protein BACCOPRO_01407 [Bacteroides coprophilus DSM 18228]
gb|EEF75913.1| hypothetical protein BACCOPRO_01407 [Bacteroides coprophilus DSM 18228]
Length = 162

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 60/165 (36%), Positives = 79/165 (47%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR A D A+ DI N YI S F T+P + + YP L+ E EG VA

Sbjct: 2 IRNARPEDAGAMTDIYNFYIRESVATFDTDPLPTTTMSRHIASASEGYPCICEEEGQVA 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G YA PWK + AY T+E+TVY+ H GLG L L+++ G ++A I

Sbjct: 62 GFCYAHWPKEKAAYRHTLETTVYLHPEHTGKGLGRQLMERLIETCRTNGSHVLIACITGG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
N+ S+ LH++LG+ G K G DV DFEL P

Sbjct: 122 NEASIALHQSLGFKQVSRFEKVGLKFGRLDV---VDFEELQVP 162

>ref|ZP_03475670.1| hypothetical protein PRABACTJOHN_01332 [Parabacteroides johnsonii DSM 18315]
gb|EEC97233.1| hypothetical protein PRABACTJOHN_01332 [Parabacteroides johnsonii DSM 18315]
Length = 165

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 55/165 (33%), Positives = 81/165 (49%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR D A+ +I N Y+ S F TEP +E + + R+P+ V E +

Sbjct: 2 IRQVELQDAKAITNIYNEYVLQSVATFDTEPVL EEEMRTIAEISSRFPYFVYEENQEIT 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G YA WK R+AY +T+E+TVY+S H G+G L L+ + G++++A I

Sbjct: 62 GYCYAHTWKERSAYRYTLETTVYLSPGHTGKGIGMLLMKKLIGACRENGYRALIACITEG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
N+ S LHE LG+ + G K W DV D+EL P

Sbjct: 122 NEASNILHEKLGFKQVSHFKKVGKLFDRWLDVA---DYELLLTP 162

>ref|ZP_08063150.1| phosphinothricin acetyltransferase [Streptococcus parasanguinis ATCC 903]
gb|EFX39156.1| phosphinothricin acetyltransferase [Streptococcus parasanguinis ATCC 903]
Length = 171

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 58/162 (35%), Positives = 91/162 (56%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP +D AA+ I Y+ + + F + T QE+ + + ++P+LVAEV+G V
 Sbjct: 3 IRPVQLSDAAAIRAIYQPYVTETAITFEVDVPTVQEFESRIAKTLTQFPYLVAEVDGKVV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 AYA + AR AYDWT E ++YV+ + G+GS LYT L + ++A+G+ +A I +P
 Sbjct: 63 AYAYASTYYARAAYDWTTELSIYVAKEARGQGIGSALYTALEEEELQARGYLRLFLACIAVP 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELP 171
 N+ S+ +H+ GY GYK WHD+ + Q+ P
 Sbjct: 123 NEASISMHKRGRYVQVAHFPGKIGYKFNKWHDIVWMQKTLNGP 164

>ref|YP_003452959.1| acetyltransferase [Azospirillum sp. B510]
 dbj|BAI76415.1| acetyltransferase [Azospirillum sp. B510]
 Length = 189

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
 Identities = 67/165 (40%), Positives = 94/165 (56%), Gaps = 9/165 (5%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-----LQDRYPWL 61
 PV IR +T D+ A+ DI ++I+ F EP P+E L+R L+ R P LV
 Sbjct: 7 PVIIRQSTELDVPAMLDIYGHIQHGLGPFIDIEPLHPEE---LKRRLKAMLRRLPHLV 62

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 AE G +AG AYA P++ R AY +TVE ++Y+ Q +G L + L+ + A G +
 Sbjct: 63 AESGGAIAAGYAYAAPFRKRPAYRYTVEHSIYIHKDFQGRRIGHQLLSTLIDACTAAGCRQ 122

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 +VAV+ N PS+RLHEA G+ G LR+ G+K G W D F QR
 Sbjct: 123 MVAVDSANIPSLRLHEACGFIQAGVLRVSGFKFGRWTDVFLQR 167

>ref|ZP_07312487.1| phosphinothricin N-acetyltransferase [Streptomyces griseoflavus
 Tu4000]
 gb|EFL40856.1| phosphinothricin N-acetyltransferase [Streptomyces griseoflavus
 Tu4000]
 Length = 172

Score = 102 bits (253), Expect = 3e-20, Method: Compositional matrix adjust.
 Identities = 59/182 (32%), Positives = 91/182 (50%), Gaps = 24/182 (13%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 M E V++RP D+ A+ D+ NHY+ + + F T TP+E R PWL
 Sbjct: 1 MPSEHEEVQVRPGEEGLRALDLYNHYVRETAITFDATFTPEE-----RLPW 50

Query: 61 VAE-VEG-----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTL 106
 ++ V+G + G A + P++ + AY +VE+TVYV+ R G+G+ L
 Sbjct: 51 LSHVPDGPYRLMVATDTGSRRILGYATSSPFRPKPAYATSVETTVYVAPDAGRGRVGTLL 110

Query: 107 YTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 Y L +++ Q A + PND S RLHE G+ GT R G K G W DV ++++
 Sbjct: 111 YKTLFEALAGQDLHAYAGVAQPNDASTRLHERFGFRHVGTYREVGRKFGRWWDVAWYEK 170

Query: 167 DF 168
 +
 Sbjct: 171 EL 172

>ref|YP_003151289.1| sortase-like acyltransferase [Cryptobacterium curtum DSM 15641]
 gb|ACU94607.1| sortase-like acyltransferase [Cryptobacterium curtum DSM 15641]
 Length = 185

Score = 101 bits (252), Expect = 3e-20, Method: Compositional matrix adjust.
Identities = 57/175 (32%), Positives = 86/175 (49%), Gaps = 1/175 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV-V 68
IR AT D AV DI Y+ TST F + + E +E +YP+LV + + V
Sbjct: 7 IRIATGDDAGAVADIYGEYVRTSTATFEEDAPSANECRLRIENTLAQYPFLVVCDSLAV 66

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
G YA + R+AY + E+T+Y+S R Q G+ + LYT L + + QG ++ A I
Sbjct: 67 VGFCYAHALRERSAYLHSAETTYLSSRAQHTGVAAALYTELERILARQGVNTNLYACITG 126

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQDRDFELPAPPRPVRPVTQI 183
N+ S+R H GY + GYK W D+ + ++ P P P +Q+
Sbjct: 127 ENEASLRFHSTCGYARCAQFNSCGYKFNRLWDIIWMEKLIADHGAPAPFIPFSQL 181

>ref|ZP_03793115.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
Pakistan 9]
gb|EEH26161.1| phosphinothricin N-acetyltransferase [Burkholderia pseudomallei
Pakistan 9]
Length = 176

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 90/163 (55%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
Sbjct: 1 MRDATEHDLEAIQAIYAHHVLTGVASFEEETPPS----VDDLRRAREAVRRHGLPYLVAEL 56

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+GVVAG AYA P++ R+AY + +E ++YV+ + G+G L L+ EA ++ ++A
Sbjct: 57 DGVVAGYAYATPYRPRSAYRYAIEDSIYVNEACRGRGIGRVLLAALIARCEAGPWRQMIA 116

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
VI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 117 VIADGGRGGSTSLHRALGFEPITGLRGVGFKHGRWIDTALMQR 159

>ref|ZP_07954371.1| acetyltransferase [Gemella moribillum M424]
gb|EFV35397.1| acetyltransferase [Gemella moribillum M424]
Length = 172

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 51/158 (32%), Positives = 81/158 (51%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR D + DI Y+E + + F E + + + + +YP+LVAE +G V
Sbjct: 3 IRDVNLEDAGRIADIYRPYVENTAITFDYEVPSVDFFEKISNTLQKYPFLVAEKDGEVL 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
G AYAG + + AY WT E T+Y+ + + G+G LY L K + +G + + I P
Sbjct: 63 GYAYAGEFYPKAAYAWTTEITIYLDEQVRGEGIGDKLYNELEKRLYDKGICRITSCISYP 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRD 167
++ SV HE G+ + GYK W+DV ++Q+D
Sbjct: 123 DEGSVSFHEKHGFRKVAHFQNVGYKFNRLWYDVVWYQKD 160

>ref|ZP_02164455.1| putative phosphinothricin N-acetyltransferase (antibiotic
resistance) protein [Hoeflea phototrophica DFL-43]
gb|EDQ35150.1| putative phosphinothricin N-acetyltransferase (antibiotic
resistance) protein [Hoeflea phototrophica DFL-43]

Length = 182

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 53/162 (32%), Positives = 83/162 (51%), Gaps = 1/162 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-QDRYPWLVAEVEG 66
++IR AT AD+ A+ I + ++ P E + + YP+LVAE +G
Sbjct: 1 MQIRDATLADVPAITRIYTESVRNGVASIELTPPGAEEMTRRFSTICNGYPYLVAEADG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G AYA ++ R AY W+VE ++Y+ + G G L L+ E GF+ ++AVI
Sbjct: 61 KVMGYAYASAFRTRPAYRWSVEDSIYLDPEARGRGYKALLHALIAGCETLGFRQMIAMI 120

Query: 127 GLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQD 168
G + S+ +H+ G+ G + +G+KHG W D F QR
Sbjct: 121 GGAHPASIAVHQKAGFVHSGMISGSGHKHGSWLDTVFMQRQL 162

>ref|YP_003332566.1| phosphinothricin acetyltransferase [Dickeya dadantii Ech586]
gb|ACZ75861.1| Phosphinothricin acetyltransferase [Dickeya dadantii Ech586]
Length = 176

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 59/163 (36%), Positives = 83/163 (50%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
+ I A +AA+ DI HY+ T F TEP E + ++ D PWLVA
Sbjct: 4 ILIEDAREEHIAAIRDIYTHYVLHGTATFETEPPEAEMLARWRKIHDAGLPWLVALENQ 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G Y G ++ R AY +T+E ++Y+ GLG L + L E QG++ VV+V+
Sbjct: 64 QVLGYCYLGFYRPRYAYRFTLEDISIYLHPEQVGRGLGKRLLEALLRAEQGYRQVSVV 123

Query: 127 GLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQD 168
N S++LH +LG+ GTLR+ G KHG W D QR
Sbjct: 124 ANSGNQASMLHLHLGFEAGTLRSVGMKHGRWLDLTALLQRSL 166

>ref|YP_575598.1| GCN5-related N-acetyltransferase [Nitrobacter hamburgensis X14]
gb|ABE61138.1| GCN5-related N-acetyltransferase [Nitrobacter hamburgensis X14]
Length = 183

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 58/158 (36%), Positives = 86/158 (54%), Gaps = 2/158 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR A AD+ A+ I +H + T F +P E L+D +P+LVAE+ G V
Sbjct: 6 IRAANEADLPATAIYDHAVRFGTATFELDPDLTEMTRRFALRDGGFPYLVAEAGAV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
G AYAGP++ R AY +TVE+++Y++ R G+G L L+ EA+G++ ++AVIG
Sbjct: 66 VGYAYAGPYRPRPAYRFTVENSIIYLAPASHRRGVGIQLLRRLIAECEARGYRQMIAVIGD 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
N S+ +H G+ GT + G K G W D Q
Sbjct: 126 SANAGSIGVHVRAGFKMIGTHPSVGLKFGRWLDTVMMQ 163

>ref|ZP_07945011.1| acetyltransferase [Bilophila wadsworthia 3_1_6]
gb|EFV43821.1| acetyltransferase [Bilophila wadsworthia 3_1_6]
Length = 170

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.

Identities = 56/168 (33%), Positives = 91/168 (54%), Gaps = 5/168 (2%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQT---PQEWIDDLERLQDRYPWLVAEVEG 66
          IRPAT AD+ A+ DI N + +T + P T ++W + E + P V E +G
Sbjct: 2   IRPATEADLQAILDIYNDAVINTTAVYTYTPHTLDMRRQWFN--EHREAGLPVVFVLEEDG 59

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAVI 126
          V+AG A G ++ AY +++E ++YV +R + + L LL++ G+ +++A I
Sbjct: 60  VIAGFATYGNFRPWPAKYKSIEHSIYVHKDFRRRHIAITRLMEKLLAANGAGYATMIAGI 119

Query: 127  GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
          N S+R+HE G+T G + AGYK G W D+ F+Q+ + P P
Sbjct: 120  DADNAASIRMHERFGFTFAGKIVKAGYKFGRWLDLVFYQKLLDGPQKQP 167
```

>ref|ZP_06053422.1| GCN5-related N-acetyltransferase [Grimontia hollisae CIP 101886]
gb|EEY70737.1| GCN5-related N-acetyltransferase [Grimontia hollisae CIP 101886]
Length = 171

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 55/161 (34%), Positives = 85/161 (52%), Gaps = 4/161 (2%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWDLLERLQDRYPWLVAEVE- 65
          IR A AD+ A+ +I NHY+ + + F +P T Q W+D L+R Y LV E E
Sbjct: 8   IRKAQHADLPAINIYNYHYVTQTCITFDYDPWTLERRQRWLDKQLQSNNGYHVLVKESES 67

Query: 66  GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAV 125
          G + G AY ++ + A++ + E T+Y+ + GLGS L LL+ + + ++
Sbjct: 68  GEIVGFAYNSEFREKQAFNVSSIEITIIYHLPERRAKGLGSELMAALLEEIASPICRAYSL 127

Query: 126  IGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
          I LPN S++LHE G+ G L GYK G +H V ++
Sbjct: 128  ITLPNTASMKLHEKFGFKQVGLLTDVGYKFGQFHSVAMLEK 168
```

>ref|YP_879394.1| phosphinothricin N-acetyltransferase [Mycobacterium avium 104]
ref|ZP_05214659.1| hypothetical protein MaviaA2_00456 [Mycobacterium avium subsp.
avium ATCC 25291]
gb|ABK66397.1| phosphinothricin N-acetyltransferase [Mycobacterium avium 104]
Length = 188

Score = 101 bits (252), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 60/157 (38%), Positives = 82/157 (52%), Gaps = 1/157 (0%)

```
Query: 28  YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTV 87
          Y+ + ++F T+ + +E L PWLV V G AYA P +AR AY W+V
Sbjct: 17  YVRDTAISFETQQPSVEEMRSRLTTTTLATLPWLITDGPVKGAYAYASPHRAREAYRWSV 76

Query: 88  ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAVIGLPNDPSPVRLHEALGYTARGT 147
          + ++Y+ R G G LYT LL + AQG+ + A I LPN SV LHEAL + G
Sbjct: 77  DVSLYLDASIHRRQGQGRRLYTALLNLLGAQGYINAYAAITLPNAASVGLHEALAFRRVGV 136

Query: 148  LRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183
          G+K W DVG+W R + PA P RP T++
Sbjct: 137  FPRVGFKQQRWWDVGWWHRLADPPAVPEEPRPWTRL 173
```

>ref|YP_003784563.1| UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
[Brachyspira pilosicoli 95/1000]
gb|ADK30062.1| UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
[Brachyspira pilosicoli 95/1000]
Length = 189

Score = 101 bits (251), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 50/157 (31%), Positives = 84/157 (53%), Gaps = 1/157 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR AT+ D + DI ++YI+T+ + F + +E+ ++ + YP+LV E +
Sbjct: 3 IRLATSEDTKQILDYISNYIDTN-ITFEYSLPSIEEFKRIKNIKVYPYLVYEENEKIL 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G AYA + R AY W E ++Y+ + H+ GLG L L+ ++ QGFK++ + +
Sbjct: 62 GYAYAHSMEREAAYKWDTLSIYMDYNHKSGLGKKLCLALINILKYQGFKTLYSRVTSG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S + H+ G+ G L GYK WHDV +++
Sbjct: 122 NVASEKFHDYFGFKKCGMLCNTGYKLSKWHDVTIYEK 158

>ref|YP_105922.1| phosphinothricin N-acetyltransferase [Burkholderia mallei ATCC 23344]
ref|ZP_00441992.2| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) [Burkholderia mallei GB8 horse 4]
ref|ZP_02266045.2| phosphinothricin N-acetyltransferase [Burkholderia mallei PRL-20]
gb|AAU46447.1| phosphinothricin N-acetyltransferase [Burkholderia mallei ATCC 23344]
gb|EEP87977.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase) (Phosphinothricin-resistance protein) [Burkholderia mallei GB8 horse 4]
gb|EES46057.1| phosphinothricin N-acetyltransferase [Burkholderia mallei PRL-20]
Length = 210

Score = 101 bits (251), Expect = 4e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 89/163 (54%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
Sbjct: 35 VRDATEHDLEAIQAIYAHVLTGVASFEETPPS----VDDLRRAREAVRRHGLPYLVAEL 90

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+GVVAG AYA P++ R+AY + +E + YV+ + G+G L L+ EA ++ ++A
Sbjct: 91 DGVVAGYAYATPYRPRSAYRYAIEDSTYVNEACRGRGIGRVLLAALIARCEAGPWRQMI 150

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
VI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 151 VIADGGRGGSTSLHRALGFEPIGTLRGVGFKHGRWIDTALMQR 193

>ref|YP_001195120.1| GCN5-related N-acetyltransferase [Flavobacterium johnsoniae UW101]
gb|ABQ05801.1| GCN5-related N-acetyltransferase [Flavobacterium johnsoniae UW101]
Length = 165

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 54/162 (33%), Positives = 86/162 (53%), Gaps = 5/162 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAE 63
V +RPAT D+ + +IVNH I +T N+ + QT + +W +D + P +VA+
Sbjct: 2 SVILRPATVNDLGKILEIVNHSILHTTANYSYDIQTIEVQTKWFED--KKAKNLPIVVAD 59

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
++G V G G ++ + Y +TVE +VYV G+GS L + L++ + QG+ ++
Sbjct: 60 LDGEVLGFGSYGQFREKIGYQYTVESVYVVDNVIGKGVGSKLLSELIRLAKEQGYHVM 119

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165

I N S+ HE G+ GT+R GYK W D+ F Q
Sbjct: 120 GAIDADNAGSIAFHEKFGFVETGTIREVGYKFDHWLDFVMQ 161

>ref|YP_003607239.1| Phosphinothricin acetyltransferase [Burkholderia sp. CCGE1002]
gb|ADG17728.1| Phosphinothricin acetyltransferase [Burkholderia sp. CCGE1002]
Length = 193

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 61/171 (35%), Positives = 95/171 (55%), Gaps = 5/171 (2%)

Query: 1 MSPERRPVE---IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR- 56
MS R P++ IR AT AD+ A+ I H++ T +F P + ++ L ++
Sbjct: 1 MSSRPPLDAPLIRDATEADLPAIQAIYAHHVLTGVASFEEIPPSVEDLRARLASVRSHG 60

Query: 57 YPWLVAEEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
P++VAE++G VAG YA P++ R AY T+E ++YV+ ++ G+G L L+ E
Sbjct: 61 LPYMVAEIDGDVAGYCYATPYRPRAAYRNTIEDSIYVNDAYRGRGIGRVLLQALIDRCET 120

Query: 117 QGFKSVVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
++ ++AVI + S+ LH LG+ GTL+A GYKHG W D QR
Sbjct: 121 GPWRQMIAVIADGGSGGSLSLHTQLGFELTGTLLKAVGYKHGRWLDTTLMQR 171

>ref|ZP_02466216.1| phosphinothricin N-acetyltransferase [Burkholderia thailandensis
MSMB43]
Length = 189

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 61/167 (36%), Positives = 90/167 (53%), Gaps = 2/167 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWL 60
+P +R AT D+ A+ I H++ T +F P + + E L+ P+L
Sbjct: 6 APAHCSAIVRDATEDDLEAIQAIYAHHVLTGVASFEETPPSVADLRARREAVLRHGLPYL 65

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
VAE++GVVAG AYA P++ R+AY + +E ++YVS + G+G L L+ EA ++
Sbjct: 66 VAELDGVVAGYAYATPYRPRSAIRYALSDSIYVSDACRGRGIGRVLLGALIRCEAGPWR 125

Query: 121 SVVAVIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
++AVI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 126 QMIAVIADGGGGSTSLHRLGFEFVGTLRGVGFKHGRWIDTALMQR 172

>ref|ZP_02926674.1| putative acetyltransferase [Verrucomicrobium spinosum DSM 4136]
Length = 162

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 61/157 (38%), Positives = 79/157 (50%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGVVA 69
+R A D+ A+ DI NHY+ ST ++TEP T +E E R+P V E EG V
Sbjct: 4 LRLARRDDLGAINDIYNHYVLHSTCTYQTEPSTLEERQAWFEVHGVRHPVTVLEEEGRVI 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G + R AY TVE++VY+ H Q GLGS L L+ G V+AVI
Sbjct: 64 GWGALNKFHPRAAYGHTVENSIVLHHDQQGRGLGSVLLADLMDRAAQLGHHVVIIVIDAS 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
PSV LH G+ G R G+K G W DV + Q+
Sbjct: 124 QAPSVGLHAKFGFVQCGHFREVGFQWLDVVYMQK 160

>ref|ZP_06641431.1| phosphinothricin acetyltransferase [Serratia odorifera DSM 4582]
 gb|EFE93883.1| phosphinothricin acetyltransferase [Serratia odorifera DSM 4582]
 Length = 178

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
 Identities = 60/162 (37%), Positives = 87/162 (53%), Gaps = 3/162 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + I AT AD+ AV DI H++ +F P T E + ++ PWLVA++EG
 Sbjct: 6 LSITDATPADLVAVADIYRHHVLHGAGSFEETPPTLAEMQQRHDSVRSAGLPWLVAKLEG 65

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 V G YA P++ R AY +TVE +VY++ Q G+G L L+ E ++ ++AV+
 Sbjct: 66 QVVGICYATPYRPRPAYRFTVEDSVYIAAGMQGRGIGKALLGALIARCERGPWRQMLAVV 125

Query: 127 G--LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
 G N S+ LH LG+ + GTL A G+K G W D QR
 Sbjct: 126 GDSANNLGSLELHRKLGFAISIGTLNAVGFKFGCWRDTHLMQR 167

>ref|NP_387329.1| putative acetyltransferase (antibiotic resistance) protein
 [Sinorhizobium meliloti 1021]
 ref|ZP_07582201.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti BL225C]
 ref|ZP_07595670.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti AK83]
 emb|CAC47802.1| Acetyltransferase [Sinorhizobium meliloti 1021]
 gb|EFN28808.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti AK83]
 gb|EFN33704.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti BL225C]
 Length = 185

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
 Identities = 56/173 (32%), Positives = 89/173 (51%), Gaps = 2/173 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVE-GV 67
 +R A AAD+ ++ +I + + P + E + + YP++VA E G
 Sbjct: 5 LRDAVAADLRSITEIYRESVLNGVATYEETPPSEAEMALRFSTITGNGYPYVVALDERGA 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 V G AYA ++ R AY + VE ++Y+S + G+G L + L+ A GF+ ++AVIG
 Sbjct: 65 VIGYAYASAFRNRTAYRFLVEDSIYLSPEARGKGIGKALLSELVGRCTALGFRQMIAVIG 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQRDFELPAPPRPVRPV 180
 + S+ LH ALG+ +G ++A G+KHG W D F QR +P V
 Sbjct: 125 GAHPSSIALHRALGFELQGLMKATGFKHGRWLDTAFMQRPLGEGTATKPTGEV 177

>ref|ZP_07376830.1| Phosphinothricin acetyltransferase [Pantoea sp. aB]
 gb|EFM21562.1| Phosphinothricin acetyltransferase [Pantoea sp. aB]
 Length = 174

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
 Identities = 59/161 (36%), Positives = 87/161 (54%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 +EI A + A+ I +++ T F TEP E LE+++ PW VA +G
 Sbjct: 1 MEITEADKRHIAIQIYAYHVLQGTATFETEPDAAEIAARLEKVRSAAGLPWFVAVEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 V G Y ++ R AY +T+E +VY+ +Q G G L +H + EA+GF+ +VAV+
 Sbjct: 61 QVRGYCYLSFYRERRAYRFTLEDSVYMDVNYQGRGTGKMLLSHAIAWAEARGFRQLVAVV 120

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
 G N S+ LH A G++ GTLR+ G+KHG W D QR
 Sbjct: 121 GNSENRGSALHSAAGFSITGTLRSVGFKHGRWLDTVILQR 161

>ref|ZP_07028623.1| Phosphinothricin acetyltransferase [Afipia sp. 1NLS2]
gb|EFI50046.1| Phosphinothricin acetyltransferase [Afipia sp. 1NLS2]
Length = 176

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 57/157 (36%), Positives = 85/157 (54%), Gaps = 2/157 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV 64
R IR ATAAD+ A+ I + T +F P E + + +P+LVAE
Sbjct: 2 RDFTIRAATAADIPAITAIYGFVREKTASFEMTPPDEAEMMRFTAITGGGFPYLVAEA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
G +AG AYAGP++ R AY +T+E++VY+ + R G+GS L L+ A+G++ ++A
Sbjct: 62 GGRIAGYAYAGPYRPRPAYRYTLENSVYLDPAYYRRGIGSALLKELIAQCTARGYRQMIA 121

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
VIG N S+ LH + G+ G G+K G W D
Sbjct: 122 VIGDSANAASIGLHRSAGFAMIGIHPNVGFKFGRWLD 158

>ref|YP_001078206.1| phosphinothricin N-acetyltransferase [Burkholderia mallei NCTC
10247]
ref|ZP_04973250.1| phosphinothricin N-acetyltransferase [Burkholderia mallei
2002721280]
gb|ABO02876.1| phosphinothricin N-acetyltransferase [Burkholderia mallei NCTC
10247]
gb|EDK84125.1| phosphinothricin N-acetyltransferase [Burkholderia mallei
2002721280]
Length = 188

Score = 101 bits (251), Expect = 5e-20, Method: Compositional matrix adjust.
Identities = 60/163 (36%), Positives = 89/163 (54%), Gaps = 10/163 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVAEV 64
+R AT D+ A+ I H++ T +F P + +DDL ++ P+LVAE+
Sbjct: 13 VRDATEHDLEAIQAIYAHHVLTVGASFEETPPS----VDDLRRARREAVRRHGLPYLVAE 68

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+GVVAG AYA P++ R+AY + +E + YV+ + G+G L L+ EA ++ ++A
Sbjct: 69 DGVVAGYAYATPYRPRSAYRYAIEDSTYVNEACRGRGIGRVLLAALIERCEAGPWRQMIA 128

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
VI S LH ALG+ GTLR G+KHG W D QR
Sbjct: 129 VIADGGRGGSTSLHRALGFEPITLGRGVGFKHGRWIDTALMQR 171

>ref|ZP_02358538.1| phosphinothricin N-acetyltransferase [Burkholderia oklahomensis
EO147]
Length = 189

Score = 100 bits (250), Expect = 6e-20, Method: Compositional matrix adjust.
Identities = 57/159 (35%), Positives = 90/159 (56%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
+R A D+ A+ I H++ T +F P + + E L+ P+LVAE++G V
Sbjct: 14 VRDAAERDLEAIQAIYAHHVLTVGASFEETPPSVADLRARREAVLRHGLPYLVAE 73

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
AG AYA P++ R+AY + +E ++YV+ ++ G+G L L++ EA ++ ++AV+
Sbjct: 74 AGYAYATPYRPRSAYRYAIEDSIYVNDAYRGRGIGRVLLAALIERCEAGPWRQMIAVVAD 133

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 + S LH ALG+ GTLRA G+KHG W D QR
 Sbjct: 134 GSGGSTSLHRALGFEPVGTLRVAVGFKHGRWIDTALMQR 172

>ref|ZP_02365602.1| phosphinothricin N-acetyltransferase [Burkholderia oklahomensis
 C6786]
 Length = 189

Score = 100 bits (250), Expect = 6e-20, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 90/159 (56%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGV 68
 +R A D+ A+ I H++ T +F P + + E L+ P+LVAE++G V
 Sbjct: 14 VRDAAERDLEAIQAIYAHHVLTVGASFEETPPSVADLRARREAVLRHGLPYLVAELDGAV 73

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 AG AYA P++ R+AY + +E ++YV+ ++ G+G L L++ EA ++ ++AV+
 Sbjct: 74 AGYAYATPYRPRSAIRYAIEDSIYVNDAYRGRGIGRVLLAALIERCEAGPWRQMIADVAD 133

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 + S LH ALG+ GTLRA G+KHG W D QR
 Sbjct: 134 GSGGSTSLHRALGFEPVGTLRVAVGFKHGRWIDTALMQR 172

>ref|ZP_02080264.1| hypothetical protein CLOLEP_01716 [Clostridium leptum DSM 753]
 gb|EDO61321.1| hypothetical protein CLOLEP_01716 [Clostridium leptum DSM 753]
 Length = 189

Score = 100 bits (250), Expect = 6e-20, Method: Compositional matrix adjust.
 Identities = 51/161 (31%), Positives = 82/161 (50%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A D + +I +Y++ + + F + + E+ +E+ RYP++V E +GV
 Sbjct: 2 INIRNAEITDAERLVEIYGYVKNITAITFEYDIPSLTEFRQRMEQTMRRYPYIVIEQDGV 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G AYAG + R AYDW+ E TVY+ ++ G+G LY L + + G ++ A I
 Sbjct: 62 IQGYAYAGAFVGRAAYDWSCEVTYLDKDKTRKHGMGRRLYEALKEKLRKMILNLYACIA 121

Query: 128 LPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 P S H LGYT G + GYK G W+++
 Sbjct: 122 YPETEDEYLTTNSADFHHLGYTKVGKFKCGYKFGRWYNM 162

>ref|YP_981695.1| GCN5-related N-acetyltransferase [Polaromonas naphthalenivorans
 CJ2]
 gb|ABM36774.1| GCN5-related N-acetyltransferase [Polaromonas naphthalenivorans
 CJ2]
 Length = 178

Score = 100 bits (250), Expect = 6e-20, Method: Compositional matrix adjust.
 Identities = 61/172 (35%), Positives = 91/172 (52%), Gaps = 7/172 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGV 68
 IRP+ D+ A+ I H++ T F TEP + +Q + P+LVAE +G +
 Sbjct: 4 IRPSRDEDIRAITAIYAHHVLHGTGTFTETPPGTSDMAARRADVQSKGLPYLVAEQDGKI 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G AY +K R AY ++VE ++Y++ QR GLG L LL EA G + V+A++G
 Sbjct: 64 LGFAYGNWFKPRPAYRYSVEDSIYLPDLQRKGLGRALLAELLARCEAAGIRKVMIAVGD 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR-----DFELPAPP 174

N SV +H ALG+ G + + G+K G W D+ Q+ D E P+ P
 Sbjct: 124 SANAGSVGVHLALGFRQVGIIESCWKFGAWRDIVIMQKTLGPGDTEPPSEP 175

>ref|ZP_05546015.1| conserved hypothetical protein [Parabacteroides sp. D13]
 gb|EEU51105.1| conserved hypothetical protein [Parabacteroides sp. D13]
 Length = 165

Score = 100 bits (250), Expect = 6e-20, Method: Compositional matrix adjust.
 Identities = 57/165 (34%), Positives = 82/165 (49%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR ++ D A+ DI N Y+ S F TEP +E + + YP+LV V
 Sbjct: 2 IRNVSSRDAKAIVDIYNEYVNVSVATFETELRVEEMEGRIAGISASYPYLVIYVDHDEVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G YA WK + AY +T+E+TVY+S ++ G+G L L++ A G+ +++A I
 Sbjct: 62 GYCYAHAWKEKAAYKYTLETTVYLSPGYKKGIGRQLMERLIEECRAGGYHALIACITEG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N+ S LHE LG+ G K G W DV D+EL P
 Sbjct: 122 NEASCSLHEKLGFRKVSHEFKVGLKFGRWLDV---VDYELIIP 162

>ref|YP_001338532.1| putative acetyltransferase [Klebsiella pneumoniae subsp. pneumoniae
 MGH 78578]
 gb|ABR80302.1| putative acetyltransferase [Klebsiella pneumoniae subsp. pneumoniae
 MGH 78578]
 Length = 178

Score = 100 bits (250), Expect = 7e-20, Method: Compositional matrix adjust.
 Identities = 63/178 (35%), Positives = 92/178 (51%), Gaps = 7/178 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + I A + A+ I H++ T +F TEP QE + ++ +Q R +PW +A
 Sbjct: 1 MHIINAEQHIPIAIRRIYAHHLVHGTGSFETEPDQTQEMLARVKNVQSRGFPWYIALQGE 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 V G Y ++ R+AY +TVE++VY+ +QR G G L H L +QG++ ++AV+
 Sbjct: 61 TVIGYCYLSRYRERHAYRFTVENSVIDPAYQRQGGKALLDHALTWARSQGYRQMIAVV 120

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-----ELPAPPRPVR 178
 G N SV LH G+T GTL+ G+KHG W D QR LP P P R
 Sbjct: 121 GDSANVASVALHLRAGFTEIGTLKDIGFKHGRWLDTVLLQRQLGKGSCTLPDSPVPGR 178

>ref|ZP_07304405.1| phosphinothricin N-acetyltransferase [Streptomyces viridochromogenes DSM 40736]
 gb|EFL32774.1| phosphinothricin N-acetyltransferase [Streptomyces viridochromogenes DSM 40736]
 Length = 172

Score = 100 bits (250), Expect = 7e-20, Method: Compositional matrix adjust.
 Identities = 60/180 (33%), Positives = 92/180 (51%), Gaps = 24/180 (13%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 MS ER V++RP D+ ++ + NHY+ + F TE TP+E R PWL
 Sbjct: 1 MSTERVEVQVRPGVEGDLVSLTGLYNHYVRETAFTFDTEIFTPEE-----RRPWL 50

Query: 61 VAE-VEG-----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTL 106
 ++ V+G + G A + P++A+ AY +VE+TVYVS R G+G+ L
 Sbjct: 51 LSHPVDGPHRLMVAVTPDSQEILGYATSSPYRAKPAYATSVETTIVYVSPHAGRRGVGTLL 110

Query: 107 YTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 Y L +++ + A I PN+ S RLHE G+ GT R G K G + DV +++
 Sbjct: 111 YEALFEALSGEDLHRAYAGIAQPNEASARLHERFGFRYVGTYREVGRKFGRYWDVAWYEK 170

>ref|ZP_03679607.1| hypothetical protein BACCELL_03968 [Bacteroides cellulosilyticus
 DSM 14838]
 gb|EEF88418.1| hypothetical protein BACCELL_03968 [Bacteroides cellulosilyticus
 DSM 14838]
 Length = 170

Score = 100 bits (250), Expect = 7e-20, Method: Compositional matrix adjust.
 Identities = 55/166 (33%), Positives = 83/166 (50%), Gaps = 7/166 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
 E+RP D ++ I N Y+ S + F TEP +E + + +P+ V E EG +
 Sbjct: 4 EVRPE---DTGSITAIYNEYVAHSVITFETEPVREEEMRSRITGIVSHFPYFVYETEGKI 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 AG YA WK R AY +T+E+TVY++ +Q G+G L L+ +G+ +++A I
 Sbjct: 61 AGYCYAHAWKERAARYTLETTVYLASEYQKGIGKQLMQTLINCEHRHGYHALIACITE 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPP 174
 N+ S LH+ LG+ G K W DV D+EL P
 Sbjct: 121 GNEASNSLHKKLGFKQVSHFEKVGLKFDRLDVF----DYELILIP 162

>ref|ZP_02032877.1| hypothetical protein PARMER_02897 [Parabacteroides merdae ATCC
 43184]
 gb|EDN85812.1| hypothetical protein PARMER_02897 [Parabacteroides merdae ATCC
 43184]
 Length = 165

Score = 100 bits (250), Expect = 7e-20, Method: Compositional matrix adjust.
 Identities = 55/165 (33%), Positives = 82/165 (49%), Gaps = 4/165 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR D A+ +I N Y+ S F TEP +E + + R+P+ V E + +
 Sbjct: 2 IRQVELQDAKAITNIYNEYVLHSVATFDTEPQVEEEMRARIAEISSRFPYFVYEEDEKEIT 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G YA WK R+AY +T+E+TVY+S H G+G L L+++ G+++++A I
 Sbjct: 62 GYCYAHTWKERSAYRYTLETTVYLSPGHTGKGIGMMLMQRLIEACRENGYRALIACITEG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPP 174
 N+ S LHE LG+ G K W DV D+EL P
 Sbjct: 122 NEASNILHERLGFKQVSRFTKVGLKFDRLDVA---DYELLLLP 162

>ref|YP_004153830.1| phosphinothricin acetyltransferase [Variovorax paradoxus EPS]
 gb|ADU35719.1| Phosphinothricin acetyltransferase [Variovorax paradoxus EPS]
 Length = 182

Score = 100 bits (249), Expect = 8e-20, Method: Compositional matrix adjust.
 Identities = 62/161 (38%), Positives = 85/161 (52%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPE-QTPQEWIDDLERLQDRYPWLVAEVEG 66
 +EI A MA+V I +HY++ +F E P E L+ P+LVA G
 Sbjct: 19 LEILDAEPHMASVQAIYSHYVQHDLCSEFEVPTVEDMQTRRTEVLRRGLPYLVALKNG 78

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VAG AYA P++AR+AY TVE ++YV+ G+G L ++ GF +VAV+

Sbjct: 79 EVAGYAYASPYRARSAYRHTVEDSIYVARGMHGHGIGMALLRAVIAHCTEGGFTQMVAVV 138

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166

G N S RLHE+LG+ G LR+ G+K G W D QR

Sbjct: 139 GNSANTGSQRLHESLGFTVGVLRVGVFKFGQWVDTVLMQR 179

>ref|ZP_08076595.1| putative phosphinothricin N-acetyltransferase

[Phascolarctobacterium sp. YIT 12067]

gb|EFY04641.1| putative phosphinothricin N-acetyltransferase

[Phascolarctobacterium sp. YIT 12067]

Length = 203

Score = 100 bits (249), Expect = 8e-20, Method: Compositional matrix adjust.
Identities = 51/153 (33%), Positives = 82/153 (53%), Gaps = 1/153 (0%)

Query: 32 STVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTV 91

S V+F E + +E+ + ++ + YP++V E EG + G YA P+ R AY W E+T+

Sbjct: 34 SDVSFEYEVPSVEEFTERIKNISADYPYIVCEHEGRLLGYVYAHPIQRAAYQWGAEATI 93

Query: 92 YVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAA 151

Y++ Q GLG +Y L + QG A I N+ SV++HEA GY GT

Sbjct: 94 YLAPEGQGCGLGKVMYAALEALLRLQGQVVVYACITASNEHSVKMHEACGYKIIGTFNNT 153

Query: 152 GYKHGGWHDVGFWRDF-ELPAPPRPVRPVTQI 183

G+KHG W D+ + ++ E P P ++ + ++

Sbjct: 154 GFKHGHWLDVMWMEKVIAEYPKQPALIKKIGEL 186

>ref|ZP_05093745.1| acetyltransferase, GNAT family [marine gamma proteobacterium
HTCC2148]

gb|EEB79741.1| acetyltransferase, GNAT family [marine gamma proteobacterium
HTCC2148]

Length = 154

Score = 100 bits (249), Expect = 8e-20, Method: Compositional matrix adjust.
Identities = 57/150 (38%), Positives = 79/150 (52%), Gaps = 1/150 (0%)

Query: 20 AVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVVAGIAYAGPWK 78

A+ +I NHYI ST F + ++ + + + PWLVAE +G V G AYA WK

Sbjct: 2 ALAEIYNHYIVNSTATFEEVVLSAEDMKQRLAVAELGLPWLVAEQGQVVGAYANRWK 61

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHE 138

R+AY ++VESTVY+ G G+ LYT L + + +V+ I LPN SV LHE

Sbjct: 62 ERSAYRFSVESTVYLLPDIGSRGWGTRLYTALFEELRTLVDHAVIGSITLPNPASVALHE 121

Query: 139 ALGYTARGTLRAAGYKHGGWHDVGFWRDF 168

+G + G+K W VG+WQ F

Sbjct: 122 KMGMSKVAEFPEVGFKNQWLTVGYWQIIF 151

>ref|YP_001117611.1| GCN5-related N-acetyltransferase [Burkholderia vietnamiensis G4]

gb|ABO58146.1| GCN5-related N-acetyltransferase [Burkholderia vietnamiensis G4]

Length = 186

Score = 100 bits (249), Expect = 9e-20, Method: Compositional matrix adjust.
Identities = 63/179 (35%), Positives = 90/179 (50%), Gaps = 7/179 (3%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWL 61

P+ +R AT AD+ A+ I H++ S +F P E + L+ P+LV

Sbjct: 2 PDAPACTVRDATDADLDIAHAIYAHVHRVSVASFEEAPPDVAELRARRDAVLRHGLPYLV 61

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121

AE +G VAG AYA P++ R+AY T+E ++Y+ + G+G L L+ EA ++
 Sbjct: 62 AECDGRVAGYAYATPYRTRSAYRHTIEDSIYIDDAQRGRGIGRALLAALIRCEAGPWRQ 121

Query: 122 VVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-----ELPAPP 174

++AVI S LH A G+ G L+A GYKHG W D QR LPA P
 Sbjct: 122 MIAVIADGGTGGSTSLHRAFGFEPAGVLKAVGYKHGRWIDTALLQRALGDGARTLPATP 180

>ref|ZP_06944043.1| toxin resistance protein [Vibrio cholerae RC385]

gb|EFH72488.1| toxin resistance protein [Vibrio cholerae RC385]

Length = 169

Score = 100 bits (249), Expect = 9e-20, Method: Compositional matrix adjust.

Identities = 57/154 (37%), Positives = 79/154 (51%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAEV 64

+EIR D+A++ DI N YIE + FR + QEW +Y VA
 Sbjct: 1 MEIRTGKFEDVASITDIFNFYIEHTNARFEEFRFTLENRQEWFSQFSS-TTKYQLYVAVE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124

GV+ G A + ++A A+D TVE TVY++ + GLGS LYT L S+ A G V++
 Sbjct: 60 NGVLLGFACSQQYRAIPAFDDTVEVTVYLAQEAKGKGLSKLYTQLFSSIRAYGVHRVLS 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158

+ LPND SV LH+ G+ G KHG +
 Sbjct: 120 GVALPNDASVALHKRFGFREVGVFNEYAKKHGQY 153

>ref|ZP_02891871.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria IOP40-10]

gb|EDT02543.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria IOP40-10]

Length = 187

Score = 100 bits (249), Expect = 9e-20, Method: Compositional matrix adjust.

Identities = 63/188 (33%), Positives = 96/188 (51%), Gaps = 15/188 (7%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR---- 56

MS +R +T D+AA+ I H++ S +F +TP + +D+L +D
 Sbjct: 1 MSATPAACVVRDSTDTDLAAIHAIYAHHRHSVASFE---ETPPD-VDELRRARRDAVLRH 56

Query: 57 -YPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115

P+LVAE +G ++G AYA P++ R+AY T+E ++Y+ + G+G L L+ E
 Sbjct: 57 GLPYLVAECDGRISGYAYATPYRTRSAYRHTIEDSIYIDDAQRGRGIGRALLAALIRCE 116

Query: 116 AQGFKSVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-----E 169

++ ++AVI S LH A G+ G L+A G+KHG W D QR
 Sbjct: 117 TGPWRQMIAVIADGGTGGSTSLHRAFGFEPAGMLKAVGFKHGRWIDTALMQRALGDGART 176

Query: 170 LPAPPRPV 177

LPA P PV
 Sbjct: 177 LPASPEPV 184

>emb|CBL25177.1| Sortase and related acyltransferases [Ruminococcus torques L2-14]

Length = 196

Score = 100 bits (249), Expect = 9e-20, Method: Compositional matrix adjust.

Identities = 56/178 (31%), Positives = 86/178 (48%), Gaps = 10/178 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR A D + + Y+ + + F E + +E+ D + + +YP+LVAE G +
 Sbjct: 5 IRFAKMEDAEELLALYTPYVTDTVITFEYEVPSLEEFKDRMRQTMKKYPYLVAEQNGEIL 64

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129

G + AG +K R AYDW VE+T+Y+ Q+ G+G LY L K + AQ ++ A IG P
 Sbjct: 65 GYSCAGAFKGRAAYDWAETTTIYIRKDRQKTGVGKKLYEAEKVLHAQNICNLYACIGYP 124

Query: 130 -----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELP--APPRPVR 178
 S + H LGY G GYK W+++ W P P+P++

Sbjct: 125 EVEDEYLTKNQAQFHAHLGYRMVGEFYHCGYKFDRWYNM-VWMEKLLDPEIKHPKPIK 181

>ref|YP_003881883.1| Phosphinothricin N-acetyltransferase [Dickeya dadantii 3937]
 gb|ADM97326.1| Phosphinothricin N-acetyltransferase [Dickeya dadantii 3937]
 Length = 187

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 60/161 (37%), Positives = 86/161 (53%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + I A A +AA+ DI H++ S F TEP E D ++++D PWLVA

Sbjct: 15 IVIEDAGAEHIAAIRDIYAHVHLHSLATFETEPPEDEAEMRDRWQKIRDAGLPWLVAATENK 74

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G Y G ++AR AY +T+E ++Y+ H G+G L + L E QG + VV+V+

Sbjct: 75 QVLGYCYLGFYRARYAYRFTLEDSIYLHPDHLGKGVGKRLLSAALLQAEQQGHRQVVSVV 134

Query: 127 GLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S++LH +LG+ G LR+ G KHG W D QR

Sbjct: 135 ADSGNQASLQLHLSLGFAQVGMLRSVGMKHGRWVDTVLLQR 175

>ref|YP_003450289.1| acetyltransferase [Azospirillum sp. B510]
 dbj|BAI73745.1| acetyltransferase [Azospirillum sp. B510]
 Length = 177

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 59/161 (36%), Positives = 90/161 (55%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + +R +T AD+ A+ + ++ T +F P E L R P+LVAE EG

Sbjct: 4 ITVRASTDADIPALTALYAQHVSHGTASFEEVPPDAAEMARRRRDLLARGLPYLVAECEG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 +AG AYAGP++ R+AY +T+E++VYV+ R G+G L L++ EA G++ ++A+I

Sbjct: 64 RLAGYAYAGPYRTRSAIRFTLENSVYVADGMGRRGIGRALMAPLIERCEAAGYRRMIAMI 123

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G N S+ LH A G+ G L A G+K G W D +R

Sbjct: 124 GDSANQGSIGLHTACGFRLVGVLPAVGFKFGRWLDGVMMER 164

>ref|YP_004223325.1| sortase [Microbacterium testaceum StLB037]
 dbj|BAJ73445.1| sortase [Microbacterium testaceum StLB037]
 Length = 203

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 61/170 (35%), Positives = 91/170 (53%), Gaps = 4/170 (2%)

Query: 3 PER-RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWL 60
 PER EIRPAT AD+ + +I N+Y+ S V F + + +W D L+ P+L

Sbjct: 23 PERPFSYEIRPATEADIPDIREIYNYVRNSVVTTFDEKAWSIKWRDKFATLKRGLPLFL 82

Query: 61 VAEV-EGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 VAE G V G A PW++++AY +TVE+++Y+ GLG L L+ + + G

Sbjct: 83 VAESPSGQVLGYALVQPWQSKSAYRYTVENSIYLGQAAAGKGLGRALLEALIAACQDLGI 142

Query: 120 KSVVAVIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
+ +VA I D S+ LHE LG+T G + G+K G W V + Q+
Sbjct: 143 REMVAAISDKGADASIALHEKLGTFEVRMGRVGFKFRWLGVVYLQKSI 192

>ref|YP_001215771.1| toxin resistance protein [Vibrio cholerae 0395]
ref|ZP_06035903.1| toxin resistance protein [Vibrio cholerae RC27]
gb|AAC38427.1| unknown [Vibrio cholerae]
gb|ABQ18834.1| toxin resistance protein [Vibrio cholerae 0395]
gb|ACP11177.1| GCN5-related N-acetyltransferase [Vibrio cholerae 0395]
gb|EEY42151.1| toxin resistance protein [Vibrio cholerae RC27]
Length = 169

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 55/154 (35%), Positives = 79/154 (51%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVAEV 64
+EIR D+A + DI N YIE + F P + +EW R +Y VA
Sbjct: 1 MEIRTGEFEDIAGITDIFNFYIEQTNRFEFFPTLENREEWFSQFSRTA-KYQIYVAVE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
GV+ G A + ++A A+D TVE +VY++ + GLGS LYT L S+ A G +++
Sbjct: 60 NGVLQGFACSQKYRAIPAFDDTVEVSVYLAQEAKGKGLGSKLYTQLFSSIRAYGVHRILS 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
+ LPND SV LH+ G+ G KHG +
Sbjct: 120 GVALPNDASVALHKRFGFREVGFIFNEYAKKHGQY 153

>ref|ZP_07475281.1| phosphinothricin N-acetyltransferase [Brucella sp. B02]
gb|EFM58716.1| phosphinothricin N-acetyltransferase [Brucella sp. B02]
Length = 179

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 57/159 (35%), Positives = 84/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AD+ + I + T T ++ EP T E D+ +P LVAE +G V
Sbjct: 4 IRDFQLADIETITAIYTQAVLTGTGSYEIEPPTMDEMAKRFATFADQGFPIILVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
G AYA ++ R AY W E ++Y++ + G+G L L+ + A GF+ ++AVIG
Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQGIGKLLRELIARISALGFRQLLAVIGD 123

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
N SV+LHE+LG+T G + +G+KHG W D Q
Sbjct: 124 GEHNIGSVKLHESLGFTHCGRIEGSGFKHGRWLDTVLMQ 162

>ref|ZP_03313133.1| hypothetical protein DESPIG_03073 [Desulfovibrio piger ATCC 29098]
gb|EEB32040.1| hypothetical protein DESPIG_03073 [Desulfovibrio piger ATCC 29098]
Length = 195

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 60/178 (33%), Positives = 87/178 (48%), Gaps = 5/178 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
++ A D+ + I Y+ ++ F E T E+ L + YPWL V G V
Sbjct: 5 LQVAGDGDIFPMLAIYAPYVRDTAITFEYEVPTAAEFGARLHHVLPYVWLVCRAPGQVL 64

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
G AYA R AY W VE +VYV + G+G LY LL+ + QG + I +P
Sbjct: 65 GYAYAHRHMERAAYGWNVESVYVLGSARGRGVGRALYGALLELLRLQGVVNAYGCIAPV 124

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE-----LPAPPRPVRPVTQ 182
 N+PS LH+A ++ G A+G+K G WHD+ ++ R + PAP RP + Q
 Sbjct: 125 NEPSEALHKATSFSLGHPASGWKQGRWHDIVWYGRCLQEDGEGEPAPLRPFGLGQ 182

>ref|ZP_07478906.1| phosphinothricin N-acetyltransferase [Brucella sp. B01]
 gb|EFM55089.1| phosphinothricin N-acetyltransferase [Brucella sp. B01]
 Length = 179

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 84/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR AD+ + I + T T ++ EP T E D+ +P LVAE +G V
 Sbjct: 4 IRDFQPADIETITTIYTQAVLTGTGSYEIEPPTMDEMAKRFAAFADQGFILVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G AYA ++ R AY W E ++Y++ + G+G L L+ + A GF+ ++AVIG
 Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQGIGKLLRELIARISALGFRQLLAVIGD 123

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N SV+LHE+LG+T G + +G+KHG W D Q
 Sbjct: 124 GEHNIGSVKLHESLGFTHCGRIEGSGFKHGRWLDTVLMQ 162

>ref|YP_003620615.1| hypothetical protein LKI_00515 [Leuconostoc kimchii IMSNU 11154]
 gb|ADG39646.1| hypothetical protein LKI_00515 [Leuconostoc kimchii IMSNU 11154]
 Length = 180

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 52/174 (29%), Positives = 87/174 (50%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT D + DI YIE +T +F + + ++ + + YP++V +
 Sbjct: 3 IRIATKEDANQLIDIYRPIENNTTSFEYDVPSLDDFKQIRIDITITYPIVMVDGETIL 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G AYA +K R+AY WTVE +VY+S Q G+G LY L + + Q +++A I
 Sbjct: 63 GYAYAHEYKERDAYQWTVEVSVYLSKNAQKGIGRRLYNSLEEYLRQHVVNIMACITGA 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQI 183
 N+ S+ HE +GY G + G+K+ W D+ + ++ P P +++
 Sbjct: 123 NETSIAFHEHMGYETVGQFKKVGFKNQWLDIYWLEKQISSSVSPEAFIPFSKL 176

>ref|NP_353896.2| acetyltransferase [Agrobacterium tumefaciens str. C58]
 gb|AAK86681.2| acetyltransferase [Agrobacterium tumefaciens str. C58]
 Length = 180

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 59/159 (37%), Positives = 86/159 (54%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-QDRYPWLVAEVEGVV 68
 IRP AD+ A+ +I + +F +P + L + YP+LVAE +G V
 Sbjct: 11 IRPCEEADIPAITEIYRDAVLHGRASFEIDPPDVATMAERRRLLVEGNYPYLVAEHDGKV 70

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
 AG AYAG ++AR AY TVE +VY+ + G+G L L+ A+GF+ ++AVIG
 Sbjct: 71 AGYAYAGAYRARPAYGATVEDSVYIDPAMKGTGIGRKLDDALIAEATARGFRQMIAVIGD 130

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N SV +H A G+ GT ++ G+KHG W + QR

Sbjct: 131 SANAASVGVHRAAGFELVGTFSIGWKHGQWLNTVLMQR 169

>ref|YP_002988528.1| Phosphinothricin acetyltransferase [Dickeya dadantii Ech703]
 gb|ACS86706.1| Phosphinothricin acetyltransferase [Dickeya dadantii Ech703]
 Length = 178

Score = 100 bits (248), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 58/161 (36%), Positives = 85/161 (52%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 + I A A +AA+ I H++ F TEP QE ++++Q PWLVA G
 Sbjct: 4 IVIEEAGAEHIAAIRQIYRHHVLHGIATFETEPPEQEMAHRVDKVQQAGLPWLVAHEG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 V G Y P++ R+AY +T+E ++Y++ GLG L + + G++ VVAVI
 Sbjct: 64 HVLGYCYLSPYRPRHAYRFTLEDSIYIAPERAGRGLGKRLQAAAFERVGQLGYRQVVAVI 123

Query: 127 GLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G N S+ +H +LG+ GTLR+ G KHG W D QR
 Sbjct: 124 GNSDNQASLGVHRSGLGDMVGTLRSVGMKHGRWVDTVIMQR 164

>ref|YP_001258130.1| phosphinothricin N-acetyltransferase [Brucella ovis ATCC 25840]
 gb|ABQ61144.1| phosphinothricin N-acetyltransferase [Brucella ovis ATCC 25840]
 Length = 179

Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 84/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR AD+ + I + T T ++ EP T E D+ +P LVAE +G V
 Sbjct: 4 IRDFQPADIETITAIYTQAVLTGTGSYEIEPPTMDEMAKRFAAFADQSFILVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 G AYA ++ R AY W E ++Y++ + G+G L L+ + A GF+ ++AVIG
 Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQIGKLLRELIARISALGFRQLLAVIGD 123

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N SV+LHE+LG+T G + +G+KHG W D Q
 Sbjct: 124 GEHNIGSVKLHESLGFTHCGRIEGSGFKHGRWLDTVLMQ 162

>ref|YP_001888617.1| GCN5-related N-acetyltransferase [Burkholderia phytofirmans PsJN]
 gb|ACD19247.1| GCN5-related N-acetyltransferase [Burkholderia phytofirmans PsJN]
 Length = 197

Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 62/165 (37%), Positives = 91/165 (55%), Gaps = 10/165 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD----RYPWLVAEV 64
 IR AT AD+ A+ I H++ T +F P + +DDL RL P++VAE+
 Sbjct: 21 IRDATEADLPAIQAIYAAHVLTGVASFEETPPS----VDDLRLMLASVRSHGLPYMVAEI 76

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +G VAG YA P++ R AY T+E ++YV+ ++ GLG L L++ E ++ +VA
 Sbjct: 77 DGEVAGYCYATPYRPRPAYRNTIEDSIYVNDAYRGRGLGRVLLQALIERCETGPWRQMV 136

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 VI + S+ LH LG+ GTL+A G+KHG W D QR
 Sbjct: 137 VIADGGSGGSLSLHTQLGFELTGTLKAVGFKHGRWLDTTLMQRTL 181

>ref|YP_585578.1| GCN5-related N-acetyltransferase [Cupriavidus metallidurans CH34]
gb|ABF10309.1| Phosphinothricin N-acetyltransferase [Cupriavidus metallidurans
CH34]
gb|EEE77719.1| predicted protein [Populus trichocarpa]
Length = 206

Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
Identities = 58/167 (34%), Positives = 87/167 (52%), Gaps = 5/167 (2%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDL-ERLQDRYPWLVAE 63
R+P +R AT D+ A+ I H+++ +F T E E L+ P++VAE
Sbjct: 29 RKPYRLRDATTTDDVPAIHAIYAHVQHGRASFEEVAPTVDEMRHRFGEVLKKGLPYIVAE 88

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
+G + G AYA ++AR+AY + +E ++Y+ HRH GLG L L+ E ++ +V
Sbjct: 89 RDGEILGYAYASSYRARSAYRFAIEDSIYIDHRHTGEGLGRALLAELITRCETGPWRQMV 148

Query: 124 AVIGLPND----PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
AV+ L SV +HE LG+ G L + G KHG W D QR
Sbjct: 149 AVVALTASGEGAGSVAVHERLGFRTVGRLESVGLKHGQWIDTLLMQR 195

>ref|NP_540775.1| phosphinothricin N-acetyltransferase [Brucella melitensis bv. 1
str. 16M]
ref|NP_697130.1| phosphinothricin N-acetyltransferase [Brucella suis 1330]
ref|YP_001591963.1| phosphinothricin N-acetyltransferase [Brucella canis ATCC 23365]
ref|YP_001626767.1| phosphinothricin N-acetyltransferase [Brucella suis ATCC 23445]
ref|ZP_03784670.1| Phosphinothricin N-acetyltransferase [Brucella ceti str. Cudo]
ref|ZP_05162729.1| phosphinothricin N-acetyltransferase [Brucella suis bv. 5 str.
513]
ref|ZP_05167094.1| phosphinothricin N-acetyltransferase [Brucella suis bv. 3 str.
686]
ref|ZP_05169039.1| phosphinothricin N-acetyltransferase [Brucella pinnipedialis
M163/99/10]
ref|ZP_05171054.1| phosphinothricin N-acetyltransferase [Brucella pinnipedialis
B2/94]
ref|ZP_05175145.1| phosphinothricin N-acetyltransferase [Brucella ceti M644/93/1]
ref|ZP_05178123.1| phosphinothricin N-acetyltransferase [Brucella ceti M13/05/1]
ref|ZP_05444380.1| phosphinothricin N-acetyltransferase [Brucella pinnipedialis
M292/94/1]
ref|ZP_05448755.1| phosphinothricin N-acetyltransferase [Brucella melitensis bv. 1
str. Rev.1]
ref|ZP_05450406.1| phosphinothricin N-acetyltransferase [Brucella neotomae 5K33]
ref|ZP_05453515.1| phosphinothricin N-acetyltransferase [Brucella melitensis bv. 3
str. Ether]
ref|YP_003106061.1| phosphinothricin N-acetyltransferase [Brucella microti CCM 4915]
ref|ZP_05756480.1| phosphinothricin N-acetyltransferase [Brucella sp. F5/99]
ref|ZP_05833652.1| phosphinotricin acetyltransferase [Brucella melitensis bv. 1 str.
16M]
ref|ZP_05837737.1| phosphinotricin acetyltransferase [Brucella suis bv. 4 str. 40]
ref|ZP_05932373.1| phosphinotricin acetyltransferase [Brucella ceti M13/05/1]
ref|ZP_05953890.1| phosphinotricin acetyltransferase [Brucella pinnipedialis
M163/99/10]
ref|ZP_05955945.1| phosphinotricin acetyltransferase [Brucella pinnipedialis B2/94]
ref|ZP_05960258.1| phosphinotricin acetyltransferase [Brucella ceti M644/93/1]
ref|ZP_05963404.1| phosphinotricin acetyltransferase [Brucella neotomae 5K33]
ref|ZP_05995125.1| phosphinotricin acetyltransferase [Brucella suis bv. 5 str. 513]
ref|ZP_05999687.1| phosphinotricin acetyltransferase [Brucella suis bv. 3 str. 686]
ref|ZP_06002914.1| phosphinotricin acetyltransferase [Brucella sp. F5/99]
ref|ZP_06100377.1| phosphinotricin acetyltransferase [Brucella pinnipedialis
M292/94/1]
ref|ZP_06104851.1| phosphinotricin acetyltransferase [Brucella melitensis bv. 1 str.
Rev.1]

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ref|ZP_06106592.1| phosphinotricin acetyltransferase [Brucella melitensis bv. 3 str.
Ether]
ref|ZP_06792167.1| acetyltransferase [Brucella sp. NVSL 07-0026]
gb|AAL53039.1| phosphinothricin n-acetyltransferase [Brucella melitensis bv. 1
str. 16M]
gb|AAN29045.1| phosphinothricin N-acetyltransferase [Brucella suis 1330]
gb|ABX61192.1| Phosphinothricin N-acetyltransferase [Brucella canis ATCC 23365]
gb|ABY37197.1| Phosphinothricin N-acetyltransferase [Brucella suis ATCC 23445]
gb|EEH15331.1| Phosphinothricin N-acetyltransferase [Brucella ceti str. Cudo]
gb|ACU47112.1| phosphinothricin N-acetyltransferase [Brucella microti CCM 4915]
gb|EEW88274.1| phosphinotricin acetyltransferase [Brucella melitensis bv. 1 str.
16M]
gb|EEW91865.1| phosphinotricin acetyltransferase [Brucella suis bv. 4 str. 40]
gb|EEX89749.1| phosphinotricin acetyltransferase [Brucella ceti M13/05/1]
gb|EEX97247.1| phosphinotricin acetyltransferase [Brucella ceti M644/93/1]
gb|EEX99467.1| phosphinotricin acetyltransferase [Brucella pinnipedialis B2/94]
gb|EEY03684.1| phosphinotricin acetyltransferase [Brucella neotomae 5K33]
gb|EEY07216.1| phosphinotricin acetyltransferase [Brucella pinnipedialis
M163/99/10]
gb|EEY27185.1| phosphinotricin acetyltransferase [Brucella sp. F5/99]
gb|EEY29095.1| phosphinotricin acetyltransferase [Brucella suis bv. 5 str. 513]
gb|EEY33657.1| phosphinotricin acetyltransferase [Brucella suis bv. 3 str. 686]
gb|EEZ10937.1| phosphinotricin acetyltransferase [Brucella melitensis bv. 3 str.
Ether]
gb|EEZ15653.1| phosphinotricin acetyltransferase [Brucella melitensis bv. 1 str.
Rev.1]
gb|EEZ30278.1| phosphinotricin acetyltransferase [Brucella pinnipedialis
M292/94/1]
gb|EFG37082.1| acetyltransferase [Brucella sp. NVSL 07-0026]
Length = 179
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Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 84/159 (52%), Gaps = 3/159 (1%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AD+ + I + T T ++ EP T E D+ +P LVAE +G V
Sbjct: 4 IRDFQPADIETITAIYTQAVLTGTGSYEIEPPTMDEMAKRFAAFADQGFILVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G AYA ++ R AY W E ++Y++ + G+G L L+ + A GF+ ++AVIG
Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQIGKLLRELIARISALGFRQLLAVIGD 123

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
N SV+LHE+LG+T G + +G+KHG W D Q
Sbjct: 124 GEHNIGSVKLHESLGFTHCGRIEGSGFKHGRWLDTVLMQ 162
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>ref|YP_003005423.1| Phosphinothricin acetyltransferase [Dickeya zeae Ech1591]
gb|ACT07944.1| Phosphinothricin acetyltransferase [Dickeya zeae Ech1591]
Length = 176
```

Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 60/161 (37%), Positives = 85/161 (52%), Gaps = 2/161 (1%)

```
Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
+ I A A +AA+ DI ++ F TE E D +++D PWLVA G
Sbjct: 4 IVIEDARAEHIAAIRDIYAQHVLHGIATFETEAPPEAEEMRDRWRKIRDAGLPWLVA TENG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G Y G ++ R AY +T+E ++Y+ H G+G L + L E QG++ VV+VI
Sbjct: 64 HVLGYCYLGFYRTRCAYRFTLEDSIYLHPDHLGKGVGKRLLSAALLQAEQQGYRQVVSVI 123

Query: 127 GLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
```

N S++LH +LG+T GTLR+ G KHG W D QR
 Sbjct: 124 ADSGNQASLQLHLSLGFLLTGTLSVGMKHGRWVDTTLLQR 164

>ref|YP_553531.1| putative phosphinothricin N-acetyltransferase [Burkholderia
 xenovorans LB400]
 gb|ABE34181.1| putative phosphinothricin N-acetyltransferase [Burkholderia
 xenovorans LB400]
 Length = 200

Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 62/165 (37%), Positives = 91/165 (55%), Gaps = 10/165 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQD---RYPWLVAEV 64
 IR AT AD+ A+ I H++ T +F P + +DDL RL P++VA+V
 Sbjct: 21 IRDATEADLPAIQAIYAHVLTGVASFEVPPS----VDDLRLARLASVRSYGLPYMVAQV 76

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +G VAG YA P++ R AY T+E ++YV+ ++ GLG L L++ E ++ +VA
 Sbjct: 77 DGEVAGYCYATPYRPRAAYRNTIEDSIYVNDAYRGRGLGRVLLQALIERCETGPWRQMV 136

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 VI + S+ LH LG+ GTL+A G+KHG W D QR
 Sbjct: 137 VIADGGSGGSLSLHTQLGFELTGTCLKAVGFKHGRWLDTTLMQRTL 181

>ref|YP_935194.1| putative N-acetyltransferase [Azoarcus sp. BH72]
 emb|CAL96308.1| putative N-acetyltransferase [Azoarcus sp. BH72]
 Length = 188

Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 69/170 (40%), Positives = 94/170 (55%), Gaps = 2/170 (1%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPW 59
 M+ R ++R ATAADM AV I HY+ ST F P + L++++D PW
 Sbjct: 11 MTDVRPAAQLRDATAADMEAVAAIYAHYVLGSTATFEETPPSADALRARLQQVRDAGLPW 70

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 LVA ++G V G YA P + R AY +TVE+++YV+ + GLG TL L++ E +
 Sbjct: 71 LVAVLDAVVGICYAAPHRRPAYRYTVENSIVYVAPGARGAGLGGTLLGALIQRCQGPW 130

Query: 120 KSVVAVI-GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 + +VAVI G N S+ LH A G+ GTL A GYK G W D QR
 Sbjct: 131 RQMVAVIGGSDNAASIALHAAHGFRPAGTLTAVGYKLGHVWDTVLMQRAL 180

>ref|ZP_04761786.1| GCN5-related N-acetyltransferase [Acidovorax delafieldii 2AN]
 gb|EER61428.1| GCN5-related N-acetyltransferase [Acidovorax delafieldii 2AN]
 Length = 173

Score = 99.8 bits (247), Expect = 1e-19, Method: Compositional matrix adjust.
 Identities = 56/159 (35%), Positives = 88/159 (55%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IRP+T D+ A+ I H++ T F +P T + + + R PWLVAE +G V
 Sbjct: 4 IRPSTDQDIPAITAIYQHHLVHGTGTFEIDPPTADMAARRKDVLAGLPWLVAEKDQGV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G AYA +K R AY ++ E ++YV+ + +G+G L L +A G + ++AVIG
 Sbjct: 64 LGFAYANWFKPRPAYRFSAESIYVADSARGMGVGRKLLAELAVQAQAAGVRKLLAVIGD 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ +H ALG+T G +R+ G+K G W D+ ++

Sbjct: 124 SANAGSIGVHRALGFTDVGVMRSVGWKFCAWRDIVLMEK 162

>ref|YP_364233.1| putative phosphinothricin N-acetyltransferase [Xanthomonas
campestris pv. vesicatoria str. 85-10]
emb|CAJ24179.1| putative phosphinothricin N-acetyltransferase [Xanthomonas
campestris pv. vesicatoria str. 85-10]
Length = 179

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 61/176 (34%), Positives = 87/176 (49%), Gaps = 3/176 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
P+E+R AD+ A+ I I P + + YP+LVAE++G
Sbjct: 2 PLELRVRDADIPAITAIYAEQIAGVNTYEYNAPSLDEMRRARVSAIVDAGYPYLVAELDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
VVAG AYA ++AR Y WTVE+++Y++ Q G+G L L+ E +GF+ ++AVI
Sbjct: 62 VVAGYAYASAFRRAGYRWTVENSIYLASAMQGRGIGKALLGELIAVCEQGRGFRQMIAMI 121

Query: 127 GLPNPDPSVR-LHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL--PAPPRPVRP 179
G + + R LHE G+ G G KHG W D QR APP +P
Sbjct: 122 GDAGNLASRHLHERFGFRTVGVFNGIGRKHGRWLDGVQMQRALSSGDTAPPSDEKP 177

>ref|YP_004278115.1| GCN5-related N-acetyltransferase [Agrobacterium sp. H13-3]
gb|ADY63795.1| GCN5-related N-acetyltransferase [Agrobacterium sp. H13-3]
Length = 180

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 54/166 (32%), Positives = 90/166 (54%), Gaps = 2/166 (1%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWL 61
P + IRP AD+ + +I + +F +P + ++ L + Y +LV
Sbjct: 4 PTISLTLIRPCEEADIPITEIYRDAVLHGRASFEIDPPSEDMMLERRRLVVEGNYSYL 63

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
AE++G +AG AYAG ++ R AY VE++VY+ + +G+G L L++ ++GF+
Sbjct: 64 AEIDGKIAGYAYAGAYRPRPAYGAAVENSVDYIDPAMKGMGIGRKLDDALIEDATSRGFRQ 123

Query: 122 VVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
++AVIG N S+ +H A G+ GT ++ G+KHG W D QR
Sbjct: 124 MIAVIGDSANAASIGVHRAAGFEHVGTFKSGIGWKHGQWLDTVLMQR 169

>ref|ZP_04858262.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA]
gb|EES75633.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39BFAA]
Length = 194

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 51/161 (31%), Positives = 85/161 (52%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR AT +D A+ +I + Y+E + + F + + +E+ ++ +YP+LVAE G
Sbjct: 7 ITIRTATLSDAQALLNIYSPYVEHTAITFEYDVPSVEEFASRIKNTLQKYPYLVAEKNR 66

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G AYA P+ R AYDW VE+++YV + G+G L+ L ++ +QG ++ A I
Sbjct: 67 LLGYAYASPFHERPAYDWAVETSIYVDQNIKHQIGIRRLHNALEDALRSQGILNMNACIA 126

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
P + SV H +GY G GYK W+++
Sbjct: 127 YPPEEDEYLDKNSVEFHTMGYRLVGEFYKCGYKFRWYNM 167

>ref|YP_297475.1| GCN5-related N-acetyltransferase [Ralstonia eutropha JMP134]
 gb|AAZ62631.1| GCN5-related N-acetyltransferase [Ralstonia eutropha JMP134]
 Length = 210

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
 Identities = 61/172 (35%), Positives = 90/172 (52%), Gaps = 13/172 (7%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-----ERLQDRYP 58
 +R+P +R A AD+ A+ I H++ +F P +DD+ E L+ P
 Sbjct: 32 QRKPFTRLRAGPADVP AIQAIYAHVHLHGRASFEETP----PGVDDMQLRMAEVLRKGLP 87

Query: 59 WLVAEEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 +LVAE +G V G AYA ++AR+AY + +E ++YV HR GLG TL L+ E
 Sbjct: 88 YLVAERDGEVLGYAYASSYRARSAYRYAIEDSIYVDHRCVGEGLGRTLLEALIARCETGP 147

Query: 119 FKSVMVAVIGLPND----PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 ++ +VAV+ S+ +HE LG+ G L A G+KHG W D QR
 Sbjct: 148 WRQMVAVVACTASGEGAGSLAVHERLGFRTVGRLEAVGFKHGQWIDTVLMQR 199

>ref|ZP_07217130.1| phosphinothricin N-acetyltransferase [Bacteroides sp. 20_3]
 gb|EFK61418.1| phosphinothricin N-acetyltransferase [Bacteroides sp. 20_3]
 Length = 164

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
 Identities = 56/161 (34%), Positives = 81/161 (50%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGVVA 69
 IR ++ D A+ DI N Y+ S F TEP +E + + YP+LV V
 Sbjct: 4 IRNVSSRDAKAIVDIYNEYVNVSVATFETEPLRVEEMEGRIAGISASYPYLVYVDHDEVV 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G YA WK + AY +T+E+TVY+S R++ G+G L L++ A G+ +++A I
 Sbjct: 64 GYCYAHAWKEKAAYKYTLETTVYLSPRYKKGKIGRQLMERLIEECRAGGYHALIACITEG 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFEL 170
 N+ S LHE LG+ G K W DV D+EL
 Sbjct: 124 NEASCSLHEKLGFKKVSHFEKVGLKFERWLDV---VDYEL 160

>ref|ZP_08079711.1| phosphinothricin acetyltransferase [Lactobacillus ruminis ATCC
 25644]
 gb|EFZ35730.1| phosphinothricin acetyltransferase [Lactobacillus ruminis ATCC
 25644]
 Length = 202

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
 Identities = 54/182 (29%), Positives = 94/182 (51%), Gaps = 8/182 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGVVA 69
 +R A D + I Y+E + + F + T E+ ++ +++YP++VAE++G +
 Sbjct: 9 LRFAEIDDANELLQIYAPYVEQTAITFEYDVPTVAEFSKRKIKNTREKYPYIVAEIDGKII 68

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G AYAG +K+R AYDW VE+++YV+ + LG G+ LY L ++ QG +V A I
 Sbjct: 69 GYAYAGTFKSRAAYDWA VETSIYVAKDDRGLGTGTLTYAALEAILKLQGITNVNACITYA 128

Query: 130 NDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRP-VRPVT 181
 + SV H+ Y G + GYK W+D+ + ++ P P ++ +
 Sbjct: 129 DQEDHLTHGSVD FHKH DYRLVGRFKKCGYKFD TWYDMIWMEKFISKHVVPMPAIIKSIIK 188

Query: 182 QI 183

+I

Sbjct: 189 EI 190

>ref|YP_003594410.1| phosphinothricin acetyltransferase [Caulobacter segnis ATCC 21756]

gb|ADG11792.1| Phosphinothricin acetyltransferase [Caulobacter segnis ATCC 21756]

Length = 185

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 61/161 (37%), Positives = 86/161 (53%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66

V IRP+ AD+ A+ +I + F P E E R P+LVAE++G

Sbjct: 5 VVIRPSVDADVPAITEIYGWNVLNGFGTFEEVPPDEAEMARRREGFLSRGLPYLVAELDG 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126

V G AYAGP++ R AY +TVE ++YVS G+G L L+++ EA G + + AVI

Sbjct: 65 KVVGYAYAGPFRRLRAAYRYTVEDSIYVSPDAVSGVGRALLKTLIEACEALGLRQMCABI 124

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166

G N S+ LH ALG+ +G G+K G W D+ + QR

Sbjct: 125 GDSGNQASIALHAALGFEEKGVFPDMGHKFGRWLDLVWMQR 165

>ref|NP_879101.1| putative acetyltransferase [Bordetella pertussis Tohama I]

emb|CAE40593.1| putative acetyltransferase [Bordetella pertussis Tohama I]

Length = 182

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 65/181 (35%), Positives = 88/181 (48%), Gaps = 16/181 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPW 59

+ IR + AD+ A+ I H++ T +F EP LE L++R P+

Sbjct: 9 ILIRDSRDADLPAIAAIYAHVHLHGHTASFELEPP-----GLEALRERRAAVLAHGLPY 61

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119

L AE G + G AYA P++ R AY TVE +VYV H G+G L L+ A G+

Sbjct: 62 LAAECGGEIVGYAYATPYRPRPAYRHTVEDSVYVRAGHAGGIGGKLLAALIDRCAAGGW 121

Query: 120 KSVVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRPVR 178

+ ++AV+G N SV LH G+ GT R+ GYKHG W D QR P R

Sbjct: 122 RQMLAVVGDSANTASVALHARHGFDITIGTFRSVGYKHGQWRDVTLMQRALGEGDATPPSR 181

Query: 179 P 179

P

Sbjct: 182 P 182

>ref|NP_882772.1| putative acetyltransferase [Bordetella parapertussis 12822]

ref|NP_886971.1| putative acetyltransferase [Bordetella bronchiseptica RB50]

emb|CAE36004.1| putative acetyltransferase [Bordetella parapertussis]

emb|CAE30920.1| putative acetyltransferase [Bordetella bronchiseptica RB50]

Length = 182

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 65/181 (35%), Positives = 89/181 (49%), Gaps = 16/181 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPW 59

+ IR + AD+ A+ I H++ T +F EP LE L++R P+

Sbjct: 9 ILIRDSRDADLPAIAAIYAHVHLHGHTASFELEPP-----GLEALRERRAAVLAHGLPY 61

Query: 60 LVAEEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 L AE G + G AYA P++ R AY TVE +VYV H G+G L L++ A G+
 Sbjct: 62 LAAECGGEIVGYAYATPYRPRPAYRHTVEDSVYVRAGHAGQGIGGKLLAALIERCAAGGW 121

Query: 120 KSVVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 + ++AV+G N SV LH G+ GT R+ GYKHG W D QR P R
 Sbjct: 122 RQMLAVVGDSANTASVALHARHGFDITIGTFRSVGYKHGQWRDVTLMQRALGEGDATPPGR 181

Query: 179 P 179
 P
 Sbjct: 182 P 182

>ref|YP_530095.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris
 BisB18]
 gb|ABD85776.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris
 BisB18]
 Length = 174

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
 Identities = 58/161 (36%), Positives = 85/161 (52%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEEVG 66
 +EIRP + AD+ A+ I + T F P E L +P+LVA G
 Sbjct: 4 LEIRPTSLADLPATAIYAEAVRCGTATFELTPPDLAEMTRRFAALTGGGFPYLVARRAG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 + G AYAGP++ R AY +TVE+++Y++ QR G+GS L L+ EA+G++ ++AVI
 Sbjct: 64 ELLGYAYAGPYRPRPAYRFTVENSIIYLAPAAQRQGVGSRLGLRLIAESEARGYRQMIAMI 123

Query: 127 GLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G N S+ LH G+ G + G+K G W D QR
 Sbjct: 124 GGSDNLGSIALHGRTGFMIGVHPSVGFKFGRWLDSVLMQR 164

>emb|CBL24674.1| Sortase and related acyltransferases [Ruminococcus obeum A2-162]
 Length = 202

Score = 99.4 bits (246), Expect = 2e-19, Method: Compositional matrix adjust.
 Identities = 53/173 (30%), Positives = 88/173 (50%), Gaps = 7/173 (4%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL 60
 MS + IR A+ D AA+ I Y+ + + F E + +E+ + ++YP+L
 Sbjct: 1 MSSAASNIHIRTASPDAAALLAIYAPYVRETAITFEYEVPSSTEEFTRRITHLTLEKYPYL 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 VAE + + G AYAGP+ R AYDW VE+++YV + G+G L+ L +++ QG
 Sbjct: 61 VAEKDHTILGYAYAGPFHERAAYDWAVENTSIYVDQNLKHSIGIGRLLHDALENALKKQGIL 120

Query: 121 SVVAVIGLP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 ++ A I N+ SV H +GY G GYK W+++ + ++
 Sbjct: 121 NMNACIACPTEDPHLNNNSVEFHTHMGYRLVGEFYQCGYKFLTWYNMVWMEK 173

>ref|YP_001368661.1| GCN5-like N-acetyltransferase [Ochrobactrum anthropi ATCC 49188]
 gb|ABS12832.1| GCN5-related N-acetyltransferase [Ochrobactrum anthropi ATCC 49188]
 Length = 193

Score = 99.0 bits (245), Expect = 2e-19, Method: Compositional matrix adjust.
 Identities = 60/174 (34%), Positives = 89/174 (51%), Gaps = 9/174 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEEGVV 68
 IR AD+ + I + T ++ EP T E + E ++ +P LVAE +G V

Sbjct: 18 IRDFQPADIETITTTIYTEAVLTGAGSYEIEPPTMDEMVKRFEAFVEQGFILVAEEDGRV 77

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G AYA ++ R AY W E ++Y++ + G+G L L+ + A GF+ ++AVIG

Sbjct: 78 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGKGIGKLLRELIDRIAALGFRQLLAVIGD 137

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ-----RDFELPAPP 174
N SV+LHE+LG+T G + +G+KHG W D Q R E PP

Sbjct: 138 GEHNIGSVKLHESLGFTHCRIEGSGFKHGRWLDTVLMQLPLNGGRSIEPGTPP 191

>ref|ZP_08188723.1| sortase-like acyltransferase [Xanthomonas perforans 91-118]
gb|EGD13644.1| sortase-like acyltransferase [Xanthomonas perforans 91-118]
Length = 179

Score = 99.0 bits (245), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 62/176 (35%), Positives = 86/176 (48%), Gaps = 3/176 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
P+E+R AD+ A+ I I P + + YP+LVAE++G

Sbjct: 2 PLELRAVRDADIPAITAIYAEQIAGVNTYEYNAPSLDEMRAVRSAIVDAGYPYLVAELDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VVAG AYA ++AR Y WTVE+++Y++ Q G+G L L+ E +GF+ ++AVI

Sbjct: 62 VVAGYAYASAFRRARAGYRWTVENSIYLASAMQGRGIGKALLGELIAVCEQGRGFRQMIAMI 121

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL--PAPPRPVRP 179
G N S LHE G+ G G KHG W D QR APP +P

Sbjct: 122 GDAGNLASRNLERHFGFRTVGVFNGIGRKHGRWLDGVQMQRALGSGDTAPPSDEKP 177

>ref|ZP_06843515.1| Phosphinothricin acetyltransferase [Burkholderia sp. Ch1-1]
gb|EFG68808.1| Phosphinothricin acetyltransferase [Burkholderia sp. Ch1-1]
Length = 197

Score = 99.0 bits (245), Expect = 2e-19, Method: Compositional matrix adjust.
Identities = 65/178 (36%), Positives = 95/178 (53%), Gaps = 12/178 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQD---RYPWLVAEV 64
IR AT AD+ A+ I H++ T +F P + +DDL RL P++VA++

Sbjct: 21 IRDATEADLPAIQAIYAHHVLTVGASFEIEPPS---VDDLRLTLASVRSYGLPYMVAQI 76

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+G VAG YA P++ R AY T+E ++YV+ ++ GLG L L++ E ++ +VA

Sbjct: 77 DGEVAGYCYATPYRPRAAYRNTIEDSIYVNDAYRGRGLGRVLLQALIERCETGPWRQMV 136

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL--PAPPRPVRP 179
VI + S+ LH LG+ GTL+A G+KHG W D QR PP V P

Sbjct: 137 VIADGGSGGSLSLHTQLGFELTGTLKAVGFKHGRWLDTTLMQRTLGKGDSTPPDDVAP 194

>ref|YP_003819401.1| Phosphinothricin acetyltransferase [Brevundimonas subvibrioides
ATCC 15264]
gb|ADL01778.1| Phosphinothricin acetyltransferase [Brevundimonas subvibrioides
ATCC 15264]
Length = 182

Score = 99.0 bits (245), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 60/173 (34%), Positives = 89/173 (51%), Gaps = 4/173 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AT AD+ A+ + + T T F +P + + E ++ + PVLVAE++G

Sbjct: 2 IRAATPADLPAIAALYGREVLTGTATFELDPPSAADMTTRFEAVRAKGLPWLVAEIDGAF 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI-- 126
AG AYA P++ R AY + VE ++YV + G+G L T L++ + A G + V+ I
Sbjct: 62 AGYAYASPFPRPAYRYGVEGSIYVEEAARGHGVGRALLTALVERVRAMGLRHVIGAISD 121

Query: 127 GLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
++ S+ LHE LG+ GT G+K W DV Q D LP P P
Sbjct: 122 SATSEASIALHERLGFRRVGTYAQVGWKFDRWIDVHLMQLDL-LPDGQPPTTP 173

>emb|CBL06841.1| Sortase and related acyltransferases [Megamonas hypermegale
ART12/1]
Length = 168

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 42/158 (26%), Positives = 80/158 (50%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
R A D + +I Y++ + + F E E+ + ++ ++P+++A + +
Sbjct: 9 FRLAKIDDAEKLVEIYAPYVKNITFEYEVPIIDEFKQRITKIMSKFPYILACIGDEIV 68

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G YA ++ R AY+W VE+++Y++ ++Q +G LYT L ++ Q ++VA I P
Sbjct: 69 GYTYASTFRERQAYNWCVETSIYINEKYQGRKIGEILYTKLEAILKLQNITNLVASITYP 128

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRD 167
N S+ HE Y GYK W+D+ F +++
Sbjct: 129 NPQSIAFHEKFNYKKIAHFTKCGYKQNCWYDMVFMEN 166

>ref|YP_001682970.1| GCN5-like N-acetyltransferase [Caulobacter sp. K31]
gb|ABZ70472.1| GCN5-related N-acetyltransferase [Caulobacter sp. K31]
Length = 185

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 61/161 (37%), Positives = 86/161 (53%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
V IRP+T AD+ A+ I + F P E D+ P+LVAE +G
Sbjct: 5 VTIRPSTDADLPAITAIYGNVFNGLGTFFEEIPPDQAEMGRRRAAFLDKGLPYLVAEQDG 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VV G AYAGP++ R AY +TVE +VYV G+G L + ++++ EA G + + AVI
Sbjct: 65 VVLGYAYAGPFRLRAAYRYTVEDSVYVGPDAVGKGVKALLSAVIEACEALGLRQMCABI 124

Query: 127 G-LPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
G N S+ LH +LG+ +G GYK G W D+ + QR
Sbjct: 125 GDSGNAASIGLHASLGFEKKGVFPDMGYKFGRWVDLVWMQR 165

>ref|ZP_03265218.1| GCN5-related N-acetyltransferase [Burkholderia sp. H160]
gb|EEA03124.1| GCN5-related N-acetyltransferase [Burkholderia sp. H160]
Length = 193

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.
Identities = 61/173 (35%), Positives = 93/173 (53%), Gaps = 10/173 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 64
+R AT AD+ A+ I H++ T +F P + +DDL RL P++VAE+
Sbjct: 13 VRDATEADLPAIQAIYAHVLTGVASFEEPPS----VDDLRLARLAAVRSHGLPYMVAEI 68

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+G +AG YA P++ R AY T+E ++YV+ ++ G+G L L++ E ++ +A

Sbjct: 69 DGEIAGYCYATPYRPRAAYRNTIEDSIYVNDAYRGRGIGRVLLQALIERCETGPWRQMIA 128

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 VI + S+ LH LG+ GTL+A GYKHG W D QR A P

Sbjct: 129 VIADGGSGGSLSLHTQLGFELTGTLKAVGYKHGRWLD'TTLMQRTLGRGASTGP 181

>ref|YP_002234420.1| putative acetyltransferase [Burkholderia cenocepacia J2315]
 emb|CAR55667.1| putative acetyltransferase [Burkholderia cenocepacia J2315]
 Length = 186

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.
 Identities = 59/172 (34%), Positives = 86/172 (50%), Gaps = 2/172 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
 +R AT AD+ A+ I H++ S +F P E + L P+LVAE +G V

Sbjct: 9 VRDATDADLEAIHAIYAHVHHSVASFEETPPDVAELRARRDAVLNHGLPYLVAECDGRV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 AG AYA P++ R+AY + +E ++Y+ + G+G L L+ E ++ ++AVI

Sbjct: 69 AGYAYATPYRTRSAYRFAIEDSIYIDDAQQRGRGIGRALLAALIARCEDGPWRQMIAVIAD 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVVP 179
 S LH A G+ G L+A G+KHG W D QR A RP P

Sbjct: 129 GGTGGSTSLHRAFGFEPAGQLKAVGFKHGRWIDTALLQRPLGEGANTRPASP 180

>ref|YP_002885911.1| GCN5-related N-acetyltransferase [Exiguobacterium sp. AT1b]
 gb|ACQ70466.1| GCN5-related N-acetyltransferase [Exiguobacterium sp. AT1b]
 Length = 170

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.
 Identities = 59/168 (35%), Positives = 88/168 (52%), Gaps = 5/168 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR D+ + I N I ST + +P T W + E+ + P +V +

Sbjct: 2 IRNCRDDLQMLHIYNDAIVNSTAVYHYQPVTLDNRVAWYE--EKKEQDCPIIIVWVEDD 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126
 VV G A GP++ AY +TVE +VYV ++ G+G L +++ EA+G K+V+ I

Sbjct: 60 VVMGFATFGPFRPWPAYHYTVEHSVYVHPGYRGKGIGNKLKEIIRIAEARGMKTIVIGI 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N S+R HE +G+ GT+R AGYK G W D+ +Q D E PA P

Sbjct: 120 DASNVTSIRAHEKVGFFVHSGTIRNAGYKFGKWLDSLQYQLDLEGPASP 167

>ref|ZP_06896375.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC
 49957]
 gb|EFH11927.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC
 49957]
 Length = 179

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.
 Identities = 70/174 (40%), Positives = 91/174 (52%), Gaps = 7/174 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 +R AT AD+ A+ I H++ T T F P T QE L R+Q + + WLVAE G V

Sbjct: 4 LRDATPADLPAITAIYAHVLTGTGTFEETPPTEQEMAARLARVQGGWAWLVAEEAGEV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G ++A+ A+ + E ++YV GLG +L LL+ EA GF+ V AVIG

Sbjct: 64 LGFGLLSAYRAQPAWRYAAEDSIYVRQDVHGGQLGKSLVAALLERAEAAAGFRQVFVIGD 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR-----DFELPAPPRP 176

N SV LH +LG+ G LR AG+K G W DV QR D LPA P

Sbjct: 124 SENVGSVGLHLSLGRQAGLLRGAGFKFGRWLDVVLQMQRPVGAADKTLPAGAAP 177

>ref|YP_002502279.1| GCN5-related N-acetyltransferase [Methylobacterium nodulans ORS 2060]

gb|ACL61976.1| GCN5-related N-acetyltransferase [Methylobacterium nodulans ORS 2060]

Length = 182

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.

Identities = 60/159 (37%), Positives = 83/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEP-QTPQEWIDDLERLQDRYPWLVAEVEGVV 68

+RP D+ AV I + T +F +P P+ + +P+L A +

Sbjct: 11 VRPCGPEDIPAVQAIYAQAVLTGRASFELDPDIPPEMLRRHAGLVGAGFPFLAAMRGTEL 70

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127

G AYAGP++AR AY TVE++VYV G+G L L+ + +GF+ +VAVIG

Sbjct: 71 LGYAYAGPYRARPAYRSTVENSVMYVDPARHGQGIGRRLGLDLIAATERGFRQMVAVIGD 130

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

N S+RLH ALG+ G LRA G+KHG W D QR

Sbjct: 131 SANTASIRLHAALGFAQVGVLRVAVGWKHGQWLDTVLMQR 169

>ref|ZP_07957845.1| acetyltransferase [Lachnospiraceae bacterium 5_1_63FAA]

gb|EFV15350.1| acetyltransferase [Lachnospiraceae bacterium 5_1_63FAA]

Length = 185

Score = 98.6 bits (244), Expect = 3e-19, Method: Compositional matrix adjust.

Identities = 56/162 (34%), Positives = 86/162 (53%), Gaps = 8/162 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVA-EVEG 66

+E+R AT D + +I +Y+E + + F E + E+ +++ RYP+L A + G

Sbjct: 1 MEVRLATPQDAEELLEIYRYVEHTAITFEYETPSITEFRQRIKQTLKRYPYLAADVGHG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126

+ G AYA +K R AYDW+VE+T+YV +R G+G LY L + + Q ++ A I

Sbjct: 61 KIVGYAYASSFKNRAAYDWSVETIYVDKDVKRQIGIGKKLYEALKEILRKQHVINDACI 120

Query: 127 GLP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

P SV+ HE LGY G +GYK G W+D+

Sbjct: 121 TDPEIEDEYVTKNVQYHEHLGYHVMVGKFKYKSGYKFGRWYDM 162

>ref|ZP_01675773.1| toxin resistance protein [Vibrio cholerae 2740-80]

ref|ZP_01970000.1| toxin resistance protein [Vibrio cholerae NCTC 8457]

ref|ZP_01973658.1| toxin resistance protein [Vibrio cholerae B33]

ref|ZP_04395947.1| toxin resistance protein [Vibrio cholerae BX 330286]

ref|ZP_04398962.1| toxin resistance protein [Vibrio cholerae B33]

ref|ZP_04406171.1| toxin resistance protein [Vibrio cholerae RC9]

ref|YP_002876658.1| toxin resistance protein [Vibrio cholerae MJ-1236]

ref|ZP_05419792.1| phosphinothricin N-acetyltransferase [Vibrio cholera CIRS 101]

ref|ZP_06028240.1| phosphinothricin N-acetyltransferase [Vibrio cholerae INDRE 91/1]

gb|EAX59669.1| toxin resistance protein [Vibrio cholerae 2740-80]

gb|EAX74676.1| toxin resistance protein [Vibrio cholerae NCTC 8457]

gb|EAX78797.1| toxin resistance protein [Vibrio cholerae B33]

gb|EEO11576.1| toxin resistance protein [Vibrio cholerae RC9]

gb|EEO18368.1| toxin resistance protein [Vibrio cholerae B33]

gb|EEO21707.1| toxin resistance protein [Vibrio cholerae BX 330286]

gb|ACQ62862.1| toxin resistance protein [Vibrio cholerae MJ-1236]
gb|EET90997.1| phosphinothricin N-acetyltransferase [Vibrio cholera CIRS 101]
gb|EEY49695.1| phosphinothricin N-acetyltransferase [Vibrio cholerae INDRE 91/1]
Length = 169

Score = 98.6 bits (244), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 55/154 (35%), Positives = 79/154 (51%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV 64
+EIR D+A + DI N YIE + F P + +EW R +Y VA
Sbjct: 1 MEIRTGEFEDIAGITDIFNFYIEQTNARFEFFPTLENREEWFSQFSRTA-KYQIYVAVE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
GV+ G A + ++A A+D TVE +VY++ + GLGS LYT L S+ A G +++
Sbjct: 60 NGVLQGFACSQKYRAIPAFDDTVEVSVYLAQEAKGKGLGSKLYTQLFSSIRAYGVHRILS 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
+ LPND SV LH+ G+ G KHG +
Sbjct: 120 GVALPNDASVALHKRFGFREVGISNEYAKKHGQY 153

>ref|YP_001779246.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia MC0-3]
gb|ACA94756.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia MC0-3]
Length = 186

Score = 98.6 bits (244), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 59/172 (34%), Positives = 86/172 (50%), Gaps = 2/172 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
+R AT AD+ A+ I H++ S +F P E + L P+LVAE +G V
Sbjct: 9 VRDATDADLDIAHAIYAHVHHSVASFEETPPDVAELRARRDAVLNHGLPYLVAECDGRV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
AG AYA P++ R+AY + +E ++Y+ + G+G L L+ E ++ ++AVI
Sbjct: 69 AGYAYATPYRTRSAYRFAIEDSIYIDDAQRGRGIGRALLDALIARCEGGPWRQMIAVIAD 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
S LH A G+ G L+A G+KHG W D QR A RP P
Sbjct: 129 GGTGGSTSLHRAFGFEPAGLLKAVGFKHGRWIDTALLQRPLGDGANTRPASP 180

>ref|YP_998663.1| GCN5-related N-acetyltransferase [Verminephrobacter eiseniae
EF01-2]
gb|ABM59645.1| GCN5-related N-acetyltransferase [Verminephrobacter eiseniae
EF01-2]
Length = 181

Score = 98.6 bits (244), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 58/159 (36%), Positives = 85/159 (53%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IRP D+ AV I H++ T F +P E + R PWLVA+ +G +
Sbjct: 5 IRPGADDDIPAVTAIYRHHVLHGTGTFFELDPPECATEMAARRADVLRGLPWLVAQEDGQI 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
G AYA +K R AY ++ E +VYV+ + GLG L L+ +A G + ++AVIG
Sbjct: 65 LGFAYANWFKPRPAYRFSAESDVYVADSARGRGLGRQLLAELVAQAQAAGVRKLLAVIGD 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+ LH ALG+T GT+R+ G+K G W D+ ++
Sbjct: 125 SANAGSIGLHRALGFTDVGTMRSVGWKFGAWRDIVLMEK 163

>ref|YP_623564.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia AU 1054]
ref|YP_838296.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia HI2424]
gb|ABF78591.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia AU 1054]
gb|ABK11403.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia HI2424]
Length = 186

Score = 98.2 bits (243), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 59/172 (34%), Positives = 86/172 (50%), Gaps = 2/172 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
+R AT AD+ A+ I H++ S +F P E + L P+LVAE +G V
Sbjct: 9 VRDATDADLDIAHAIYAHVHHSVASFEETPPDVAELRARRDAVLSHGLPYLVAECDGRV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
AG AYA P++ R+AY + +E ++Y+ + G+G L L+ E ++ ++AVI
Sbjct: 69 AGYAYATPYRTRSAYRFAIEDSIYIDDAQRGRGIGRALLDALIARCEGGPWRQMIAVIAD 128

Query: 128 LPNDPSVRLHEALGYTARGLTARAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
S LH A G+ G L+A G+KHG W D QR A RP P
Sbjct: 129 GGTGGSTSLHRAFGFEPAGLLKAVGFKHGRWIDTALLQRPLGDGANTRPASP 180

>ref|ZP_05180120.1| phosphinothricin N-acetyltransferase [Brucella sp. 83/13]
ref|ZP_06096003.1| phosphinothricin acetyltransferase [Brucella sp. 83/13]
ref|ZP_07470127.1| phosphinothricin N-acetyltransferase [Brucella sp. NF 2653]
gb|EEZ32121.1| phosphinothricin acetyltransferase [Brucella sp. 83/13]
gb|EFM63885.1| phosphinothricin N-acetyltransferase [Brucella sp. NF 2653]
Length = 179

Score = 98.2 bits (243), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 56/159 (35%), Positives = 84/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AD+ + I + T T ++ EP E D+ +P LVAE +G V
Sbjct: 4 IRDFQPADIETITAIYTQAVLTGTGSYEIEPPAMDEMAKRFAAFADQGFILVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G AYA ++ R AY W E ++Y++ + G+G+ L L+ + A GF+ ++AVIG
Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQGIGNLLLRKLIARISALGFRQLLAVIGD 123

Query: 129 P--NDPSVRLHEALGYTARGLTARAAGYKHGGWHDVGFQW 165
N SV+LHE+LG+T G + +G+KHG W D Q
Sbjct: 124 GEHNIGSVKLHESLGFTHCGRIEGSGFKHGRWLDTVLMQ 162

>ref|YP_002287583.1| phosphinothricin N-acetyltransferase [Oligotropha
carboxidovorans
OM5]
gb|ACI91718.1| phosphinothricin N-acetyltransferase [Oligotropha carboxidovorans
OM5]
Length = 185

Score = 98.2 bits (243), Expect = 4e-19, Method: Compositional matrix adjust.
Identities = 57/155 (36%), Positives = 83/155 (53%), Gaps = 2/155 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVAEVEG 66
+ IR ATAAD+ A+ I + T +F E L +P+LVA V+G
Sbjct: 13 LTIRSATAADIPAITAIYGFVREKTASFELTAPDEAEMARRFTALTGGFPYLVATVDG 72

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
+AG AYAGP++ R+AY +TVE +VY+ + G+G L T L+ +GF+ ++AVI
Sbjct: 73 HLAGYAYAGPYRPRSAYRYTVEDSVYLDPAYYHRGIGRALLTELIAECTMRGFRQIIAVI 132

Query: 127 G-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHD 160
 G N S+ LH + G+ GT G+K G W D
 Sbjct: 133 GDSANAASIGLHRSAGFAMIGTHPNVGFKFGRWLD 167

>ref|NP_900042.1| resistance protein [Chromobacterium violaceum ATCC 12472]
 gb|AAQ58050.1| probable resistance protein [Chromobacterium violaceum ATCC 12472]
 Length = 174

Score = 98.2 bits (243), Expect = 4e-19, Method: Compositional matrix adjust.
 Identities = 58/163 (35%), Positives = 88/163 (53%), Gaps = 6/163 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEV 64
 ++IR AT D+AA+ DI N I T+T + +P TP E W D R YP L+AE
 Sbjct: 1 MQIREATLEDLAAILDYNEVIATTTAVYNDDPLTPGEFAVWFQD--RAAAGYPVLLAED 58

Query: 65 E-GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 E G G + G ++AR Y +TVE +V+++ + G+G+ L L +A G +++
 Sbjct: 59 EDGRALGFSSFGDFRARPGRYFTVEHSVHLTADARGKGIGTALVQALFPRAQALGKHTML 118

Query: 124 AVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 + N+ S+R HE LG+ G L G+K G W D+ + QR
 Sbjct: 119 GAVDADNEASIRFHEKLGFGVQVGRLPQVGFKFGRWLDLVYLQR 161

>ref|YP_004012611.1| phosphinothricin acetyltransferase [Rhodocrobium vanniellii
 ATCC
 17100]
 gb|ADP71512.1| Phosphinothricin acetyltransferase [Rhodocrobium vanniellii ATCC
 17100]
 Length = 190

Score = 98.2 bits (243), Expect = 4e-19, Method: Compositional matrix adjust.
 Identities = 65/177 (36%), Positives = 90/177 (50%), Gaps = 7/177 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR-TEPQTPQEWIDDLERLQDRYPWLVAEVE 65
 V +R A DMAAV I H++ +F P + + L P+LVAE
 Sbjct: 11 AVSVRDARECDMAAVHAIYAHHVLDGLASFEEVAPSVEEMAMRRESVLASGLPYLVAERG 70

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G AYAG ++ R+AY +T+E +VYV+ + G+GS L LL EA ++ +VAV
 Sbjct: 71 GAVVGYAYAGLYRLRSAYRYTIEDSVYVADGLRGCGIGSVLLAELLARCEAGPWRQMVAV 130

Query: 126 IG-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR-----DFELPAPPRP 176
 IG N S+ LH+ +G+ G L +AG+K G W D QR D LP R
 Sbjct: 131 IGDSGNAGSIALHKRMGFHPAGVLVSAGFKFGRWVDSVLMQRRLEGDRTLPESDRA 187

>ref|YP_002123860.1| Phosphinothricin N-acetyltransferase [Streptococcus equi subsp.
 zooepidemicus MGCS10565]
 gb|ACG62847.1| Phosphinothricin N-acetyltransferase [Streptococcus equi subsp.
 zooepidemicus MGCS10565]
 Length = 225

Score = 98.2 bits (243), Expect = 5e-19, Method: Compositional matrix adjust.
 Identities = 62/176 (35%), Positives = 84/176 (47%), Gaps = 8/176 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT AD + DI Y+E + V F + E+ L + YP LV E EG +
 Sbjct: 33 IRLATLADAKTLLDIYRYPVEETAVTFEYTVPSLTFEERRLSDIMVFYPCLVVEEEGGIL 92

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + AR AY W+ E T+Y++ + GLGS LY L ++ G + A I P

Sbjct: 93 GYAYASRFHARAAYAWSAEVTIYLAQEARGRGLGSALYHRLLESYLGKMGILNCNACIASP 152

Query: 130 -----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF-ELPAPPRPV 177
 + S HE LGY G +GYK W D+ + ++ E PPRPV

Sbjct: 153 AHATPYLTNSSQVFHEKLGRLVGRFHQSGYKFNQWFDVMWMEKLLGEHDVPPRPV 208

>ref|ZP_02438997.1| hypothetical protein CLOSS21_01461 [Clostridium sp. SS2/1]
 gb|EDS21498.1| hypothetical protein CLOSS21_01461 [Clostridium sp. SS2/1]
 Length = 185

Score = 98.2 bits (243), Expect = 5e-19, Method: Compositional matrix adjust.
 Identities = 56/162 (34%), Positives = 86/162 (53%), Gaps = 8/162 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-EVEG 66
 +E+R AT D + +I +Y+E + + F E + E+ +++ RYP+L A + G

Sbjct: 1 MEVRLATPQDAEELLEIYRYVEHTAITFEYETPSITEFRQRIKQTLKRYPYLAADVGHG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AYA +K R AYDW+VE+T+YV +R G+G LY L + + Q ++ A I

Sbjct: 61 KIVGYAYASSFKNRAAYDWSVETTIYVDKDVRRQGIGKKLYEALKEILRKQHVINLDACI 120

Query: 127 GLP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 P SV+ HE LGY G +GYK G W+D+

Sbjct: 121 TDPEIEDEYVTKNSVQYHEHLGYHMGKFKYKSGYKFGRWYDM 162

>ref|ZP_05456648.1| phosphinothricin N-acetyltransferase [Brucella ceti M490/95/1]
 ref|ZP_05459707.1| phosphinothricin N-acetyltransferase [Brucella ceti B1/94]
 ref|ZP_05935601.1| phosphinothricin acetyltransferase [Brucella ceti B1/94]
 ref|ZP_06109837.1| phosphinothricin acetyltransferase [Brucella ceti M490/95/1]
 gb|EEX86557.1| phosphinothricin acetyltransferase [Brucella ceti B1/94]
 gb|EEZ07738.1| phosphinothricin acetyltransferase [Brucella ceti M490/95/1]
 Length = 179

Score = 97.8 bits (242), Expect = 5e-19, Method: Compositional matrix adjust.
 Identities = 56/159 (35%), Positives = 83/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR AD+ + I + T T ++ EP T E D+ +P LVAE +G V

Sbjct: 4 IRDFQPADIETITAIYTQAVLTGTGSYEIEPPTMDEMAKRFAAFADQGFPI LVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G AYA ++ R AY W E ++Y++ + G+G L L+ + A GF+ ++AVIG

Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQIGKLLRELIARISALGFRQLLAVIGD 123

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 N SV+LHE+LG+ G + +G+KHG W D Q

Sbjct: 124 GEHNIGSVKLHESLGFHCGRIEGSGFKHGRWLDTVLMQ 162

>ref|NP_793104.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato str. DC3000]
 gb|AA056799.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato str. DC3000]
 Length = 179

Score = 97.8 bits (242), Expect = 6e-19, Method: Compositional matrix adjust.
 Identities = 60/161 (37%), Positives = 84/161 (52%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEG 66
 + +R A DM AV I ++ +F EP T E ++ + L P+LVAE

Sbjct: 5 LTLRDARDDMPAVQAIYADHVLHGISSFELEPPTLAELLERRSQVLAKGLPYLVAERAK 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G Y P++ R AY +TVE +VYV LG+G L + L+K E G++ ++AVI
 Sbjct: 65 EVVGYGYVTPYRPRAAYRFTVEDSVYVRDGMGLGIGQALLSELIKRCETGGWRQMIAVI 124

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G N S+RLHE LG+ G + G+KHG W D QR
 Sbjct: 125 GNSENIASLRLHERLGFGRVGVFESVGFKHGRWVDTVLMQR 165

>ref|YP_001832727.1| GCN5-related N-acetyltransferase [Beijerinckia indica subsp. indica

ATCC 9039]

gb|ACB95238.1| GCN5-related N-acetyltransferase [Beijerinckia indica subsp. indica

ATCC 9039]

Length = 180

Score = 97.8 bits (242), Expect = 6e-19, Method: Compositional matrix adjust.
 Identities = 59/160 (36%), Positives = 82/160 (51%), Gaps = 6/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL---QDRYPWLVAEVEG 66
 +R D+ A+ I +H++ F P P E + R +RYP++VAE E
 Sbjct: 12 LRDCDENDIPAITAIYSHHVLNGFGTFEIVP--PGAEEMKIRRRVMSTNRYPIVAEFER 69

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G AY ++ R AY TVE ++Y+ Q G+G L + LL GF+ VVAVI
 Sbjct: 70 KVVGFAYVNSYRQRPAYSKTVEDSIYIRDGLQGQIGQRLLSRLAETAGAGFRQVAVI 129

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
 G N S+RLHE LG+ GTL+ G+K+G W D Q
 Sbjct: 130 GDSENHASIRLHEKLGFGHAGTLKTVGWKNGRWLDTVLMQ 169

>ref|NP_642621.1| phosphinothricin N-acetyltransferase [Xanthomonas axonopodis pv. citri str. 306]

gb|AAM37157.1| phosphinothricin N-acetyltransferase [Xanthomonas axonopodis pv. citri str. 306]

Length = 179

Score = 97.8 bits (242), Expect = 6e-19, Method: Compositional matrix adjust.
 Identities = 59/162 (36%), Positives = 86/162 (53%), Gaps = 3/162 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIE-TSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE 65
 P+E+R AD+ A+ I + +T +R P + + YP+LVAE++
 Sbjct: 2 PLELRAVRNADIPAITAIYAEQVAGVNTYEYRA-PSLDEMRAVSAIVDAGYPYLVAELD 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 GVVAG AYA ++AR Y WIVE+++Y+S Q G+G L L+ E +GF+ ++AV
 Sbjct: 61 GVVAGYAYASAFRAGYRWTVENSIIYLSAAMQGRGIGKALLGELIAVCEQGRGFRQMIAV 120

Query: 126 IGLPNDPSVR-LHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 IG + + R LHE G+ G G KHG W D QR
 Sbjct: 121 IGDAGNLASRHLHERFGFRTVGVFNGIGRKHGRWLDGVQMQR 162

>ref|ZP_02376770.1| GCN5-related N-acetyltransferase [Burkholderia ubonensis Bu]
 Length = 184

Score = 97.8 bits (242), Expect = 6e-19, Method: Compositional matrix adjust.
 Identities = 62/179 (34%), Positives = 92/179 (51%), Gaps = 4/179 (2%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWL 60
 +P+ +R +T D+ A+ I H++ S +F P E + L+ P+L

Sbjct: 4 TPDTVSCIVRDSTGDGLDAIQAIYAHVHRHSVASFEETPPDVAELRARRDTVLRHGLPYL 63

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120

VAE +G VAG AYA P++ R+AY +T+E ++Y+ + G+G L L+ EA ++

Sbjct: 64 VAEHDGRVAGYAYATPYRTRSAYRYTIEDSIYIDDARRGRGIGRALLAALIARCEAGPWR 123

Query: 121 SVVAVIG-LPNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA--PPRP 176

+VAVI S LH A G+ GTL+A G+KHG W D QR A PRP

Sbjct: 124 QMVAVIADGGTGGSTSLHRAFGFEPITGLKAVGFKHGRWIDTALLQRPLGEGAHDAAPRP 182

>ref|YP_417853.1| phosphinothricin N-acetyltransferase [Staphylococcus aureus RF122]

emb|CAI82091.1| probable phosphinothricin N-acetyltransferase [Staphylococcus aureus RF122]

Length = 163

Score = 97.4 bits (241), Expect = 6e-19, Method: Compositional matrix adjust.

Identities = 55/163 (33%), Positives = 85/163 (52%), Gaps = 5/163 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66

IR A D+ A+ I N I +T + EPQT E W + +R D P V E G

Sbjct: 2 IRCAKKEDLNAILAIYNDAIINTTAVYTYEPQTIDERVAVFETKQRKHD--PIFVFEENG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS SVVAVI 126

V G A G ++ AY +T+E ++YV +R G+ S L HL+ +A+G++++VA I

Sbjct: 60 SVLG FATFGSFRPW PAYLYTIEHSIYVDASARRKGIASQLLHHLIVEAKAKGYRALVAGI 119

Query: 127 GLPNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169

N S++LH+ + GTL G+K W D+ F++ D +

Sbjct: 120 DASNKASIQHLHQKFAFKHAGTLTNVGFKNQWLDLAFYELDLQ 162

>ref|NP_863380.1| hypothetical protein R64_p025 [Salmonella enterica subsp. enterica serovar Typhimurium]

dbj|BAB91588.1| sortase and related acyltransferases [Salmonella enterica subsp. enterica serovar Typhimurium]

Length = 178

Score = 97.4 bits (241), Expect = 6e-19, Method: Compositional matrix adjust.

Identities = 51/163 (31%), Positives = 92/163 (56%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66

++I A + A+ DI H++ T +F TEP E + L+++++ PW+VA E

Sbjct: 1 MKIVNAEEKHIPAIRDIYAHHVHLHGTA SFETEPDTHMLTRLKKIRNQALPWVVALEEE 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS SVVAVI 126

V G Y ++ R AY T+E ++Y+ QR G G L +++ + G++ ++A++

Sbjct: 61 KVIGYCYLTRYRERYAYRHTLEDSIYIHPDAQRRGTGKALLRYVISWAKTHGYRQMIAIV 120

Query: 127 GLPNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168

G N+ S+++H+ +G+T GTL+ G+KHG W D QR+

Sbjct: 121 GDSNNQGS LKVHQVGFTEIGTLKNIGFKHGRWLDTVLLQRNL 163

>ref|YP_002562667.1| GNAT family acetyltransferase [Streptococcus uberis 0140J]

emb|CAR42959.1| acetyltransferase (GNAT) family protein [Streptococcus uberis 0140J]

Length = 202

Score = 97.4 bits (241), Expect = 7e-19, Method: Compositional matrix adjust.

Identities = 51/161 (31%), Positives = 82/161 (50%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 67

Sbjct: 3 V I R A +D A+ DI Y+E + + F + + + + + ++ +Q RYP+LVAE G+
VTIRIAKESDAKALLDIYKPYVEKTAITFDYDIPSLENFKNRMKDIQKRYPFLLVAEESGM 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G AYA P+ R AY W+ E ++Y+ + G+G LY L + GF ++ A +

Sbjct: 63 ILGYAYASPFHPRAAYAWSCEVSIYLEESCRGRGIGQQLYQSLESYLRQMGFLNLNACLA 122

Query: 128 LPN-----DPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
+ S HE LG+ GT +GYK W D+

Sbjct: 123 SSSIETPYLTQASQHFHEKLGFKKVGTFHHSYKGFQHWFD 163

>ref|ZP_07093254.1| acetyltransferase, GNAT family [Lactobacillus delbrueckii subsp.
bulgaricus PB2003/044-T3-4]
gb|EFK31322.1| acetyltransferase, GNAT family [Lactobacillus delbrueckii subsp.
bulgaricus PB2003/044-T3-4]
Length = 190

Score = 97.4 bits (241), Expect = 7e-19, Method: Compositional matrix adjust.
Identities = 56/176 (31%), Positives = 91/176 (51%), Gaps = 10/176 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E+R A D + +I Y+E + + F E E+ + + + YP+LVA +G

Sbjct: 4 LELRRANVGDAERLLEIYAPYVEKTAITFEDEVPPIGEFQNRILKTLRIYPYLVALKDGK 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G AYA +K R AYD +VE ++YV + +G +LY + ++ QGF ++ A I

Sbjct: 64 IVGYAYASAFKERAAYDHSVELSIYVDANVRHQHVGRSLYDAIEDCLKKQGFLLNACIA 123

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ---DFELPAP 173
P +D S+R HE LGY G GYK G W+D+ + ++ + +PAP

Sbjct: 124 APIGEDPYLDDNSIRFHEHLGYNFVGRFHQCGYKFGRWYDMVWMEKMLGEHTVPAP 179

>ref|NP_627417.1| phosphinothricin acetyltransferase [Streptomyces coelicolor A3(2)]
ref|ZP_05525601.1| phosphinothricin acetyltransferase [Streptomyces lividans TK24]
ref|ZP_06530447.1| phosphorinothricin n-acetyltransferase [Streptomyces lividans
TK24]
sp|P21861.2|PAT_STRCO RecName: Full=Phosphinothricin N-acetyltransferase; Short=PPT
N-acetyltransferase; AltName:
Full=Phosphinothricin-resistance protein
gb|AAA26705.1| phosphorinothricin n-acetyltransferase [Streptomyces coelicolor]
emb|CAB90987.1| phosphinothricin acetyltransferase [Streptomyces coelicolor A3(2)]
gb|EFD68697.1| phosphorinothricin n-acetyltransferase [Streptomyces lividans TK24]
Length = 171

Score = 97.4 bits (241), Expect = 7e-19, Method: Compositional matrix adjust.
Identities = 57/173 (32%), Positives = 86/173 (49%), Gaps = 24/173 (13%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG- 66
V++RP D+ + D+ NHY+ + + F TEP TP+E R PWL++ E

Sbjct: 7 VQVRPGVEEDLKPLTDLYNHVRETPIITFDTEPFTPEE-----RRPWLLSHPEDG 56

Query: 67 -----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
+ G A + P++A+ AY +VE+TVYV+ G+GS LY L +

Sbjct: 57 PYRLRVATDAESQEILGYATSSPYRAKPAYATSVETTVYVAPGAGGRGIGSLLYASLFDA 116

Query: 114 MEAQGFKSVAVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 166
+ A+ A I PN+ S RLH G+ GT R G K G + DV ++R

Sbjct: 117 LAAEDLHRAYAGIAQPNEASARLHARFGFRHVGTYREVGRKFGRYWDVAWYER 169

>ref|ZP_07904920.1| phosphinothricin acetyltransferase [Eubacterium saburreum DSM 3986]
 gb|EFU76127.1| phosphinothricin acetyltransferase [Eubacterium saburreum DSM 3986]
 Length = 190

Score = 97.4 bits (241), Expect = 8e-19, Method: Compositional matrix adjust.
 Identities = 47/159 (29%), Positives = 85/159 (53%), Gaps = 7/159 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A D + +I +Y+ + ++F TE + +E+ +E++ YP+LVA+
 Sbjct: 5 ISIRSAEPEDANELLNIIYAYVSETAISFETEVPSVKEFKIRMEKVMKNYPYLVAQKNNE 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G AY P+ R AY+ + E+T+Y++ +++G+G LY+ L +AQ ++ + IG
 Sbjct: 65 ILGYAYLHPFVGRKAYELSAETTIYLNQDKKKMGIGKKLYSVLEDIAKAQNITNLYSCIG 124

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWH 159
 N+ SV+ HE +GY G G+K G W+
 Sbjct: 125 YVDKEDEYLNNSVQFHEHMGYRMVGKFENCCHKFGRWY 163

>ref|NP_637556.1| phosphinothricin N-acetyltransferase [Xanthomonas campestris pv. campestris str. ATCC 33913]
 ref|YP_243001.1| phosphinothricin N-acetyltransferase [Xanthomonas campestris pv. campestris str. 8004]
 gb|AAM41480.1| phosphinothricin N-acetyltransferase [Xanthomonas campestris pv. campestris str. ATCC 33913]
 gb|AAY48981.1| phosphinothricin N-acetyltransferase [Xanthomonas campestris pv. campestris str. 8004]
 Length = 175

Score = 97.4 bits (241), Expect = 8e-19, Method: Compositional matrix adjust.
 Identities = 58/161 (36%), Positives = 80/161 (49%), Gaps = 1/161 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 PVE+R AD+ A+ I I P Q + YP+LVAE +G
 Sbjct: 2 PVELREVRDADIPAITAIYAEQIAGCNTYEYVAPSAEQMRGRVRAIVDAGYPYLVAERDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126
 V G AYA ++AR Y WTVE+++Y++ Q G+GS L L+ E +G++ ++AVI
 Sbjct: 62 AVIGYAYASSYRARAGYRWTVENSIYLA AAAAQCGIGSQLLGALIAVCEQGRYRQMIAVI 121

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 G N S+RLHE + G G KHG W D QR
 Sbjct: 122 GDATNQASLRLHERFEFRTVGVFTGLGRKHGRWLDVAVQMQR 162

>ref|YP_003941113.1| Phosphinothricin acetyltransferase [Enterobacter cloacae SCF1]
 gb|ADO47829.1| Phosphinothricin acetyltransferase [Enterobacter cloacae SCF1]
 Length = 184

Score = 97.4 bits (241), Expect = 8e-19, Method: Compositional matrix adjust.
 Identities = 59/172 (34%), Positives = 90/172 (52%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVAEVEG 66
 +EIR A D A+ + ++ +F P + E +++++ +D +PWLVA G
 Sbjct: 12 IEIRDAVPDDAHAIAALYAWHVLNGRASFEVPPSVDEMTRMKKITRDGFPWLVALYRG 71

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126
 ++ G YA P++ R AY +T+E ++YV GLGS L L+ E ++ +VAVI
 Sbjct: 72 IIVGYCYASPYRPRPAYRYTLEESIIYVDASMAGRLGSALLARLIDICEQGPWRQMVAVI 131

Query: 127 GLPNDP--SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR-----DFELP 171

G N+ S+RLH+ G+ G LR+ GYK G W D QR D+ LP
Sbjct: 132 GDGNNNTGSLRLHKKHGFVDVVGQLRSVGYKLGDWDRDTVIMQRPLNDGDWTLPL 183

>ref|NP_824872.1| phosphinothricin N-acetyltransferase [Streptomyces avermitilis MA-4680]
dbj|BAC71407.1| putative phosphinothricin N-acetyltransferase [Streptomyces avermitilis MA-4680]
Length = 172

Score = 97.4 bits (241), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 59/182 (32%), Positives = 89/182 (48%), Gaps = 24/182 (13%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
M ER V++R AD+ A+ DI NHY+ + + F T TP+E R PWL
Sbjct: 1 MPSERTEVQVRSGVEADLKALTDIYNHYVRETPITFDTAFTPEE-----RRPWL 50

Query: 61 VAEVEG-----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTL 106
++ E + G A + P++A+ AY +VE TVYV+ G+G+ L
Sbjct: 51 LSHPEDGPHRLMVATGADSQEILGYATSSPFRAKPAYTTSVEVTYVAPDAAGRGIGTLL 110

Query: 107 YTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
Y L +++ + A I PN+ S RLHE G+ GT R G K G + DV ++R
Sbjct: 111 YGALFEALAGEDLHRAYAGIAQPNASTRLHERFGRHVGTYREVGRKFGRYWDVAWYER 170

Query: 167 DF 168
+
Sbjct: 171 EL 172

>ref|ZP_01114119.1| putative phosphinothricin N-acetyltransferase [Reinekea sp. MED297]
gb|EAR09826.1| putative phosphinothricin N-acetyltransferase [Reinekea sp. MED297]
Length = 167

Score = 97.1 bits (240), Expect = 8e-19, Method: Compositional matrix adjust.
Identities = 58/158 (36%), Positives = 81/158 (51%), Gaps = 5/158 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
+ IRP +D+ A+ I+NHYI + V F T+ T + W R+ LVAE
Sbjct: 3 ITIRPVNQSDLNALVTILNHYISKTAFTDTQTYTAETRMFWFSQFAE-TGRHQCLVAEA 61

Query: 65 E-GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 123
+ G + G A +G + + AYD +VE +VY H++ GLGS LY L + +
Sbjct: 62 DNGQILGYANSGLTRPKAAYDTSVEVSVYTDHQNSVKGLGSKLYEALFLRLADEDVHRAH 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
A+I LPND SV LH G+ GTL AG K +H V
Sbjct: 122 ALITLPNDASVGLHRKFGFYDVGTLHEAGRKFDLYHSV 159

>ref|YP_002283223.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv. trifolii WSM2304]
gb|ACI56997.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv. trifolii WSM2304]
Length = 185

Score = 97.1 bits (240), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 52/159 (32%), Positives = 83/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVAE-VEGV 67
+R A+ AD+ A+ DI + T ++ P + E + +YP++ A +G
Sbjct: 5 LRDAQADIPAADIYRESVLNGTSSYEIAPPSEAEMAQRFAAIVGQQYPYIAAGADGG 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA ++ R AY W VE ++Y++ + G+G TL L+ + GF+ ++AVIG
Sbjct: 65 LLGYAYASAFVRVPAYRWMVEDSIYLAPEARGRGIGKTLMAELIDRCTSLGFRQMIAVIG 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+ S+ LH G+ G +R AGYKHG W D QR
Sbjct: 125 GASPASIALHLKAGFVEVGLMRGAGYKHGRWLDTMLMQR 163

>ref|YP_001328738.1| GCN5-related N-acetyltransferase [Sinorhizobium medicae WSM419]
gb|ABR61903.1| GCN5-related N-acetyltransferase [Sinorhizobium medicae WSM419]
Length = 185

Score = 97.1 bits (240), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 55/159 (34%), Positives = 84/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVE-GV 67
+R A AAD+ + I + ++ P T E + YP++VA E G
Sbjct: 5 LRDAVAADLPVITGIYRESVLNGVASYEETPTEAEMALRFSTITGSGYPYVVALDEAGA 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G AYA ++ R+AY + VE ++Y+S + G G L + L+ A GF+ ++AVIG
Sbjct: 65 VIGYAYASAFNRNSAYRFVVEDSIYLSAARGKGTGKALLSELIGRCTALGFRQMIAVIG 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+ S+ LH ALG+ +G ++A G+KHG W D F QR
Sbjct: 125 GAHPLSIALHRALGFEQQGLIKATGFKHGRWLDTVFMQR 163

>emb|CBL33399.1| Sortase and related acyltransferases [Eubacterium siraeum V10Sc8a]
Length = 172

Score = 97.1 bits (240), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 84/161 (52%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+EIR AT D + I ++YIE + V + E + +++ +E+ +YP++VAE +G
Sbjct: 4 IEIRTATPFD AEELLGIYSYIENTAVTYELEVPSAEDFRRRIEKTLLKYPYIVAERDGR 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYAG +K R AY+ + E+++YV +R G G+ LY L K + G ++ A I
Sbjct: 64 ITGYAYAGVFKDRAAYERSAETSIYVDVNKKRHGTGTALYRELEKRLADMGVRNAYACIA 123

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N S+R HE GYT G K G +D+
Sbjct: 124 STDKDDEYLNHDSIRFHEKQGYTLVGKFHKCAEKF GREYDM 164

>ref|YP_001757052.1| GCN5-related N-acetyltransferase [Methylobacterium radiotolerans
JCM 2831]
gb|ACB26369.1| GCN5-related N-acetyltransferase [Methylobacterium radiotolerans
JCM 2831]
Length = 192

Score = 97.1 bits (240), Expect = 9e-19, Method: Compositional matrix adjust.
Identities = 60/174 (34%), Positives = 93/174 (53%), Gaps = 6/174 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-----YPWLVA 62
+ IRP++ AD+ A+ I H+I + + + DDL+R + P LVA
Sbjct: 19 IVIRPSSDADVEAMVAIYEHHSIRGSVSDVGVAEED-RLLPDDLKRRRKTRKKRPLHLVA 77

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122

+ +G VAG AYA P++ R AY +T++ ++YV H G+G L L+++ A G++ +
 Sbjct: 78 DRDGAVAGYAYAVPFRKRPAYRYTLKHSIYVHPDHLHAGIGRRLLPALIEACAAGGYRQM 137

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176

 + I N S+RLHEA G+ G LRA G+K+G W D QR + RP
 Sbjct: 138 IGYIDAENAASRLHEACGFERVGYLRAVGFKYGHWSDSVMVQRALGTGSEDRP 191

>ref|YP_001339364.1| GCN5-like N-acetyltransferase [Marinomonas sp. MWYL1]
 gb|ABR69429.1| GCN5-related N-acetyltransferase [Marinomonas sp. MWYL1]
 Length = 170

Score = 97.1 bits (240), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 55/163 (33%), Positives = 86/163 (52%), Gaps = 4/163 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64

 V+IRPA D+ A+ D+ NHYI + F EP T + W RY LVAE
 Sbjct: 3 VQIRPAVIEDLPALTDLYNHYIVNTATTDFIEPYTLEGRAVWFSQFAP-TGRYRLLVAEQ 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124

 +G + G A +G +K + AY+ +VE ++Y+ + GLG+ LY L + +E + A
 Sbjct: 62 DGEILGYACSGQFKPKRAYETSVEVSIYLPNTKGRGLGTALYLELFEQLETEDVHRAYA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRD 167

 I LPN+ S +HE G+ + G G K G + DV +++++
 Sbjct: 122 GITLPNEASHIIHEKFGFESVGVYLEVGRKFGQYWDVEWFEKE 164

>ref|YP_002961972.1| phophinothricin N-acetyltransferase [Methylobacterium extorquens
 AM1]

ref|YP_003066775.1| phophinothricin N-acetyltransferase [Methylobacterium extorquens
 DM4]

gb|ACS38695.1| phophinothricin N-acetyltransferase [Methylobacterium extorquens
 AM1]

emb|CAX22757.1| phophinothricin N-acetyltransferase [Methylobacterium extorquens
 DM4]

Length = 204

Score = 97.1 bits (240), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 58/162 (35%), Positives = 88/162 (54%), Gaps = 4/162 (2%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETS---TVNFRTPEQTPQEWIDDLERLQD-RYP 58

 P V IRP++ AD++A+ I +I T +F E P E + ++ R P
 Sbjct: 9 PTHAEVVIRPSSDADVSAMIAIYERHIRKGVGDTGDFEERLLPDELRRRRKTMRSKRLP 68

Query: 59 WLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 118

 LVAE G +AG AYA P++ R AY + ++ ++YV H G+G L L+++ A G
 Sbjct: 69 HLVAERGGQIAGYAYAVPFRKRPAYRYALKHSIYVHPDHLHAGIGRRLLPALIEACAAG 128

Query: 119 FKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

 ++ ++ I N+ S+RLHEA G+ G L A GYK+G W D
 Sbjct: 129 YRQMIGYIDASNEASRLHEACGFARVGYPALGYKYGRWSD 170

>ref|YP_002007021.1| phosphinothricin n-acetyltransferase [Cupriavidus taiwanensis
 LMG

 19424]
 emb|CAQ70960.1| Phosphinothricin N-acetyltransferase [Cupriavidus taiwanensis LMG
 19424]
 Length = 197

Score = 97.1 bits (240), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 60/177 (33%), Positives = 89/177 (50%), Gaps = 5/177 (2%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAE 63
 R +R AT AD+ A+ I H+++ +F P + E L ++ + P+LVAE
 Sbjct: 20 RHAFTLRDATPADIPAIHAIYAHVQHGRASFEEVPPSADEMQLRLAEVRRKGLPYLVAE 79

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 +G V G AYA ++AR+AY + +E ++Y+ HR GLG L L+ E ++ +V
 Sbjct: 80 RDGEVLGYAYASAYRARSAYRFAIEDSIYIDHRRVGEGLGQALLAALIARCETGPWRQMV 139

Query: 124 AVIGLP----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRP 176
 AVI S+ +HE LG+ G L A G+KHG W D QR A P
 Sbjct: 140 AVIACAAAGGAGSLAVHERLGFRTVGRLEAVGFKHGQWIDTVLMQRMGLGAGATTLP 196

>ref|ZP_04996481.1| conserved hypothetical protein [Streptomyces sp. Mg1]
 gb|EDX20992.1| conserved hypothetical protein [Streptomyces sp. Mg1]
 Length = 172

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 62/160 (38%), Positives = 81/160 (50%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
 RPV +R A + D+ + I NH IE ST + Q+P E L +R VAEVE
 Sbjct: 9 RPVTVRRALSGDVETIRAIRNHAIEHSTALWTQILQSPAEEAAWLAHLERGSFAFVAEVE 68

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G AG GPW+ ++ Y TVE +VYV LG+GS L L+ S G +VA
 Sbjct: 69 GETAGFGVYGPWREKGYRHTVEDSVYVRDGMVGLGIGSALLAELISSARDAGHHVMVAG 128

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQ 165
 I N S+RLH+ G+ GT+ AG K G W D+ Q
 Sbjct: 129 IEAENTASIRLHKRYGFRLVGTVPAGTKFGRWLDLTLMQ 168

>gb|ADL24342.1| acetyltransferase, GNAT family [Staphylococcus aureus subsp. aureus
 JKD6159]
 Length = 163

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 54/161 (33%), Positives = 85/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
 IR A D+ A+ I N I +T + EPQT E I E Q + P V E +G V
 Sbjct: 2 IRCAKKEDLNAILAIYNDAIINTTAVTYTEPQTIDERIAWFETKQHNHEPIFVFESDGNV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G++++A I
 Sbjct: 62 LGFATFGSFRPWPAYQYIEHSIYVDASARGKGIASQLLQHLIVEAKAKGYRALIAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFE 169
 N S++LH+ G+ GTL G+K W D+ F++ D +
 Sbjct: 122 SNKASIQLHQKFGFKHAGTLTNVGFKNQWLDLAFYELDLQ 162

>gb|ADY85178.1| Phosphinothricin acetyltransferase [Lactobacillus delbrueckii
 subsp. bulgaricus 2038]
 Length = 190

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 56/176 (31%), Positives = 90/176 (51%), Gaps = 10/176 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +E+R A D + +I Y+E + + F E E+ + + + YP+LVA +G

Sbjct: 4 LELRRANVGDAERLLEIYAPYVEKTAITFEDEVPPIGEFQNRILKTLRIYPYLVALKD GK 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA +K R AYD +VE ++YV + +G LY + ++ QGF ++ A I

Sbjct: 64 IVGYAYASAFKERAAYDHSVLSIYVDANVRHQHVGRFLYDAMENCLKKQGFLNLNACIA 123

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR---DFELPAP 173
P +D S+R HE LGY G GYK G W+D+ + ++ + +PAP

Sbjct: 124 APIGEDPYLDDNSIRFHEHLGYKFVGRFHQCGYKFGRWYDMVWMEKMLGEHTVPAP 179

>ref|ZP_01259639.1| toxin resistance protein [Vibrio alginolyticus 12G01]
gb|EAS76986.1| toxin resistance protein [Vibrio alginolyticus 12G01]
Length = 169

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 54/154 (35%), Positives = 77/154 (50%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV 64
+EIR D+ + DI N YIE + F P + Q+W +Y VA

Sbjct: 1 MEIRTGKLEDDVTGITDIFNFYIEHTNARFEEVPFTLENRQKWFSQFSS-NTKYQLYVAIE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
G + G A + ++A +A+D TVE TVY++ + GLGS LYT L S+ A G V++

Sbjct: 60 NGELLGFACSQQYRAISAFDDTVEVTYLAQEAQKGLGSKLYTQLFSSIRAYGVHRVLS 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
+ LPND SV LH+ G+ G KHG +

Sbjct: 120 GVALPNDASVALHKRFGFREVGVFNEYAKKHGQY 153

>ref|ZP_03301026.1| hypothetical protein BACDOR_02398 [Bacteroides dorei DSM 17855]
ref|ZP_04555308.1| conserved hypothetical protein [Bacteroides sp. D4]
gb|EEB25151.1| hypothetical protein BACDOR_02398 [Bacteroides dorei DSM 17855]
gb|EEO46642.1| conserved hypothetical protein [Bacteroides dorei 5_1_36/D4]
Length = 161

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 54/161 (33%), Positives = 81/161 (50%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR D A+ I N Y+E S F TEP ++ + + R+P+ V E EG V

Sbjct: 2 IRRVELQDAKAITTIYNEYVEHSVATFETEPLEEDMRSRIGIAVRFYPFYVEEEGKV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G YA WK R AY +T+E+TVY++ ++ G+G L L++ G++++A +

Sbjct: 62 GYCYAHLWKERTAYRYTLETTVYLAPGYEGKGIGRELMEERLIEECRRDGYRALIACVTEG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFEL 170
N S LH LG+ + G K G W DV D+EL

Sbjct: 122 NAASDALHLRLGFKKVSHFKKVGKFGRWLDV---VDYEL 158

>ref|YP_001339360.1| GCN5-like N-acetyltransferase [Marinomonas sp. MWYL1]
gb|ABR69425.1| GCN5-related N-acetyltransferase [Marinomonas sp. MWYL1]
Length = 167

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 55/162 (33%), Positives = 85/162 (52%), Gaps = 4/162 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEV 64
V+IRPA D+ A+ D+ NHYI + F EP T + W RY LVAE

Sbjct: 3 VQIRPAVIEDLPALTDLYNHYIVNTATTFDIEPYTLEGRAVWFSQFAP-TGRYRLVAEQ 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +G + G A +G +K + AY+ +VE ++Y+ + GLG+ LY L + +E + A
 Sbjct: 62 DGEILGYACSGQFKPKRAYETSVEVSIYLPNTKGRGLGTALYLELFEQLETEDVHRAYA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 I LPN+ S +HE G+ + G G K G + DV ++++
 Sbjct: 122 GITLPNEASRIIEKFGFESVGVYLEVGRKFGQYWDVEWFQEK 163

>ref|YP_300460.1| putative acetyltransferase [Staphylococcus saprophyticus subsp.
 saprophyticus ATCC 15305]
 dbj|BAE17515.1| putative acetyltransferase [Staphylococcus saprophyticus subsp.
 saprophyticus ATCC 15305]
 Length = 163

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 51/162 (31%), Positives = 85/162 (52%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR AT +D+ + DI N I +T + +PQT W ++ + Q+ P V E +G
 Sbjct: 2 IRHATKSDLNILDYNDAILNTTAVYSYKPTLASREIWFEN--KSQNNPIFVFEEQG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 A G ++ AY +++E ++YV+ H+ G+ S L L+ + +G+K++VA I
 Sbjct: 60 EAVAFATYGSFRDWPAYQYSIEHSIYVNEHHRGKGIASQLLKQLINHAQVEGYKTLVAGI 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDF 168
 ND S+ LH+ + GT++ GYK W D+ F+Q D
 Sbjct: 120 DATNDNSIYLHKKFDFQHSGTIQNVGYKFDKWLDLAFYQLDL 161

>ref|YP_002731861.1| phosphinothricin N-acetyltransferase [Brucella melitensis ATCC
 23457]
 ref|ZP_05467392.1| phosphinothricin acetyltransferase [Brucella melitensis bv. 2 str.
 63/9]
 gb|ACN99906.1| Phosphinothricin N-acetyltransferase [Brucella melitensis ATCC
 23457]
 gb|EEZ18942.1| phosphinothricin acetyltransferase [Brucella melitensis bv. 2 str.
 63/9]
 gb|ADZ65167.1| phosphinothricin N-acetyltransferase [Brucella melitensis M28]
 gb|ADZ86031.1| phosphinothricin N-acetyltransferase [Brucella melitensis M5-90]
 Length = 179

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
 Identities = 56/159 (35%), Positives = 83/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR AD+ + I + T T ++ EP T E D+ +P LVAE +G V
 Sbjct: 4 IRDFQPADIETITAIYTQAVLTGTGSYEIEPPTMDEMAKRFAAFADQGFILVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G AYA ++ R AY W E ++Y++ + G+G L L+ + A GF+ ++AVIG
 Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSIYIAPDAKGQGIGKLLRELIARISALGFRQLLAVIGD 123

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N SV+LHE+LG+T G + +G+KH W D Q
 Sbjct: 124 GEHNIGSVKLHESLGFTHCGRIEGSGFKHERWLDTVLMQ 162

>ref|ZP_02243592.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv.
 oryzicola BLS256]
 Length = 179

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 65/181 (35%), Positives = 90/181 (49%), Gaps = 13/181 (7%)

```
Query: 7   PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-----LQDRYPWL 61
          PVE+R   AAD+ A+  I    I          + P      +DD+      +   YP+LV
Sbjct: 2   PVELRAVRAADIPAITAIYAEQIAGVNTYEYSAPS-----LDDMRARVSAIVDAGYPYL 56

Query: 62  AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 121
          AE++GVVAG A A  ++AR Y WTVE+++Y++  Q  G+G +L  L+  E +GF
Sbjct: 57  AELDGVVAGYADASAFRARAGYRWTVENSIIYLATAMQGRGIGKSLLGELIAVCEQRGFLQ 116

Query: 122 VVAVIG-LPNDPVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFEL--PAPPRPVR 178
          ++AVIG  N S +LHE  G+  G    G KHG W D  QR      APP
Sbjct: 117 MIAVIGDADNLASRQLHERFGFRTVGVFTGIGRKHGRWLDGVQMQRALGSGNTAPPSDEN 176

Query: 179 P 179
          P
Sbjct: 177 P 177
```

>ref|ZP_04540039.1| conserved hypothetical protein [Bacteroides sp. 9_1_42FAA]
gb|EE062335.1| conserved hypothetical protein [Bacteroides sp. 9_1_42FAA]
Length = 161

Score = 96.7 bits (239), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 54/161 (33%), Positives = 81/161 (50%), Gaps = 4/161 (2%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR      D A+  I N Y+E S  F TEP  ++    +  +  R+P+ V E EG V
Sbjct: 2   IRRVELQDAKAITTIYNEYVEHSVATFETEPLREEDMRSRIAGIAIRFPYFVYEEEGKV 61

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
          G YA  WK R AY +T+E+TVY++  ++  G+G  L  L++    G+++++A +
Sbjct: 62  GYCYAHLWKERAARYRTLETTVYLAPGYEGKGIGRELMEERLIEECRRDGYRALIACVTED 121

Query: 130 NDPVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFEL 170
          N S  LH  LG+      +  G K G W DV      D+EL
Sbjct: 122 NAASDALHLRLGFKKVSHFKVGLKFGRWLDVV----DYEL 158
```

>ref|ZP_06412786.1| Phosphinothricin acetyltransferase [Frankia sp. EUN1f]
gb|EFC84422.1| Phosphinothricin acetyltransferase [Frankia sp. EUN1f]
Length = 201

Score = 96.3 bits (238), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 63/157 (40%), Positives = 90/157 (57%), Gaps = 5/157 (3%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR--YPWLVAEVEGV 67
          +RPA +D A+  I  Y+  + + F  E  P E +    R+  R  PW VAE+EG
Sbjct: 18  VRPARLSDATAIRAIYAPYVLETPITFEVE--VPSEAVMR-ARMTGRPLMPWFVAEIEGE 74

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
          VAG AYA  + R AY W+  + ++Y++ R +R GLG  LYT L+  +  G+ ++ A I
Sbjct: 75  VAGYAYASQHRERAAYRWSADVSIYLAARQRRRGLGRLLYTRLIDEVRTLGYVALFAGIA 134

Query: 128 LPNDPVRRLHEALGYTARGLRAAGYKHGGWHDVGF 164
          LPN+ SV LH ALG+  G  A G+K G WHDVG++
Sbjct: 135 LPNEASVGLHTALGFRPVGYPVAVGHKAGRWHDVGWY 171
```

>ref|YP_728012.1| phosphinothricin N-acetyltransferase [Ralstonia eutropha H16]
emb|CAJ94644.1| Phosphinothricin N-acetyltransferase [Ralstonia eutropha H16]

Length = 193

Score = 96.3 bits (238), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 60/177 (33%), Positives = 89/177 (50%), Gaps = 5/177 (2%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAE 63
R+P +R AT AD+ A+ I H++ +F P + E + + P+LVA
Sbjct: 16 RKPFTLRDATPADVPAIHAIYAHHVHLHGRASFEETPPSLDEMQLRFAEVHRKGLPYLVAV 75

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
+G V G AYA ++AR+AY + +E ++Y+ HR GLG L L+ E ++ +V
Sbjct: 76 RDGEVLGYAYASSYRARSAYRFAIEDSIYIDHRRVGEGLGQALLAELVARCETGPWRQMV 135

Query: 124 AVI----GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
AVI G S+ +HE LG+ G L A G+KHG W D QR + A P
Sbjct: 136 AVIAC TAGGEGAGSLAVHERLGFRTVGRLEAVGFKHGQWIDTVLMQVRVLGVGATTLP 192

>ref|NP_769816.1| acetyltransferase [Bradyrhizobium japonicum USDA 110]
dbj|BAC48441.1| acetyltransferase [Bradyrhizobium japonicum USDA 110]
Length = 194

Score = 96.3 bits (238), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 57/166 (34%), Positives = 82/166 (49%), Gaps = 5/166 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETST---VNFRTPEQTPQEWIDDLERL-QDRYPWLVA 62
PV++RP+ +D+ A+ I H++ V P+ P + D + L Q R P LVA
Sbjct: 15 PVQVRPSRES DVEAMLAIYRHHVRNGVPRDVEGTGAPE-PDDLRRRKNLQKQTRLPHLVA 73

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
G V G AYA ++ R AY +T + ++YV H H G+G L L+ A GF+ +
Sbjct: 74 TYRGEVVGAYAVLFRKRPAYRYTAKHSIVVHHAHLGRGVGRLLQLQELVDVCAAAGFRQM 133

Query: 123 VAVIGLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
+ I N PS+ LHE G+ G L Y+HG W D QR
Sbjct: 134 IGYIDADNAPSLALHEKFGFARAGLLCGVAYRHGRWSDTVMVQRSL 179

>ref|ZP_04941465.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia PC184]
gb|EAY64636.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia PC184]
Length = 186

Score = 96.3 bits (238), Expect = 1e-18, Method: Compositional matrix adjust.
Identities = 59/172 (34%), Positives = 86/172 (50%), Gaps = 2/172 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
+R AT AD+ A+ I H++ S +F P E + L P+LVAE +G V
Sbjct: 9 VRDATDADLDIAIHAIYAHHVHHSVASFEETPPDVAELRARRDAVLNHGLPYLVAEWDGRV 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
AG AYA P++ R+AY + +E ++Y+ + G+G L L+ E ++ ++AVI
Sbjct: 69 AGYAYATPYRTRSAYRFAIEDSIYIDDAQRGRGIGRALLEALIRCEGGPWRQMI AVIAD 128

Query: 128 LPNDPVRRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVVP 179
S LH A G+ G L+A G+KHG W D QR A RP P
Sbjct: 129 GGTGGSTSLHRAFGFEPAGLLKAVGFKHGRWIDTALLQRPLGDGANTRPASP 180

>ref|YP_004088834.1| phosphinothricin acetyltransferase [Asticcacaulis excentricus CB 48]
gb|ADU14683.1| Phosphinothricin acetyltransferase [Asticcacaulis excentricus CB 48]
Length = 180

Score = 96.3 bits (238), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 68/179 (37%), Positives = 86/179 (48%), Gaps = 21/179 (11%)

```
Query: 9  EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE-----WIDDLERLQDRYPWLVA 62
          EIR      D AA+ DI      +   T F TEP P E      W   LE      P+LVA
Sbjct: 3  EIRKVQVTDFAAIADIYKDGVLNGTGTDFTEP--PGEDAMRARW--LELQSMNLPYLVA 57

Query: 63  EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
          G V G AYA P++AR AY + VE ++YV  H+  G+G L   L+ +   GF ++
Sbjct: 58  TEGGSVIGYAYASPFRARIAYRYGVEDSIYVHPAHKGKGVGKALLEALIAASTEAGFYAM 117

Query: 123  VAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
          AVIG  N  S+RLHE  G+   G L  AGYK   W DV F      +P+RP
Sbjct: 118  YAVIGDAENTGSIRLHEQAGFEHTGKLPKAGYKFDRWLDVIFMS-----KPLRPT 167
```

>ref|ZP_02919852.1| hypothetical protein STRINF_00704 [Streptococcus infantarius subsp.
infantarius ATCC BAA-102]
gb|EDT48137.1| hypothetical protein STRINF_00704 [Streptococcus infantarius subsp.
infantarius ATCC BAA-102]
Length = 234

Score = 96.3 bits (238), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 56/187 (29%), Positives = 94/187 (50%), Gaps = 8/187 (4%)

```
Query: 5  RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE WIDDLERLQDRYPWLVAEV 64
          R  + IR A+  D  A+ DI  +Y+E + + F  + T +E+  + +   YP+LVAE
Sbjct: 44  RMAITIRLASLDDAKALLDIYRYVEETAITFEYDVPTLEEF TGRMRSIMAFYPYLVAEE 103

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
          +G + G AYA  +  R AY W+ E+TVY+  +  G+G +Y L   +   G ++ A
Sbjct: 104  DGKILGYAYASKFHPRAAYAWSAEATVYLDKAARGKGVGRQIYGKLEDYLTQMGILNLNA 163

Query: 125  VIGLPN-----DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRP 176
          I   +      + S + H ALGY + G   +GYK   W+D+ + ++   E A  P
Sbjct: 164  CIASTDVEDAYLTNGSEKFHRALGYQSVGKFHDSGYKFNRWYDMIWMEKMLGEHGADVAP 223

Query: 177  VRPVTQI 183
          V+ + +I
Sbjct: 224  VKSIHEI 230
```

>ref|YP_002770383.1| phosphinothricin acetyltransferase [Brevibacillus brevis NBRC 100599]
dbj|BAH41879.1| putative phosphinothricin acetyltransferase [Brevibacillus brevis NBRC 100599]
Length = 163

Score = 96.3 bits (238), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 52/158 (32%), Positives = 85/158 (53%)

```
Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE WIDDLERLQDRYPWLVAEVEGV 67
          ++IR A  +D+ A+  I N+ +E      F  EPQT  +      +   R+P +VAE EG
Sbjct: 2  LQIRDAVLSDLPAMLAIYNYAVENLVATFDLEPQT LAQREVWFHKKHGRHPIIVA EYEGN 61

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
          V G      ++ + AY  + E ++Y++      G+G+TL + +L+      + ++V+ I
Sbjct: 62  VIGYCSLSVFREKPAYQKSTELSIYIAPDQSGKGVGTTLMSAILERARQLEYHTIVSGIV 121

Query: 128  LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
          ND SV+LHE  G+T  G  +   G+K G WHDV F+Q
```

Sbjct: 122 GGNDASVKLHEKFGLTAGRFQEVGFKFGEWHHDVHFYQ 159

>ref|YP_001638468.1| GCN5-related N-acetyltransferase [Methylobacterium extorquens PA1]

gb|ABY29397.1| GCN5-related N-acetyltransferase [Methylobacterium extorquens PA1]
 Length = 191

Score = 96.3 bits (238), Expect = 2e-18, Method: Compositional matrix adjust.
 Identities = 56/155 (36%), Positives = 86/155 (55%), Gaps = 4/155 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETS---TVNFRTEPQTPQEWIDDLERLQD-RYPWLVAEVE 65

IRP++ AD++A+ I +I T+F E P E + ++ R P LVAE

Sbjct: 3 IRPSSDADVSAMIAIYERHIRKGVGDTGDFEERLLPDELRRRRKTMRSKRLPHLVAERG 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125

G +AG AYA P++ R AY + ++ ++YV H G+G L L+++ A G++ ++

Sbjct: 63 GQIAGYAYAVPFRKRPAYRYALKHSIYVHPDHLHAGIGRLLPALIEACAAGGYRQMIGY 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

I N+ S+RLHEA G+ G L A GYK+G W D

Sbjct: 123 IDASNEASLRLHEACGFARVGYLPAIGYKYGRWSD 157

>ref|ZP_07726498.1| acetyltransferase, GNAT family [Streptococcus downei F0415]

gb|EFQ56200.1| acetyltransferase, GNAT family [Streptococcus downei F0415]
 Length = 197

Score = 96.3 bits (238), Expect = 2e-18, Method: Compositional matrix adjust.
 Identities = 54/159 (33%), Positives = 81/159 (50%), Gaps = 7/159 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR D++ + I YIE + ++F E + QE+ + + YP+LV E EG +

Sbjct: 5 IRNTKKTDLSQLLAIIYAPYIEKTAISFEYEVPSLQEFQQRWQGIVQTYPYLVLEQEGQIL 64

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL- 128

G AYA + R AY W E ++Y++ + Q GLG Y L ++AQG S +A I

Sbjct: 65 GYAYASAFHPREAYQWLAEVSIYLAPQAQKGLGKLFYQKLEACLKAQGVLSALACIATT 124

Query: 129 --PND----PSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

PND S H+ LG+ G + +GYK G W+D+

Sbjct: 125 DQPN DYLSNNSFDFHKHLGFREVGHFKKSGYKFGHWYDM 163

>ref|YP_003638725.1| Phosphinothricin acetyltransferase [Cellulomonas flavigena DSM 20109]

gb|ADG76526.1| Phosphinothricin acetyltransferase [Cellulomonas flavigena DSM 20109]
 Length = 168

Score = 96.3 bits (238), Expect = 2e-18, Method: Compositional matrix adjust.
 Identities = 56/161 (34%), Positives = 85/161 (52%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-QDRYPWLVAEVEG 66

V++R AT+ D+A + I +HY+ TST F +P W+D L+ + +P+ VA ++G

Sbjct: 3 VQVRAATSGDVAGLARIYDHYVATSTATFELDPPGEAVWVDKLDVVAAGWPFEVALLDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

VAG AY GPW+ R AY TVE T+Y+ G+G+ L +L+ A G + V+AV+

Sbjct: 63 QVAGFAYVGPWRPRPAYAHTVEDTIYLDPAATGRGIGTRLLASVLEQAAAAGAREVIAVV 122

Query: 127 GLPND-PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166

+ S+ LH G+ G L G K W Q+

Sbjct: 123 ADGDTAASLALHRRAGFDPAGRLERVGRKFDRLWLTLLQK 163

>ref|YP_200814.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae KACC10331]
ref|YP_451073.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae MAFF 311018]
ref|YP_001913577.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae PX099A]
gb|AAW75429.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae KACC10331]
dbj|BAE68799.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae MAFF 311018]
gb|ACD59045.1| phosphinothricin N-acetyltransferase [Xanthomonas oryzae pv. oryzae PX099A]
Length = 179

Score = 95.9 bits (237), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 58/161 (36%), Positives = 83/161 (51%), Gaps = 1/161 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
P+E+R AAD+ A+ I I + P + + Y +LVAE++G
Sbjct: 2 PLELRAVRAADIPAITAIYAEQIAGVNTYEYSAPSLDEMRAVSAIVDAGYSYLVAELDG 61
Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VVAG AYA ++AR Y WTVE+++Y++ Q G+G +L L+ E +GF ++AVI
Sbjct: 62 VVAGYAYASAFRARAGYRWTVENSIIYLATAMQGRGIGKSLGELIACEQRFGLQMIAMI 121
Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
G N S +LHE G+ G G KHG W D QR
Sbjct: 122 GDADNLASRQLHERFGFRTVGLFTGIGRKHGRWLDGVQMQR 162

>ref|YP_003968115.1| Phosphinothricin acetyltransferase [Ilyobacter polytropus DSM 2926]
gb|ADO83767.1| Phosphinothricin acetyltransferase [Ilyobacter polytropus DSM 2926]
Length = 161

Score = 95.9 bits (237), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 48/156 (30%), Positives = 83/156 (53%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR D ++ +I N+Y+E +T P + + + ++ + YPWL V E +
Sbjct: 3 IRYVEDRDAESIAEIIYNYVENTTFTGDETFPSKEHMKNKIKDISKDYPWLVLVLEENSQIL 62
Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G Y W+ R+AY + E +VY+ + + GLGS L++ LLK ++ + +++++ I LP
Sbjct: 63 GYIYLNQWRFRSAYRHSALSVYIRNGVRTNGLGSKLFSSLLKELKKKNLHTIISAIVLP 122
Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
N+ S+ LHE G+ GYK W D+G+W+
Sbjct: 123 NNASINLHEKFGFKKVAHFSEVGYKFEKWLDLGYWE 158

>ref|ZP_06089820.1| conserved hypothetical protein [Bacteroides sp. 3_1_33FAA]
gb|EEZ20450.1| conserved hypothetical protein [Bacteroides sp. 3_1_33FAA]
Length = 161

Score = 95.9 bits (237), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 81/161 (50%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

```

IR      D A+ I N Y+E S F TEP  ++  +  + R+P+ V E EG V
Sbjct: 2  IRRVELQDAKAITTIYNEYVEHSVATFETEPLREEDMRSRIAGIAIRFPYFVYEEEGKV 61

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
          G YA WK R AY +T+E+TVY++ ++ G+G L L++ G+++++A +
Sbjct: 62  GYCYAHLWKERAARYRTLETTVYLAPGYEGKGIGRELMEERLIEECRRDGYRALIACVTED 121

Query: 130  NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170
          N S LH +G+ + G K G W DV D+EL
Sbjct: 122  NAASDALHLRMGFKKVSHFKKVLKFGRWLDVV---DYEL 158

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>ref|NP_232781.1| toxin resistance protein [Vibrio cholerae O1 biovar eltor str.
N16961]
gb|AAF96293.1| toxin resistance protein [Vibrio cholerae O1 biovar El Tor str.
N16961]
Length = 169

```

Score = 95.9 bits (237), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 54/154 (35%), Positives = 78/154 (50%), Gaps = 4/154 (2%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEP---QTPQEWIDDLERLQDRYPWLVAEV 64
          +EI D+A + DI N YIE + F P + +EW R +Y VA
Sbjct: 1  MEIXTGFEFEDIAGITDIFNFYIEQTNARFEFFFTLENREEWFSQFSRTA-KYQIYVAVE 59

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
          GV+ G A + ++A A+D TVE +VY++ + GLGS LYT L S+ A G +++
Sbjct: 60  NGVLQGFACSQKYRAIPAFDDTVEVSVYLAQEAQKGLGSKLYTQLFSSIRAYGVHRILS 119

Query: 125  VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
          + LPND SV LH+ G+ G KHG +
Sbjct: 120  GVALPNDASVALHKRFGFREVGISNEYAKKHGQY 153

```

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>gb|EFA85466.1| hypothetical protein PPL_01423 [Polysphondylium pallidum PN500]
Length = 208

```

Score = 95.9 bits (237), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 55/170 (32%), Positives = 87/170 (51%), Gaps = 9/170 (5%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQ-DRYPWLVAE--- 63
          + IR A D+ A+C+I HY+ S F T + + L+ D P+ VAE
Sbjct: 26  IVIREAVVDDVKAICEIYGHYVRESVATFEEVVPVPTLDDMLSRFNSLKADGMPYFVAEQAA 85

Query: 64  ----VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
          V V+ G YAG ++ R+AY +T+E ++Y+ ++ G+GS L L+ +GF
Sbjct: 86  VDNSVSPVIVGYCYAGLYRTRSAYRTLEDSEIYLDPNYRARGVGSMLLRRLIDESTKRGF 145

Query: 120  KSVVAVI-GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          + ++AVI G N S++LHE LG+ + L + G K W DV Q +
Sbjct: 146  RQMIAVIGSDNLGSIKLHERLGFKKHILYSVGLKFEKWVDVVTLEL 195

```

```

>ref|YP_619073.1| acyltransferase [Lactobacillus delbrueckii subsp. bulgaricus ATCC
11842]
emb|CAI97967.1| Acyltransferase [Lactobacillus delbrueckii subsp. bulgaricus ATCC
11842]
Length = 190

```

Score = 95.9 bits (237), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 55/176 (31%), Positives = 91/176 (51%), Gaps = 10/176 (5%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVAEEGV 67

```

```

      +E+R A   D   + +I   Y+E + + F   + +   E+ + + +   YP+LVA +G
Sbjct: 4   LELRRANVGDAERLLEIYAPYVEKTAITFEDKVPSIGEFQNRILKTLRIYPYLVALKD GK 63

Query: 68   VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIG 127
      + G AYA +K R AYD +VE ++YV      +   +G LY +   ++ QGF ++ A I
Sbjct: 64   IVGYAYASAFKERAAYDHSVELSIYVDANVRHQHVGRFLYDAIEDCLKKQGF LNLNACIA 123

Query: 128   LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR---DFELPAP 173
      P           +D S+R HE LGY   G       GYK G W+D+ + ++   + +PAP
Sbjct: 124   APIGEDPYLDDNSIRFHEHLGYKFVGRFHQC GYK FGRWYDMVWMEKMLGEHTVPAP 179

```

```

>ref|YP_004006032.1| gnat acetyltransferase [Rhodococcus equi 103S]
emb|CBH47347.1| GNAT acetyltransferase [Rhodococcus equi 103S]
      Length = 162

```

Score = 95.9 bits (237), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 56/159 (35%), Positives = 83/159 (52%), Gaps = 5/159 (3%)

```

Query: 10   IRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
      IR AT D+   + +I N I +T           +   + W+DD R D +P LVA+V+G
Sbjct: 3   IRDATTGDLPGILEIHNEAIANTTAIWDETLADLDERRRWLDD--RRADGF PVLVADVDG 60

Query: 67   VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVI 126
      VAG A G W+A++ Y +TVE++VYV   H R G+ + L T L++   A G   +VA +
Sbjct: 61   AVAGYASYGVWRAKSGYRYTVENS VYVHVDHRRGIATALMTALIERARAGGIHVIVASV 120

Query: 127   GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 165
      N S+ LHE G+       +   G K G W D+ + Q
Sbjct: 121   ESSNTTSIALHERFGFRIVAQMPEVGRKFGRWLDMTYLQ 159

```

```

>gb|EGD28189.1| phosphinothricin acetyltransferase [Lactobacillus delbrueckii
      subsp. lactis DSM 20072]
      Length = 190

```

Score = 95.5 bits (236), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 56/176 (31%), Positives = 89/176 (50%), Gaps = 10/176 (5%)

```

Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
      +E+R A   D   + +I   Y+E + + F   E       E+ + + +   YP+LVA +G
Sbjct: 4   LELRRANVGDAERLLEIYAPYVEKTAITFEDEVPPIGEFQNRILKTLQIYPYLVALKD GK 63

Query: 68   VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIG 127
      + G AYA +K R AYD +VE ++YV      +G LY +   ++ QGF ++ A I
Sbjct: 64   IVGYAYASAFKERAAYDHSVELSIYVDANVCHQHVGRFLYDAIEDCLKKQGF LNLNACIA 123

Query: 128   LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR---DFELPAP 173
      P           +D S+R HE LGY   G       GYK G W+D+ + ++   + +PAP
Sbjct: 124   APIGEDPYLDDNSIRFHEHLGYKFVGRFHQC GYK FGRWYDMVWMEKMLGEHTVPAP 179

```

```

>ref|ZP_05736877.1| phosphinothricin N-acetyltransferase [Granulicatella adiacens
ATCC
      49175]
gb|EEW38147.1| phosphinothricin N-acetyltransferase [Granulicatella adiacens ATCC
      49175]
      Length = 186

```

Score = 95.5 bits (236), Expect = 2e-18, Method: Compositional matrix adjust.
Identities = 48/164 (29%), Positives = 84/164 (51%), Gaps = 7/164 (4%)

```

Query: 10   IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

```


IR AT D + +I Y+ + + F + +E+ + + + + +P+LV E E +
 Sbjct: 6 IRVATVEDARYIQEIYAPYVLNTAITFEEVVPSEEFQERIAKTLEAFPYLVLEEEKEIV 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129

G AYAG + R A+DW+ E ++Y+S HQR G G LYT L K + G++++ A + +P
 Sbjct: 66 GYAYAGRFSQRAAFDWSTEVSIYISLEHQKRGFGKLLYTELEKQLLKLGYQNIYACVAVP 125

Query: 130 -----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

+ S+ H+ LG+ G G K W+ + + Q+
 Sbjct: 126 EVEDEYLTTNNSLSYHQYLGFKECGRFENCCKFNRYHIVWLQK 169

>ref|ZP_04449569.1| hypothetical protein GCWU000282_00798 [Catonella morbi ATCC 51271]
 gb|EEP23058.1| hypothetical protein GCWU000282_00798 [Catonella morbi ATCC 51271]
 Length = 166

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
 Identities = 50/161 (31%), Positives = 80/161 (49%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IR A D ++ I Y+E + ++F E + + +++ YP+LVAE+EG
 Sbjct: 6 IVIRSANPQDAPSLRAIYRPYVERTVISFEYEVPSVSGFRQRIKQTLAHYPYLVAEELEGE 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

V G AY + R AY + E +VY+ + G+G+ LY L +++ QG + V A +
 Sbjct: 66 VVGAYAGSAFHPRAAYQYVAEVSVYLKRSVRGQGIGAKLYAALEALRQQGIRRVTVACVA 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDF 168

P + SV H GY GYK W DV ++Q+D
 Sbjct: 126 YPEGGSVEFHLKQGYHQVALFEKVGKFDQVAVFQKDL 166

>ref|YP_001903385.1| Putative phosphinothricin N-acetyltransferase [Xanthomonas
 campestris pv. campestris str. B100]
 emb|CAP51333.1| Putative phosphinothricin N-acetyltransferase [Xanthomonas
 campestris pv. campestris]
 Length = 175

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
 Identities = 57/161 (35%), Positives = 79/161 (49%), Gaps = 1/161 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66

PVE+R AD+ A+ I I P Q + YP+LVAE +
 Sbjct: 2 PVELREVRDADIPAITAIYAEQIAGCNTYIEYVAPSAEQMCGRVRAIVDAGYPYLVAERDD 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

V G AYA ++AR Y WTVE+++Y++ Q G+GS L L+ E +G++ ++AVI
 Sbjct: 62 AVVGAYAYASSYRARAGYRWTVENSIIYLAQAQCGIGSQLLGALIAVCEQRYRQMIAMI 121

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

G N S+RLHE + G G KHG W D QR
 Sbjct: 122 GDATNQASLRLHERFEFRTVGVFTGLGRKHGRWLDVAVQMQR 162

>ref|ZP_06684576.1| phosphinothricin N-acetyltransferase [Achromobacter piechaudii
 ATCC 43553]
 gb|EFF78489.1| phosphinothricin N-acetyltransferase [Achromobacter piechaudii ATCC
 43553]
 Length = 212

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
 Identities = 64/170 (37%), Positives = 92/170 (54%), Gaps = 2/170 (1%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEW-IDDLERLQDRYPW 59
MSP V IR + AD+ A+ I H++E T +F EP + E + L+ P+
Sbjct: 32 MSPHTPTVLIRDSADADLPAIKTIYAHVHEGTASFELEPPSINEMRLRRASVLEREMPY 91

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
LVAE++G V G AY ++ R AY TVE +VYV LG+G L L++ A G+
Sbjct: 92 LVAEIDGEVVGAYVTAYRPRPAYRHTVEDSVYVKTGRAGLGIGGKLLGALVERCTAAGW 151

Query: 120 KSVVAVIGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
+ ++AV+G N S+ LH + G+ GTLR+ G+KHG W D QR
Sbjct: 152 RQMLAVVGDSRNAASLALHASQGFHPVGTLSVGHKHGEWRD TVLMQQRSL 201

>ref|YP_003144489.1| sortase-like acyltransferase [Slackia heliotrinireducens DSM 20476]
gb|ACV23140.1| sortase-like acyltransferase [Slackia heliotrinireducens DSM 20476]
Length = 210

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 60/182 (32%), Positives = 90/182 (49%), Gaps = 8/182 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR AT AD A + I Y+E + + F + + +E+ + ++YP+LVAE +
Sbjct: 19 IRAATPADAAELLAIYAFYVENTAITFEYDVPSVEEFARRIAGTLEKYPYLVAESSDGIQ 78

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G AY G + AR AYDW VE++VYV + G G LY L K + AQG ++ A I
Sbjct: 79 GYAYVGQFHARPAYDWAVETS VYVRRDGRTRGTGRALYDALEKVLAAQGIINLEACIAYA 138

Query: 130 -----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVT 181
+ SV H+ +GY G G+K W+D+ + ++ E A PVR
Sbjct: 139 PVEDEYLTTNSVGFHDHMGYRMVGRFEKCGFKFNRWYDMVWMEKLIGEHCADQPPVRWFP 198

Query: 182 QI 183
Q+
Sbjct: 199 QV 200

>emb|CAQ50959.1| hypothetical acetyltransferase YncA [Staphylococcus aureus subsp. aureus ST398]
Length = 163

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 55/161 (34%), Positives = 84/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
IR A D+ A+ I N I +T + EPQT E I E Q + P V E G V
Sbjct: 2 IRCAKKEDLNAILAIYNDAIINTTAVYTYEPQTIDERIAWFETKQRNHEPIFVFEENGSV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G++++VA I
Sbjct: 62 LGFATFGSFRPWPAYQYTIHESIYVDASARGKGIASQLLQHLIVEAKAKGYRTLAVAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
N+ S++LH+ + GTL GYK W D+ F++ D +
Sbjct: 122 SNEASIKLHQKFNFKHAGTLTNVGYKFDYWLDLAFYELDLK 162

>ref|YP_784856.1| acetyltransferase [Bordetella avium 197N]
emb|CAJ47923.1| acetyltransferase [Bordetella avium 197N]
Length = 178

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 58/161 (36%), Positives = 82/161 (50%), Gaps = 7/161 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER---LQDRYPWLVAEVE 65
IR + D+ + I H++ T +F +P D +R L P+LVAE +
Sbjct: 7 IRDSAETDLDP IQAIYAHVHLGHTSSFELDPPGIH---DIFQRRAAVLAQGLPYLVAERD 63

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G + G AYA ++ R AY T E +VYV LG+G L L+ A G++ ++AV
Sbjct: 64 GEIVGYAYATLYRPRAAYRHTCEDSVYVREGRHGLGIGRGLDRTLVARCAAAGWRQMLAV 123

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+G N S+ LH G+ GTL+A GYKHG W D F QR
Sbjct: 124 VGDNNPASLALHARC GF EVAGTLKAVGYKHGQWRD TTFMQR 164

>emb|CBA28717.1| Phosphinothricin N-acetyltransferase [Curvibacter putative symbiont
of Hydra magnipapillata]
Length = 174

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 56/173 (32%), Positives = 89/173 (51%), Gaps = 2/173 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
+RP+T +D++A+ I H++ T T F T P + + + L P+LVAEV+G V
Sbjct: 1 MRPSTESDISAITAIYAHVLTGTGTFTETPPSESMDQRRADVLSKGLPYLVAEVDGEV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
G AY +K R AY ++ E ++Y++ GLG L L+ E G + ++AVIG
Sbjct: 61 IGFAYCNWFKPRPAYRFS AEDSIY LAPNAHGKGLGKLLLIELMSQAERC GVRKLI AVIGD 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPPRPVRPV 180
N S+ +H + GY G + A G+K W D+ ++ + PV PV
Sbjct: 121 SANAGSIGVHTSCGYDKVGVISACGWKFDRWLDIVLMEKTIGAGSSTPPVDPV 173

>ref|YP_003830359.1| GNAT family acetyltransferase [Butyrivibrio proteoclasticus B316]
gb|ADL33777.1| acetyltransferase GNAT family [Butyrivibrio proteoclasticus B316]
Length = 190

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 58/184 (31%), Positives = 90/184 (48%), Gaps = 15/184 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-EVEG 66
++I T D + DI Y+ + + F + + E+ + + + ++P++ A + G
Sbjct: 1 MKIEKVT'TEDARELLDIYTPYVTDTAITFEYDVPSLSEFEERIRNISAKFPYIKAVDDNG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+ G AYA +K R+AYDW+VE+TVYV +R G+GS LY L KS+ G + A I
Sbjct: 61 AILGYAYASTFKGRSAYDWSVETTVYVRKDSKRCGVGSMLYDTLEKSLAKMGILNANACI 120

Query: 127 G-----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF--ELPAPP 174
L ND S HE GY GT +G+K W+D+ W + + P
Sbjct: 121 AYLKEGATDEHLTND-SKYFHEKHGYKLVGTFHDSGFKFNTWYDM-IWMEKYLGHQHTTSP 178

Query: 175 RPVR 178
PVR
Sbjct: 179 APVR 182

>emb|CBK74492.1| Sortase and related acyltransferases [Butyrivibrio fibrisolvens
16/4]
Length = 175

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 52/161 (32%), Positives = 90/161 (55%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-G 66
+ IR A +D AA+C+I +Y + V F + + + + + + YP++VA E G
Sbjct: 3 ITIRDAQVSDAAAICEIYGYYAAHTFVTFTEDNPSVEAYERSILETKKAYPYIVACDETG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRH-QRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
V G+AYAG + +AY ++VEST+Y + ++ G+G+ LY L K + G+K + V
Sbjct: 63 KVVGMAYAGRVRQHDAYRFSVESTIYTAVDAPKQQGIGTLLYDELEKRLSDMGYKFMYG 122

Query: 126 IGLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
I N+PS++ H+A G+ G GYK G W + +++
Sbjct: 123 ITDDNEPSIQFHKARGFEEVGHFENIGYKFGQWKGVVYRK 163

>ref|YP_003101768.1| GCN5-related N-acetyltransferase [Actinosynnema mirum DSM 43827]
gb|ACU37922.1| GCN5-related N-acetyltransferase [Actinosynnema mirum DSM 43827]
Length = 169

Score = 95.5 bits (236), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 60/160 (37%), Positives = 81/160 (50%), Gaps = 1/160 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
V +RPATA D+ AV I HY+ STV F P T +W + R P+L+A+
Sbjct: 6 VTVRPATADDLEAVAAIYAHYVHHSTVTFDLVPPTVDDWRRKHGEVTARGLPFLIADQGS 65

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G AY PW+A+ AY T E T+Y++ G G+ L LL ++ G + +AVI
Sbjct: 66 EVVGFAYLAPWRAPAYRHTAEDTIYLAPTATGRGTGAALLEALLALADSSGIRQTIAVI 125

Query: 127 GLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
+ S+ LH G+T G L A GYKH W QR
Sbjct: 126 TEDGEGSLVLHRRFGFTEAGRLEAVGYKHERWIGTILMQR 165

>ref|ZP_01996698.1| hypothetical protein DORLON_02716 [Dorea longicatena DSM 13814]
gb|EDM61934.1| hypothetical protein DORLON_02716 [Dorea longicatena DSM 13814]
Length = 205

Score = 95.1 bits (235), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 57/190 (30%), Positives = 94/190 (49%), Gaps = 8/190 (4%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
+ E++ + IR A D + I YIE + + + + T +E+ + + +RYP+LV
Sbjct: 3 TNEKKEITIRIAKEEDAELLAIYAPYIEHTVITYEYDVPTVEEFRGRIRHVLERYPYLV 62

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
AEV G + G AYA + R A W VE+++YV + +G+G+ LY L K ++ Q +
Sbjct: 63 AEVNGEICGYAYASAFHERPAGGWNVETSIYVDQNKKGMGIGTKLYDMLEKILKRQNVLN 122

Query: 122 VVAVIGLP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF-ELPAP 173
+ A I + S+ HE LGY G GYK W+++ + +++ E A
Sbjct: 123 MNACIACTEHEDEYLTNASIHYHEHLGYRMVGWFTNCGYKFHRWYNLAWMEKEIGEHVAD 182

Query: 174 PRPVRPVTQI 183
PV T I
Sbjct: 183 QPPVIAFTDI 192

>ref|ZP_02862900.1| hypothetical protein ANASTE_02127 [Anaerofustis stercorihominis DSM

17244]
gb|EDS72411.1| hypothetical protein ANASTE_02127 [Anaerofustis stercorihominis DSM
17244]
Length = 199

Score = 95.1 bits (235), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 47/178 (26%), Positives = 90/178 (50%), Gaps = 2/178 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++IR A D + DI YI ++ F + +E+ + + + YP+LV ++
Sbjct: 4 IKIRFAEENDSNEILDIYTPYILNTPITFEYDRPDEEEFKNRIVKTKKLYPYLVYTIDSR 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA +K R AYD+T E ++Y+ ++ +G LY L++ ++ Q + + A I
Sbjct: 64 IIGYAYASQYKNRKAYDYTAEISYIYKEGYKGKHIGQNLVMSLIEILKLQNLQLLYACIT 123

Query: 128 L-PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAPPRPVRPVTQI 183
+ P S H+ LG+ G +G+K G W+D ++ + + P+ P+ +I
Sbjct: 124 IHPTLKSSDFHKKLGFKYGEKSGFKDQWYDTAWYSLEIGDFKPNPKEFIPINKI 181

>ref|ZP_08185887.1| sortase-like acyltransferase [Xanthomonas gardneri ATCC 19865]
gb|EGD16518.1| sortase-like acyltransferase [Xanthomonas gardneri ATCC 19865]
Length = 173

Score = 95.1 bits (235), Expect = 3e-18, Method: Compositional matrix adjust.
Identities = 55/167 (32%), Positives = 88/167 (52%), Gaps = 2/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWL-VAEVEGV 67
I + A +A+ DI N I ST + +P+ P+ + + +P + V + +G
Sbjct: 4 IDCSEARHASAILDIFNDAIANSTALYDYKPRPPESMVGWGFATKRAGGFPVIGVEDADGT 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G A G ++A A+ ++VE ++YV H+ GLG TL L+ + + +G +V I
Sbjct: 64 LMGFASYGTFRAPPAFKYSVEHSIYVDRDHRGKGLGRTLQALIAAAQERGVHVLVGGID 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
N S+ LHE G+T GT+R AG+K G W D+ F+QR PA P
Sbjct: 124 ASNQASIALHEQFGFTHAGTVREAGFKFGRWLDLAFYQRILATPADP 170

>ref|YP_003910913.1| phosphinothricin acetyltransferase [Burkholderia sp. CCGE1003]
gb|ADN61622.1| Phosphinothricin acetyltransferase [Burkholderia sp. CCGE1003]
Length = 184

Score = 95.1 bits (235), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 62/168 (36%), Positives = 91/168 (54%), Gaps = 2/168 (1%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWL 61
P P IR AT AD+ A+ I H++ T +F P E L ++ P++V
Sbjct: 6 PASAPALIRDATEADLPAIQAIYAAHVLTGVASFEEVPPCVDELRLRRLTSVRSHGLPYMV 65

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
AE++G VAG YA P++ R AY T+E ++YVS ++ GLG L L++ EA ++
Sbjct: 66 AEIDGEVAGYCYATPYRPRAAYRHTIEDSIYVSDAYRGRGLGRLLLQALIERCEAGPWRQ 125

Query: 122 VVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
+VAVI + S+ LH+ G+ GTL+A G+KHG W D QR
Sbjct: 126 MVAVIADGGSGGSLSLHKQSGFELTGTLKAVGFKHGRWLDTTLMQRTL 173

>ref|ZP_07818891.1| acetyltransferase, GNAT family [Eremococcus coleocola
ACS-139-V-Col8]

gb|EFR31267.1| acetyltransferase, GNAT family [Eremococcus coleocola
ACS-139-V-Col8]
Length = 195

Score = 95.1 bits (235), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 58/182 (31%), Positives = 88/182 (48%), Gaps = 8/182 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR A D AA+ I Y+E + + F TE T ++ + YP+LV E EG +
Sbjct: 2 IRYAQVTDAAAILAIYKPYVENTAITFETEIPTVADFEGRIAATLKHYPYLVLEEEGQIL 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G AYA ++ R AYDW VE ++Y+ + G G LY L K + QG + A I
Sbjct: 62 GYAYASRYRTRAAYDWVVELSIYMDMNARDQKGKGRFLYEALEKLLRVQGLTAYACITGA 121

Query: 130 ND-----PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFE-LPAPPRPVRPVT 181
++ S + +EALGY GYK G W D+ + ++ L PP+ ++ +
Sbjct: 122 DEQEAYVTGASPKFYEALGYQYICHFPKIGYKFGQWFDILWMYKELAPLANPPQTLKSM 181

Query: 182 QI 183
Q+
Sbjct: 182 QL 183

>ref|YP_002516357.1| phosphinothricin N-acetyltransferase [Caulobacter crescentus
NA1000]
gb|ACL94449.1| phosphinothricin N-acetyltransferase [Caulobacter crescentus
NA1000]
Length = 183

Score = 95.1 bits (235), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 60/161 (37%), Positives = 83/161 (51%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
V IR +T AD+ A+ I + F P E + DR P+LVAE+ G
Sbjct: 3 VVIRASTDADIPAITAIYGNVNLGLTGFEEVPPDAAEMARRRQGFLLDRGLPYLVAELNG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G YAGP++ R AY +TVE +VYVS G+G L + L+ + E G + + AVI
Sbjct: 63 KVVGYCYAGPFRRLRAAYRYTVEDSVYVSPEAVGAGVGKALLSALISACEDLGVQMC 122

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
G N S+ LH ALG+ +G G+K G W D+ + QR
Sbjct: 123 GDSGNAASIGLHAALGFEEKGVFPDMGHKFGRWVDLVWMQR 163

>ref|YP_003613927.1| GCN5-related N-acetyltransferase [Enterobacter cloacae subsp.
cloacae ATCC 13047]
gb|ADF62978.1| GCN5-related N-acetyltransferase [Enterobacter cloacae subsp.
cloacae ATCC 13047]
Length = 184

Score = 95.1 bits (235), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 60/172 (34%), Positives = 89/172 (51%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
VE+R A D+ A+ I + ++ +F P T E L+ + D PWLVA G
Sbjct: 12 VEVVDALPDDVHAISAIYSWHVLHGRASFEEIPPTVDEMRKRLKNVTDNGLPWLVALYRG 71

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+V G YA P++ R+AY +T+E ++YV G GS L L++ E ++ ++AV+
Sbjct: 72 IVVGYCYATPYRPRHAYRFTLEESIYVDASTTGRGFGSALMDALIERCEQGPWRQMI 131

Query: 127 --GLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR----DFELP 171
 G N S+RLH+ G+ G LR+ GYK G W D QR D+ LP
 Sbjct: 132 GDGHNNAGSLRLHKKHGFVVGQLRSVGYKKGDWRDTLIMQRPLNDGDWTL 183

>ref|YP_004034059.1| sortase related acyltransferase [Lactobacillus delbrueckii subsp.
 bulgaricus ND02]
 gb|ADQ61082.1| Sortase related acyltransferase [Lactobacillus delbrueckii subsp.
 bulgaricus ND02]
 Length = 194

Score = 95.1 bits (235), Expect = 4e-18, Method: Compositional matrix adjust.
 Identities = 55/176 (31%), Positives = 90/176 (51%), Gaps = 10/176 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +E+R A D +I Y+E + + F + E+ + + + YP+LVA +G
 Sbjct: 8 LELRRANVGDAERLLEIYAPYVEKTAITFEDKVPPIGEFQNRILKTLRIYPYLVALKD 67

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G AYA +K R AYD +VE ++YV + +G LY + ++ QGF ++ A I
 Sbjct: 68 IVGYAYASAFKERAAYDHSVELSIYVDANVRHQHVGRFLYDAIEDCLKKQGFNLNACIA 127

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR---DFELPAP 173
 P +D S+R HE LGY G GYK G W+D+ + ++ + +PAP
 Sbjct: 128 APIGEDPYLDDNSIRFHEHLGYNFVGRFHQCGYKFGRWYDMVWMEKMLGEHTVPAP 183

>ref|ZP_04676812.1| phosphinothricin acetyltransferase [Staphylococcus warneri L37603]
 gb|EEQ81039.1| phosphinothricin acetyltransferase [Staphylococcus warneri L37603]
 Length = 167

Score = 94.7 bits (234), Expect = 4e-18, Method: Compositional matrix adjust.
 Identities = 50/161 (31%), Positives = 88/161 (54%), Gaps = 5/161 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A +D+ ++ DI N I +T + +P +E W + + Q+ P V E +
 Sbjct: 2 IRQAQQSDLTSLDIYNDAIINTTAVYTYQPTNIEERQAWFN--HKQQNGDPFVFEKDD 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126
 +V G A G ++ AY +T+E ++YV +++ G+ S L L++ + F++++A I
 Sbjct: 60 IVQGFATYQFRDWPAYLYTIEHSIYVHPKYRHHGSIASQLLIKLEIEAKDNNFRTLIAGI 119

Query: 127 GLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRD 167
 N S++LHE G++ GT++ AGYK W D+ F+Q D
 Sbjct: 120 DASNTGSIKLHEKFGFSHSGTIKYAGYKFDQWLDLTFYQLD 160

>ref|YP_002943286.1| phosphinothricin acetyltransferase [Variovorax paradoxus S110]
 gb|ACS18020.1| Phosphinothricin acetyltransferase [Variovorax paradoxus S110]
 Length = 177

Score = 94.7 bits (234), Expect = 4e-18, Method: Compositional matrix adjust.
 Identities = 61/167 (36%), Positives = 86/167 (51%), Gaps = 16/167 (9%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWL 60
 EI A A M +V I + Y+ +F +E + +E +Q R P+L
 Sbjct: 15 EILDAGAHMPSVQAIYSRYVLHDLCSF-----EEEVPSVEEMQARRAGVLARGLPYL 67

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 VA +G VAG AYA P+++R+AY TVE ++YV+ Q G+G L L++ GF
 Sbjct: 68 VALKDGEVAGYAYASPYRSRAYSRTVEDSIYVAEGMQGRGIGRALLQELIRRCTDGGFA 127

Query: 121 SVVAVIG-LPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

+VAVIG N S R+H+ LG+ G LR G+K G W D QR
Sbjct: 128 QMVAVIGNSANAGSQRVHQGLGFETAGVLRNVGFKFGQWVDTVLMQR 174

>ref|YP_062723.1| phosphinothricin acetyltransferase protein [Leifsonia xyli subsp.
xyli str. CTCB07]
gb|AAT89618.1| phosphinothricin acetyltransferase protein [Leifsonia xyli subsp.
xyli str. CTCB07]
Length = 192

Score = 94.7 bits (234), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 58/163 (35%), Positives = 80/163 (49%), Gaps = 3/163 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV-EGV 67
IR A A D+ V +I NHY+ STV F + T EW L P++VAE G
Sbjct: 30 IREARAEDLPHVREIYNHYVANSTVTFTDEDAMTLPEWKSFKGYLHKLGMPPFIVAESPQG 89

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
V G A PWK + AY +TVE+++Y+ GLG L L+ +A G K ++AVI
Sbjct: 90 VLGVALVSPWKQKRAYRYTVENSIYLGAASTGKGLGPALLQELIDRSKAAGLKEMIAVIA 149

Query: 128 LPN-DPSVRLHEALGYTARGLTIRAAGYKHGGWHDVGFWRQDFE 169
+ S+ +HE G+T G + GYK W QR +
Sbjct: 150 DKGAESITMHNENFGFTEIGRMGRVGYKFERWLGTVLMQRSLK 192

>ref|YP_002637715.1| acetyltransferase [Salmonella enterica subsp. enterica serovar
Paratyphi C strain RKS4594]
gb|ACN46274.1| putative acetyltransferase [Salmonella enterica subsp. enterica
serovar Paratyphi C strain RKS4594]
Length = 171

Score = 94.7 bits (234), Expect = 4e-18, Method: Compositional matrix adjust.
Identities = 64/170 (37%), Positives = 89/170 (52%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
+ IR A AD AA+ +I NH + T+T+ N RT + W + + L YP LV+E
Sbjct: 1 MTIRFADKADCAAITEIYNHAVLHTATIWNDRVTVDNRLAWYEARQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
GVVAG A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA
Sbjct: 59 NGVVAGYASFGDWRSFDGFRYTVESVYVHPAHQKGKGLGRKLLSRLIDEARRCGKHVMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGLTIRAAGYKHGGWHDVGFWRQDFELPAPP 174
I N S+RLH +LG+T + G K G W D+ F Q + A P
Sbjct: 119 GIESQNAASIRLHHS LGFTVTAQMPQVGKFGRWLDLTFMQLQLDEHAAP 168

>ref|YP_003695517.1| phosphinothricin acetyltransferase [Starkeya novella DSM 506]
gb|ADH90898.1| Phosphinothricin acetyltransferase [Starkeya novella DSM 506]
Length = 194

Score = 94.7 bits (234), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 59/172 (34%), Positives = 88/172 (51%), Gaps = 7/172 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVAEVEGVV 68
+R A DMAAV +I H++ F P + E + D P+LVAE+EG +
Sbjct: 18 VRDAREEDMAAVTEIYAHVNLGLATFEEVPPSLAEMSRRRAAILDLNLPYLVAEIEGRI 77

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
G +YA ++ R AY +TVE+++Y++ QR G+GS L L+ + ++ ++AVIG
Sbjct: 78 VGYSYATSYPRPAYRYTVENSIYIAPGQQRRGIGSALLDALIARCSSGPWRQMLAVIGD 137

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-----ELPAPP 174
N S+ +H G+ GTL G+K G W D QR LPA P
Sbjct: 138 SGNAGSLAVHRRAGFQPVGTLSCVGFKFGRWVDTVLMQRPLGEGSATLPASP 189

>ref|YP_002943389.1| phosphinothricin acetyltransferase [Variovorax paradoxus S110]
gb|ACS18123.1| Phosphinothricin acetyltransferase [Variovorax paradoxus S110]
Length = 174

Score = 94.7 bits (234), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 58/161 (36%), Positives = 87/161 (54%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRT-EPQTPQEWIDDLERLQDRYPWLVAEVEG 66
+ IRP+ D+AA+ I H++ T T F TE P + L P+LVAE +G
Sbjct: 3 LTIRPSRDQDIAAITAIYAHVLTGTGTFTFETEAPSAADMAARRADVGLKNLPYLVAEEDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
V G AY +K R AY ++ E ++Y+S + GLG+ L L ++ EA G + ++AVI
Sbjct: 63 EVLGFAFCNWFKPRPAYRFSAEFSIYMSEAARGKGLGAQLLAALSQAEEAVGVRKLIAMI 122

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
G N SV +H + G+T G L+ G+K G W DV ++
Sbjct: 123 GDSANAGSVGVHRSQGFTHVGVLKDCGKFGQWRDVLMEK 163

>ref|YP_813066.1| sortase related acyltransferase [Lactobacillus delbrueckii subsp.
bulgaricus ATCC BAA-365]
gb|ABJ58628.1| Sortase related acyltransferase [Lactobacillus delbrueckii subsp.
bulgaricus ATCC BAA-365]
Length = 190

Score = 94.7 bits (234), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 55/176 (31%), Positives = 90/176 (51%), Gaps = 10/176 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRT-EPQTPQEWIDDLERLQDRYPWLVAEVEG 67
+E+R A D + +I Y+E + + F + E+ + + + YP+LVA +G
Sbjct: 4 LELRRANVGDAERLLEIYAPYVEKTAITFEDKVPPIGEFQNRILKTLRIYPYLVALKDGK 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 127
+ G AYA +K R AYD +VE ++YV + +G LY + ++ QGF ++ A I
Sbjct: 64 IVGYAYASAFKERAAYDHSVELSIYVDANVRHQHVGRFLYDAIEDCLKKQGFNLNACIA 123

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR---DFELPAP 173
P +D S+R HE LGY G GYK G W+D+ + ++ + +PAP
Sbjct: 124 APIGEDPYLDDNSIRFHEHLGYKFVGRFHQCGYKFGRWYDMVWMEKMLGEHTVPAP 179

>ref|YP_001570427.1| hypothetical protein SARI_01387 [Salmonella enterica subsp.
arizonae serovar 62:z4,z23:-- str. RSK2980]
gb|ABX21285.1| hypothetical protein SARI_01387 [Salmonella enterica subsp.
arizonae serovar 62:z4,z23:--]
Length = 172

Score = 94.7 bits (234), Expect = 5e-18, Method: Compositional matrix adjust.
Identities = 63/174 (36%), Positives = 86/174 (49%), Gaps = 5/174 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTV--NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
+ IR A AD AA+ +I NH + + N RT + W + + L YP LV+E
Sbjct: 1 MTIRFADKADCAAITEIYNHAVLNTAAIWNDRVTVDNRLAWYETRQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
GVV G A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA
Sbjct: 59 NGVVTGYASFGDWRSFDGFRYTVESHSVYVHPAHQKGLGRKLLSRLIDEARRCGKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 178
 I N S+RLH ALG+T + G K G W D+ F Q + A P R
 Sbjct: 119 GIESQNAASIRLHHALGFTVTAQMPQVGVKFGRWLDLTFMQLQLDERAAPDVCR 172

>ref|YP_004155971.1| phosphinothricin acetyltransferase [Variovorax paradoxus EPS]
 gb|ADU37860.1| Phosphinothricin acetyltransferase [Variovorax paradoxus EPS]
 Length = 173

Score = 94.4 bits (233), Expect = 5e-18, Method: Compositional matrix adjust.
 Identities = 59/161 (36%), Positives = 85/161 (52%), Gaps = 2/161 (1%)

Query: 16 ADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVE-GVVAGIAY 73
 A A+ I+N I TST + +P+TP+ + + + +P + AE E G + G A
 Sbjct: 10 AHAGAILAILNDAIVTSTALYDYKPRTPENMVAVFATKRANGFPVIGAEDENGKLLGFAS 69

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPS 133
 G ++A AY +TVE +VYV H+ GLG TL ++ A+ +V I N S
 Sbjct: 70 YGSFRAFPAKYKTVEHSVYEAGHRGAGLGRITLMEAIIEAIARDVHVMVGAIDAANAGS 129

Query: 134 VRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 + LHE LG+ GT+R AG+K G W DV F+QR P P
 Sbjct: 130 IGLHERLGFHSGTVRQAGFKFGRWLDVAFYQRILATPLNP 170

>ref|YP_002744002.1| acetyltransferase (GNAT) family protein [Streptococcus equi
 subsp.
 zooepidemicus]
 emb|CAW98359.1| acetyltransferase (GNAT) family protein [Streptococcus equi subsp.
 zooepidemicus]
 Length = 193

Score = 94.4 bits (233), Expect = 5e-18, Method: Compositional matrix adjust.
 Identities = 62/177 (35%), Positives = 81/177 (45%), Gaps = 10/177 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT AD + DI Y+E + V F + E+ L + YP LV E EG +
 Sbjct: 4 IRLATLADAKTLLDIYRYPVEETAVTFEYTVPSLTFEERRLSDIMVFYPCLVVEEEGGIL 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 G AYA + AR AY W+ E T+Y++ + GLGS LY L ++ G + A I P
 Sbjct: 64 GYAYASRFHARAAYAWSAEVTIYLAQEARGRGLGSALYHRLEGYLKGMGILNCNACIASP 123

Query: 130 -----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF--ELPAPPRPV 177
 + S HE LGY G +GYK W D+ W E PRPV
 Sbjct: 124 AHATPYLTNSSQAFHEKLGRLVGRFHSQGYKFNQWFDL-IWMEKLLGEHDVRRPV 179

>ref|YP_004255451.1| Phosphinothricin acetyltransferase [Deinococcus proteolyticus
 MRP]
 gb|ADY25834.1| Phosphinothricin acetyltransferase [Deinococcus proteolyticus MRP]
 Length = 178

Score = 94.4 bits (233), Expect = 6e-18, Method: Compositional matrix adjust.
 Identities = 67/172 (38%), Positives = 94/172 (54%), Gaps = 7/172 (4%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVAE 63
 PV IRPATAAD+ A+ DI NH + +T + P Q+ +EW +R + +P LVAE
 Sbjct: 4 PVSIRPATAADLPAILDIYNHAVLHTTATYDHTPVSLQSREEWFAGRQR--EGFPVLVAE 61

Query: 64 VEG-VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 +G V G A GP++ + Y TVE +VY+S Q GLG L L+ +G+ +

Sbjct: 62 DDGGAUVGWASYGPFPRPKLGYSTRTEHVSVYLSPAAQGGQLGGLLEALIAQATTEGYHLM 121

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF-ELPAP 173
 + V+ ND S+R HE G++ G L AG+K G W D F R E+ AP

Sbjct: 122 IGVVDAENDGSLRFHERHGFSEAGRLPQAGHKFGRWLDATFVVRRLQEMDAP 173

>ref|NP_419751.1| phosphinothricin N-acetyltransferase [Caulobacter crescentus CB15]
 gb|AAK22919.1| phosphinothricin N-acetyltransferase [Caulobacter crescentus CB15]
 Length = 180

Score = 94.4 bits (233), Expect = 6e-18, Method: Compositional matrix adjust.
 Identities = 59/159 (37%), Positives = 82/159 (51%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR +T AD+ A+ I + F P E + DR P+LVAE+ G V
 Sbjct: 2 IRASTDADIPAITAIYGWNVNLGLGTFFEEVPPDAAEMARRRQGFLLDRGLPYLVAELNGKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G YAGP++ R AY +TVE +VYVS G+G L + L+ + E G + + AVIG
 Sbjct: 62 VGYCYAGPFRRLRAAYRYTVEDSVYVSPEAVGAGVGKALLSALISACEDLGVRQMCAVIGD 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 N S+ LH ALG+ +G G+K G W D+ + QR
 Sbjct: 122 SGNAASIGLHAALGFEEKGVFPDMGHKFGRWVDLVWMQR 160

>ref|ZP_06703408.1| phosphinothricin N-acetyltransferase [Xanthomonas fuscans subsp.
 aurantifolii str. ICPB 11122]
 gb|EFF45047.1| phosphinothricin N-acetyltransferase [Xanthomonas fuscans subsp.
 aurantifolii str. ICPB 11122]
 Length = 179

Score = 94.4 bits (233), Expect = 6e-18, Method: Compositional matrix adjust.
 Identities = 59/176 (33%), Positives = 84/176 (47%), Gaps = 3/176 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 P+E+R D+ + I I P + YP+LVAE++G
 Sbjct: 2 PLELRAVRNTDIPTITAIYAEQIAGVNTYIEYKAPSLDEMRRARVSAIVDAGYPYLVAELDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VVAG AYA ++AR Y WTV+++Y++ Q G+G L L+ E +GF+ ++AVI
 Sbjct: 62 VVAGYAYASAFRRAGYRWTVENSIYLAAMQGRGIGKALLGELIAVCEQGRFRQMIAMI 121

Query: 127 GLPNDPSVR-LHEALGYTARGTLRAAGYKHGGWHDVGFWRDFEL--PAPPRPVRP 179
 G + + R LHE G+ G G KHG W D QR APP P
 Sbjct: 122 GDAGNLASRHLHERFGFRTVGVFNIGRKHGRWLDGMMQMRALGSGDTAPPSDENP 177

>ref|ZP_03398208.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato T1]
 ref|ZP_07229851.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato Max13]
 ref|ZP_07250895.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato K40]
 ref|ZP_07258977.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato NCPPB 1108]
 gb|EEB58743.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 tomato T1]
 Length = 179

Score = 94.4 bits (233), Expect = 6e-18, Method: Compositional matrix adjust.
 Identities = 59/161 (36%), Positives = 83/161 (51%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEG 66
 + +R A DM AV I ++ +F EP T E ++ + L P+LVAE
 Sbjct: 5 LTLRDARDDMPAVQAIYADHVLHGSSFELEPPTLAELLERSQVLAKGLPYLVAERAK 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 V G Y P++ R AY +TVE +VYV LG+G L + L+K E G++ ++AVI
 Sbjct: 65 EVVGYGYVTPYRPRAAYRFTVEDSVYVRDGMGGLGIGQALLSELIKRCETGGWRQMIAMI 124

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 G N S+RLHE LG+ G + +KHG W D QR
 Sbjct: 125 GNSENIASLRLHERLGFGRVGVFESVEFKHGRWVDTVLMQR 165

>ref|YP_002746939.1| acetyltransferase (GNAT) family protein [Streptococcus equi subsp.
 equi 4047]
 emb|CAW94759.1| acetyltransferase (GNAT) family protein [Streptococcus equi subsp.
 equi 4047]
 Length = 193

Score = 94.4 bits (233), Expect = 7e-18, Method: Compositional matrix adjust.
 Identities = 64/178 (35%), Positives = 82/178 (46%), Gaps = 12/178 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT AD A+ DI Y+E + V F + E+ L + YP LV E EG +
 Sbjct: 4 IRLATLADAKALLDIYRPYVEETAVTFEYTPVPSLTFEERRLSDIMVFYPCLVVEEEGGIL 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG-- 127
 G AYA + AR AY W+ E T+Y++ + GLGS LY L ++ G + A I
 Sbjct: 64 GYAYASRFHARAAYAWSAEVTIYLAQEARGRGLGSALYHRLEGYLKGMGILNCNACIAST 123

Query: 128 -----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF--ELPAPPRPV 177
 L N V HE LGY G +GYK W D+ W E PRPV
 Sbjct: 124 AHATPYLTNSSQV-FHEKLGRLVGRFHQSGYKFNQWFDW-IWMEKLLGEHDVVRPRPV 179

>gb|ADW05103.1| Phosphinothricin acetyltransferase [Streptomyces flavogriseus ATCC 33331]
 Length = 192

Score = 94.0 bits (232), Expect = 7e-18, Method: Compositional matrix adjust.
 Identities = 57/166 (34%), Positives = 87/166 (52%), Gaps = 8/166 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP--WLVAEVE 65
 +++RP AD+ A+ DI NHY+ + + F T TP+E + L + P LVA
 Sbjct: 7 LQVRPGVEADLEALTDIYNHYVRETVLTFDTVAFTPEERLPWLRSHPEDGPHRLLLVALDP 66

Query: 66 GV-----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 G V G A + P++ + AY +VE +VY + G+G+ LY L +++ +
 Sbjct: 67 GTRQNAPHVLGYATSSPYRPKAAYSTSVEVSVCAPGATGRGVGTLLYRTLFEALADEDL 126

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 165
 A I LPN+PSVRLHEA G+ GT G K G + DV +++
 Sbjct: 127 HRAYAAIALPNEPSVRLHEAFGRFLVGTYGEVGRKLGRYLDVSWYE 172

>ref|ZP_08156293.1| phosphinothricin acetyltransferase [Rhodococcus equi ATCC 33707]
 gb|EGD22477.1| phosphinothricin acetyltransferase [Rhodococcus equi ATCC 33707]
 Length = 162

Score = 94.0 bits (232), Expect = 8e-18, Method: Compositional matrix adjust.
 Identities = 55/159 (34%), Positives = 83/159 (52%), Gaps = 5/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT D+ + +I N I +T + + W+DD R + +P LVA+V+G
 Sbjct: 3 IRDATTGDLPGILEIHNEAIANTTAIWDETLADLDERRRWLDD--RRANGFPVLVADVDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VAG A G W+A++ Y +TVE++VYV H R G+ + L T L++ A G +VA +
 Sbjct: 61 AVAGYASYGVWRKASGYRYTVENSYYVHVDHRRGIATALMTALIERARAGGIHVIVASV 120

Query: 127 GLPNDPVSRLEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N S+ LHE G+ + G K G W D+ + Q
 Sbjct: 121 ESSNTTSIALHERFGFRIVAQMPEVGRKFGRWLDMTYLQ 159

>emb|CBK97049.1| Sortase and related acyltransferases [Eubacterium siraeum 70/3]
 Length = 172

Score = 94.0 bits (232), Expect = 8e-18, Method: Compositional matrix adjust.
 Identities = 52/161 (32%), Positives = 84/161 (52%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +EIR AT D + I ++YI + V + + + +++ +E+ +YP++VAE +G
 Sbjct: 4 IEIRTATPFDAEELLGIYSYIINTAVTYEIDVPSAEDFRRRIEKTLLKYPYIVAERDGR 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYAG +K R AY+ + E+++YV +R G G+ LY L K + G ++ A I
 Sbjct: 64 IMGYAYAGVFKDRAAYERSAETSIYVDVNEKRHGTGTALYRELEKRLADMGVRNAYACIA 123

Query: 128 -----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 N S+R HE GYT GT K G +D+
 Sbjct: 124 STDKDDEYLNHDSIRFHEKQGYTLVGTFFHKCADKFGREYDM 164

>ref|ZP_04589637.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 oryzae str. 1_6]
 Length = 209

Score = 94.0 bits (232), Expect = 8e-18, Method: Compositional matrix adjust.
 Identities = 60/169 (35%), Positives = 84/169 (49%), Gaps = 2/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 +R A DM AV I ++ +F EP + E + + L P+LVAE G V
 Sbjct: 37 LRDALDDMPAVQTIYADHVLHGIISSFELEPPSLAELLQRRQVLAKGLPYLVAEHAGEV 96

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 G Y P++ R AY +TVE +VYV LG+G L L+K E G++ ++AVIG
 Sbjct: 97 VGYGYVTPYRPRPAYRFTVEDSVYVRAGMGLGIGHALLGELIKRCETGGWRQMIAVIGN 156

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 N S+RLHE + + G + G+KHG W D QR + RP
 Sbjct: 157 SENIASLRLHERMDFRRVGVFESVGFKHGRWVDTVLMQALGDGSCSRP 205

>ref|YP_427494.1| GCN5-related N-acetyltransferase [Rhodospirillum rubrum ATCC 11170]
 gb|ABC23207.1| GCN5-related N-acetyltransferase [Rhodospirillum rubrum ATCC 11170]
 Length = 195

Score = 94.0 bits (232), Expect = 8e-18, Method: Compositional matrix adjust.
 Identities = 63/166 (37%), Positives = 88/166 (53%), Gaps = 8/166 (4%)

Query: 8 VEIRPATAADMA-AVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-QDRYPWLVAEVE 65
 + IRPA D A A+ I Y+ TST F P + + L L + YP LVAE
 Sbjct: 4 LTIRPARPDDDALAIQAIYAPYVLTSTATFENVPPSVDDMAGRLRTLVEGGYPVLVAEES 63

Query: 66 GV-----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
 G + G AYAGP+ R AY T+E+++YV + +R G+G+ L T LL +GF+
 Sbjct: 64 GEGAPPRIVGYAYAGPYHKRPAYRATLENSIYVDSQCRRGGVGAALMTRLLAEAAERGFR 123

Query: 121 SVVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 V+AVIG N S + H G+ G + A G+K G W DV ++Q
 Sbjct: 124 QVIAVIGDADNTASRQFHLRQGFREAGMIAAVGWKFGRWLDVFFYYQ 169

>ref|ZP_04560308.1| yceA [Citrobacter sp. 30_2]
 gb|EEH94351.1| yceA [Citrobacter sp. 30_2]
 Length = 178

Score = 94.0 bits (232), Expect = 8e-18, Method: Compositional matrix adjust.
 Identities = 55/163 (33%), Positives = 94/163 (57%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 ++I A + A+ DI H++ T +F T+P E + LE+++ PW+VA E
 Sbjct: 1 MKIVNAEEKHILAIRDIYAHHLVHGTGSFETDPPDAHEMLARLEKIRSLGLPWVVALQED 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G Y ++ R AY +T+E ++Y++ QR G+G L H++ EAQG++ ++A++
 Sbjct: 61 KVIGYCYLTRYRERYAYRYTLEDSIYIAPTAQRQGVGKALLRHVIGWAEAQGYRQLIAIV 120

Query: 127 GLPNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 G N+ S+++H+ G+T GTL+ G+KHG W D QR+
 Sbjct: 121 GDSNNQGS�KVHQAGFTQIGTLKNIGFKHGLWLDTVLLQRNL 163

>ref|ZP_04776030.1| phosphinothricin N-acetyltransferase [Gemella haemolysans ATCC
 10379]
 gb|EER69121.1| phosphinothricin N-acetyltransferase [Gemella haemolysans ATCC
 10379]
 Length = 167

Score = 94.0 bits (232), Expect = 9e-18, Method: Compositional matrix adjust.
 Identities = 46/160 (28%), Positives = 80/160 (50%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR D + +I Y+E + + F + E+ + + + RYP+LVA
 Sbjct: 2 INIRTVELEDAEQLVNIYRPVYHTAITFDYTVPSVHEFEKISKSIQRYPFVLVATEGND 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA + ++AY WT E T+Y+ + + G+G LY+ L K + +G + + I
 Sbjct: 62 ILGYAYASEFYPKDAYKWTAETIYLDKARGKGVGKLYSELEKQLYDRGICRLTSCIA 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRD 167
 P++ S+ HE G+ GYK W+DV ++Q+D
 Sbjct: 122 YPDEGSISFHEKRGFRKVAHFEKVGKFNRYDVVVYQKD 161

>ref|YP_003766391.1| acetyltransferase [Amycolatopsis mediterranei U32]
 gb|ADJ45989.1| acetyltransferase [Amycolatopsis mediterranei U32]
 Length = 162

Score = 94.0 bits (232), Expect = 9e-18, Method: Compositional matrix adjust.
 Identities = 57/160 (35%), Positives = 80/160 (50%), Gaps = 3/160 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 I AT AD + + Y S V F T P T ++W + + +P+LV G V
 Sbjct: 4 IAEATEADAEGIAAVFAPYATDSVVTFTTPTAEQWRKIR--ESAWPFLVLAEEAGEVL 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G A A PW+ + AY ++VE+T+Y++ + G G L LLK G + +AVI
 Sbjct: 62 GYALAAPWRPKPAYRFSVETIYLAPQAAGRGHGRRLLDELLKRCGDAGARQAIIVIDS 121

Query: 130 NDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDF 168
 +P S RLH A G+T G LR G+KH W D QR+
 Sbjct: 122 GNPASQRLHAAAGFTDAGVLRGVGFKHDRWLDTLQMREL 161

>ref|ZP_06492287.1| putative phosphinothricin N-acetyltransferase [Xanthomonas
 campestris pv. musacearum NCPPB4381]
 Length = 173

Score = 93.6 bits (231), Expect = 9e-18, Method: Compositional matrix adjust.
 Identities = 57/161 (35%), Positives = 82/161 (50%), Gaps = 1/161 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 PVE+R AD+ A+ I I + P + +P+LVAE++G
 Sbjct: 2 PVELRAVRDADIPAITAIYADQICGVNTYEYSAPSLDEMRRARVSAIVDAGHPYLVAELDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 VAG AY ++AR Y WTV E+++Y++ Q G+G L L+ E +GF+ ++AVI
 Sbjct: 62 AVAGYAYVSAFRARAGYRWTVENSIYLAAMQGRGIGKALLGELIAVCEQGRGFRQMIAVI 121

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQR 166
 G N S +LHE G+ G L G KHG W D QR
 Sbjct: 122 GDAGNLASRQLHERFGFRTVGVLTGIGRKHGRWLDGVQMQR 162

>ref|YP_003518666.1| Pat [Pantoea ananatis LMG 20103]
 gb|ADD75538.1| Pat [Pantoea ananatis LMG 20103]
 Length = 223

Score = 93.6 bits (231), Expect = 9e-18, Method: Compositional matrix adjust.
 Identities = 56/161 (34%), Positives = 84/161 (52%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 +EI A + + A+ I H++ T +F P E LE+L+ PW VA EG
 Sbjct: 51 MEIILAEDSHVPAIQIYAHHVLTGSGSFEIVPPDEAEIASRLEKLRAAGLPWFVASEG 110

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 V G Y ++ R AY +T+E ++Y++ Q G+G L H + E++GF+ +V +
 Sbjct: 111 QVCGYCYLSFYRPRYAYRFTLEDSLYIAPAFQGGKIGKRLLAHAIHWAESRGFRQMVGNV 170

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQR 166
 G N S+ LH A G+T GTL + G+KHG W D QR
 Sbjct: 171 GDSANVASIALHRAAGFTVTGTLTSVGFKHGRWLDTVLMQR 211

>emb|CBL38504.1| Sortase and related acyltransferases [butyrate-producing bacterium
 SSC/2]
 Length = 185

Score = 93.6 bits (231), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 56/163 (34%), Positives = 86/163 (52%), Gaps = 10/163 (6%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG- 66
 +E+R AT D + +I +Y+E + + F E + E+ +++ YP+L A V+G
 Sbjct: 1 MEVRLATPQDAEELLEIYRYVEHTAITFEYETPSITEFRQRIKQTLKCYPLAA-VDGH 59

Query: 67 -VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
 + G AYA +K R AYDW+VE+T+YV +R G+G LY L + + Q ++ A
 Sbjct: 60 RKIVGYAYASSFKNRAAYDWSVETIYVDKDKVRQGIGKKLYEALKEILRKQHVINLDAC 119

Query: 126 IGLP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 I P SV+ HE LGY G +GYK G W+D+
 Sbjct: 120 ITDPEIEDEYVTKNSVQYHEHLGYHMGKFKYKSGYKFGRWYDM 162

>ref|YP_002548913.1| Phosphinothricin acetyltransferase [Agrobacterium vitis S4]
 gb|ACM35907.1| Phosphinothricin acetyltransferase [Agrobacterium vitis S4]
 Length = 168

Score = 93.6 bits (231), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 58/155 (37%), Positives = 85/155 (54%), Gaps = 5/155 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT AD+AA+ +I NH +E +T + + W++ L R + +P LVAEV+G
 Sbjct: 7 IRDATEADLAAIVEIYNHAVEHTTAIWNEALIDVDNRRRAWLE-LRRARG-FPVLVAEVDG 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VAG A G W++ + Y TVE +VY+ H+ GLG L L++ +A ++A I
 Sbjct: 65 RVAGYASYGDWRSFDGYRHTVEHSVYIDKDHGAGLGKALMLALIERAKAGNVHVMIAAI 124

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 N S+ LHE LG+ G R G K G W D+
 Sbjct: 125 EAGNAASIALHEKLGFLVGIHREVGTGKGRWLDL 159

>gb|EFZ06201.1| putative acyltransferase [Salmonella enterica subsp. enterica
 serovar Choleraesuis str. A50]
 Length = 171

Score = 93.6 bits (231), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 63/170 (37%), Positives = 88/170 (51%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IR A AD AA+ +I NH + T+ + N RT + W + + L YP LV+E
 Sbjct: 1 MTIRFADKADCAAITEIYNHAVLHTAAIWNDRTVDTNRLAWYEARQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 GVVAG A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA
 Sbjct: 59 NGVVAGYASFGDWRSFDGFRYTVVEHSVYVHLAHQKGLGRKLLSRLIDEARRCGKHVMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+RLH +LG+T + G K G W D+ F Q + A P
 Sbjct: 119 GIESQNAASIRLHHSGLGFTVTAQMPQVGKFGRWLDLTFMQLQLDEHAAP 168

>ref|ZP_07603383.1| Phosphinothricin acetyltransferase [Streptomyces violaceusniger
 Tu

4113]
 gb|EFN20884.1| Phosphinothricin acetyltransferase [Streptomyces violaceusniger Tu
 4113]
 Length = 184

Score = 93.6 bits (231), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 70/177 (39%), Positives = 86/177 (48%), Gaps = 12/177 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEV---- 64
 IR AT D+ A+ I +HY+ + V F P T +W L L DR P+LVAEV
 Sbjct: 8 IRDATHTDLGAIAAIFSHYVTETVVTFFEEVPPTVDDWARRLAELTDRGLPFLVAEVPEVA 67

Query: 65 ---EG---VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 118
 EG V G AYAGPW+ + AY T E +Y++ GLG+ L LL G
 Sbjct: 68 EVAEGAGRTVVGAYAGPWRPKPAYRHTAEDAIY LAPGRTGAGLGAALLGALLTHCAEAG 127

Query: 119 FKSVVAVIG-LPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQ RDFELPAPP 174
 + VVAVI +D S LH G+T G L G KHG W D QRD A P
 Sbjct: 128 VRQVVAVIADSGSDASAAALHRRFGFTPAGKLAGVGRKHGRWIDTHLMQRDLTTGANP 184

>ref|YP_468767.1| phosphinothricin acetyltransferase (antibiotic resistance) protein
 [Rhizobium etli CFN 42]
 gb|ABC90040.1| probable phosphinothricin acetyltransferase (antibiotic resistance)
 protein [Rhizobium etli CFN 42]
 Length = 171

Score = 93.6 bits (231), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 58/158 (36%), Positives = 79/158 (50%), Gaps = 5/158 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 V +R AT AD+ A+ DI NH +E +T R + + +EW+ R +P +VAE
 Sbjct: 4 AVLLRDATEADLPAIRDIYNHAVEHTTAIWNETRVDLENRREWLS--ARKGRGFPVVVAE 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VV 123
 G VAG A G W+A Y TVE +VYV H+ G+G L L+ A ++
 Sbjct: 62 RSGKVAGYASYGDWRAFEGYRHTVEHSVYVDKDHGAGIGEALMRELIARAAAANIHVMI 121

Query: 124 AVIGLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 A I N S+RLHE LG+ G G K G W D+
 Sbjct: 122 AGIEADNTASIRLHEKLGFRIGRFSEVGTKFGRWLDL 159

>ref|ZP_01772202.1| Hypothetical protein COLAER_01204 [Collinsella aerofaciens ATCC
 25986]
 gb|EBA39618.1| Hypothetical protein COLAER_01204 [Collinsella aerofaciens ATCC
 25986]
 Length = 196

Score = 93.6 bits (231), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 54/177 (30%), Positives = 88/177 (49%), Gaps = 10/177 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR AT D A+ I Y+ + + E + +E+ +ER RYP+LV E++G
 Sbjct: 9 IRLATPDDAPALLAIYEPYVRQTAITCEYEVPSVEEFAGRIERTLKRYPYLVMELDGRPV 68

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIGLP 129
 G AY P +R AYDW+VE+++Y++ + GLG L+ L + + A G ++ A+I +P
 Sbjct: 69 GYAYVSPLSREAYDWSVETSIYLARDVRHGGLGRKLHDALKQCLIAMGITNM CALI AVP 128

Query: 130 NDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQ RDF--ELPAPPRP 176
 +D S H +GY G K G W+D+ + + +P P+P
 Sbjct: 129 HDKDDEYLTHNSQDFHAHMGYRLVGAFDRCAQKFGRWYDMCWMELVLAERVPNQPKP 185

>ref|YP_002827727.1| putative GCN5-related N-acetyltransferase [Sinorhizobium fredii
 NGR234]
 gb|ACP26974.1| putative GCN5-related N-acetyltransferase [Sinorhizobium fredii
 NGR234]
 Length = 185

Score = 93.2 bits (230), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 51/158 (32%), Positives = 84/158 (53%), Gaps = 2/158 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVE-GV 67
 +R A AAD+ A+ +I + + P + E + YP++ A E G+
 Sbjct: 5 LRDAVAADLPAITEIYRESVLNGVATYELTPPSEAEMALRFSTITGSGYPYVA AVDERGI 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G AYA ++ R AY + VE ++Y++ + G+G L L++ A GF+ +VAVIG
 Sbjct: 65 VLGAYAYAFARTRAAAYRFLVEDSIYLAPEARGRGIGRALLEELVRRSTALGFRQMVAVIG 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 + S+ +H A+G+ +GT++A G+KHG W D Q
 Sbjct: 125 GAHPASIAVHRAVGFAHQGTMKATGFKHGRWLDTAIMQ 162

>ref|YP_275243.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 phaseolicola 1448A]
 gb|AAZ34956.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 phaseolicola 1448A]
 gb|EFW83894.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 glycinea str. race 4]
 Length = 179

Score = 93.2 bits (230), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 58/159 (36%), Positives = 84/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 +R A D+ AV I ++ +F +P + E + + L + P+LVAE+ G V
 Sbjct: 7 LRDACDQDIPAVQAIYADHVLHGIISSFELDPSPVAELLQRRQVVLNGLPYLVAELAGEV 66

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 G YA P++ R AY +TVE +VYV G+G L L++ E G++ +VAVIG
 Sbjct: 67 VGYGYATPYRPRPAYRFTVEDSVYVRDGMGGRGIGLALLGELVQRCEQGGWRQMVAVIGN 126

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+RLHE LG+ G + G+KHG W D QR
 Sbjct: 127 SENIASLRLHERLGFRRVGVFESVGFKHGRWVDTVLMQR 165

>ref|YP_001020299.1| putative phosphinothricin acetyltransferase [Methylibium
 petroleiphilum PM1]
 gb|ABM94064.1| putative phosphinothricin acetyltransferase [Methylibium
 petroleiphilum PM1]
 Length = 190

Score = 93.2 bits (230), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 59/161 (36%), Positives = 86/161 (53%), Gaps = 6/161 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWI---DDLRLQDRYPWLVAEVEG 66
 +RP+ AAD+ A+ + + + F E + +E DD+ L PVLVAE G
 Sbjct: 12 LRPSAAADLPALTALYGWHARHSGTFELEGPSLEEMARRRDDV--LAKGLPWLVAERHG 69

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G AYA P++ R AY + +E ++Y++ R G+G L L+ EA G + + AVI
 Sbjct: 70 DLLGYAYAAPFRPRLAYRFALEDISIYLAPHAHRQGVGRALLAELIARCEAWGARQMFVAI 129

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G N S+ LH ALG+ GT+ AAG+K W DV QR
 Sbjct: 130 GDSTNAASIGLHRALGFADVGMTMAAGWKFRWLDVVIMQR 170

>gb|ADI99011.1| probable phosphinothricin N-acetyltransferase [Staphylococcus
 aureus subsp. aureus ED133]
 Length = 163

Score = 93.2 bits (230), Expect = 1e-17, Method: Compositional matrix adjust.
 Identities = 53/161 (32%), Positives = 84/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLRLQDRY-PWLVAEVEGVV 68

```

IR A  D+ A+ I N I  +T + EPQT E + E Q ++ P V E G V
Sbjct: 2  IRCARKEDLNAILAIYNDAIINTTAVTYTEPQTIDERVAVFETKQRKHEPIFVFEKNGSV 61

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
          G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G++++VA I
Sbjct: 62  LGFATFGSFRPWPAYLYTIEHSIYVDASARGKGIASQLLHHLIVEAKAKGYRALVAGIDA 121

Query: 129  PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQWRDQFE 169
          N S++LH+ + GTL G+K W D+ F++ D +
Sbjct: 122  SNKASIQLHQKFQFKHAGTTLTNVGFKNQWLDLAFYELDLQ 162

```

>dbj|BAI77989.1| phosphinothricin N-acetyltransferase [*Pseudomonas cichorii*]
Length = 199

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 55/159 (34%), Positives = 82/159 (51%), Gaps = 2/159 (1%)

```

Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
          +R A  DM V I  ++ +F EP + +E + + D+ P+ VAE +G V
Sbjct: 27  LRDARDDDMPTVQAIYAEHVLGGISSFELEPPSLEEMLRRRADVLDKGLPYRVAERQGEV 86

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
          G Y P++ R Y +TVE +VYV H LG+G L L++ G++ ++A+IG
Sbjct: 87  VGYGYVTPYRPRPGYRFTVEDSVYVRHGLGGLGIGQALLGELIEHCVQGGWRQMIAIIGN 146

Query: 128  LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQWR 166
          N S+RLHE LG+ G + G+KHG W D QR
Sbjct: 147  SENLASIRLHERLGFHRVGVFESVGFKHGRWVDTVLMQR 185

```

>ref|ZP_05687808.1| acetyltransferase [*Staphylococcus aureus* A9635]
gb|EEV68814.1| acetyltransferase [*Staphylococcus aureus* A9635]
Length = 163

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 54/161 (33%), Positives = 83/161 (51%), Gaps = 1/161 (0%)

```

Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
          IR A  D+ A+ I N I  +T + EPQT E I E Q + P V E G V
Sbjct: 2  IRCARKEDLNAILAIYNDAIINTTAVTYTEPQTIDERIAWFETKQRNHEPIFVFEENGSV 61

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
          G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G++++VA I
Sbjct: 62  LGFATFGSFRPWPAYLYTIEHSIYVDASARGKGIASQLLQHLLAEAKAKGYRALVAGIDA 121

Query: 129  PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQWRDQFE 169
          N S++LH+ + GTL G+K W D+ F++ D +
Sbjct: 122  SNKASIQLHQKFTFKHAGTTLTNVGFKNQWLDLAFYELDLQ 162

```

>ref|ZP_03290892.1| hypothetical protein CLONEX_03111 [*Clostridium nexile* DSM 1787]
gb|EEA81006.1| hypothetical protein CLONEX_03111 [*Clostridium nexile* DSM 1787]
Length = 196

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 53/159 (33%), Positives = 80/159 (50%), Gaps = 7/159 (4%)

```

Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR A  D + I Y++ + + F E T +E+ D +E + R+P+L AE +G +
Sbjct: 6  IRIAKPEDAEELLKIYAPYVKHTAITFEYEVPTVEEFDRIEHILKRHPYLAERDGEI 65

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129

```

G AYAG + R A D +VE+ +YV ++ G+G LY L K + Q ++ A I
 Sbjct: 66 GYAYAGVFNERAACDRSVETAIYVRQDGRKDGIGRMLYEALEKILSEQNILNLNACIAYV 125

Query: 130 NDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 +D SV H +GY G R GYK G W+D+

Sbjct: 126 DDDDPYLTKNSEFHNHMGYRFVGRFRRCGYKFGRWYDL 164

>ref|YP_216574.1| putative acyltransferase [Salmonella enterica subsp. enterica
 serovar Choleraesuis str. SC-B67]
 gb|AA65493.1| putative acyltransferase [Salmonella enterica subsp. enterica
 serovar Choleraesuis str. SC-B67]
 Length = 171

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 63/170 (37%), Positives = 88/170 (51%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IR A AD AA+ +I NH + T+ + N RT + W + + L YP LV+E

Sbjct: 1 MTIRFADKADCAAITEIYNHAVLHTAAIWNDRVTDTNRLAWYEARQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 GVVAG A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA

Sbjct: 59 NGVVAGYASFGDWRSFDGFRYTVESHVYVHPAHQGLGRKLLSRLIDEARRCGKHVMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+RLH +LG+T + G K G W D+ F Q + A P

Sbjct: 119 GIESQNAASIRLHSLGFTVTAQMPQVGKFGRWLDLTFMQLQLDEHAAP 168

>ref|YP_002363145.1| GCN5-related N-acetyltransferase [Methylocella silvestris BL2]
 gb|ACK51783.1| GCN5-related N-acetyltransferase [Methylocella silvestris BL2]
 Length = 195

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 84/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNH-YIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 IR A DMA I H++ F P T E+ L+ P+L+A ++G +

Sbjct: 18 IRDADEKDMAPALAIYAHVHLGLATFEETPPTIGFEFAARRAAALEQGLPFLIAALDGTI 77

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G +YA ++AR AY T+E +VYV+ G+G+ L L++ EA ++ ++AVIG

Sbjct: 78 VGYSYAAEYRARTAYRHTIEDSVYVAVGLGGRGVGTMLLAALIERCEAGPWRQMIAVIGD 137

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ LH+ LG+ RGTLR+ G K G W D QR

Sbjct: 138 SGNAGSIALHKNLGFHRGTLRSVGRKLGQWIDTVLMQR 176

>ref|YP_041954.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus
 subsp. aureus MRSA252]
 ref|ZP_05600435.1| acetyltransferase family protein [Staphylococcus aureus subsp.
 aureus 55/2053]
 ref|ZP_05603089.1| acetyltransferase family protein [Staphylococcus aureus subsp.
 aureus 65-1322]
 ref|ZP_05605709.1| acetyltransferase [Staphylococcus aureus subsp. aureus 68-397]
 ref|ZP_05608333.1| acetyltransferase [Staphylococcus aureus subsp. aureus E1410]
 ref|ZP_05610981.1| acetyltransferase [Staphylococcus aureus subsp. aureus M876]
 ref|ZP_06310330.1| toxin-antitoxin system, toxin component, GNAT family
 [Staphylococcus aureus subsp. aureus C160]
 ref|ZP_06314711.1| acetyltransferase GNAT family protein [Staphylococcus aureus
 subsp.

aureus Btn1260]

ref|ZP_06317645.1| acetyltransferase family protein [Staphylococcus aureus subsp. aureus WW2703/97]

ref|ZP_06319883.1| acetyltransferase family protein [Staphylococcus aureus subsp. aureus WBG10049]

ref|ZP_06323160.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus M899]

ref|ZP_06328823.1| acetyltransferase [Staphylococcus aureus subsp. aureus C427]

ref|ZP_06333664.1| acetyltransferase [Staphylococcus aureus subsp. aureus C101]

ref|ZP_06376739.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus A017934/97]

ref|ZP_06665634.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus 58-424]

ref|ZP_06670054.1| acetyltransferase [Staphylococcus aureus subsp. aureus M809]

ref|ZP_06672639.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus M1015]

ref|ZP_06821729.1| acetyltransferase [Staphylococcus aureus subsp. aureus EMRSA16]

ref|ZP_06948037.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus MN8]

emb|CAG41588.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus MRSA252]

gb|EEV05126.1| acetyltransferase family protein [Staphylococcus aureus subsp. aureus 55/2053]

gb|EEV07769.1| acetyltransferase family protein [Staphylococcus aureus subsp. aureus 65-1322]

gb|EEV10390.1| acetyltransferase [Staphylococcus aureus subsp. aureus 68-397]

gb|EEV12981.1| acetyltransferase [Staphylococcus aureus subsp. aureus E1410]

gb|EEV15642.1| acetyltransferase [Staphylococcus aureus subsp. aureus M876]

gb|EFB43249.1| acetyltransferase [Staphylococcus aureus subsp. aureus C101]

gb|EFB45904.1| acetyltransferase [Staphylococcus aureus subsp. aureus C427]

gb|EFB51438.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus M899]

gb|EFB54099.1| acetyltransferase family protein [Staphylococcus aureus subsp. aureus WBG10049]

gb|EFB56714.1| acetyltransferase family protein [Staphylococcus aureus subsp. aureus WW2703/97]

gb|EFB59283.1| acetyltransferase GNAT family protein [Staphylococcus aureus subsp. aureus Btn1260]

gb|EFC01855.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus C160]

gb|EFC27717.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus A017934/97]

gb|EFD96090.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus M1015]

gb|EFE26969.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus 58-424]

gb|EFF08514.1| acetyltransferase [Staphylococcus aureus subsp. aureus M809]

gb|EFG56510.1| acetyltransferase [Staphylococcus aureus subsp. aureus EMRSA16]

gb|EFH96620.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus MN8]

gb|ADQ76124.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus TCH60]

gb|EFU25415.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus CGS00]

gb|EGA98300.1| phosphinothricin N-acetyltransferase [Staphylococcus aureus 011]

gb|EGB00503.1| phosphinothricin N-acetyltransferase [Staphylococcus aureus 046]

Length = 163

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 84/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLRLQDRY-PWLVAEVEGVV 68
IR A D+ A+ I N I +T + EPQT E + E Q ++ P V E G V

Sbjct: 2 IRC AKKEDLNAILAIYNDAINTTAVYTYEPQTIDERVAVFETKQRKH EPIFVFEENGSV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G++++VA I

Sbjct: 62 LGFATFGSFRPWPAFLYLTIEHSIYVDASARGKGIASQLLHHLIVEAKAKGYRALVAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRDFE 169
 N S++LH+ + GTL G+K W D+ F++ D +

Sbjct: 122 SNKASIQLHQKFAFKHAGTLTNVGFKNQWLDLAFYELDLQ 162

>ref|ZP_06458335.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv. aesculi str. NCPPB3681]

ref|ZP_06480234.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv. aesculi str. 2250]

Length = 179

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 84/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 +R A D+ AV I ++ +F +P + E + + L + P+LVAE+ G V

Sbjct: 7 LRDACDQDIPAVQAIYADHVLHGIISSFELDPSPVAELLQRRQVVLVNGLPYLVAELAGEV 66

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 G YA P++ R AY +TVE +VY+ G+G L L++ E G++ +VAVIG

Sbjct: 67 VGYGYATPYRPRPAYRFTVEDSVYIRDGMGGRGIGLALLGELVQRCEQGGWRQMVAVIGN 126

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
 N S+RLHE LG+ G + G+KHG W D QR

Sbjct: 127 SENIASRLRLHERLGFRRVGVFESVGFKHGRWVDTVLMQR 165

>ref|ZP_07291989.1| GNAT family toxin-antitoxin system, toxin component [Streptomyces hygroscopicus ATCC 53653]

gb|EFL20358.1| GNAT family toxin-antitoxin system, toxin component [Streptomyces hygroscopicus ATCC 53653]

Length = 172

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 63/154 (40%), Positives = 79/154 (51%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V +R A D A+ I NH IE ST + PQ+P E L +R VAE EG

Sbjct: 11 VAVRRARPGDAEAIIRAIRNHAIEHSTALWTQTPQSPAEGAAWLAGHLERGSFAVVAEAGE 70

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 +AG A GPW+ + Y TVE +VYV LG+GS L L+ S G + V+A I

Sbjct: 71 LAGFAVYGPWRELDGYRHTVEDSVYVREDRHGLGIGSALLAALIASAREAGHRVVIADIE 130

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 N PSVRLHE G+ GT+ G K G W D+

Sbjct: 131 AENAPSVRLHERFGFHHVGTVSEVGTKFGRWLDL 164

>ref|ZP_05613409.1| phosphinothricin N-acetyltransferase [Faecalibacterium prausnitzii A2-165]

gb|EEU98245.1| phosphinothricin N-acetyltransferase [Faecalibacterium prausnitzii A2-165]

Length = 282

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.

Identities = 61/179 (34%), Positives = 91/179 (50%), Gaps = 6/179 (3%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA- 62
 E+ + AT AD A + DI N Y+ T F+ P + E+ D ++ + P L+A
 Sbjct: 91 EKNLPRLSLATRADAAEILDYINWYVLHHTATFQVTPSSLPEYEDWVDSTRALIPLLLAR 150

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 122
 + +G + G A A + R AYDW VEST+Y + + G+G TLY LL ++ G+ +V
 Sbjct: 151 DGDGKLLGYACAHRYHPREAYDWAVESTIYCAPDARGFGVGD TLYRALLDILDMGYWNV 210

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFW----QRDFELPAPRPV 177
 A++ PN S R+H LG+T G YK GW + W +R E P P P+
 Sbjct: 211 YALVADPNPASERIHARLGFTCVGREPHTAYKF-GWLGLSTWWLPLRRGNEKPEPTHPL 268

>ref|YP_002419800.1| GCN5-related N-acetyltransferase [Methylobacterium
 chloromethanicum
 CM4]
 gb|ACK81872.1| GCN5-related N-acetyltransferase [Methylobacterium chloromethanicum
 CM4]
 Length = 204

Score = 92.8 bits (229), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 56/162 (34%), Positives = 86/162 (53%), Gaps = 4/162 (2%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETS---TVNFRTPEQTPQEWIDDLERLQD-RYP 58
 P V IRP++ AD++A+ +I T +F E P E + ++ R P
 Sbjct: 9 PTHAEVIRPSSDADVSAMI AKYERHIRKGVGDTGDFEERLLPDELRRRRKTMRSKRLP 68

Query: 59 WLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 LVAE G +AG AYA P++ R AY + ++ ++YV H G+G L L+++ A G
 Sbjct: 69 HLVAERGQGIAGYAYAVPFRKRPAYRYALKHSIYVHPDHLHAGIGRRLLPALIEACAAGG 128

Query: 119 FKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 ++ ++ I N+ S+RLHE G+ G L A GYK+G W D
 Sbjct: 129 YRQMIGYIDASNEASRLRHETCGFARVGYLPAIGYKYGRWSD 170

>gb|EGC37188.1| hypothetical protein DICPUDRAFT_150275 [Dictyostelium purpureum]
 Length = 171

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 51/160 (31%), Positives = 87/160 (54%), Gaps = 8/160 (5%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVA----- 62
 ++R A D+ ++ +I + Y+E F E + E + + + YP++VA
 Sbjct: 4 KLRAANEGDIKSIQEIYSFYVEFEICTFEEIIPSEDEILKRYKSITGNGYPYIVATTKSA 63

Query: 63 -EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 E V G AYA ++ R AY +TVE ++Y+S ++ LG+G L + L+K + +G+K
 Sbjct: 64 DESSETVVGAYASAFRPRIAYRYTVEDSIYISKDYKGLGVGKLLSELIKLCKEKGYKQ 123

Query: 122 VVAVI-GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 +VAVI G N S+ LHE LG+ + L+ G+K + D
 Sbjct: 124 MVAVIGGFENVGSIVLHEKLGFGNKSLLKDVGFKFDKFD 163

>ref|YP_004153949.1| phosphinothricin acetyltransferase [Variovorax paradoxus EPS]
 gb|ADU35838.1| Phosphinothricin acetyltransferase [Variovorax paradoxus EPS]
 Length = 174

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 57/171 (33%), Positives = 89/171 (52%), Gaps = 2/171 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPE-QPTPQEWIDDLERLQDRYPWLVAEVEG 66
 + IRP+ D+AA+ I H++ T F TE P + L P+LVAE +G
 Sbjct: 3 LSIRPSRDDDVAITAIYAHVHLHGTGTGFETEAPSATDMAARRADVLSKNLPYLVAEEDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVI 126
 V G AY +K R AY ++ E ++Y++ + GLG+ L L ++ EA G + ++AVI
 Sbjct: 63 EVLGFAYCNWFKPRPAYRFSAEFSIYMAQSARGKGLGAKLLAALSQAEEAVGVRKLIIVI 122

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 G N SV +H + G+T G L+ G+K G W DV ++ + +P
 Sbjct: 123 GDSANAGSVGVHRSQGFTHVGVLDKCGWKFGWDRDVLMEKVLGEGSTTKP 173

>ref|YP_970241.1| GCN5-related N-acetyltransferase [Acidovorax avenae subsp. citrulli
 AAC00-1]
 gb|ABM32467.1| GCN5-related N-acetyltransferase [Acidovorax citrulli AAC00-1]
 Length = 197

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 57/168 (33%), Positives = 89/168 (52%), Gaps = 2/168 (1%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQPTPQEWIDDLERLQDR-YPW 59
 +S RR IRP+ D+ A+ I H++ T F T+P + + + R P+
 Sbjct: 19 ISTSRMPNIRPSRDEDLPAITAIYAHVHLHGTGTGFETDPPSATDMAARRADVLRGLPY 78

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 LVAE + + G AYA +K R AY ++ E ++YV+ + G+G L L + EA G
 Sbjct: 79 LVAAEQEEILGFAYANWFKPRPAYRFSAEFSIYVADAARGRGVGRLLLDALCGAAEAAGV 138

Query: 120 KSVVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 166
 + ++AVIG N SV +H A G+T G +R+ G+K G W DV ++
 Sbjct: 139 RKLLAVIGDSANAGSVGVHRAAGFTEIGVMRSVGWKGAWRDVVLMEK 186

>ref|ZP_07735846.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor
 lactoaceticus 6A]
 gb|EFR13676.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor
 lactoaceticus 6A]
 Length = 161

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.
 Identities = 48/158 (30%), Positives = 81/158 (51%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQPTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR AT +D+ + I N+ + ST F P+T ++++ L+ ++YP VAE
 Sbjct: 1 MNIRKATISDIPDLLYIYNYEVLNSTSTFDIHPKTTEDFLKLLDSHSNKYPIYVAEENST 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVIG 127
 + G Y P+ + AY TVE T+Y+ H+ G+G + LL+ + G +++A +
 Sbjct: 61 ILGYGLSPFSEKEAYSITVEDTIYIHLHRGKGIGKQILKFLLERAKDTGAANIIAKVC 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
 N S+ LH++ G+ G L G K G + DV Q
 Sbjct: 121 AENYISLHLKSFSGFVEVGKLIKVGSKFGRFLDVIIILQ 158

>ref|ZP_06586877.1| conserved hypothetical protein [Streptomyces roseosporus NRRL
 15998]
 gb|EFE77338.1| conserved hypothetical protein [Streptomyces roseosporus NRRL
 15998]
 Length = 212

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 65/169 (38%), Positives = 86/169 (50%), Gaps = 3/169 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV 64
+PV IRPA AD+ AV +I HY+ + + F P W L+ L R P+LV E+
Sbjct: 37 KPV-IRPAVPADLDAVAEIYTHYVRHTVITFEENPPPVAAWHQRLDDLAARDLPFLVVEL 95

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
G V G AYA PW+ + AY TVE+++Y++ GLG L LL + + ++A
Sbjct: 96 SGEVVGAYAAAPWRPKPAYRNTVENSILAPGRTGRGLGGALLEALLTACAGTHVRQMI 155

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA 172
VI D S LH G+T G L A GYKH W D QR PA
Sbjct: 156 VIADAGTDTSAALHRRYGFTDAGRLTAVGYKHDRWIDTLLMQRTLGHQA 204

>ref|NP_647266.1| hypothetical protein MW2449 [Staphylococcus aureus subsp. aureus MW2]
ref|YP_044528.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus MSSA476]
ref|ZP_06926043.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus ATCC 51811]
ref|ZP_07128111.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus TCH70]
dbj|BAB96314.1| MW2449 [Staphylococcus aureus subsp. aureus MW2]
emb|CAG44230.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus MSSA476]
gb|EFH24721.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus ATCC 51811]
gb|EFK83377.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus TCH70]
Length = 163

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 84/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
IR A D+ A+ I N I +T + EPQT E + E Q ++ P V E G V
Sbjct: 2 IRYAKKEDLNAILAIYNDAIINTTAVYTYEPQTIDERVAWFETKQRKHEPIFVFEENGSV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G++++VA I
Sbjct: 62 LGFATFGSFRPWPAFLYTIHESIYVDASARGKGIASQLLHHLIVEAKAKGYRALVAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
N S++LH+ + GTL G+K W D+ F++ D +
Sbjct: 122 SNKASIQLHQKFQAFKHAGTLTNVGFKNQWLDLAFYELDLQ 162

>ref|YP_001923646.1| GCN5-related N-acetyltransferase [Methylobacterium populi BJ001]
gb|ACB79111.1| GCN5-related N-acetyltransferase [Methylobacterium populi BJ001]
Length = 204

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.
Identities = 58/157 (36%), Positives = 89/157 (56%), Gaps = 4/157 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETS---TVNFRTPEQTPQEWIDDLERLQD-RYPWLVAE 63
V IRP++ AD+AA+ I +I T +F E P+E + ++ R P LVAE
Sbjct: 14 VVIRPSSDADVAAMIAIYERHIRKGVGDTGDFEERLLPEELRRRRKTMRSKRLPHLVAE 73

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 123
+G +AG AYA P++ R AY + ++ ++YV H G+G L L+++ A G++ ++
Sbjct: 74 RDGQIAGYAYVPFRKRPAYRYALKHSIYVHPDHLHAGIGRLLPALIEACAAGGYRQMI 133

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

I N+ S+RLHEA G+ G L A GYK+G W D

Sbjct: 134 GYIDASNEASLRLHEACGFARVGYLPAIGYKYGRWSD 170

>ref|ZP_07005548.1| GCN5-related N-acetyltransferase [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]

gb|EFH99095.1| GCN5-related N-acetyltransferase [Pseudomonas savastanoi pv. savastanoi NCPPB 3335]

Length = 179

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.

Identities = 57/159 (35%), Positives = 84/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68

+R A D+ AV I ++ +F +P + E + + L + P+LVAE+ G V

Sbjct: 7 LRDACDQDIPAVQAIYADHVLHGISSFELDPSPVAELLQRRAQVLVNGLPYLVAELAGEV 66

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127

G YA P++ R AY +TVE +VY+ G+G L L++ E G++ +VAVIG

Sbjct: 67 VGYGYATPYRPRPAYRFTVEDSVYIRDGMGGRGIGLALLGELVQRCEQGGWRQMVAVIGN 126

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166

N S+RLHE LG+ G + G+KHG W D QR

Sbjct: 127 SENIASLRLHEHLGFRRVGVFESVGFKHGRWVDTVLMQR 165

>ref|YP_003658700.1| GCN5-related N-acetyltransferase [Segniliparus rotundus DSM 44985]

gb|ADG97869.1| GCN5-related N-acetyltransferase [Segniliparus rotundus DSM 44985]

Length = 174

Score = 92.4 bits (228), Expect = 2e-17, Method: Compositional matrix adjust.

Identities = 50/141 (35%), Positives = 70/141 (49%)

Query: 28 YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTV 87

Y+ + ++F P T +E +E Y WL V E EG V G AY G + R AY ++

Sbjct: 29 YVLDTAISFEEVPPTTEEMAARIENALQEYAWLVLEREGAVVGYAYGGRFAPRAAYRYSC 88

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPSVRLHEALGYTARGT 147

E +VY+ G G LY T LL + +G++ LPN S LH ++G+ G

Sbjct: 89 EVSVYLKLGEVVGKGGGRALYTELLDLRAQRGYQQAFGGYVLPNLASEALHRSMGFRLAGV 148

Query: 148 LRAAGYKHGGWHDVGFQWRDF 168

R G+K G W DV + QRD

Sbjct: 149 NRKVGHKLGAWRDVAWVQRDL 169

>ref|YP_236225.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae B728a]

gb|AA38187.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae B728a]

Length = 179

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.

Identities = 57/160 (35%), Positives = 83/160 (51%), Gaps = 2/160 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGV 67

++R A DM AV I ++ +F EP E + L P++VAE+ G

Sbjct: 6 DLRDARDDMPAVQAIYADHVLHGISSFELEPPDLAELLQRRRMVLAKGLPYMVAERDGD 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127

+ G AY P++ R Y +TVE +VYV G+G L + L++ EA G++ ++AVIG
 Sbjct: 66 IVGYAYVTPYRPRPGYRFTVEDSVYVRDLGGQGIGQALLSALVQHCEAGGWRQMIAVIG 125

Query: 128 -LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

N S+RLHE LG+ G + G+KHG W D QR
 Sbjct: 126 NSQNIASLRLHERLGFRRVGVFESVGFKHGRWVDTVLMQR 165

>ref|ZP_07047827.1| acetyltransferase yncA [Lysinibacillus fusiformis ZC1]
 gb|EFI70664.1| acetyltransferase yncA [Lysinibacillus fusiformis ZC1]
 Length = 166

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 57/159 (35%), Positives = 81/159 (50%), Gaps = 5/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66

IR D+ V I N I TS +R E QT E W + + L + P LV E G
 Sbjct: 2 IRFMEEKDIPVLAIYNDIILTSAVYRYEIQTDFEKVQWFKEQQALDN--PLLVFEDNG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

+VAG A ++ Y +T+E +VYV H + G+ + L L+ E G K++VA I
 Sbjct: 60 LVAGFATYSQFRPYPGYKYMTEHSVYVHKEHYQKGIATKLMNKLIAMAEENGVKTLVAGI 119

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165

N S++ HE LG+ GT++ AGYK W D+ F+Q
 Sbjct: 120 DGENIGSIKAHEKLGFEYAGTIKNAGYKFEQWLDLVFYQ 158

>ref|ZP_06325630.1| acetyltransferase [Staphylococcus aureus subsp. aureus D139]
 ref|ZP_06340523.1| acetyltransferase [Staphylococcus aureus subsp. aureus H19]
 gb|EFB48525.1| acetyltransferase [Staphylococcus aureus subsp. aureus D139]
 gb|EFC08571.1| acetyltransferase [Staphylococcus aureus subsp. aureus H19]
 Length = 163

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 53/161 (32%), Positives = 84/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68

IR A D+ A+ I N I +T + EPQT E + E Q ++ P V E G V
 Sbjct: 2 IRCACKEDLNAILAIYNDIAINTTAVYPYEPQTIDERVAVFETKQRKHEPIFVFEENGSV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128

G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G+++VA I
 Sbjct: 62 LGFATFGSFRPWPAVLYTIEHSIYVDASARGKGIASQLLHHLIVEAKAKGYRALVAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFE 169

N S++LH+ + GTL G+K W D+ F++ D +
 Sbjct: 122 SNKASIQHLHQKFAFKHAGTLTNVGFKNQWLDLAFYELDLQ 162

>ref|YP_003930830.1| acetyltransferase [Pantoea vagans C9-1]
 gb|ADO09381.1| putative acetyltransferase [Pantoea vagans C9-1]
 Length = 222

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 51/163 (31%), Positives = 85/163 (52%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66

+EI A + A+ I ++ T +F T P E + + ++Q PW +A +G
 Sbjct: 50 MEIFDADERHIPAIQQIYAWHVLNGTGSFETVPPDAAEMGERMRKIQAGLPWFIAVSDG 109

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

V G Y P++ R+AY T+E ++Y+ Q+ G GS L H ++ E +G++ ++A +

Sbjct: 110 DVRGFCYLAPYRPRHAYRHTLEDSIYIDPGFQKRGAGSRLLLEHTIQWAEQKGYRQLIANV 169

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168

G N S+ +H+A G+ G LR+ G+K G W D F QR

Sbjct: 170 GDSENRGSIAVHQAGFEMTGILRSVGFKQGRWLDTVFMQRSL 212

>ref|ZP_04711138.1| GCN5-related N-acetyltransferase [Streptomyces roseosporus NRRL 11379]
Length = 180

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 65/169 (38%), Positives = 86/169 (50%), Gaps = 3/169 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV 64

+PV IRPA AD+ AV +I HY+ + + F P W L+ L R P+LV E+

Sbjct: 5 KPV-IRPAVPADLDAVAEIYTHYVRHTVITFEENPPPVAAWHQRLDDLAARDLPFLVVEL 63

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124

G V G AYA PW+ + AY TVE+++Y++ GLG L LL + + ++A

Sbjct: 64 SGEVVGAYAAAPWRPKPAYRNTVENSIIYAPGRTGRGLGGALLEALLTACAGTHVRQMIA 123

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPA 172

VI D S LH G+T G L A GYKH W D QR PA

Sbjct: 124 VIADAGTDTSAALHRRYGFTDAGRLTAVGYKHDRWIDTLLMQRTLGHQA 172

>ref|YP_002977838.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv. trifolii WSM1325]

gb|ACS58299.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv. trifolii WSM1325]

Length = 200

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 49/159 (30%), Positives = 80/159 (50%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVA-EVEGV 67

+R A+ AD+ A+ DI + ++ P + E + +YP++ A +G

Sbjct: 20 LRASNADIPAIAIDIYRESVLNGVASYEIVPPSEAEMAQRFAAIVGQQYPYIAAIGTDGA 79

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G AYA ++ R AY W VE ++Y++ + + G+G L L+ GF+ + AVIG

Sbjct: 80 LLGYAYASAFRTRPAYRWLVEDSIYLAPQARGRGIGKALLAELIIRCTTLGFRQMAAVIG 139

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166

+ S+ LH G+ G ++ GYKHG W D F QR

Sbjct: 140 GASPASIALHRTAGFEEVGLMKGTGYKHGRWLDTMFMQR 178

>ref|YP_187333.1| acetyltransferase [Staphylococcus aureus subsp. aureus COL]

ref|YP_495102.1| acetyltransferase [Staphylococcus aureus subsp. aureus USA300_FPR3757]

ref|YP_501294.1| hypothetical protein SAOUHSC_02836 [Staphylococcus aureus subsp. aureus NCTC 8325]

ref|YP_001333461.1| acetyltransferase, GNAT family protein [Staphylococcus aureus subsp. aureus str. Newman]

ref|YP_001576383.1| acetyltransferase [Staphylococcus aureus subsp. aureus USA300_TCH1516]

ref|ZP_03566428.1| acetyltransferase [Staphylococcus aureus subsp. aureus str. JKD6009]

ref|ZP_04864370.1| possible Phosphinothricin acetyltransferase [Staphylococcus aureus

subsp. aureus USA300_TCH959]

ref|ZP_05699498.1| acetyltransferase [Staphylococcus aureus A5948]
 ref|ZP_06023032.1| hypothetical protein SAD30_1836 [Staphylococcus aureus D30]
 ref|ZP_06024654.1| hypothetical protein SA930_1172 [Staphylococcus aureus 930918-3]
 ref|ZP_06330844.1| acetyltransferase [Staphylococcus aureus A9765]
 ref|ZP_06379946.1| acetyltransferase [Staphylococcus aureus subsp. aureus 132]
 ref|ZP_06790371.1| acetyltransferase [Staphylococcus aureus A9754]
 ref|ZP_07362461.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus ATCC BAA-39]
 gb|AAW37317.1| acetyltransferase, GNAT family [Staphylococcus aureus subsp. aureus COL]
 gb|ABD22256.1| acetyltransferase, GNAT family [Staphylococcus aureus subsp. aureus USA300_FPR3757]
 gb|ABD31837.1| conserved hypothetical protein [Staphylococcus aureus subsp. aureus NCTC 8325]
 dbj|BAF68699.1| acetyltransferase, GNAT family protein [Staphylococcus aureus subsp. aureus str. Newman]
 gb|ABX30504.1| acetyltransferase [Staphylococcus aureus subsp. aureus USA300_TCH1516]
 gb|EES94743.1| possible Phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus USA300_TCH959]
 gb|EEV83584.1| acetyltransferase [Staphylococcus aureus A5948]
 gb|EEW44689.1| hypothetical protein SA930_1172 [Staphylococcus aureus 930918-3]
 gb|EEW46336.1| hypothetical protein SAD30_1836 [Staphylococcus aureus D30]
 emb|CBI50514.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus TW20]
 gb|EFB98208.1| acetyltransferase [Staphylococcus aureus A9765]
 gb|EFG39861.1| acetyltransferase [Staphylococcus aureus A9754]
 gb|ADL66566.1| acetyltransferase, GNAT family [Staphylococcus aureus subsp. aureus str. JKD6008]
 gb|EFM07602.1| phosphinothricin acetyltransferase [Staphylococcus aureus subsp. aureus ATCC BAA-39]
 gb|EFU27469.1| acetyltransferase [Staphylococcus aureus subsp. aureus CGS01]
 gb|EFW30817.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus MRSA131]
 gb|EFW36298.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus aureus subsp. aureus MRSA177]
 Length = 163

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 53/161 (32%), Positives = 84/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
 IR A D+ A+ I N I +T + EPQT E + E Q ++ P V E G V
 Sbjct: 2 IRYAKKEDLNAILAIYNDAIINTTAVTYTEPQTIDERVAVFETKQRKHEPIFVFEENGSV 61
 Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRQRGLGLSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G A G ++ AY +T+E ++YV + G+ S L HL+ +A+G+++VA I
 Sbjct: 62 LGFATFGSFRPWPAFLYIEHSIYVDASARGKGIASQLLHHLIVEAKAKGYRALVAGIDA 121
 Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFE 169
 N S++LH+ + GTL G+K W D+ F++ D +
 Sbjct: 122 SNKASIQHLHQKFAFKHAGTLTNVGFKNRWLDLAFYELDLQ 162

>ref|ZP_07379546.1| Phosphinothricin acetyltransferase [Pantoea sp. aB]
 gb|EFM19211.1| Phosphinothricin acetyltransferase [Pantoea sp. aB]
 Length = 174

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
 Identities = 56/173 (32%), Positives = 85/173 (49%), Gaps = 2/173 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 +EI A + A+ I ++ T +F T P + + ++Q PW VA EG

Sbjct: 1 MEIFEADERHITAIQQIYAWHVINGTGSFETVPPDADAIGERIGKVQQAGLPWFVAVSEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVI 126
V G Y P++ R+AY T+E ++Y+ Q+ G GS L H ++ E G++ ++A I

Sbjct: 61 DVRGFCYLAPYRPRHAYRHTLEDSIYIDPGFQKRGAGSHLLAHAIRWAEQAGYRQLIANI 120

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
G N S+ LH A G+ G LR+ G+K G W D F QR L P +

Sbjct: 121 GDSENQGSIALHRAAGFEMTGILRSVGFQGRWLDTVFMQRTLGLGDSALPSK 173

>ref|ZP_01857922.1| hypothetical acetyltransferase YncA [Planctomyces maris DSM 8797]
gb|EDL56205.1| hypothetical acetyltransferase YncA [Planctomyces maris DSM 8797]
Length = 165

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 52/159 (32%), Positives = 83/159 (52%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
+ IR AT AD+ A+ +I N I T+T F EP T E + E +R+P VA V+

Sbjct: 3 AMNIRLATLADLDAMTEIYNEAILTTTATFDMEPMTRDERLPWFESHDERHPIFVAVVDN 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVI 126
+AG A W+ R AY T E++ YV H+ G+G L +++ G+ +++A +

Sbjct: 63 QIAGWACLSQWRPRQAYADTAETSFYVKASHRGRGIGRQLKQAIIEEARRLGYHTLIAGV 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
N+ S+ L+++ G+ GT + G K G DV + Q

Sbjct: 123 AEGNEVSLHLNQSFGEVVGTFKEVGKKFGKVLDTYTLQ 161

>ref|ZP_04695956.1| GCN5-related N-acetyltransferase [Streptomyces roseosporus NRRL
15998]
Length = 177

Score = 92.0 bits (227), Expect = 3e-17, Method: Compositional matrix adjust.
Identities = 65/169 (38%), Positives = 86/169 (50%), Gaps = 3/169 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEV 64
+PV IRPA AD+ AV +I HY+ + + F P W L+ L R P+LV E+

Sbjct: 2 KPV-IRPAVPADLDAVAEIYTHYVRHTVITFEENPPPVAAWHQRLDDLAARDLPFLVVEL 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
G V G AYA PW+ + AY TVE+++Y++ GLG L LL + + ++A

Sbjct: 61 SGEVVGAYAAPWRPKPAYRNTVENSIIYLAPGRTGRGLGGALLEALLTACAGTHVRQMIA 120

Query: 125 VIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA 172
VI D S LH G+T G L A GYKH W D QR PA

Sbjct: 121 VIADAGTDTSAALHRRYGFTDAGRLTAVGYKHDRWIDTLLMQRTLGHPA 169

>ref|ZP_04839299.1| hypothetical protein SauraC_08067 [Staphylococcus aureus subsp.
aureus str. CF-Marseille]
Length = 163

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 84/161 (52%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
IR A D+ A+ I N I +T + +PQT E I E Q + P V E G V

Sbjct: 2 IRCAKKEDLNAILAIYNDAIINTTAVYTYKPTIDERIAWFETKQRNHEPIFVFEENGSV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVIGL 128

G+A G ++ AY +T+E ++YV + G+ S L L+ +A+G++++VA I
 Sbjct: 62 LGVATFGSFRPWPAYQYTIHESIYVDASARGKGIASQLLQRLIVEAKAKGYRTLVA GIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFFE 169

N+ S++LH+ + GTL GYK W D+ F++ D +
 Sbjct: 122 SNEASIKLHQKFNFKHAGTTLTNVGYKFDYWLDLAFYELDLK 162

>ref|YP_003597722.1| GNAT family acetyltransferase [Bacillus megaterium DSM 319]
 gb|ADF39372.1| acetyltransferase, GNAT family [Bacillus megaterium DSM 319]
 Length = 163

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
 Identities = 50/159 (31%), Positives = 81/159 (50%), Gaps = 4/159 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66

IR A D+ + +I N ++TS F P T ++ W D+ + +P +VAE +G
 Sbjct: 3 IRYAKEEDLPMLVEIYNQSVQTSAAATFDLTPVTVEQRRSWFDN-HISNELFPLIVAERDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

VVAG A ++ + AY TVE ++Y+ Q G+G L +L+ + V++ I
 Sbjct: 62 VVAGYASLSSYRDKEAYIQTVELSIYIDKNQQGYGIGKQLMKRILELAKELNHHVVISGI 121

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQW 165

ND S+++HE +T G + G+K W DV F+Q
 Sbjct: 122 TKGNDISIKMHEQFNFTFCGEFKEVGWKFQWQDVLFYQ 160

>ref|YP_003447536.1| acetyltransferase [Azospirillum sp. B510]
 dbj|BAI70992.1| acetyltransferase [Azospirillum sp. B510]
 Length = 166

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
 Identities = 60/160 (37%), Positives = 83/160 (51%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66

IR AT AD+ A+ I+N I T+T + P T ++ W+ ERL + P LV+E++G
 Sbjct: 5 IRAATEADLPAIVAILNEAILTTTAVWSLTPTTLEQRRVWMA--ERLANGMPVLVSEIDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

VAG A G ++ Y TVE ++YV + G G L T LL +G +VA I
 Sbjct: 63 EVAGFASYGEFRPWEGYRHTVEHSIYVETGLRGRGQGRALLTALLDDATLKGHRMMVAGI 122

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQW 166

N S+RLH LG+ G LR G K W D+ F Q+
 Sbjct: 123 EAENAASIRLHAGLGFVEAGCLRQVGRKFDRWLDLLFMQK 162

>ref|YP_049065.1| putative acetyltransferase [Pectobacterium atrosepticum SCRI1043]
 emb|CAG73868.1| putative acetyltransferase [Pectobacterium atrosepticum SCRI1043]
 Length = 175

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
 Identities = 56/161 (34%), Positives = 83/161 (51%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEG 66

+EI A + A+ I +++ T F TEP E L++ L PW V EG
 Sbjct: 1 MEITEADERHIPAIQIYAYHVLHGATATFETEPDAVEMAIRLKKVLAAGLPWFVVDVDEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

V G Y ++ R AY +T+E ++Y+ Q G+G L + + EA+GF+ +VAV+
 Sbjct: 61 QVRGYCYLSFYRERFAYRFTLEDSIYIDPTFQGRGIGKRLLSRAVMWAEARGFRQLVAVV 120

Query: 127 G-LPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 G N S+ LH A G++ GTL + G+KHG W D QR
 Sbjct: 121 GNSENTASLALHRAAGFSITGTLT SVGFKHGRWLDTVILQR 161

>ref|YP_001977481.1| probable phosphinothricin acetyltransferase (antibiotic resistance)
 protein [Rhizobium etli CIAT 652]
 gb|ACE90303.1| probable phosphinothricin acetyltransferase (antibiotic resistance)
 protein [Rhizobium etli CIAT 652]
 Length = 171

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
 Identities = 62/173 (35%), Positives = 85/173 (49%), Gaps = 9/173 (5%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAE 63
 V IR AT AD+ A+ +I NH +E +T + + +EW+ R +P +VAE
 Sbjct: 4 AVLIRDATDADLPAIREIYNHAVEHTTAIWNETLVLDNRREWMR--ARQGRGFPIIVAE 61

Query: 64 VEGV VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + G VAG A G W+A + Y TVE +VYV + G+G TL L+ A ++
 Sbjct: 62 LSGKVAGYASYGDWRAFDGYRHTVEHSVYVDKDCRGAGIGETLMRELIVRAAAADVHVM 121

Query: 124 AVIGLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRP 176
 A I N S+RLHE LG+ G G K G W D+ EL P RP
 Sbjct: 122 AGIEAENTASIRLHEKLGFRAGRFSEVGTKFGRWLDLTC----MELRLPARP 170

>ref|YP_004235746.1| phosphinothricin acetyltransferase [Acidovorax avenae subsp. avenae]
 ATCC 19860]
 gb|ADX47179.1| Phosphinothricin acetyltransferase [Acidovorax avenae subsp. avenae]
 ATCC 19860]
 Length = 173

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
 Identities = 55/160 (34%), Positives = 86/160 (53%), Gaps = 2/160 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEEVEGV 67
 IRP+ D+ A+ I H++ T F T+P + + + R P+LVAE +G
 Sbjct: 3 NIRPSRDELDPAITAIYAHVHLHGTGTFTDPPSAADMAARRADVLARGLPYLVAEEQGE 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA +K R AY ++ E ++YV+ + G+G L L + EA G + ++AVIG
 Sbjct: 63 ILGFAYANWFKPRPAYRFSAECSIYVADAARGRGVGRLLLDALCGAAEAAAGVRKLLAVIG 122

Query: 128 -LPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 N SV +H A G+T G +R+ G+K G W DV ++
 Sbjct: 123 D SANAGSVGVHRAAGFTEIGVMRSVGWKF GAWRDVVLMEK 162

>ref|YP_001177449.1| GCN5-related N-acetyltransferase [Enterobacter sp. 638]
 gb|ABP61398.1| GCN5-related N-acetyltransferase [Enterobacter sp. 638]
 Length = 184

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
 Identities = 61/176 (34%), Positives = 89/176 (50%), Gaps = 16/176 (9%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDL-ERLQD----RYPWLVA 62
 VE+R A D+ A+ I ++ +F P ID++ +R++D PWLVA
 Sbjct: 12 VEV RDAQPD DVHAI AAIYAWHVLNGRASFEVPPA----IDEMRQMRDIAAEGLPWLVA 67

Query: 63 EVEGV VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122

GVV G YA ++AR AY +T+E ++YV G GS L L+ E ++ +
Sbjct: 68 LYRGVVVGICYASLYRARPAYRYTLEESIYVDASATGRGFGSALMDALIARCEQGHWRQI 127

Query: 123 VAVI--GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR----DFELP 171

+AV+ G N S+RLH+ G+ G LR+ GYK G W D QR D+ LP
Sbjct: 128 IAVVGDGHNNSGSIRLHKKKHGFEVAGQLRSVGYKKGNWRDTLIMQRPLNDGDWTLTP 183

>ref|ZP_08176212.1| sortase-like acyltransferase [Xanthomonas vesicatoria ATCC 35937]
gb|EGD11565.1| sortase-like acyltransferase [Xanthomonas vesicatoria ATCC 35937]
Length = 173

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 51/158 (32%), Positives = 82/158 (51%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWL-VAEVEGVVAGIAYAGP 76

+A+ DI N I ST + P+ P+ + + +P + V + +G + G A G
Sbjct: 13 SAILDIFNEAIANSTALYDYRPLPESMVGWFAAKRAGGFPVIGVEDADGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136

++A A+ ++VE +YV H+ GLG L L+ + E +G +V I N S+ L
Sbjct: 73 FRAWPAFKYSVEHAIIYVHQDHRGKGLGRVLLQALIAAAEERGVHVLVGGIDASNQASIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174

H+ G+T GT+R AG+K G W D+ F+QR P+ P
Sbjct: 133 HQQFGFTHAGTVREAGFKFGRWLDLAFYQRILATPSDP 170

>ref|YP_004023921.1| GCN5-like N-acetyltransferase [Caldicellulosiruptor
kronotskyensis
2002]

gb|ADQ46102.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor
kronotskyensis 2002]
Length = 161

Score = 91.7 bits (226), Expect = 4e-17, Method: Compositional matrix adjust.
Identities = 47/158 (29%), Positives = 79/158 (50%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IR AT +D+ + I N+ + ST F P+T ++++ + RYP VAE
Sbjct: 1 MNIRKATISDITNMLYIYNYEVLNSTSTFDIHPKTTEDFLKLFDSHSHRYPIYVAEENST 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G Y P+ + AY TVE T+Y+ H+ G+G + L++ + G +++A +
Sbjct: 61 ILGYGYLSPFSEKEAYSITVEDTIYIHPLHRGKGIGKQILKFLIEKAKDTGAANIIAKVC 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165

N S+ LH++ G+ G L G K G + DV Q
Sbjct: 121 AENYISLHLHKSFGFVEVGKLIKVGSKFGRFLDVIIQ 158

>ref|YP_002280388.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv.
trifolii WSM2304]

gb|ACI54162.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv.
trifolii WSM2304]
Length = 169

Score = 91.3 bits (225), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 57/158 (36%), Positives = 81/158 (51%), Gaps = 5/158 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR--TEPQTPQEWIDDLERLQDRYPWLVAE 63

PV +R AT AD+ A+ DI NH +E +T + + +EW+ R +P +VAE
Sbjct: 4 PVLRLDATEADLPAIRDIYNHAVEHTTAIWNETLVDLENRREWMK--ARKARGFPVIVAE 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123

+ G VAG A G W+A + Y TVE +VYV + G+G L L+ A ++

Sbjct: 62 LSGKVAGYASYGDWRAFDGYRHTVEHSVYVDKDCRGAGIGERLMRELIVRAAAGNIHVMI 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

A I N S+RLHE LG+ G G K G W D+

Sbjct: 122 AGIEAENTASIRLHEKLGFRAGRFSEVGTKFGRWLDL 159

>ref|NP_460549.1| acyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]
 ref|YP_150539.1| acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
 ref|ZP_02343696.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]
 ref|ZP_02573850.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]
 ref|ZP_02655059.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191]
 ref|ZP_02660762.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]
 ref|ZP_02666066.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]
 ref|ZP_02682196.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]
 ref|ZP_02696902.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
 ref|YP_002040837.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL254]
 ref|YP_002045632.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]
 ref|ZP_03075615.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
 ref|YP_002114615.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]
 ref|YP_002146445.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Agona str. SL483]
 ref|ZP_03165638.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]
 ref|YP_002142025.1| acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
 ref|YP_002215556.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]
 ref|ZP_03216403.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]
 ref|ZP_03218813.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433]
 ref|YP_002226528.1| acetyltransferase [Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91]
 ref|YP_002243566.1| acetyltransferase [Salmonella enterica subsp. enterica serovar Enteritidis str. P125109]
 ref|ZP_04655662.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Tennessee str. CDC07-0191]
 gb|AAL20508.1| putative acyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]
 gb|AAV77227.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
 gb|ACF63334.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL254]
 gb|ACF69055.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]
 gb|EDX44834.1| phosphinothricin acetyltransferase [Salmonella enterica subsp.

enterica serovar Kentucky str. CVM29188]

gb|ACF89322.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

gb|EDX52246.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Newport str. SL317]

emb|CAR59350.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]

gb|ACH50175.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Agona str. SL483]

gb|EDY26439.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]

gb|EDY30563.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]

gb|ACH76859.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]

gb|EDZ00783.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]

gb|EDZ08150.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433]

emb|CAR37400.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91]

gb|EDZ12889.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]

gb|EDZ15774.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]

gb|EDZ22028.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191]

gb|EDZ25934.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]

gb|EDZ37527.1| phosphinothricin acetyltransferase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]

emb|CAR33044.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Enteritidis str. P125109]

emb|CBG24597.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. D23580]

gb|ACY88396.1| putative acyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. 14028S]

emb|CBW17615.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. SL1344]

dbj|BAJ36552.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. T000240]

gb|EFX49278.1| Putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. TN061786]

gb|EFY11766.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 315996572]

gb|EFY16162.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 495297-1]

gb|EFY19936.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 495297-3]

gb|EFY25172.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 495297-4]

gb|EFY31521.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 515920-1]

gb|EFY35339.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 515920-2]

gb|EFY37613.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 531954]

gb|EFY41978.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. NC_MB110209-0054]

gb|EFY48037.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. OH_2009072675]

gb|EFY50755.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. CASC_09SCPH15965]

gb|EFY57501.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 19N]
 gb|EFY61237.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 81038-01]
 gb|EFY63954.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MD_MDA09249507]
 gb|EFY67916.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 414877]
 gb|EFY73224.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 366867]
 gb|EFY76217.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 413180]
 gb|EFY81390.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 446600]
 gb|ADX17290.1| putative acyltransferase [Salmonella enterica subsp. enterica serovar Typhimurium str. 4/74]
 gb|EFZ79909.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 609458-1]
 gb|EFZ84996.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 556150-1]
 gb|EFZ87533.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 609460]
 gb|EFZ90757.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 507440-20]
 gb|EFZ95521.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 556152]
 gb|EGA02750.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB101509-0077]
 gb|EGA03788.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB102109-0047]
 gb|EGA12237.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB110209-0055]
 gb|EGA16090.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. MB111609-0052]
 gb|EGA18597.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 2009083312]
 gb|EGA22020.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 2009085258]
 gb|EGA27456.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. 315731156]
 gb|EGA30442.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2009159199]
 gb|EGA37571.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008282]
 gb|EGA39226.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008283]
 gb|EGA44378.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008284]
 gb|EGA50045.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008285]
 gb|EGA54708.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Montevideo str. IA_2010008287]
 Length = 171

Score = 91.3 bits (225), Expect = 5e-17, Method: Compositional matrix adjust.
 Identities = 62/170 (36%), Positives = 87/170 (51%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IR A AD AA+ +I NH + T+ + N RT + W + + L YP LV+E
 Sbjct: 1 MTIRFADKADCAAITEIYNHAVLHTAAIWNDRITVDTDNRLAWYEARQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 GVV G A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA

Sbjct: 59 NGVVTGYASFGDWRSFDGFRYTVVEHSVYVHPAHQKGKGLGRKLLSRLIDEARRCGKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174

I N S+RLH +LG+T + G K G W D+ F Q + A P

Sbjct: 119 GIESQNAASIRLHSLGFTVTAQMPQVGKFGRWLDLTFMQLQLDEHAAP 168

>ref|YP_770098.1| acetyltransferase [Rhizobium leguminosarum bv. viciae 3841]
emb|CAK10017.1| putative acetyltransferase [Rhizobium leguminosarum bv. viciae 3841]
Length = 200

Score = 91.3 bits (225), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 49/159 (30%), Positives = 80/159 (50%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVA-EVEGV 67

+R A+ AD+ A+ DI + ++ P + E + +YP++ A +G
Sbjct: 20 LRDASNADIPAIADIYRESVLNGVASYEIVPPSEAEMALRFSIAIVGQQYPYIAAIGADGT 79

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

+ G AYA ++ R AY W VE ++Y++ + + G+G L L+ GF+ + AVIG
Sbjct: 80 LLGYAYASAFRTRPAYRWLVEDSIYLAPQARGRGIGKALLAELIIRCTTLGFRQMAAVIG 139

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

+ S+ LH G+ G ++ GYKHG W D F QR
Sbjct: 140 GASPASIALHRTAGFEEVGLMKGTYKHGRWLDTMFMQR 178

>ref|YP_004118289.1| phosphinothricin acetyltransferase [Pantoea sp. At-9b]
gb|ADU71733.1| Phosphinothricin acetyltransferase [Pantoea sp. At-9b]
Length = 171

Score = 91.3 bits (225), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 79/161 (49%), Gaps = 2/161 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66

+EI A + + I H++ F T+P + L + PW VA +G
Sbjct: 1 MEILQAEQHIPGIQIYAHVHLHGCATFETDPPDDATLLARLHNITAAGLPWFVALEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126

VV G Y W+ R AY +++E +VY+ R G+G L L+ E G++ +V VI
Sbjct: 61 VVLGYCYLSRWRRERFAYRFSLEDSVYIDPRLTGRGIGRQLLAQALQWAEQHGYRQMVGV 120

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

G N S+ LH + G+T GTL++ G+KHG W D QR
Sbjct: 121 GNSENSASIALHRSAGFTVTGTLQSVGFKHGRWLDTVIMQR 161

>emb|CBK84854.1| Sortase and related acyltransferases [Enterobacter cloacae subsp. cloacae NCTC 9394]
Length = 172

Score = 91.3 bits (225), Expect = 5e-17, Method: Compositional matrix adjust.
Identities = 61/168 (36%), Positives = 82/168 (48%), Gaps = 5/168 (2%)

Query: 10 IRPATAADMAAVCDIVNH-YIETSTVNFRTPEQTPQE--WIDDLERLQDRYPWLVAEVEG 66

+R A D AA+ +I NH + T+ + T T W + R YP LV+E EG
Sbjct: 3 VRHACKEDCAAIGEIYNHAVLHTAAIWNDDTVTDNRIAWFE--ARTLLGYPVVLVSEEEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126

VV G A G W+A + + TVE +VYV HQ G+G L T L+K G +VA I
Sbjct: 61 VVTGYASFGDWRAFDGFRHTVEHSVYVHPDHQKGIGRLLMTELIKEARQIGKHMVAGI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N S+ LHE LG+ G + G K G W D+ F Q + + P
 Sbjct: 121 EAQNQASIHLETGLGFVTTGNMPQVGTGKGRWLDLTFMQLQLDERSDP 168

>ref|ZP_04868204.1| possible Phosphinothricin acetyltransferase [Staphylococcus aureus
 subsp. aureus TCH130]
 gb|EES96680.1| possible Phosphinothricin acetyltransferase [Staphylococcus aureus
 subsp. aureus TCH130]
 Length = 163

Score = 91.3 bits (225), Expect = 6e-17, Method: Compositional matrix adjust.
 Identities = 52/161 (32%), Positives = 83/161 (51%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
 IR A D+ A+ I N I +T + +PQT E I E Q + P V E G V
 Sbjct: 2 IRCAKKEDLNAILAIYNDAINTTAVYTYKPTIDERIAWFETKQRNHEPIFVFEENGSV 61
 Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G A G ++ AY +T+E ++YV + G+ S L L+ +A+G+++VA I
 Sbjct: 62 LGFATFGSFRPWPAYQYTIHESIYVDASARGKGIASQLLQRLIVEAKAKGYRTLVAIGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N+ S++LH+ + GTL G+K W D+ F++ D +
 Sbjct: 122 SNEASIKLHQKFAPKHAGTTLTNVGFKFNQWLDLAFYELDLQ 162

>ref|ZP_07374561.1| toxin-antitoxin system, toxin component, gnat family [Ahrensia sp.
 R2A130]
 gb|EFL89611.1| toxin-antitoxin system, toxin component, gnat family [Ahrensia sp.
 R2A130]
 Length = 171

Score = 91.3 bits (225), Expect = 6e-17, Method: Compositional matrix adjust.
 Identities = 55/161 (34%), Positives = 84/161 (52%), Gaps = 8/161 (4%)

Query: 16 ADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVVAGIAYA 74
 +++AA+ I H++E +F + +E L LQ+ YP L+A + G AYA
 Sbjct: 11 SEVAAITAIYGHVWENGIAFELDVPDEEEMNRRLSGLQEAGYPILIAREGNEITGYAYA 70
 Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL----- 128
 ++ R AY TVE TVYVS Q G G L T L+++ + + ++ ++AVI
 Sbjct: 71 SAYRPRPAYGATVEDTVYVSPSQQGTGTGRALLTALIEACKDRKYRQIIAVIACEAASDA 130

Query: 129 PND-PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 P+ S+RLH LG+ + G LR+ G KH W D QR+
 Sbjct: 131 PDKMASIRLHAKLGFRSAGRLRSIGRKHDRWLDTVLMQREL 171

>ref|YP_002299686.1| phosphinothricin N-acetyltransferase [Rhodospirillum centenum SW]
 gb|ACJ00874.1| phosphinothricin N-acetyltransferase [Rhodospirillum centenum SW]
 Length = 180

Score = 91.3 bits (225), Expect = 6e-17, Method: Compositional matrix adjust.
 Identities = 65/155 (41%), Positives = 88/155 (56%), Gaps = 2/155 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVAEVEG 66
 V +RPATAAD AA+ I + + ++ EP E L ++ P+LVA++ G
 Sbjct: 10 VRVRPATAADAAALAAIYAPEVLHACASYELEPPDAAEMARRLA AVEACGLPFLVADMAG 69
 Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 V G AYA P++ R AY +TVE +VYV+ Q GLG L L+ A G++ +VAVI

Sbjct: 70 QVLGYAYASPFRQRPAYRYTVEDSVYVAAGAQRGLGRLLLEALIGRCTALGYRRMVAVI 129

Query: 127 G-LPNDPVRLHEALGYTARGTLRAAGYKHGGWHD 160

G N SVRLH +LG+ G L AG+KHG W D

Sbjct: 130 GDAGNAASVRLHRS LGFAEVGLLPAGAGFKHGRWLD 164

>ref|YP_003490867.1| N-acetyltransferase [Streptomyces scabiei 87.22]
 emb|CBG72325.1| putative N-acetyltransferase [Streptomyces scabiei 87.22]
 Length = 172

Score = 90.9 bits (224), Expect = 6e-17, Method: Compositional matrix adjust.
 Identities = 56/182 (30%), Positives = 88/182 (48%), Gaps = 24/182 (13%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL 60

MS E V++RP A D+AA+ DI NHY+ + + F T TP+E R PWL

Sbjct: 1 MSGESTEVQVRPGVATDLAALTDIYNHYVRETPITFDTAVLTPEE-----RRPWL 50

Query: 61 VAEVEG-----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTL 106

++ E + G A + ++ + AY +VE +VY++ G+G+ L

Sbjct: 51 LSHPEDGPHRLMVATAKDSQRILGYATSSAFRPAAYGTSVEVSVYLAPDAGGRGVGTLL 110

Query: 107 YTHLLKSMEAQGFKS VVAVIGLPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166

Y L ++ + A I PN+ S RLHE G+ GT R G K G + DV ++++

Sbjct: 111 YRALFAALATEDVHRAYAGIAQPNEASTRLHERFGFRYVGTYREVGRKFGRYWDVAWYEK 170

Query: 167 DF 168

+

Sbjct: 171 EL 172

>ref|YP_001298770.1| putative sortase and related acyltransferase [Bacteroides vulgatus
 ATCC 8482]
 ref|ZP_05255628.1| conserved hypothetical protein [Bacteroides sp. 4_3_47FAA]
 ref|ZP_07994456.1| sortase and like acyltransferase [Bacteroides sp. 3_1_40A]
 gb|ABR39148.1| putative sortase and related acyltransferase [Bacteroides vulgatus
 ATCC 8482]
 gb|EET16020.1| conserved hypothetical protein [Bacteroides sp. 4_3_47FAA]
 gb|EFV69487.1| sortase and like acyltransferase [Bacteroides sp. 3_1_40A]
 Length = 161

Score = 90.9 bits (224), Expect = 6e-17, Method: Compositional matrix adjust.
 Identities = 53/161 (32%), Positives = 80/161 (49%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR D A+ I N Y+ S F TEP ++ + + + R+P+ V E EG V

Sbjct: 2 IRRVELQDAKAITTIYNEYVGH SVATFETEPLREEDMRNRIAGIAVRFPYFVYEEEGKV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIGLP 129

G YA WK R AY T+E+TVY++ ++ G+G L L++ G++++A +

Sbjct: 62 GYCYAHLWKERAAYRHTLET TVYLAPGYEGKGIGRELMEERLIEECRRDGYRALIACVTEG 121

Query: 130 NDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFEL 170

N S LH LG+ + G K G W DV D+EL

Sbjct: 122 NVVSDALHLRLGFKKVSHFKKVGLKFGRWLDV---VDYEL 158

>ref|NP_373053.1| N-acetyltransferase [Staphylococcus aureus subsp. aureus Mu50]
 ref|NP_375641.1| hypothetical protein SA2317 [Staphylococcus aureus subsp. aureus
 N315]
 ref|YP_001247905.1| GCN5-related N-acetyltransferase [Staphylococcus aureus subsp.
 aureus JH9]

ref|YP_001317714.1| GCN5-related N-acetyltransferase [Staphylococcus aureus subsp. aureus JH1]
ref|YP_001443103.1| hypothetical protein SAHV_2513 [Staphylococcus aureus subsp. aureus Mu3]
ref|ZP_05145902.2| hypothetical protein SauraM_12550 [Staphylococcus aureus subsp. aureus Mu50-omega]
ref|ZP_05643289.1| conserved hypothetical protein [Staphylococcus aureus A9781]
ref|ZP_05680486.1| conserved hypothetical protein [Staphylococcus aureus A9763]
ref|ZP_05685035.1| conserved hypothetical protein [Staphylococcus aureus A9719]
ref|ZP_05688146.1| N-acetyltransferase [Staphylococcus aureus A9299]
ref|ZP_05691485.1| conserved hypothetical protein [Staphylococcus aureus A8115]
ref|ZP_05693690.1| N-acetyltransferase [Staphylococcus aureus A6300]
ref|ZP_05697168.1| GNAT family acetyltransferase [Staphylococcus aureus A6224]
ref|ZP_05701689.1| conserved hypothetical protein [Staphylococcus aureus A5937]
ref|YP_003283430.1| acetyltransferase [Staphylococcus aureus subsp. aureus ED98]
ref|ZP_06303143.1| hypothetical protein SGAG_02263 [Staphylococcus aureus A8117]
ref|ZP_06334648.1| acetyltransferase [Staphylococcus aureus A10102]
ref|ZP_06815034.1| acetyltransferase [Staphylococcus aureus A8819]
ref|ZP_06857484.1| acetyltransferase [Staphylococcus aureus subsp. aureus MR1]
ref|ZP_06928169.1| acetyltransferase [Staphylococcus aureus A8796]
dbj|BAB43620.1| SA2317 [Staphylococcus aureus subsp. aureus N315]
dbj|BAB58691.1| similar to N-acetyltransferase [Staphylococcus aureus subsp. aureus Mu50]
gb|ABQ50329.1| GCN5-related N-acetyltransferase [Staphylococcus aureus subsp. aureus JH9]
gb|ABR53427.1| GCN5-related N-acetyltransferase [Staphylococcus aureus subsp. aureus JH1]
dbj|BAF79396.1| hypothetical protein [Staphylococcus aureus subsp. aureus Mu3]
gb|EEV26622.1| conserved hypothetical protein [Staphylococcus aureus A9781]
gb|EEV65578.1| conserved hypothetical protein [Staphylococcus aureus A9763]
gb|EEV65991.1| conserved hypothetical protein [Staphylococcus aureus A9719]
gb|EEV73749.1| N-acetyltransferase [Staphylococcus aureus A9299]
gb|EEV75538.1| conserved hypothetical protein [Staphylococcus aureus A8115]
gb|EEV78687.1| N-acetyltransferase [Staphylococcus aureus A6300]
gb|EEV80640.1| GNAT family acetyltransferase [Staphylococcus aureus A6224]
gb|EEV86939.1| conserved hypothetical protein [Staphylococcus aureus A5937]
gb|ACY12424.1| acetyltransferase [Staphylococcus aureus subsp. aureus ED98]
gb|EFB96144.1| acetyltransferase [Staphylococcus aureus A10102]
gb|EFC02851.1| hypothetical protein SGAG_02263 [Staphylococcus aureus A8117]
gb|ADC38676.1| Phosphinothricin N-acetyltransferase [Staphylococcus aureus 04-02981]
gb|EFG46184.1| acetyltransferase [Staphylococcus aureus A8819]
gb|EFH38302.1| acetyltransferase [Staphylococcus aureus A8796]
emb|CBX35710.1| acetyltransferase (GNAT) family protein [Staphylococcus aureus subsp. aureus ECT-R 2]
gb|EFT86808.1| hypothetical protein CGSSa03_11970 [Staphylococcus aureus subsp. aureus CGS03]
Length = 163

Score = 90.9 bits (224), Expect = 6e-17, Method: Compositional matrix adjust.
Identities = 53/161 (32%), Positives = 83/161 (51%), Gaps = 1/161 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
IR A D+ A+ I N I +T + +PQT E I E Q + P V E G V
Sbjct: 2 IRCAKKEDLNAILAIYNDAIINTTAVYTYKPTIDERIAWFETKQRNHEPIFVFEENGSV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRQLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A G ++ AY +T+E ++YV + G+ S L L+ +A+G++++VA I
Sbjct: 62 LGFATFGSFRPWPAYQYTIHESIYVDASARGKGIASQLLQRLIVEAKAKGYRTLAVAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFE 169
N+ S++LH+ + GTL GYK W D+ F++ D +

Sbjct: 122 SNEASIKLHQKFNFKHAGTLTNVGYKFDYWLDLAFYELDLK 162

>ref|ZP_07922338.1| phosphinothricin acetyltransferase [Pseudoramibacter alactolyticus

ATCC 23263]

gb|EFV00563.1| phosphinothricin acetyltransferase [Pseudoramibacter alactolyticus

ATCC 23263]

Length = 204

Score = 90.9 bits (224), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 56/164 (34%), Positives = 80/164 (48%), Gaps = 8/164 (4%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
+ + IR AT AD A+ + Y++ + V F T ++ + RYP+LVA+

Sbjct: 5 KTMAIRMATPADAEALLAVYAPYVQNTAVTFETAVPVAADFRRRIAATLPRYPYLVAQDA 64

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
VAG AY G + R AY W+ E ++Y++ + G G LY L AQG ++ A

Sbjct: 65 RGVAGYAYTGAFVGRAAYAWSAEVSIYLAADRRGRGWGRRLYAALETLSRAQGITNLYAC 124

Query: 126 IGLPNDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDV 161

IG+P DP S H LGY GT R GYK W+D+

Sbjct: 125 IGMPADPNDPYLTDASATFHAHLGYRRAGTFRRCGYKFARWYDM 168

>ref|ZP_06258790.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella parvula ATCC 17745]

gb|EFB86507.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella parvula ATCC 17745]

Length = 166

Score = 90.9 bits (224), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 52/153 (33%), Positives = 81/153 (52%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
IRP T D+A DI N+ + EP+T EW + E D + P +V V+G+V

Sbjct: 6 IRPITRNDIAPCLDIYNYEVVNGVATLDLEPRTLPEWQEWYESHSDHHPIVVGTVDGIV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG-FKSVVAVIG 127
AG A P++ + AY TVE ++Y+ ++ G+ + L TH+L+ + +VV+VI

Sbjct: 66 AGYASLSPYRPKEAYKSTVELSIYIHQDYRGRGIATQLMTHILEIAKNNPLLHNVSIVIT 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

N+ S +LH G+T G G+KHG + D

Sbjct: 126 AGNEGSTKLHARFGFTYCGLTPQVGFKHGTQD 158

>ref|YP_002554139.1| gcn5-like n-acetyltransferase [Acidovorax ebreus TPSY]

gb|ACM34139.1| GCN5-related N-acetyltransferase [Acidovorax ebreus TPSY]

Length = 173

Score = 90.9 bits (224), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 55/159 (34%), Positives = 83/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
IR + D+AA+ I H++ T F +P T Q+ + L P+LVAE G V

Sbjct: 4 IRASRDKDVAAITAIYTHHVLHGTGTFEIDPPTAQDMAARRADVLAAGLPYLVAAEEAGQV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
G AY +K R AY ++ E ++YV+ + GLG L L EA G + ++AVIG

Sbjct: 64 LGFAYCNWFKPRPAYRFSAEYSIYVADAARGRLGRQLLEALAMQAEAAAGVRKLLAVIGD 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+ +H A G+T G +R+ G+K G W D+ ++
Sbjct: 124 SANAGSIGVHRAAGFTDVGVMRSVGWKFAGWRDIVLMEK 162

>ref|YP_002944112.1| GCN5-related N-acetyltransferase [Variovorax paradoxus S110]
gb|ACS18846.1| GCN5-related N-acetyltransferase [Variovorax paradoxus S110]
Length = 173

Score = 90.9 bits (224), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 57/161 (35%), Positives = 82/161 (50%), Gaps = 2/161 (1%)

Query: 16 ADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVE-GVVAGIAY 73
A A+ I+N I ST + +P+TP+ + + +P + AE E G + G A
Sbjct: 10 AHAGAILAILNEAIAINSTALYDYKPRTPESMVAVFATKRANGFPVIGAEDESGKLLGFAS 69

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPS 133
G ++A AY +TVE +VYV H+ GLG L ++ A +V I N S
Sbjct: 70 YGTFRAFPAYKYTVEHSVYVEAGHRGAGLGRRLTEAIIAEAVAHDVHVMVGAIDAANAGS 129

Query: 134 VRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPAPP 174
+ LHE LG+ GT+R AG+K G W DV F+QR P P
Sbjct: 130 IGLHERLGFEGHAGTVRQAGFKFGRWLDVAFYQRILSTPLNP 170

>emb|CAJ88465.1| putative acetyltransferase [Streptomyces ambofaciens ATCC 23877]
Length = 200

Score = 90.9 bits (224), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 63/165 (38%), Positives = 83/165 (50%), Gaps = 2/165 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IRPA AD+ AV +I HY+ + + F P W L+ L P+LVAE+ G V
Sbjct: 28 IRPAVPADLNAVAEIFTHYVCHTVITFEETPPPVAAWRQRLDDLAQNLPFLVAELSGDV 87

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
G AYA PW+ + AY TVE+++Y++ GLG L LL + + ++AVI
Sbjct: 88 VGYAYAAPWRPKPAYRHTVENSIIYLAPGRTGRGLGGALLDALLDACARTHVRQMIAVIAD 147

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPA 172
D SV LH G+T G L GYKH W D QR PA
Sbjct: 148 ADTDASVALHRRYGFTDVGRLATVGYKHDRWIDTLLMQRTLGRPA 192

>ref|ZP_07261654.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv.
syringae
642]
Length = 179

Score = 90.9 bits (224), Expect = 7e-17, Method: Compositional matrix adjust.
Identities = 58/160 (36%), Positives = 80/160 (50%), Gaps = 2/160 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGV 67
++R A DM AV I ++ +F EP E + L P+LVAE G
Sbjct: 6 DLRDARDDMPAVQAIYADHVLHGISSFELEPPDLAELLQRRCTVLAKGLPYLVAERAGE 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
+ G Y P++ R Y +TVE +VYV G+G L L+K EA G++ ++AVIG
Sbjct: 66 ILGYGYVTPYRPRPGYRFTVEDSVYVRDGLGGQGIGHALLNALVKHCEAGGWRQMIAVIG 125

Query: 128 -LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+RLHE LG+ G + G+KHG W D QR
Sbjct: 126 NSQNIASLRRLHERLGFRRVGVFESVGFKHGRWVDTVLMQR 165

>ref|ZP_04679268.1| Phosphinothricin N-acetyltransferase [Ochrobactrum intermedium LMG

3301]

gb|EEQ94774.1| Phosphinothricin N-acetyltransferase [Ochrobactrum intermedium LMG

3301]

Length = 196

Score = 90.5 bits (223), Expect = 8e-17, Method: Compositional matrix adjust.

Identities = 55/159 (34%), Positives = 83/159 (52%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68

IR AD+ + I + + T ++ EP T E L + +P LVAE +G V

Sbjct: 17 IRDFQPADIETITAIYSEAVLTGAGSYEIEPPTADEMARRFAALVAQGFILVAEHDGRV 76

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128

G AYA ++ R AY W E ++Y++ + G+G L L++ + A GF+ ++AVIG

Sbjct: 77 LGYAYASHFRVRPAYRWLAEDSIYIAPDAKKGKIGKLLLRALIERISALGFRQLLAVIGD 136

Query: 129 P--NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165

N SVRLHE+LG+ G + +G+K G W D Q

Sbjct: 137 GERNIGSVRLHESLGFACGRIEGSGFKLGRWLDTVLMQ 175

>ref|ZP_08078774.1| acetyltransferase, GNAT family [Succinatimonas hippei YIT 12066]

gb|EFY06781.1| acetyltransferase, GNAT family [Succinatimonas hippei YIT 12066]

Length = 160

Score = 90.5 bits (223), Expect = 8e-17, Method: Compositional matrix adjust.

Identities = 49/161 (30%), Positives = 75/161 (46%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR +D A+ I N+Y++ +TV F P T E D + + YP+ V E +

Sbjct: 2 IRLVKISDAPAIARIYNYVVKETTTFEYAPLTNNEMADRINSISASYPYFVYEENDCIL 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129

G YA PWK R AY T E ++Y++ G+GS L L+ +++A I

Sbjct: 62 GYCYAHPWKERAAYAQTYEISYILAKEATGQGIGSKLLKRLVDECRKINCHALIACTAE 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170

N S+R H G+ + + G+K + DV D+EL

Sbjct: 122 NAGSIRFHLRHGFKQVSSFKEVGFKFNRYLDVN---DYEL 158

>ref|ZP_08091588.1| GNAT family Toxin-antitoxin system [Clostridium symbiosum WAL-14163]

ref|ZP_08108134.1| hypothetical protein HMPREF9475_02997 [Clostridium symbiosum WAL-14673]

gb|EGA92848.1| GNAT family Toxin-antitoxin system [Clostridium symbiosum WAL-14163]

gb|EGB17870.1| hypothetical protein HMPREF9475_02997 [Clostridium symbiosum WAL-14673]

Length = 163

Score = 90.5 bits (223), Expect = 9e-17, Method: Compositional matrix adjust.

Identities = 52/160 (32%), Positives = 83/160 (51%), Gaps = 6/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66

IR A +D+ ++ DI N+ + T +F P++ +E W + +R R+P +VAE +

Sbjct: 3 IRWAEKSDLQSLVDIFNYEVLNGTASFIRSLEERTVWFEQHDR--GRFPLIVAEDK 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG-FKSVVAV 125

G A ++ +AY TVE +VYV H ++ +G L LL+ + G ++++V
 Sbjct: 61 RAVGYASLSVYRDNDAYAAATVELSVYVDHEYRGRKIGDALMEELLRIAKENGVEVHAIISV 120

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 I N S+RLHE G+ G R G K G W D F+Q

Sbjct: 121 ITADNAASIRLHEKFGFQFCGITREVGRKFGRWLDAAFYQ 160

>ref|ZP_04826272.1| possible Phosphinothricin acetyltransferase [Staphylococcus epidermidis BCM-HMP0060]
 ref|ZP_06283961.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus epidermidis SK135]
 ref|ZP_06613872.1| GNAT family toxin-antitoxin system [Staphylococcus epidermidis M23864:W2(grey)]
 gb|EES57253.1| possible Phosphinothricin acetyltransferase [Staphylococcus epidermidis BCM-HMP0060]
 gb|EFA88374.1| toxin-antitoxin system, toxin component, GNAT family [Staphylococcus epidermidis SK135]
 gb|EFE59137.1| GNAT family toxin-antitoxin system [Staphylococcus epidermidis M23864:W2(grey)]
 Length = 164

Score = 90.5 bits (223), Expect = 9e-17, Method: Compositional matrix adjust.
 Identities = 51/162 (31%), Positives = 85/162 (52%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A D+ + I N I +T + +PQ E W ++ + P V E EG

Sbjct: 2 IRFARLEDLQGILTIYNDAILNTTAVYTYKPPQLDERLQWYQSKAKINE--PIWVYEKEG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVAIVI 126
 V G A G ++ AY +T+E ++YV +++ LG+ S L +L++ + QG++++VA I

Sbjct: 60 KVVGFATYGSFRQWPAYLYTIEHSIYVHQYRGLGIASQLLENLIRYAKEQGYRTIVAGI 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQD 168
 N S+ LH+ ++ GT++ GYK W D+ F+Q D

Sbjct: 120 DASNMDSIALHKKFDFSHAGTIKNVGYKFDRLDLDFYQYDL 161

>dbj|BAI77993.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
 Length = 199

Score = 90.5 bits (223), Expect = 9e-17, Method: Compositional matrix adjust.
 Identities = 57/169 (33%), Positives = 83/169 (49%), Gaps = 5/169 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 +R A DM V I ++ +F EP + +E + E L P+ +AE +G V

Sbjct: 27 LRDARDDDDMPMVQSIYAEHVLEGISSFELEPPSLEEMLRRAEVLAKGLPYRIAHEHQGEV 86

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G Y P++ R Y +TVE +VYV LG+G L L++ G++ ++A+IG

Sbjct: 87 VGYGYVTPYRPRPGYRFTVEDSVYVRSGMGLGIGQALLAELVEHCVQGGWRQMIAIIGN 146

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ---DFELPAP 173
 N S+RLHE LG+ G + G+KHG W D QR D L P

Sbjct: 147 SENTASIRLHERLGFHRVGVFESVGFKHGRWVDTVLMQALGDGSLSTP 195

>ref|ZP_06709676.1| GNAT family toxin-antitoxin system, toxin component [Streptomyces sp. e14]

gb|EFF92798.1| GNAT family toxin-antitoxin system, toxin component [Streptomyces sp. e14]

Length = 168

Score = 90.5 bits (223), Expect = 9e-17, Method: Compositional matrix adjust.
Identities = 64/161 (39%), Positives = 82/161 (50%), Gaps = 2/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
+R A AD+ V I HY S F EP+ +W + + R P+LVAE G +
Sbjct: 8 VRAALRADLPEVARIYGHYALHSVATFDEEPRPLAQWELKYDEIAGRGLPFLVAEEAGRI 67

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
AG AYAGPW+ + AY TVE TVY+ GLG+ L LL G + V+AVI
Sbjct: 68 AGFAYAGPWRPKPAYRNTVEDTVYLDPAATGRGLGAALLAELLAECARAGVRQVIAVITA 127

Query: 129 P-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
P ++ S LH LG+T G L G+KHG W D QR
Sbjct: 128 PGSEASAALHRRLLGFTEAGRLTEVGHKHGRWLDTVLLQRTL 168

>dbj|BAI77992.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
Length = 199

Score = 90.5 bits (223), Expect = 9e-17, Method: Compositional matrix adjust.
Identities = 55/159 (34%), Positives = 80/159 (50%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
+R A DM V I ++ +F EP + +E + E L P+ VAE +G V
Sbjct: 27 LRDARDDMPMVQAIYAEHVLEGISSFELEPPSLEEMLRRAEVLAKGLPYRVAEHQGEV 86

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
G Y P++ R Y +TVE +VYV LG+G L L++ G++ ++A+IG
Sbjct: 87 VGYGYVTPYRPRPGYRFTVEDSVYVRSMMGLGIGQALLAELVEHCVQGGWRQMIAIIGN 146

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+RLHE LG+ G + G+KHG W D QR
Sbjct: 147 SENTASIRLHERLGFHRVGVFESVGFKHGRWVDTVLMQR 185

>ref|YP_004042835.1| gcn5-related N-acetyltransferase [Paludibacter propionicigenes
WB4]

gb|ADQ79850.1| GCN5-related N-acetyltransferase [Paludibacter propionicigenes WB4]
Length = 175

Score = 90.5 bits (223), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 53/170 (31%), Positives = 87/170 (51%), Gaps = 6/170 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVE 65
+++P T A + + I N I ST + + +T + W D +++ YP + A +
Sbjct: 5 QLKPCTEAQLPEILAI FNDAILNSTALYEYKVRTLERMNAWYAD--KIKGDYPVVGAFQAQ 62

Query: 66 -GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
G + G + G ++ + AY +TVE +VYV + GLG L ++K + Q + S++
Sbjct: 63 DGKLLGFSTYGMFRVQPAYKYTVEHSVYVRSMDRGRGLGKVL LLDIIKRAQE QNYHSLIG 122

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
VI N S++LHE G+ G L+ AGYK G W D F+Q + P P
Sbjct: 123 VIDADNTVSIKLHENEGFVLTGVLKEAGYKFGRWLDAAFYQLLLKTPEVP 172

>gb|ADY39465.1| GCN5-related N-acetyltransferase [bacterium enrichment culture
clone P69-9E]
Length = 184

Score = 90.5 bits (223), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 53/165 (32%), Positives = 84/165 (50%), Gaps = 3/165 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 +E+R A D+ A+ I ++ +F P T E ++ + + PWL+A G
 Sbjct: 12 MEVRDALPDDVHAIAAIYAWHLHGRASFEEVPPTIDEMRQRMKSVAESGLPWLIALYRG 71

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 +V G YA P++ R+AY +T+E ++YV G GS L L+ E ++ ++AV+
 Sbjct: 72 IVVGICYATPYRPRHAYRYTLEESIVDASITGRGFGSALMDALIARCEQGPWRQMIADV 131

Query: 127 GLPNDP--SVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFE 169
 G N+ S+RLH+ G+ G LR+ GYK G W D QR
 Sbjct: 132 GDGNNSGSLRLHKKHGFVIVGQLRSVGYKKGDWRDVTIMQSLN 176

>ref|YP_471413.1| putative phosphinothricin N-acetyltransferase (antibiotic
 resistance) protein [Rhizobium etli CFN 42]
 gb|ABC92686.1| putative phosphinothricin N-acetyltransferase (antibiotic
 resistance) protein [Rhizobium etli CFN 42]
 Length = 185

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 80/161 (49%), Gaps = 2/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVA-EVEGV 67
 +R A+ AD+ A+ +I + ++ P E + +YP++ A + +G
 Sbjct: 5 LRDSQADIPAITEIYRDSVLNGVASYEIAPPYEAEMAQRFSIAIVSQQYPYVAATDADGK 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA ++ R AY W VE ++Y++ + G+G L L+ A GF+ +VAVIG
 Sbjct: 65 LLGYAYASAFRTRPAYRWMVEDSIYLAPEARGRGVGKALMAELIDRCTLGFRQMVAVIG 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDF 168
 + S+ LH G+ G ++ GYKHG W D QR
 Sbjct: 125 GASPASIALHLKAGFVEVGLMKGTGYKHGRWLDTLMQRL 165

>ref|YP_117898.1| putative acetyltransferase [Nocardia farcinica IFM 10152]
 dbj|BAD56534.1| putative acetyltransferase [Nocardia farcinica IFM 10152]
 Length = 177

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 63/172 (36%), Positives = 85/172 (49%), Gaps = 8/172 (4%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWL 61
 R P IR AT D+ A+ ++ N I TST + E ++ W D R P LV
 Sbjct: 7 RPPAVIRDATEDDLPAILELHNANIATSTAIWDVEQVGLDRLAWFGD--RTGAGMPIIV 64

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF-K 120
 AEV+G AG A G W+ + Y +TVE++VY+ R QR GL + L L+ A G
 Sbjct: 65 AEVDGEFAGYASYGRWRPKVGYRFTVENSVIYVDRFQRRGLAAALLRELIDRATASGRVH 124

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFELPA 172
 +++A I N S+ LHE G+ G L G K G W D+ Q LPA
 Sbjct: 125 AMIAAIESSNTASIALHERFGFVEVGRLEPEVGRKFGRWMDLTLLQ--LTLPA 174

>ref|NP_765632.1| N-acetyltransferase [Staphylococcus epidermidis ATCC 12228]
 gb|AAO05719.1|AE016751_14 N-acetyltransferase [Staphylococcus epidermidis ATCC 12228]
 Length = 164

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 51/162 (31%), Positives = 85/162 (52%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66

IR A D+ + I N I +T + +PQ E W ++ + P V E EG
 Sbjct: 2 IRFARLEDLQDILTIYNDAILNTTAVYTYKPPQLDERLQWYQSKAKINE--PIWVYEKEG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

V G A G ++ AY +T+E ++YV +++ LG+ S L +L++ + Q ++++VA I
 Sbjct: 60 KVVGFATYGSFRQWPAYLYTIEHSIYVHQYRGLGIASQLLENLIRYAKEQSYRTIVAGI 119

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168

N S+ LH+ ++ GT++ GYK G W D+ F+Q D
 Sbjct: 120 DASNMDSIALHKKFDFSHAGTIKNVGYKFGRWLDLSFYQYDL 161

>ref|ZP_00943431.1| Phosphinothricin N-acetyltransferase [Ralstonia solanacearum UW551]

ref|YP_002261060.1| antibiotic resistance (acetyltransferase) protein [Ralstonia solanacearum IPO1609]

gb|EAP74046.1| Phosphinothricin N-acetyltransferase [Ralstonia solanacearum UW551]

emb|CAQ63002.1| antibiotic resistance (acetyltransferase) protein [Ralstonia solanacearum IPO1609]

Length = 182

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 57/160 (35%), Positives = 80/160 (50%), Gaps = 6/160 (3%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVA-EVEGVVAGIAYA 74

AA+ DI+N I ST + P+ PQ W D + +P + A + G + G A
 Sbjct: 22 AAILDILNEAIVNSTALYDYTPRPPQAMATWFD--AKRAGGFVVGAVDASGKLLGFASW 79

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 134

G ++A AY +TVE +VYV H + GLG L +++ A +V I N S
 Sbjct: 80 GTFRAFPAYKYTVEHSVYVHHACRGRGLGERLLREMIRRARAALHVLVGCIDAANFASA 139

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPP 174

LH LG+ GT+R AG+K G W D F+Q + E PA P
 Sbjct: 140 GLHTRLGFVHAGTIREAGFKFGRWLDAAFYQLNLETPAQP 179

>ref|XP_003088197.1| hypothetical protein CRE_05355 [Caenorhabditis remanei]

gb|EF092792.1| hypothetical protein CRE_05355 [Caenorhabditis remanei]

Length = 379

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 58/179 (32%), Positives = 88/179 (49%), Gaps = 12/179 (6%)

Query: 1 MSPERRPV-----EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQT---PQEWIDDLER 52

+SP+ R IRPA A+D+ + I NH I T + ++ +T Q+W LE
 Sbjct: 203 ISPDTRLYLGVESIRPAQASDLTEIMRIYNHEIATGLATWNSQLKTFADYQQWF--LEL 260

Query: 53 LQDRYPWLVAEVEGV--VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110

Q ++P VAE +AG A ++A N Y +TVE +VY+ + R GLG L L
 Sbjct: 261 QQQQFPLFVAEETATHAIAGYADYASFRAINGYLYTVEHSVYIDPKFTRQGLGKRLMLKL 320

Query: 111 LKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFE 169

++ + +VA I N S+ LH+ LG+ G + G K G W D+ Q +F+
 Sbjct: 321 IEHAQQHNIHVMVAIDHENTGSIYHLHQQLGFKQTGYMPQVGQKFGKWRDLVLMQLNFD 379

>ref|ZP_02421681.1| hypothetical protein EUBSIR_00512 [Eubacterium siraeum DSM 15702]

gb|EDS01608.1| hypothetical protein EUBSIR_00512 [Eubacterium siraeum DSM 15702]

Length = 180

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 51/161 (31%), Positives = 82/161 (50%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +EIR AT D + I ++YIE + V + + +++ +E+ +YP++VAE +G
 Sbjct: 12 IEIRTATPFDAEELLGIYSYIENTAVTYEIDVPFAEDFRRRIEKTLMKYPYIVAERDGR 71

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVIG 127
 + G AYAG +K R AY+ + E+++YV +R G G+ LY L K + G ++ A I
 Sbjct: 72 IIGYAYAGVFKDRAAYERSAETSIYVDVNEKRYGTGTALYRELEKRLADMGVRNAYACIA 131

Query: 128 -----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 N S+ HE GYT G K G +D+
 Sbjct: 132 STDKDDEYLNHDSIWFHEKQGYTLVGKFKHCAEKFGREYDM 172

>ref|YP_003182713.1| GCN5-related N-acetyltransferase [Eggerthella lenta DSM 2243]
 gb|ACV56324.1| GCN5-related N-acetyltransferase [Eggerthella lenta DSM 2243]
 Length = 213

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 63/180 (35%), Positives = 86/180 (47%), Gaps = 5/180 (2%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 SP +R A D A+ + Y+ET V F T + E+ + YP L
 Sbjct: 3 FSPCATSANVRIAARGDAEAMRAVYAPYVETP-VTFDTVAPSAEFAARMADAMAAYPCL 61

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 V E +G V G AYA +R AY W E +VY+ G G TLY LLK + AQG K
 Sbjct: 62 VLEQDGRVVGFAAYAHQAASRAAYRWNAELSVYLEQGATGGGRGRTLYDALLKLLRAQGVK 121

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF----ELPAPPRP 176
 S ++ +PN+ S RLH G+ AG+K G WHDV ++ ++ + PA P P
 Sbjct: 122 SAYGLVTPNEASERLHAGCGFQRCWVQSHAGWKAGSWHDVTWYVKELAPFDDDDPADPVP 181

>ref|YP_001616270.1| putative acetyltransferase [Sorangium cellulosum 'So ce 56']
 emb|CAN95790.1| putative acetyltransferase [Sorangium cellulosum 'So ce 56']
 Length = 333

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 62/160 (38%), Positives = 79/160 (49%), Gaps = 1/160 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-EVEG 66
 V IR AT AD+AA+ +I Y+E ST F T TP E L +P VA E +G
 Sbjct: 162 VRIRLATEADLAAIEEIYAFYVERSTCTFATTVPPTAERRAWLAAGPLHPATVAVEGDG 221

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSUVAVI 126
 V G W R AY +VE++VYV R GLG + L+ + G ++++A I
 Sbjct: 222 TVVGWGSLSQWNPRAAYARSVENSIVYVRDGLHRRGLGRRILADLVSRRAISLGHRTIIAQI 281

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166
 SV LH ALG+ G LR GYK W DV QR
 Sbjct: 282 AGDQAASVALHRLGFEAGVLRDVGKFDRLDVLDMQR 321

>ref|XP_002416063.1| phosphinothricin N-acetyltransferase, putative [Ixodes
 scapularis]
 gb|EEC19730.1| phosphinothricin N-acetyltransferase, putative [Ixodes scapularis]
 Length = 164

Score = 90.1 bits (222), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 61/161 (37%), Positives = 89/161 (55%), Gaps = 2/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68


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      IR AT  DM AV +I  +++  ST  F    P    QE      +++++  PVLVAE++G +
Sbjct: 3  IRHATLDDMVAVQNIYAYHVLHSTATFEQSPDEQEMGARYIQVREQNLPWLVAELDQGI 62

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI-G 127
          G AYAG +++R AY +TVE ++Y++          GLG  L   LL   E   ++ +VA+I  G
Sbjct: 63  VGYAYAGTYRSRPAYRFTVEDSIYLAQGGIGKGLGKALLEQLLLECEKGPWRQMVAIISG 122

Query: 128  LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
          +  S+ LH +LG+   GT  A GYK   W DV   QR
Sbjct: 123  HDSRGSIALHRS LGFAHVGTPAVGYKFQQWIDVVMQRS 163

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>ref|YP_189646.1| phosphinothricin acetyltransferase, putative [Staphylococcus
epidermidis RP62A]
gb|AAW52944.1| phosphinothricin acetyltransferase, putative [Staphylococcus
epidermidis RP62A]
Length = 164

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Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 51/162 (31%), Positives = 85/162 (52%), Gaps = 5/162 (3%)

```

Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
          IR A   D+  +  I N  I  +T  +  +PQ   E   W      ++  +  P  V E EG
Sbjct: 2   IRFARLEDLQDILTIYNDAILNTTAVYTYKQQOLDERLQWYQSKAKINE--PIWVYEKEG 59

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          V G A   G  ++   AY +T+E ++YV   +++ LG+ S L   +L++   + QG++++VA I
Sbjct: 60  KVVGFATYGSFRQWPAYLYTIEHSIYVHQYRGLGIASQLLENLIRYAKEQGYRTIVAGI 119

Query: 127  GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
          N  S+ LH+   ++  GT++  GYK   W D+ F+Q D
Sbjct: 120  DASNMDSIALHKKFDFSHAGTIKNVGYKFDRWLDLSFYQYDL 161

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>ref|ZP_07947262.1| acetyltransferase [Eggerthella sp. 1_3_56FAA]
gb|EFV33764.1| acetyltransferase [Eggerthella sp. 1_3_56FAA]
Length = 213

```

Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 63/180 (35%), Positives = 86/180 (47%), Gaps = 5/180 (2%)

```

Query: 1   MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
          SP      +R A   D  A+  +   Y+ET  V F T   +  E+  +   YP L
Sbjct: 3   FSPCATSANVRIAARGDAEAMRAVYAPVETP-VTFDTPVAPSRAEFAARMADAMVDYPCL 61

Query: 61  VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
          V E +G V G AYA   +R AY W   E +VY+          G G TLY  LLK + AQG K
Sbjct: 62  VLEQDGRVIGFAYAHAQASRAAYRWNAELSVYLEQGATGGGRGRTLYDALLKLLRAQGVK 121

Query: 121  SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF----ELPAPPRP 176
          S   ++ +PN+ S RLH   G+          AG+K G WHDV ++ ++   + PA P P
Sbjct: 122  SAYGLVTPNEASERLHAGCGFQRCWVQSHAGWKAGSWHDTVWYVKELAPFDDDDPADPVP 181

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>ref|YP_002573340.1| GCN5-like N-acetyltransferase [Caldicellulosiruptor bescii DSM
6725]
gb|ACM60567.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor bescii DSM
6725]
Length = 161

```

Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 46/158 (29%), Positives = 80/158 (50%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR AT +D+ + I N+ + ST F P+T ++++ L+ ++Y VAE
 Sbjct: 1 MNIRKATISDITNMLYIYNYEVLNSTSTFDIHPKTTEDFLKLLDSHSNKYSIYVAEENST 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G Y P+ + AY TVE T+Y+ H+ G+G + L++ + G +++A +
 Sbjct: 61 ILGYGYLSPFSEKEAYSITVEDTIYIHPLHRGKGIGKQILKFLIEKAKDTGAANIIAKVC 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N S+ LH++ G+ G L G K G + DV Q
 Sbjct: 121 AENYISLHLHKSFGFVEVGKLIKVGSKFGRFLDVIIILQ 158

>ref|YP_001587924.1| hypothetical protein SPAB_01697 [Salmonella enterica subsp.
 enterica serovar Paratyphi B str. SPB7]
 gb|ABX67091.1| hypothetical protein SPAB_01697 [Salmonella enterica subsp.
 enterica serovar Paratyphi B str. SPB7]
 Length = 171

Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 61/170 (35%), Positives = 86/170 (50%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IR A AD A + +I NH + T+ + N RT + W + + L YP LV+E
 Sbjct: 1 MTIRFADKADCATITEIYNHAVLHTAAIWNDRVTVDNRLAWYEARQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 GVV G A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA
 Sbjct: 59 NGVVTGYASFGDWRSFDGFRYTVVEHSVYVHPAHQKGKGLGRKLLSRLIDEARRCGKHVMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+RLH +LG+T + G K G W D+ F Q + A P
 Sbjct: 119 GIESQNAASIRLHSLGFTVTAQMPQVGKFGRWLDLTFMQLQLDEHAAP 168

>ref|YP_002543819.1| phosphinothricin acetyltransferase (antibiotic resistance)
 protein
 [Agrobacterium radiobacter K84]
 gb|ACM25893.1| phosphinothricin acetyltransferase (antibiotic resistance) protein
 [Agrobacterium radiobacter K84]
 Length = 168

Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
 Identities = 54/157 (34%), Positives = 79/157 (50%), Gaps = 5/157 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAEV 64
 V +R A AD+ A+C+I NH + +T + + EW+ R +P +VAE
 Sbjct: 5 VLLRDAIEADLPAICEIYNHAVVHTTAIWNDTLVDVDNRIEWLK--ARRARGFPVVVAEK 62

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +G VAG A G W+A + Y TVE+++YV H+ LG+G L L+ ++A
 Sbjct: 63 DGKVAGYASYGDWRAFDGYRHTVENSIIYVDKDHRLGIGEGLLRELVAACAKGNVHVMIA 122

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 I N S+RLHE LG+ G G K G W D+
 Sbjct: 123 AIETGNAVSIRLHEKLGFRAGQFSEVGTGKFGRWLDL 159

>ref|YP_001832067.1| GCN5-related N-acetyltransferase [Beijerinckia indica subsp.
 indica
 ATCC 9039]
 gb|ACB94578.1| GCN5-related N-acetyltransferase [Beijerinckia indica subsp. indica
 ATCC 9039]

Length = 186

Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 54/166 (32%), Positives = 85/166 (51%), Gaps = 3/166 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQ--EWIDDLERLQDR-YPWLVA 62
+ V IRP+ D+ A+ +I +I + TPQ + D + L++R +P LVA
Sbjct: 5 QAVVIRPSQDKDVEAMLEIYRRHIRRGIEEGVDDSGTPQPDDLRRRKNLRNRRFPHLVA 64

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
+ G V G AY ++ R AY +TV+ ++YV H H G+G L L+ + A GF+ +
Sbjct: 65 MLGGEVIGYAYVVLFRKRPAAYRYTVKHSIYVHHEHLGQGIGRLLMQGLIDACAAAGFRQM 124

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168
+ I N S+ LHE G++ G L + Y++G W D QR
Sbjct: 125 IGYIDADNAASLGLHETFGFSRVGVLPVAVRYGHWADTIMVQRSL 170

>ref|YP_002252427.1| antibiotic resistance (acetyltransferase) protein [Ralstonia
solanacearum MolK2]
emb|CAQ17746.1| antibiotic resistance (acetyltransferase) protein [Ralstonia
solanacearum MolK2]
Length = 182

Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 55/158 (34%), Positives = 79/158 (50%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWLVA-EVEGVVAGIAYAGP 76
AA+ DI+N I ST + P+ PQ + + +P + A + G + G A G
Sbjct: 22 AAILDILNEAIVNSTALYDYTPRPPQAMVTWFAAKRAGGFPVVGAVDASGKLLGFASWGT 81

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++A AY +TVE +VYV H + GLG L +++ A +V I N S L
Sbjct: 82 FRAFPAYKYTVEHSVYVHHACRGRGLGERLLREMIRRARAQLHVLVGCIDAANSASAGL 141

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPP 174
H LG+ GT+R AG+K G W D F+Q + E PA P
Sbjct: 142 HTRLGFVHAGTIREAGFKFGRWLDAAFYQLNLETPAQ 179

>ref|ZP_06355097.1| toxin-antitoxin system, toxin component, GNAT family [Citrobacter
youngae ATCC 29220]
gb|EFE06630.1| toxin-antitoxin system, toxin component, GNAT family [Citrobacter
youngae ATCC 29220]
Length = 174

Score = 89.7 bits (221), Expect = 1e-16, Method: Compositional matrix adjust.
Identities = 54/163 (33%), Positives = 90/163 (55%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
++I A + A+ DI H++ T +F T P E + LE++ PW+VA EG
Sbjct: 1 MKIVNAEVKHIPAIRDIYAHHVHGTGSFETAPPDNNEMLARLEKIHRLGLPWVVALQEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G Y ++ R AY +T+E ++Y+ QR G+G L H++ E G++ ++A++
Sbjct: 61 KVIGYCYLTRYRERYAYRYTLEDSIYIDPAAQRQGVGKALLRHVIDWAETHGYRQLIAMV 120

Query: 127 GLPNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168
G N+ S+++H+ +GY GTL+ G+KHG W D QR+
Sbjct: 121 GDSNNQGSLSKVHQVGYREIGTLKDVGFKHGRWLDTVVLQRNL 163

>ref|ZP_07842937.1| toxin-antitoxin system, toxin component, GNAT family

[Staphylococcus hominis subsp. hominis C80]
gb|EFS19890.1| toxin-antitoxin system, toxin component, GNAT family
[Staphylococcus hominis subsp. hominis C80]
Length = 168

Score = 89.7 bits (221), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 49/161 (30%), Positives = 85/161 (52%), Gaps = 5/161 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
IR A D+ + +I N I +T + PQ+ E W + ++ P V E++
Sbjct: 5 IREAERKDLDPDIFNINNDAILNTTAVTYHPQSLNEREVWFE--TKVLANEPIFVFEIDN 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
VAG A G ++ AY +++E ++YV+ ++R G+ S L HL+ + + +++VA I
Sbjct: 63 KVAGFATYQDFRHWPAYLSIEHSIYVKNKYRRRGVASHLLEHLIDDAKHRQYRTIVAGI 122

Query: 127 GLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRD 167
N+ S++LHE + GT+ GYK W D+ F+Q D
Sbjct: 123 DTLNEASIKLHETFNFKHAGTIENVGYKFERWLDLAFYQYD 163

>ref|ZP_07743896.1| putative acetyltransferase [Vibrio caribbenthicus ATCC BAA-2122]
gb|EFP95772.1| putative acetyltransferase [Vibrio caribbenthicus ATCC BAA-2122]
Length = 166

Score = 89.7 bits (221), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 49/168 (29%), Positives = 85/168 (50%), Gaps = 10/168 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEV 64
+EIR A D+ + + N+YIE + F + ++ +EW + + +Y +VA
Sbjct: 1 MEIRHAERPDLPIQITALFNYYIEHTNARFEEQAFSVESRKEWFNQFSN-ETKYQIVVACE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+V G A + P++ A+ TVE+++Y++ ++ GLG LY HL ++ ++
Sbjct: 60 NDIVIGFACSQPYRGSKAFSETVETSIYINSYKGRGLGKALYRHLFANIGKYKIHRALS 119

Query: 125 VIGLPNDPVSRLHEALGYTARGTLRAAGYKHG-----GWHDVGFQWQRD 167
I LPN+ S+ LHE G+ GT KHG W++ W+RD
Sbjct: 120 GIALPNEASIALHEHFGFKKVGTFDEYAKKHGQYISSAWYEKT-WKRD 166

>ref|ZP_06917734.1| phosphinothricin N-acetyltransferase [Streptomyces sviveus ATCC 29083]
gb|EDY53486.1| phosphinothricin N-acetyltransferase [Streptomyces sviveus ATCC 29083]
Length = 169

Score = 89.7 bits (221), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 55/179 (30%), Positives = 87/179 (48%), Gaps = 28/179 (15%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA----- 62
+++RP D+ A+ D+ NHY+ + + F T TP+E R PWL++
Sbjct: 1 MQVRPGVEGDLKALADLYNHVRETPIFTDAVFTPEE-----RRPWLLSHPEDG 50

Query: 63 -----EVEGV---VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTH 109
E G + G A + P++A+ AY +VE TVYV+ G+G+ LY
Sbjct: 51 PYRLMVATDTESTGTSTQIRILGYATSSPFRAKAAYATSVEVTYVYVAPDAGGRGVGTLLYKA 110

Query: 110 LLKSMEAQGFKSVAVIGLPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRD 168
L +++ + A I PN+ S RLHE G+ GT R G K G + DV ++++D
Sbjct: 111 LFEALAGEDVHAYAGITQPNEASTRLHERFGFRYVGTYEVGRKFGRYWDVAWYEKDL 169

>ref|ZP_01721887.1| hypothetical protein BB14905_06898 [Bacillus sp. B14905]
 gb|EAZ87894.1| hypothetical protein BB14905_06898 [Bacillus sp. B14905]
 Length = 162

Score = 89.7 bits (221), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 53/152 (34%), Positives = 81/152 (53%), Gaps = 5/152 (3%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEGVVAGIAY 73
 D+ V +I N I TS +R E Q+ E W D + L + P V + G+VAG A
 Sbjct: 5 DIPEVLEIYNDIILTSKAVYRYEIQSLDEKKKWFSDQQALGN--PLFVYDDNGMVAGFAT 62

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133
 ++ Y +T+E +VYV H + G+ + L L++ + QG K++VA I N S
 Sbjct: 63 YSQFRPYPGYKYTMEHSVYVHKDHYQKGIATNLMLKLIKAKEQGVKTLVAGIDGENIGS 122

Query: 134 VRLHEALGYTARGTLRAAGYKHGGWHDVGFWQ 165
 ++ HE LG+ GT++ AGYK W D+ F+Q
 Sbjct: 123 IKAHEKLGFEYAGTIKNAGYKFEQWLDLVFYQ 154

>ref|YP_166358.1| phosphinothricin N-acetyltransferase, putative [Ruegeria pomeroyi
 DSS-3]
 gb|AAV94407.1| phosphinothricin N-acetyltransferase, putative [Ruegeria pomeroyi
 DSS-3]
 Length = 164

Score = 89.7 bits (221), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 57/163 (34%), Positives = 80/163 (49%), Gaps = 4/163 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEG 66
 ++IRPA A D A + I NHYI + V F TE + P+ D+ R P +LVAE G
 Sbjct: 1 MKIRPARALDAADIAGIANHYIRDTLVTFTTELRRPEAVAGDI---AARAPAYLVAEAAAG 57

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G A GP++A Y T E ++ + + G G L T L + A+G +VA I
 Sbjct: 58 AILGFATYGPFRAGPGYACTREHSILLDPGARGQGAGRALMTELERVARAEGVHVLVAGI 117

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDFE 169
 N +V H ALG+ G L G K G W D+ Q+ +
 Sbjct: 118 SGANPGAVAFHRALGFAEVGRLPQVGRKEGRWLDLVLQMOKILD 160

>dbj|BAI77990.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
 Length = 199

Score = 89.7 bits (221), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 56/159 (35%), Positives = 79/159 (49%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 +R A DM V I ++ +F EP + +E + E L P+ VAE G V
 Sbjct: 27 LRDARDDMPMVQAIYAEHVLEGISSFELEPPSLEEMLRRAEVLAKGLPYRVAERLGEV 86

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 G Y P++ R Y +TVE +VYV LG+G L L++ G++ ++AVIG
 Sbjct: 87 VGYGYVTPYRPRPGYRFTVEDSVYVRSMMGLGIGQALLAEVHCVCQGWQMIAVIGN 146

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 N S+RLHE LG+ G + G+KHG W D QR
 Sbjct: 147 SENTASIRLHERLGFHRVGVFESVGFKHGRWVDTVLMQR 185

>ref|ZP_08164878.1| putative phosphinothricin N-acetyltransferase [Eggerthella sp.
 HGA1]

gb|EGC88981.1| putative phosphinothricin N-acetyltransferase [Eggerthella sp.
HGA1]
Length = 213

Score = 89.7 bits (221), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 61/180 (33%), Positives = 86/180 (47%), Gaps = 5/180 (2%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL 60
SP +R A D A+ + Y+ET V F T + E+ + YP L
Sbjct: 3 FSPCATSANVRIAARGDAEAMRAVYAPYVETP-VTFDTVAPSRAEFAARMADAMVDYPCL 61

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
V E +G V G AYA +R AY W E +VY+ G G LY+ LL+ + AQG K
Sbjct: 62 VLEQDGRVVGFAAQAASRAAYRWNAELSVYLEQGATGGGRGRALYSALLELLRAQGVK 121

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF----ELPAPPRP 176
S ++ +PN+ S RLH G+ AG+K G WHDV ++ ++ + PA P P
Sbjct: 122 SAYGLVTVPNEASERLHAGCGFQRCWVQSHAGWKAGSWHDTVWYVKELAPFDDDDPADPVP 181

>ref|ZP_01915320.1| phosphinothricin N-acetyltransferase [Limnobacter sp. MED105]
gb|EDM83503.1| phosphinothricin N-acetyltransferase [Limnobacter sp. MED105]
Length = 182

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 56/160 (35%), Positives = 81/160 (50%), Gaps = 2/160 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY-PWLVAEVEGV 67
+IR AT ADM AV + HY+ F P T +E + + D + P+LVA ++ V
Sbjct: 10 DIRDATLADMPAVQALYAHYVLKELATFELVPPTHEEMCARRQAILDSHLPYLVAHIDDV 69

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
+ G AYA ++ R AY +TVE +VY+S H G+G+ L L++ E ++ +VAVI
Sbjct: 70 IVGYAYAVSYRPRPAYRYTVEDSVYLSPNHTGKGIGAAALLNELIRRCEQGPWRQMVAVIT 129

Query: 128 LPNDP-SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
S LH LG+ G + GYK W QR
Sbjct: 130 QGGTAGSAELHRKLGFGQEVGRMPNVGYKFNWVGTLIMQR 169

>ref|ZP_04060141.1| phosphinothricin acetyltransferase [Staphylococcus hominis SK119]
gb|EEK11640.1| phosphinothricin acetyltransferase [Staphylococcus hominis SK119]
Length = 168

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 49/163 (30%), Positives = 86/163 (52%), Gaps = 5/163 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66
IR A D+ + +I N I +T + PQ+ E W + ++ P V E++
Sbjct: 5 IREAERKDLDPDILNIYNDAILNTTAVYTYHPQSLNEREVWFE--TKVLANEPIFVFEIDH 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
VAG A G ++ AY +++E ++YV+ ++R G+ S L HL+ + + ++++VA I
Sbjct: 63 KVAGFATYGGFRHWPAYLYSIEHSIYVKNKYRRRGVASHLLEHLIDDAKHRQYRTIVAGI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
N+ S++LHE + GT+ GYK W D+ F+Q D +
Sbjct: 123 DTLNEASIKLHETFNFKHAGTIENVGYKFERWLDLAFYQYDLK 165

>ref|YP_004026569.1| GCN5-like N-acetyltransferase [Caldicellulosiruptor
kristjanssonii
177R1B]

gb|ADQ40956.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor
kristjanssonii 177R1B]
Length = 161

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 47/158 (29%), Positives = 80/158 (50%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR AT +D+ + I N+ + ST F P+T ++++ L+ ++Y VAE
Sbjct: 1 MNIRKATISDIPDLLYIYNYEVLNSTSTFDIHPKTTEDFLKLLDSHSNKYSIYVAEENST 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G Y P+ + AY TVE T+Y+ H+ G+G + LL+ + G +++A +
Sbjct: 61 ILGYGYLSPFSEKEAYSITVEDTIYIHPLHRGKGIGKQILKFLLEAKDTGAANIIAKVC 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
N S+ LH++ G+ G L G K G + DV Q
Sbjct: 121 AENYISLHLHKSFGFVEVGKLIKVGSKFGRFLDVIIILQ 158

>ref|NP_639084.1| phosphinothricin acetyltransferase [Xanthomonas campestris pv.
campestris str. ATCC 33913]
ref|YP_244869.1| phosphinothricin acetyltransferase [Xanthomonas campestris pv.
campestris str. 8004]
ref|YP_001905325.1| N-acetyltransferase [Xanthomonas campestris pv. campestris str.
B100]
gb|AAM42996.1| phosphinothricin acetyltransferase [Xanthomonas campestris pv.
campestris str. ATCC 33913]
gb|AA50849.1| phosphinothricin acetyltransferase [Xanthomonas campestris pv.
campestris str. 8004]
emb|CAP53287.1| N-acetyltransferase [Xanthomonas campestris pv. campestris]
Length = 173

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 53/158 (33%), Positives = 82/158 (51%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
A+ DI N I ST + P+ + Q +P + V + +G + G A G
Sbjct: 13 GAILDIFNDIAHSTALYDYRPRPAESMAGWFATKQAGGFPVIGVEDADGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRL 136
++A A+ ++VE ++YV H+ GLG TL L+ + +A+G +V I N S+ L
Sbjct: 73 FRAWPAFKYSVEHSIYVHRDHRGKGLGRITLLQLLIDAAQARGVHVLVGGIDASNAASIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQRFELPAPP 174
HE G+T GT+R AG+K G W D+ F+QR P+ P
Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILSTPSDP 170

>ref|YP_001796181.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
[Cupriavidus taiwanensis]
emb|CAP63987.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
[Cupriavidus taiwanensis LMG 19424]
Length = 179

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 59/176 (33%), Positives = 84/176 (47%), Gaps = 6/176 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVA-E 63
+ IR AT DM AVC I N +E +T + +W+ R + P LVA +
Sbjct: 5 ITIRDATPEDMEAVCAIYNDAVENTTAIWNEVLVDVANRLDWLS--ARRKAGLPVLVALD 62

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 123

GVV G A G W+A + Y TVE +VYV + G+ +L L++ G +V
 Sbjct: 63 ATGVVVGYSFGDWRAFDGYRHTVEHSVYVRTDQRGKGIAGSLMKALIERAGELGKHIIIV 122

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179

+ I N S+RLHE LG+ G ++ G K G W D+ F Q + + A P R
 Sbjct: 123 SAIEAGNASSIRLHEKLGFEQVGLMKEVGTKFGKWLDLVMQLNIDHRADPDGARK 178

>ref|ZP_03500072.1| GCN5-related N-acetyltransferase [Rhizobium etli Kim 5]
 Length = 159

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 57/158 (36%), Positives = 81/158 (51%), Gaps = 5/158 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR--TEPQTPQEWIDDLERLQDRYPWLVAE 63

V IR AT AD+ A+ +I NH +E +T + + + +EW+ R +P +VAE
 Sbjct: 4 TVLIRDATEADLPAIREIYNHAVEHTTAIWNETLVDLENRREWLR--ARKGRGFPVIVAE 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123

+ G VAG A G W+A + Y TVE +VYV + G+G TL L+ A ++
 Sbjct: 62 MSGKVAGYASYGDWRAFDGYRHTVEHSVYVDKDCRGAGIGETLMRELIARAAAGNVHVM 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

A I N S+RLHE LG+ G G K G W D+
 Sbjct: 122 AGIEAENTASIRLHEKLGFRAGRFSEVGTKFGRWLDL 159

>ref|YP_001695941.1| acetyltransferase yncA [Lysinibacillus sphaericus C3-41]
 gb|ACA37811.1| Hypothetical acetyltransferase yncA [Lysinibacillus sphaericus
 C3-41]
 Length = 165

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 55/162 (33%), Positives = 84/162 (51%), Gaps = 5/162 (3%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTEPQTPQE--WIDDLERLQDRYPWLVAEVEGVVAGIAY 73

D+ V +I N I TS +R E Q+ E W + + L + P LV + G+VAG A
 Sbjct: 5 DIPEVLEIYNDIILTSKAVYRYEIQSLDEKVKWFREQQALGN--PLLVFDDNGMVAGFAT 62

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133

++ Y +T+E +VYV H + G+ + L L++ + QG K++VA I N S
 Sbjct: 63 YSQFRPYPGYKYTMEHSVYVHKEHYQKGIATNLMLQLIEIAKEQGVKTLVAGIDGENIGS 122

Query: 134 VRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175

++ HE LG+ GT++ AGYK W D+ F+Q P R
 Sbjct: 123 IKAHEKLGFEYAGTIKNAGYKFEQWLDLVFYQLHLTGPIHKR 164

>ref|YP_003365800.1| putative acetyltransferase [Citrobacter rodentium ICC168]
 emb|CBG89001.1| putative acetyltransferase [Citrobacter rodentium ICC168]
 Length = 184

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 58/172 (33%), Positives = 86/172 (50%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-QDRYPWLVAEVEG 66

+ +R A D+ A+ + ++ +F P T +E + ++ Q PWLVA G
 Sbjct: 12 IVVRNALPGDVEAISALYAWHVLNGRASFEIIPPTVEEMRQMRKVAQYELPWLVALYRG 71

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

VV G YA ++ R AY +T+E ++YV G+GS L L+ E ++ +VAVI
 Sbjct: 72 VVVGICYATQYRPRPAYRYTLEESIYVDTSMGTGQIGISLLMHTLISRCEEGPWRQMVAVI 131

Query: 127 --GLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR-----DFELP 171
 G N S+RLH+ G+ G LR+ GYK G W D QR D+ LP
 Sbjct: 132 GDGYNNPGSLRLHKKHGFIEAGQLRSVGYKKGDWRDTLIMQRPLNEGDWTL 183

>gb|ABA47267.1| phosphinothricin N-acetyltransferase [*Pseudomonas cichorii*]
 Length = 199

Score = 89.4 bits (220), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 56/159 (35%), Positives = 80/159 (50%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 +R A DM AV I ++ +F EP + E + E L P+ VAE +G V
 Sbjct: 27 LRDARDDDDMPAVQAIYAEHVLEGISSFELEPPSLAEMLRRAEVLAKGLPYRVAEHQGEV 86

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127
 G Y P++ R Y +TVE +VYV LG+G L L++ G++ ++A+IG
 Sbjct: 87 VGYGYVTPYRPRPGYRFTVEDSVYVRSMMGLGIGQALLAGLVEHCVEGGWRQMIAIIGN 146

Query: 128 LPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+RLHE LG+ G + G+KHG W D QR
 Sbjct: 147 SENVASIRLHERLGFHRVGVFESVGFKHGRWVDTVLMQR 185

>ref|ZP_07289232.1| phosphorinothricin n-acetyltransferase [*Streptomyces* sp. C]
 gb|EFL17601.1| phosphorinothricin n-acetyltransferase [*Streptomyces* sp. C]
 Length = 165

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 54/173 (31%), Positives = 83/173 (47%), Gaps = 22/173 (12%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL----- 60
 +EIRP D+ + I NHY+ + + F EP TP + R PWL
 Sbjct: 3 MEIRPGVEDDLDELTRIYNHYVIETPITFDVEPFTPDQ-----RRPWLLAHPTSG 52

Query: 61 -----VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
 VAE G + G A + ++ + AY +VE++VY++ H G+G LYT L + +
 Sbjct: 53 PHRLLVAAEGGKLLGYATSSAFRPPKPAYATSVETSVYLAPEHVGRGIGGLLYTSLFEVLA 112

Query: 116 AQGFKSVAVAVIGLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDF 168
 + + +A I +PN S RLHE G+ G L G K + DV ++Q+
 Sbjct: 113 QEDVHTALAGIAMPNQASQRLHERFGFRQVGLLEQVGRKFDRFWDVAWFQKSL 165

>emb|CBL20923.1| Sortase and related acyltransferases [*Ruminococcus* sp. SR1/5]
 Length = 195

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 80/161 (49%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR A D A + +I ++Y+E + + F E + +E+ + ++ +YP++VAE +G
 Sbjct: 1 MQIRVAEEKDAATLLEIYSYVEKTAITFEYETPSIEEFTQRIHDIKVKYPYIVAEKE 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G AY + R AY W E +VYV H + G G LY L + G ++ A I
 Sbjct: 61 ILGYAYGSAFHPRAAYGWAEMS VYVHRDRSGAGGRLYRALESLLAEMGILNLNACIA 120

Query: 128 L-PND-----PSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 + P D SV H+ GY G GYK W+++
 Sbjct: 121 VAPKDDEYLTSASVDFHKHFGYKRVGEFHRGCGYKFNRWYNM 161

>ref|ZP_06758377.1| acetyltransferase, GNAT family [Veillonella sp. 6_1_27]
 ref|ZP_06759874.1| acetyltransferase, GNAT family [Veillonella sp. 3_1_44]
 gb|EFG22475.1| acetyltransferase, GNAT family [Veillonella sp. 3_1_44]
 gb|EFG24540.1| acetyltransferase, GNAT family [Veillonella sp. 6_1_27]
 Length = 166

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 50/153 (32%), Positives = 79/153 (51%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
 IRP T D+A DI N+ + EP T EW + E D + P +V ++G+V
 Sbjct: 6 IRPITKGDIAPCLDIYNYEVVNGVATLDLEPHTLSEWQEWHEHSHSDEHHPIVVGTIDGIV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVAVIG 127
 AG A P++ + AY TVE ++Y+ ++ G+ + L H+L+ + +VV+VI
 Sbjct: 66 AGYASLSPYRPKEAYKSTVELSIYIHQDYRGRGIATQLMAHILEIAKNDPLLHNVSIVIT 125

Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHD 160
 N+ S +LH G+T G G+KHG + D
 Sbjct: 126 AGNEGSTKLHARFGFTYCGLTPOVGFKHKGKYQD 158

>ref|YP_003741598.1| Phosphinothricin N-acetyltransferase [Erwinia billingiae Eb661]
 emb|CAX59751.1| Phosphinothricin N-acetyltransferase [Erwinia billingiae Eb661]
 Length = 174

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 54/160 (33%), Positives = 82/160 (51%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP-WLVAEVEG 66
 +EI A AA +A + I ++ F TEP T E + L ++Q+ WLVA E
 Sbjct: 1 MEIVTAQAAHVAGIQIYAWHVLNGLATFETEPPTADEMLARLAKVQESGGFWLVALEEH 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 V G Y P++ R AY +T+E ++Y+ G+G L L+ + GF+ V+ V+
 Sbjct: 61 RVVGYCYLAPYRPRYAYRFTLEDSIYLDPCAGRGIGRALLGEGLRQAQEAGFRQVMTVV 120

Query: 127 G-LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQW 165
 G N S+ LH +LG+ G L++ G+KHG W D Q
 Sbjct: 121 GSENVASLALHRSLSLGFELTGVLKSVGFKHGRWVDTVMMQ 160

>ref|YP_001525936.1| acetyltransferase [Azorhizobium caulinodans ORS 571]
 dbj|BAF89018.1| acetyltransferase [Azorhizobium caulinodans ORS 571]
 Length = 181

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 58/177 (32%), Positives = 83/177 (46%), Gaps = 8/177 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYI---ETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 + IRP D+ A+ I H+I E + EP ++ +L+ R P + A
 Sbjct: 7 IVIRPTRDEVDAMLAIYRHHIRRGVEEGVDDGSPEPDDLKDRRKNLK--NRRLPHIAAL 64

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
 G V G AY P++ R AY + V+ ++YV H H G+G L L+ + A GF+ ++
 Sbjct: 65 FNGEVVGYAYVVPFRKRPAYRYAVKHSIYVHHDHTGRGIGRDLMQGLVDACAAAGFRQMI 124

Query: 124 AVIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPA--PPRPVR 178
 I N S+ LHE G+T G L Y+ G W D QR L A PP P R
 Sbjct: 125 GYIDADNSASLTHERFGFTRVGILPGVAYRFRGWADTVMVQRAIGLGATTPPPPSR 181

>ref|ZP_06729691.1| phosphinothricin N-acetyltransferase [Xanthomonas fuscans subsp.

aurantifolii str. ICPB 10535]
gb|EFF49178.1| phosphinothricin N-acetyltransferase [Xanthomonas fuscans subsp.
aurantifolii str. ICPB 10535]
Length = 178

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 59/176 (33%), Positives = 84/176 (47%), Gaps = 4/176 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
P+E+R D+ A+ I I P + + YP+LVAE++G
Sbjct: 2 PLELRAVRNTDIPAITAIYAQQIAGVNTYIEYKAPSLDEMRAVSAIVDAGYPYLVAELDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VVAG AYA ++AR Y WTVE+++Y++ Q G+ L L+ E +GF+ ++AVI
Sbjct: 62 VVAGYAYASAFRARAGYRWTVENSIYLAAMQGRGI-EALLGELIAVCEQRFGRQMIAMI 120

Query: 127 GLPNDPSVR-LHEALGYTARGTLRAAGYKHGGWHDVGFWRDFEL--PAPPRPVRP 179
G + + R LHE G+ G G KHG W D QR APP P
Sbjct: 121 GDAGNLASRHLHEHFGFRTVGVFNGIGRKHGRWLDGMQMQRALGSGDTAPPSDENP 176

>ref|YP_002541986.1| phosphinothricin N-acetyltransferase (antibiotic resistance)
protein [Agrobacterium radiobacter K84]
gb|ACM30389.1| phosphinothricin N-acetyltransferase (antibiotic resistance)
protein [Agrobacterium radiobacter K84]
Length = 198

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 61/183 (33%), Positives = 91/183 (49%), Gaps = 7/183 (3%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPW 59
+S ER IR A+ DM A+ DI H++ F P + E L P+
Sbjct: 12 ISIERDRPAIRDASDGDMEAIRDIYTHHVLHGLATFEEVPPSADELRSRRASVLGVGLPY 71

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
LVAE+ G + G +YA ++ R AY +++E +VYV+ G+GS L L+ E +
Sbjct: 72 LVAELNGEIVGYSYATAYRPRPAYRFSIEDSVYVADGLGGRGVGSALLQELIARCEKGPW 131

Query: 120 KSVVAVIGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ-----DFELPAP 173
+ ++AVIG N S+ LH +G+ GT ++AG+K G W D QR D PA
Sbjct: 132 RQMLAVIGNSGNAGSLALHRRMGFQPIGTFKSAGFKLGRWVDTVLMQRALGEGDQTTPAQ 191

Query: 174 PRP 176
+P
Sbjct: 192 NKP 194

>ref|YP_252457.1| hypothetical protein SH0542 [Staphylococcus haemolyticus JCSC1435]
dbj|BAE03851.1| unnamed protein product [Staphylococcus haemolyticus JCSC1435]
Length = 164

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
Identities = 50/162 (30%), Positives = 81/162 (50%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
IR A D+ A+ I N I +T + + QT E W D + + P V E G
Sbjct: 2 IREAKIEDLPAILSIYNDAILHTTAVYTYDIQTLDERKAWFDMKNKANE--PIFVFEQAG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
G A G ++ AY +++E ++YV ++ G+ S L HL++ + ++++VA I
Sbjct: 60 KAVGFATYGGFRNWPAYLYSIEHSIYVDKSNRGKGIASQLLQHLIEDARTRNYRTIVAGI 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168

ND S++LHE + GT++ GYK W D+ F+Q D
 Sbjct: 120 DASNDSSIKLHEKFNFKHAGTIQNVGYKFDRWLDLAFYQYDL 161

>gb|EFV88451.1| acetyltransferase, GNAT family [Staphylococcus epidermidis FRI909]
 Length = 164

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 51/162 (31%), Positives = 84/162 (51%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A D+ + I N I +T + +PQ E W ++ + P V E EG
 Sbjct: 2 IRFARLEDLQDILTIYNDAILNTTAVYTYKPPQLDERIQWYQSKAKINE--PIWVYEKEG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A G ++ AY +T+E ++YV +++ LG+ S L +L+ + QG++++VA I
 Sbjct: 60 KVVGFATYGSFRQWPAYLYTIEHSIYVHQYRGLGIASQLLENLIHYAKEQGYRTIVAGI 119

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 N S+ LH+ ++ GT++ GYK W D+ F+Q D
 Sbjct: 120 DASNMDSIALHKKFDFSHAGTIKNGYKFNRLDLSFYQYDL 161

>ref|ZP_01694880.1| acetyltransferase, gnat family [Microscilla marina ATCC 23134]
 gb|EAY24149.1| acetyltransferase, gnat family [Microscilla marina ATCC 23134]
 Length = 163

Score = 89.0 bits (219), Expect = 2e-16, Method: Compositional matrix adjust.
 Identities = 52/162 (32%), Positives = 78/162 (48%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A D+ A+ +I N+ + S N T P T +E W ++ ++ P LV EV+G
 Sbjct: 2 IRLAKKEDLGAINIYNYEVAHSIYNVDTRPVTQEERLLWYEN--HPKNELPILVKEVKG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 A W Y T E ++V+ R GLG L +L++ E +KS+V+ I
 Sbjct: 60 ETIAWASLSQWTTGGYSKTAEVAIFVARNVHRQGLGKELLRLNIEKAETLEYKSLVSRI 119

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 N PS++LH+ G+ G +R K W DV WQ+D
 Sbjct: 120 VAGNTPSIKLHQLFGFKYVGMRRRIACKLDQWVDVQIWQKDL 161

>ref|ZP_08192665.1| GCN5-related N-acetyltransferase [Clostridium papyrosolvens DSM
 2782]
 gb|EGD47704.1| GCN5-related N-acetyltransferase [Clostridium papyrosolvens DSM
 2782]
 Length = 164

Score = 89.0 bits (219), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 49/159 (30%), Positives = 81/159 (50%), Gaps = 5/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A AD+ + DI N +E +T +F PQT ++ W + R+P +V
 Sbjct: 5 IREAIEADLPKITDIYNWAVENTTASFDINPQTIEQRAVWFVSHYK--GSRFPLIVFKNE 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VAG A ++A+ Y T E +VYV +Q++G+G L +++ G+ +++ I
 Sbjct: 63 EVAGYACLSQFRAKEGYRNTCEMSVYVHPEYQKMGIGKKLMDYVIALGREAGYHVIISCI 122

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 165
 N S+++HE G+ G L+ GYK G + D F+Q
 Sbjct: 123 TTDNIVSIKMHEDAGFKLCGELKEVGYKFGRYLDCLFYQ 161

>ref|YP_001980331.1| putative phosphinothricin N-acetyltransferase (antibiotic resistance) protein [Rhizobium etli CIAT 652]
 gb|ACE93153.1| putative phosphinothricin N-acetyltransferase (antibiotic resistance) protein [Rhizobium etli CIAT 652]
 Length = 185

Score = 89.0 bits (219), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 80/161 (49%), Gaps = 2/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-QDRYPWLVA-EVEGV 67
 +R A+ AD++A+ I + ++ P E + +YP++ A + +G
 Sbjct: 5 LRDASEADISAITGIYRDSVLNGVASYEITPPPEAEMAQRFTAIVGQQYPYIAAIDDDGS 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 G AYA ++ R AY W VE ++Y++ + G+G L + L+ A GF+ +VAVIG
 Sbjct: 65 FLGYAYASAFRTRPAYRWMVEDSIYLAPEARGQGIGKALMSELIDRCTALGFRQMVAVIG 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 + S+ LH G+ G ++ GYKHG W D QR
 Sbjct: 125 GASPASIALHLKAGFVEVGLMQGTGYKHGRWLDTMLMQRS 165

>ref|YP_003311091.1| GCN5-related N-acetyltransferase [Veillonella parvula DSM 2008]
 gb|ACZ23811.1| GCN5-related N-acetyltransferase [Veillonella parvula DSM 2008]
 Length = 166

Score = 89.0 bits (219), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 50/153 (32%), Positives = 80/153 (52%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
 IRP T D+A DI N+ + EP+T EW + E D + P +V ++G+V
 Sbjct: 6 IRPITRNDIAPCLDIYNYEVVNGVATLDLEPRTLSEWQEWYESHSDHEHPPIVVGITIDGIV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVAVIG 127
 AG A P++ + AY TVE ++Y+ ++ G+ + L H+L+ + +VV+VI
 Sbjct: 66 AGYASLSPYRPKEAYKSTVELSIYIHQDYRGRGIATQLMAHILEIAKNDPPLLHNVSIVIT 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 N+ S +LH G+T G G+KHG + D
 Sbjct: 126 AGNEGSTKLHARFGFTYCGLTQPQVGFKHGKYQD 158

>ref|ZP_08040600.1| phosphinothricin acetyltransferase [Streptococcus equinus ATCC 9812]
 gb|EFW89780.1| phosphinothricin acetyltransferase [Streptococcus equinus ATCC 9812]
 Length = 187

Score = 89.0 bits (219), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 82/161 (50%), Gaps = 7/161 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V +R A D + +I +Y+E + V F + + +E+ + + + YP+LVAE +
 Sbjct: 3 VTVRFAALEDAEKLLIYTYVEDTAVTFEYDVPSLEEFTERMRSIMTFYPYLVAEEDDK 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G AYA + R AY W+ E+TVY+ + G+G LYT L + ++ G ++ A I
 Sbjct: 63 ILGYAYASKFHPRAAYAWSAEATVYLDKNARGKGVGRQLYTCLEEYLYKQMGILNLNACIA 122

Query: 128 LPN-----DPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 + + S + H ALGY G +GYK W+D+

Sbjct: 123 STDVEDAYLTNGSEKFHRALGYQLVGKFHHSGYKFNRWYDM 163

>emb|CBK87248.1| Sortase and related acyltransferases [Enterobacter cloacae subsp. cloacae NCTC 9394]
Length = 184

Score = 89.0 bits (219), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 57/172 (33%), Positives = 85/172 (49%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
+E+R A D A+ I ++ +F P T E ++ + D PWLVA G
Sbjct: 12 IEVRDALPDDAHASAIYAWHVLHGRASFEEIPPTVDEMQRMSVTDGSLPWLVALYRG 71

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
+V G YA ++ R AY +T+E ++YV G GS L L+ E ++ ++AV+
Sbjct: 72 IVVGICYATFYRPRQAYRYTLEESIVDASTTGRGFGSALLQALIARCEQGPWRQMIADV 131

Query: 127 GLPNDP--SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR-----DFELP 171
G N+ S+RLH+ G+ G LR+ GYK G W D QR D+ LP
Sbjct: 132 GDGNNNAGSLRLHKKHGFVVGQLRSVGYKKGDWRDTLIMQRPLNDGDWTL 183

>ref|YP_003562993.1| GNAT family acetyltransferase [Bacillus megaterium QM B1551]
gb|ADE69559.1| acetyltransferase, GNAT family [Bacillus megaterium QM B1551]
Length = 163

Score = 89.0 bits (219), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 50/159 (31%), Positives = 80/159 (50%), Gaps = 4/159 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
IR A D+ + +I N ++TS F T ++ W D+ + +P +VAE +G
Sbjct: 3 IRYAKEEDLPLMVEIYNQSVQTSATFDLTTVTVEQRRSWFDN-HISNELFPLIVAEDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
VVAG A ++ + AY TVE ++Y+ Q G+G L +L+ + V++ I
Sbjct: 62 VVAGYASLSSYRDKEAYIQTVLSIYIDKNQQGHGIGKQLMKRILELAKELNHHVVISGI 121

Query: 127 GLPNDP--SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 165
ND SV++HE +T G + G+K W DV F+Q
Sbjct: 122 TKGNDISVKMHEQFNFTFCGEFKEVGWKFDQWQDVLFYQ 160

>pdb|3DR8|A Chain A, Structure Of Ynca, A Putative Acetyltransferase From
Salmonella Typhimurium With Its Cofactor Acetyl-CoA
pdb|3DR8|B Chain B, Structure Of Ynca, A Putative Acetyltransferase From
Salmonella Typhimurium With Its Cofactor Acetyl-CoA
pdb|3DR6|A Chain A, Structure Of Ynca, A Putative Acetyltransferase From
Salmonella Typhimurium
pdb|3DR6|B Chain B, Structure Of Ynca, A Putative Acetyltransferase From
Salmonella Typhimurium
pdb|3DR6|C Chain C, Structure Of Ynca, A Putative Acetyltransferase From
Salmonella Typhimurium
Length = 174

Score = 88.6 bits (218), Expect = 3e-16, Method: Compositional matrix adjust.
Identities = 62/168 (36%), Positives = 84/168 (50%), Gaps = 5/168 (2%)

Query: 10 IRPATAADMAAVCDIVNHYI-ETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR A AD AA+ +I NH + T+ + N RT + W + + L YP LV+E G
Sbjct: 6 IRFADKADCAAITEIYNHAVLHTAAIWNDRVTDTNRLAWYEARQLLG--YPVLVSEENG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126

VV G A G W++ + + +TVE +VYV HQ GLG L + L+ G VA I
 Sbjct: 64 VVTGYASFGDWRSFDGFRYTVVEHSVYVHPAHQKGKGLGRKLLSRLIDEARRCGKHVXVAGI 123

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N S+RLH +LG+T G K G W D+ F Q + A P

Sbjct: 124 ESQNAASIRLHHSLGFTVTAQXPQVGKFGRWLDLTFXQLQLDEHAAP 171

>ref|YP_001415549.1| GCN5-related N-acetyltransferase [Xanthobacter autotrophicus Py2]
 gb|ABS65892.1| GCN5-related N-acetyltransferase [Xanthobacter autotrophicus Py2]
 Length = 186

Score = 88.6 bits (218), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 57/170 (33%), Positives = 85/170 (50%), Gaps = 7/170 (4%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWDIDL-ERLQD---RYP 58
 + + V +RP+ AD+ A+ I H+I + TPQ DDL ER ++ R+P
 Sbjct: 3 QEQAVVVRPSREADVDAMLAIYRHHIRRGVEEGVDDGDTQP--DDLRERRKNLKSRRFP 60

Query: 59 WLVAEEGEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 LVA VV G AY ++ R AY ++V+ ++YV H H G+G L L+ + A G
 Sbjct: 61 HLVATRGEVVVGAYVVLFRKRPAYRYSVKHSIYVHHAHLGEGIGRHLMRGLIDACAAAG 120

Query: 119 FKSVAVAVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 F+ ++ I N S+ LHE G+ G L Y++G W D QR
 Sbjct: 121 FRQMIGYIDADNTASLTLEHKFGFVRVGHLPGVAYRYGRWSDSVMVQRSL 170

>ref|YP_003086840.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM
 18053]
 gb|ACT93675.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM 18053]
 Length = 167

Score = 88.6 bits (218), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 45/163 (27%), Positives = 83/163 (50%), Gaps = 5/163 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEEVG 66
 IR A D+ ++ DI+NH I +T + EP+T ++ W + + D P +VAE+EG
 Sbjct: 5 IRSAAPKDLPSLLDIINHAILNTTAIYDYEPRTLEQQKAWFEQM--FYDGMPPVIVAELEG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVAI 126
 V G ++ + Y ++VE ++Y+ + + +G+G L L++ + G +++ I
 Sbjct: 63 EVIGYGSYNIFRPKIGYKFSVEHSIYLDEKSRGMVGKLLGSLIQRAKESGLHTMIGCI 122

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N S+ H+ G+ +G L+ YK W D+ + Q E
 Sbjct: 123 DASNRASIEFHKKYGFVEKGYLKEVAYKFDQWLDLIYMQLLLE 165

>ref|YP_001901044.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12J]
 gb|ACD28612.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12J]
 Length = 171

Score = 88.6 bits (218), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 61/169 (36%), Positives = 84/169 (49%), Gaps = 5/169 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEEVG 66
 +R AT AD+ A+ I N I TS + P T ++ W+ R YP LVA+ +G
 Sbjct: 3 LRDATQADLPAILAIYNDVIATSNAIYTETPVTLEDRTAWL--ALRATQGYPPVLVADDDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVAI 126
 VAG+A G ++ + TVE +V++ + GLGS L L+ A G +V I
 Sbjct: 61 QVAGVASFGDFRPYPGFRFTTVEHSVHIHRDWRGKGLGSLLEALCERAAALGKHLMVGA I 120

Query: 127 GLPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175
 N S+RLHE LG+ G + A KHG W D+ F QR E P R
 Sbjct: 121 DGANAGSIRLHEKLGFKVGRMPEAAIKHGQWLDLVMQWLEAPGTVR 169

>ref|YP_001859565.1| GCN5-related N-acetyltransferase [Burkholderia phymatum STM815]
 gb|ACC72519.1| GCN5-related N-acetyltransferase [Burkholderia phymatum STM815]
 Length = 188

Score = 88.6 bits (218), Expect = 3e-16, Method: Compositional matrix adjust.
 Identities = 61/170 (35%), Positives = 90/170 (52%), Gaps = 9/170 (5%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER---LQDRY 57
 SP P+ IR AT AD A+ I H++ T +F +TP D L+R L
 Sbjct: 5 SPAAAPL-IRDATHADFHAIQAIYAHHVLTGVASFE---ETPPSADDLLQRRRAVLAHGL 60

Query: 58 PWLVAEVEGGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
 P++VA V+G VAG AYA ++ R AY +T+E ++Y+ + G+G L L++ E
 Sbjct: 61 PYIVAVVDGKVAGYAYATLYRPRVAYRYTIEDSIYMDDAFRGRGVGRALLAALIERCEQG 120

Query: 118 GFKSVVAVIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 ++ +VAVI S+ LH + G+ GTL+A G+K G W D QR
 Sbjct: 121 PWRQMVAVIADGGRGGSLSLHRSAGFELVGTCLKAVGFKQGRWLDSTLMQR 170

>ref|ZP_02831369.1| phosphinothricin acetyltransferase [Salmonella enterica subsp.
 enterica serovar Weltevreden str. HI_N05-537]
 gb|EDZ30579.1| phosphinothricin acetyltransferase [Salmonella enterica subsp.
 enterica serovar Weltevreden str. HI_N05-537]
 emb|CBY95697.1| putative acyltransferase [Salmonella enterica subsp. enterica
 serovar Weltevreden str. 2007-60-3289-1]
 Length = 171

Score = 88.6 bits (218), Expect = 4e-16, Method: Compositional matrix adjust.
 Identities = 61/170 (35%), Positives = 86/170 (50%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IR A AD AA+ +I NH + T+ + N RT + W + + L YP LV+E
 Sbjct: 1 MTIRFADKADCAAITEIYNHAVLHTAAIWNDRVTDTNRLAWYEQRLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 GVV G A G W++ + + +TVE +VYV H GLG L + L+ G +VA
 Sbjct: 59 NGVVTGYASFGDWRSDGFRYTVESVYVHPAHLGKGLGRKLLSRLIDEARRCGKHMVA 118

Query: 125 VIGLPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+RLH +LG+T + G K G W D+ F Q + A P
 Sbjct: 119 GIESQNAASIRLHSLGFTVTAQMPQGVKFGRWLDLTFMQLQLDEHAAP 168

>ref|NP_455906.1| acetyltransferase [Salmonella enterica subsp. enterica serovar
 Typhi str. CT18]
 ref|NP_805286.1| acetyltransferase [Salmonella enterica subsp. enterica serovar
 Typhi str. Ty2]
 ref|ZP_03346163.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. E00-7866]
 ref|ZP_03353682.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. E01-6750]
 ref|ZP_03358988.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. E02-1180]
 ref|ZP_03364644.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. E98-0664]
 ref|ZP_03370807.1| putative acetyltransferase [Salmonella enterica subsp. enterica

serovar Typhi str. E98-2068]
 ref|ZP_03380303.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. J185]
 ref|ZP_03382633.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. M223]
 ref|ZP_06544815.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. E98-3139]
 pir||AE0670 probable acetyltransferase (EC 2.3.1.-) [imported] - Salmonella
 enterica subsp. enterica serovar Typhi (strain CT18)
 emb|CAD01734.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi]
 gb|AA069135.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. Ty2]
 Length = 171

Score = 88.2 bits (217), Expect = 4e-16, Method: Compositional matrix adjust.
 Identities = 61/170 (35%), Positives = 86/170 (50%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IR A AD AA+ +I N + T+ + N RT + W + + L YP LV+E
 Sbjct: 1 MTIRFADKADCAAITEIYNRAVLHTAAIWNDRITVDTNRLAWYEARQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 GVV G A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA
 Sbjct: 59 NGVVTGYASFGDWRSFDGFRYTVEHSVYVHPAHQKGKGLGRKLLSRLIDEARRCGKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPP 174
 I N S+RLH +LG+T + G K G W D+ F Q + A P
 Sbjct: 119 GIESQNAASIRLHHSLGFTVTAQMPQVGKFGRWLDLTFMQLQLDEHAAP 168

>ref|YP_002974830.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv.
 trifolii WSM1325]
 gb|ACS55291.1| GCN5-related N-acetyltransferase [Rhizobium leguminosarum bv.
 trifolii WSM1325]
 Length = 183

Score = 88.2 bits (217), Expect = 4e-16, Method: Compositional matrix adjust.
 Identities = 56/158 (35%), Positives = 79/158 (50%), Gaps = 5/158 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 V +R AT AD++A+ DI NH +E +T + + + EW R +P +VAE
 Sbjct: 16 AVLRLDATEADLSAIRDIDYHNAVEHTTAIWNDRITVLDLENRLLEWFK--ARKARGFPVIVAE 73

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 123
 + G VAG A G W+A + Y TVE +VYV + G+G L L+ A ++
 Sbjct: 74 MSGKVAGYASYGDWRAFDGYRHTVEHSVYVDKDCRGGGIGERLMRELIVRAAAGNIHVMI 133

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 A I N S+RLHE LG+ G G K G W D+
 Sbjct: 134 AGIEAENTASIRLHEKLGFRFAGRFSEVGTFKFGRWLDL 171

>ref|ZP_03518748.1| probable phosphinothricin acetyltransferase (antibiotic
 resistance)
 protein [Rhizobium etli IE4771]
 Length = 171

Score = 88.2 bits (217), Expect = 4e-16, Method: Compositional matrix adjust.
 Identities = 56/158 (35%), Positives = 80/158 (50%), Gaps = 5/158 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAE 63
 V IR AT AD+ A+ +I NH +E +T + + + +EW+ R +P +VAE

Sbjct: 4 TVLIRDATEADLPAIREIYNHAVEHTTAIWNETLVDLENRREWLR--ARKGRGFPIIVAE 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + G VAG A G W+A + Y TVE +VYV + G+G TL L+ ++

Sbjct: 62 MSGKVAGYASYGDWRAFDGYRHTVEHSVYVDRDCRGAGIGETLMRELIARAATGNVHVMI 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 A I N S+RLHE LG+ G G K G W D+

Sbjct: 122 AGIEAENTASIRLHEKLGFRAGRFSEVGTKFGRWLDL 159

>ref|YP_003777936.1| sortase/acetyltransferase [Herbaspirillum seropedicae SmR1]
 gb|ADJ66028.1| sortase/acetyltransferase (antibiotic resistance) protein
 [Herbaspirillum seropedicae SmR1]
 Length = 173

Score = 88.2 bits (217), Expect = 4e-16, Method: Compositional matrix adjust.
 Identities = 57/161 (35%), Positives = 80/161 (49%), Gaps = 5/161 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEV 64
 ++IR A AD+A + I N + +T + + + ++W+ R Q YP LVA

Sbjct: 1 MQIRDAELADIAGITPIYNDAVANTTAIWNETLVDDRNRDNL--TARRQSGYPVLVAVA 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +G V G A G W+A + Y TVE +VYV H+ GLG L L+ A G +VA

Sbjct: 59 DGKVLGYASFQDWRAFDGYRHTVEHSVYVHKDHRGEGLGRALMEALIARARALGKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 I N S+ LH+ LG+ G L G K G W D+ F Q

Sbjct: 119 GIDASNSGSINLHKKLGFEQVGYLPQVGTKFGKWLDLAFLQ 159

>ref|ZP_02902668.1| acetyltransferase, GNAT family [Escherichia albertii TW07627]
 gb|EDS91912.1| acetyltransferase, GNAT family [Escherichia albertii TW07627]
 Length = 172

Score = 88.2 bits (217), Expect = 4e-16, Method: Compositional matrix adjust.
 Identities = 56/172 (32%), Positives = 83/172 (48%), Gaps = 1/172 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +G

Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNQTVADNRIDAWFEARTLSGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V+ G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I

Sbjct: 61 VITGYASFQDWRSFDGFRHTVEHSVYVHPDHQKGLGRKLLSRLIDEARGCGKHMVAVI 120

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N S+ LH++LG+ + G K G W D+ F Q + + P +R

Sbjct: 121 ESQNQASLHLHQSLGFVTTAQMPQVGTKFGRWLDLTFMQLQLDDRSEPDALR 172

>ref|YP_004002606.1| GCN5-like N-acetyltransferase [Caldicellulosiruptor owensensis
 OL]
 gb|ADQ04806.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor owensensis
 OL]
 Length = 161

Score = 88.2 bits (217), Expect = 4e-16, Method: Compositional matrix adjust.
 Identities = 46/158 (29%), Positives = 78/158 (49%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR AT +D+ + I N+ + ST F P+T ++++ + RYP AE

Sbjct: 1 MNIRKATISDIPHLLYIYNYEVLNSTSTFDIHPKTTEDFLKLFDSHSHRYPIYAAEENST 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G Y P+ + AY TVE T+Y+ ++ G+G + L+K + G +++A +

Sbjct: 61 ILGYGYLSPFSEKEAYSITVEDTIYIHPLYRGRGIGKQILKFLIKRAKDTGATNIIAKVC 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
N S+ LH++ G+ G L G K G + DV Q

Sbjct: 121 AENYISLHLHKSFGFVEVGKLTKVGSKFRFLDVIIQ 158

>ref|ZP_01619614.1| putative phosphinothricin N-acetyltransferase [Lyngbya sp. PCC 8106]
gb|EAW38582.1| putative phosphinothricin N-acetyltransferase [Lyngbya sp. PCC 8106]
Length = 168

Score = 88.2 bits (217), Expect = 4e-16, Method: Compositional matrix adjust.
Identities = 50/161 (31%), Positives = 88/161 (54%), Gaps = 5/161 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR----TEPQTPQEWIDDLERLQDRYPWLVAEVE 65
IR + +D+ + +I N+YI + + F T + +EW + RY VAEVE

Sbjct: 5 IRFSQPSDIFQLTEIYNYIILNTAITFDLKLFTVERRTEEWEFHYSS-TGRYQLFVAEVE 63

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G A + ++A+ AY+ ++E++VYV + + G+GS LY+ L +S++ + A

Sbjct: 64 GQVVGAYASSRFRKAAAYETSIETSVYVHPKTIKKIGISLLYSALFESLKTEDVHRAYAG 123

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
I LPN S+ +H+ G+ + G R G K + DV ++++

Sbjct: 124 ITLPNPASIAVHQKFGFQSVGVNREVGRKFDRYWDVEWFEK 164

>ref|ZP_05902359.1| phosphinothricin N-acetyltransferase [Leptotrichia hofstadii F0254]
gb|EEX73623.1| phosphinothricin N-acetyltransferase [Leptotrichia hofstadii F0254]
Length = 196

Score = 88.2 bits (217), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 50/184 (27%), Positives = 84/184 (45%), Gaps = 1/184 (0%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL 60
M ++ + R A D + I YIE +T+ F E +E+ + + YP++

Sbjct: 1 MELKKENLVFRFAAEEDAELKILKIYPYIENTTITFEYEVPAVEEFKVRIRETLEEYPYI 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
V E +AG AYA R AY W E +VY + G+G LY L++ ++ Q

Sbjct: 61 VCECGNEIAGYAYAHRIWTRAAYQWDAELSVYTDGKFAGNGIGKKLYKILIEILKLQIV 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELP-APPRPVRP 179
+V ++ PN+ S +LH + GYK G W V ++++ L P V+

Sbjct: 121 NVYGLVTYPNENSEKLHNYFEFKRVAFFEKTGYKFGQWIGVTWFEKAINLHFETPVSVKK 180

Query: 180 VTQI 183
+++I

Sbjct: 181 ISEI 184

>ref|YP_782081.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris BisA53]
gb|ABJ07101.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris BisA53]
Length = 180

Score = 87.8 bits (216), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 59/175 (33%), Positives = 85/175 (48%), Gaps = 7/175 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQD---RYPWLVA 62
V IRP+ AD+ + I HYI + TPQ DDL ER ++ R+P LVA
Sbjct: 7 VLIRPSRDADVEDMLAIYRHYIRRLDEGVDDSGTPQP--DDLRRERRKNLNRNRRPPLVA 64

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
G + G AY ++ R AY +TV+ ++YV H G+G L L+ + A GF+ +
Sbjct: 65 TRGGAILGYAYVVLFRKRPAYRFTVKHSIYVHPDHLGRGIGRLLMQELIDACAAAGFRQI 124

Query: 123 VAVIGLPNDPSVRLHEALGYTARGLTAAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
+ I N S+ LH+A ++ G L A Y+ G W D QR + PV
Sbjct: 125 IGYIDADNAASLALHQAADFISIVGRPLPAVAYRFRWSDSVMVQVRSGLGAGSTAPPV 179

>ref|YP_001515135.1| acetyltransferase, putative [Acaryochloris marina MBIC11017]
gb|ABW25821.1| acetyltransferase, putative [Acaryochloris marina MBIC11017]
Length = 175

Score = 87.8 bits (216), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 56/177 (31%), Positives = 83/177 (46%), Gaps = 9/177 (5%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRT---EPQTPQEWIDDLERLQDRYPWL 60
+ PV+IR +T+AD AA+ I N I T ++ F T E Q W++ + DR L
Sbjct: 3 DSEPQVIRASTADYAAIASIYNEAIATGTSITFDTRQFEASDIQAWVN--KFCDCRECLL 59

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
V E + V G + R Y E+++Y++ + GLG + T LL+ + G+
Sbjct: 60 VIERQQQVLGWGIVKQYSDRPGYRICCETSIYLTFAEKGQGLGKMMQTALLQKVVLGYH 119

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGLTAAAGYKHGGWHDVGFQWQDFELP-APPRP 176
VV I ND S+ H++ G+ G R G+ W DV Q LP PP P
Sbjct: 120 HVVVKIVATNDDSI AFHKSFGFEMGVQREVGHVADRWQDVAIMQ--LILPQVPPYP 174

>ref|ZP_08139853.1| GCN5-related N-acetyltransferase [Pseudomonas sp. TJI-51]
gb|EGB98871.1| GCN5-related N-acetyltransferase [Pseudomonas sp. TJI-51]
Length = 171

Score = 87.8 bits (216), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 58/169 (34%), Positives = 80/169 (47%), Gaps = 5/169 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVE 65
++R A AD+ + DI N + T+T + P Q W + R Q YP LVA +
Sbjct: 4 QLRDALPADVPGLDIYNDVVRTTTAIWNETPVDLANRQAWFE--ARTQQGYPIVAVDD 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
V G A G W+ + TVE +VY+ + GLG+ L L++ + G +VA
Sbjct: 62 TGVLYASFGDWRPFEGFRLTVEHSVYIRGDQRGKGLGAVLMAALIERAQCGKHVMVAA 121

Query: 126 IGLPNDPSVRLHEALGYTARGLTAAAGYKHGGWHDVGFQWQDFELPAPP 174
I N SVRLHE LG+ G + G K G W D+ F QR A P
Sbjct: 122 IESGNAASVRLHERLGFVVTGQMPQVGKFGRWLDLTFMQRVLNPGAEP 170

>ref|YP_002504394.1| GCN5-related N-acetyltransferase [Clostridium cellulolyticum H10]
gb|ACL74414.1| GCN5-related N-acetyltransferase [Clostridium cellulolyticum H10]
Length = 164

Score = 87.8 bits (216), Expect = 5e-16, Method: Compositional matrix adjust.
Identities = 49/159 (30%), Positives = 81/159 (50%), Gaps = 5/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A D+ + DI N I+ +T +F PQT ++ W DR+P +V +G
 Sbjct: 5 IREAIEEDLPKITDIYNWAIKNTTASFINDPQTIEQRAVWFVSHYG--GDRFPLIVYIEDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VAG A ++ + Y T E +VYV Q+ G+G L ++++ G+ ++++ I
 Sbjct: 63 EVAGYASLSEFRTKEGYKNTCELSVYVQPDFQKQKQIGKKLMDYIIQLGRDVGYNHNIISCI 122

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N S+++HE G+ G L+ GYK G + D F+Q
 Sbjct: 123 TTDNIISIQMHEKKGFKLCGELKEVGKFGRYLDCLFYQ 161

>ref|ZP_06274580.1| Phosphinothricin acetyltransferase [Streptomyces sp. ACTE]
 gb|EFB65124.1| Phosphinothricin acetyltransferase [Streptomyces sp. ACTE]
 Length = 200

Score = 87.8 bits (216), Expect = 6e-16, Method: Compositional matrix adjust.
 Identities = 54/184 (29%), Positives = 86/184 (46%), Gaps = 35/184 (19%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-- 65
 V+++P D+AA+ D+ NHY+ + + F T+ TP+E R PWL + E
 Sbjct: 8 VQVKPGVETDLAALTDLYNHVRETALTFDTAFTPEE-----RLPWLRSHPEDG 57

Query: 66 -----GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGL 102
 + G A + P++A+ AY +VE +VY + G+
 Sbjct: 58 PHRLLVAWEAAGGPDDGTDGAASRIVGYATSSPFRAKAAYRTSVEVSVYCAPEAVGRGI 117

Query: 103 GSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVG 162
 G+ LY L +++ + A I PN+PSVRLH A G+ GT G K G + DV
 Sbjct: 118 GTLLYQALFEALADEVDHAYAGIAQNPSPVRLHAAFGRHVGTAEVGRKFGRFWDVS 177

Query: 163 FWQR 166
 +++R
 Sbjct: 178 WYER 181

>ref|ZP_01064186.1| toxin resistance protein [Vibrio sp. MED222]
 ref|YP_002416894.1| putative acetyltransferase [Vibrio splendidus LGP32]
 gb|EAQ54443.1| toxin resistance protein [Vibrio sp. MED222]
 emb|CAV18422.1| putative acetyltransferase (Phosphinothricin-resistance protein)
 [Vibrio splendidus LGP32]
 Length = 168

Score = 87.8 bits (216), Expect = 6e-16, Method: Compositional matrix adjust.
 Identities = 48/154 (31%), Positives = 76/154 (49%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEV 64
 +EIR T D+A + DI N YIE + F E + Q+W Q +Y VA
 Sbjct: 1 MEIRVGTLPDIAGITDIFNFYIEHTNARFEEKLSLENRQQWFSSQFSS-QSKYQLYVATE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 + G A + ++ +A++ T E T+Y++ Q GLGS LY+ L S+ G V++
 Sbjct: 60 GDALLGFACSQQYRVMSAFEDTAEVTIYLA TEAQGKGLGSKLYSQLFASISDYGVHRVLS 119

Query: 125 VIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGW 158
 + LPN+ S+ LH+ G+ G K+G +
 Sbjct: 120 GVALPNEASIALHKRFGFREVGVFNEYAKKNGQY 153

>ref|ZP_07360833.1| acetyltransferase [Actinomyces viscosus C505]
 Length = 182

Score = 87.8 bits (216), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 60/170 (35%), Positives = 84/170 (49%), Gaps = 9/170 (5%)

```
Query: 6  RPVEIRPATAADMAAVCDIVNHYIETST---VNFRTPEQTPQEWIDDLERLQDRYPWLVA 62
          RP IRPAT +D A+ I N + S + + + W L + R LVA
Sbjct: 16 RPYRIRPATMSDSPAIRIRNTAVRESLAIWTSIEQDHAGAEAW---LAPMVQRTALVA 72

Query: 63 EVEGV---VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
          V G V G A AGPW + Y TVE ++Y+S Q GLG+ L L+++ G
Sbjct: 73 HVSQEPQDVVGFAVAGPWHSEYEGYARTVEDSIYLSPSAQKGLGARLLAALIEASRRAGD 132

Query: 120 KSVVAVIGLPLNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFE 169
          ++++A+I N SVRLHE G+T GT+ AG KHG D+ R +
Sbjct: 133 RTMIALIEAGNATSVRLHERYGFTTVGTVPQAGEKHGQILDLTLMRSRLQ 182
```

```
>ref|YP_003610973.1| putative acetyltransferase [Enterobacter cloacae subsp. cloacae
          ATCC 13047]
gb|ADF60024.1| putative acetyltransferase [Enterobacter cloacae subsp. cloacae
          ATCC 13047]
          Length = 176
```

Score = 87.8 bits (216), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 56/174 (32%), Positives = 86/174 (49%), Gaps = 7/174 (4%)

```
Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
          +EI A ++A+ I ++ T F TEP E + + PW VA G
Sbjct: 1  MEITEADERHISAIQIYAWHVLHGTATFETEPDVAEMTARQKNHAAGLPWFVATENG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          V G Y ++ R AY +T+E +VY++ Q G+G+ L + ++ E GF+ ++AV+
Sbjct: 61 EVLGICYLSLYRERCAYRFTLEDSVYIAPAFQGRGIGTLLLSRVVAAEEHGFRLIAVV 120

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDR----DFELPAPP 174
          G N S+ LH + G+ GTL++ G+KHG W D QR D LP P
Sbjct: 121 GNSENIASLSLHRSAGFRHTGTLKSVGFKHGRWLDTVILQRTLGAAGDVTLPDIP 174
```

```
>ref|ZP_03527994.1| GCN5-related N-acetyltransferase [Rhizobium etli CIAT 894]
          Length = 170
```

Score = 87.8 bits (216), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 48/150 (32%), Positives = 76/150 (50%), Gaps = 2/150 (1%)

```
Query: 21 VCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA-EVEGVVAGIAYAGPWK 78
          + DI + T ++ P + E + + YP++ A + +G + G AYA ++
Sbjct: 1 ITDIYRESVLNGTSSYEIMPPSEAEMAQRFAAIVGQHYPYISAVDADGTLGAYASAFR 60

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPLNDPSVRLHE 138
          R AY W VE ++Y++ + G+G L + L+ S GF+ +VAVIG + S+ LH
Sbjct: 61 TRPAYRWMVEDSIYLAPEARGRGIGKALMSELIDSCTGLGFRQMVAVIGGASPASIALHL 120

Query: 139 ALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
          G+ G +R AGYKHG W D QR
Sbjct: 121 KAGFVEVGLMRGAGYKHGRWLDTPMQRTL 150
```

```
>dbj|BAG06876.1| phosphinothricin acetyltransferase [Nocardia sp. AB2253]
          Length = 177
```

Score = 87.8 bits (216), Expect = 6e-16, Method: Compositional matrix adjust.
Identities = 55/162 (33%), Positives = 83/162 (51%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 +R A +D+ + I N+ I +T + TE E W R +P L+AE+ G
 Sbjct: 10 VRDARESDLPEILVIHNNAIAETTAIWDELADIHEREAWF--AARTGAGHPVLIAEIHG 67

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 VAG A G ++ ++ Y ++VE++VYVS R G+ + L LL+ E G +++A I
 Sbjct: 68 KVAGYASYGQFRPKSGYRFSVENSVMYSDIFHRRGVATALMRALLERAHEHGGVHAMIAAI 127

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 N S+ LHE G+T G L G+K G W D+ QR F
 Sbjct: 128 ESSNRTSIGLHEKFGFTTVGQLPEVGFKFGRWMDLTLMQRTF 169

>ref|ZP_06743498.1| acetyltransferase, GNAT family [Bacteroides vulgatus PC510]
 gb|EFG16688.1| acetyltransferase, GNAT family [Bacteroides vulgatus PC510]
 Length = 161

Score = 87.8 bits (216), Expect = 6e-16, Method: Compositional matrix adjust.
 Identities = 52/161 (32%), Positives = 79/161 (49%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR D A+ I Y+ S F TEP ++ + + + R+P+ V E EG V
 Sbjct: 2 IRRVELQDAKAITTIYYEYVGHVSATFETEPLEEDMRNRIAGIAVRFPYFVYEEEGKV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G YA WK R AY T+E+TVY++ ++ G+G L L++ G++++A +
 Sbjct: 62 GYCYAHLWKERAAYRHTLETTVYLAPGYEGKGIGRELMEERLIEECRRDGYRALIACVTEG 121

Query: 130 NDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170
 N S LH LG+ + G K G W DV D+EL
 Sbjct: 122 NVVSDALHLRLGFKKVSHPKVKGLKFGRWLDV---VDYEL 158

>ref|ZP_04798151.1| possible Phosphinothricin acetyltransferase [Staphylococcus
 epidermidis W23144]
 gb|EES35117.1| possible Phosphinothricin acetyltransferase [Staphylococcus
 epidermidis W23144]
 Length = 164

Score = 87.4 bits (215), Expect = 7e-16, Method: Compositional matrix adjust.
 Identities = 50/162 (30%), Positives = 84/162 (51%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A D+ + I N I +T + +PQ E W ++ + P V E +G
 Sbjct: 2 IRFARLEDLQDILTIYNDAILNTTAVYTYKPKQLDERLQWYQSKAKINE--PIWVYEKKG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 V G A G ++ AY +T+E ++YV +++ LG+ S L +L+ + QG++++VA I
 Sbjct: 60 KVVGFATYGSFRQWPAYLYTIEHSIYVHQYRGLGIASQLLENLIHYAKEQGYRTIVAGI 119

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 N S+ LH+ ++ GT++ GYK W D+ F+Q D
 Sbjct: 120 DASNMDSIALHKKFDFSHAGTIKNVGYKFNRLDLDFYQYDL 161

>ref|NP_885641.1| hypothetical protein BPP3481 [Bordetella parapertussis 12822]
 emb|CAE38765.1| conserved hypothetical protein [Bordetella parapertussis]
 Length = 184

Score = 87.4 bits (215), Expect = 7e-16, Method: Compositional matrix adjust.
 Identities = 59/163 (36%), Positives = 84/163 (51%), Gaps = 8/163 (4%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQ---TPQEWIDDLERLQDRYPWLVAE-VEGVVAGIAYA 74
 AA+ DI N I TST + +P+ + + W L + Q +P + E GV+ G A
 Sbjct: 24 AAILDIFNDAILTSTALYDYQPRALASMEAWF--LAKRQGGFPVVGFEAAGVLMGFASY 81

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 134
 G ++A AY ++VE +VYV R++ GLG L L++ Q +V I N SV
 Sbjct: 82 GTFRAWPAYKYSVEHSVYVDRRYRGRGLGEALLRALIERARLQQVHVLVGGIDATNAGSV 141

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRPV 177
 LH LG+ GT+ AG+K G W D+ F+Q L P RPV
 Sbjct: 142 ALHRKLGfVHAGTITQAGFKFGRWLDLAFYQ--LTLDTPLRPV 182

>ref|ZP_03928954.1| acyltransferase [Acidaminococcus sp. D21]
 gb|EEH90184.1| acyltransferase [Acidaminococcus sp. D21]
 Length = 199

Score = 87.4 bits (215), Expect = 7e-16, Method: Compositional matrix adjust.
 Identities = 52/165 (31%), Positives = 82/165 (49%), Gaps = 10/165 (6%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 P+ IRPA+ D A + I YI+ + + F + +E+ + + +YP+LV E
 Sbjct: 9 PLVIRPASDDAALLRLIYAPYIQTETAITFEKTVPSLKEFRERIVHTLQQYPYLVCEENQ 68

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G AY + R+AY E+++YV + G+G LY L KS ++ G ++ A I
 Sbjct: 69 EVVGAYYLSAFNPRSAYRHAETSIIYVKKNMRHHGVGKALYQALEKSAQSMGILNLNACI 128

Query: 127 GLPN-----DPSVRL-----HEALGYTARGTLRAAGYKHGGWHDV 161
 P+ DP + L HE LGYT G G+K G ++D+
 Sbjct: 129 AYPSENEKADPFLSLDSPHFHEHLYTVVGRFHQCGFKFGRYYDM 173

>ref|ZP_05968426.2| toxin-antitoxin system, toxin component, GNAT family
 [Enterobacter
 cancerogenus ATCC 35316]
 gb|EFC55914.1| toxin-antitoxin system, toxin component, GNAT family [Enterobacter
 cancerogenus ATCC 35316]
 Length = 191

Score = 87.4 bits (215), Expect = 8e-16, Method: Compositional matrix adjust.
 Identities = 56/172 (32%), Positives = 85/172 (49%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 V++R A D A+ I ++ +F P T E ++ + D+ PWLV G
 Sbjct: 19 VDVRDALPDDAHAISAIYAWHVLHGRASFEEVPPTVDEMQRMQNVADKGLPWLVLVLYRG 78

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 +V G YA ++ R AY +T+E ++YV G GS L L+ E ++ ++AV+
 Sbjct: 79 IVVGICYATYYRPRPAYRFTLEESIYVDASTTGRGFGSALMDALIARCEKGPWRQMIADV 138

Query: 127 GLPNDP--SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ----DFELP 171
 G N+ S+RLH+ G+ G LR+ GYK G W D QR D+ LP
 Sbjct: 139 GDGNNNAGSLRLHKKHGFVVGQLRSVGYKKGDWRDTLIMQRPLNDGDWTLIP 190

>ref|ZP_05036885.1| acetyltransferase, GNAT family [Synechococcus sp. PCC 7335]
 gb|EDX85620.1| acetyltransferase, GNAT family [Synechococcus sp. PCC 7335]
 Length = 169

Score = 87.4 bits (215), Expect = 8e-16, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 83/161 (51%), Gaps = 5/161 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQT---PQEWIDDLERLQDRYPWLVAEVE 65
 IR +D+ A+ I N YIE +T+ F P T + W+ R+ LVAE +
 Sbjct: 5 IRNFHPSDIEALVHIYNRYIEETTITFDITPHTIEYRREHWM SHYH-ASGRHRL LVAECD 63

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VAV 125
 V G A + ++ + AYD +VE+++Y+ + G+G+ LYT L ++ + A
 Sbjct: 64 RKVVG YASSQFRTKAAYDTSVETSIYLDMSFRAKGIGTQLYTALFGALAKEDVHRAYAG 123

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 I LPND S+ +H+ G+ G + G K G + DV ++++
 Sbjct: 124 ITLPNDV SIGIHQKFGFEQVGLFKEVGRKFGKYWDVAWFEK 164

>ref|ZP_08034621.1| toxin-antitoxin system, toxin component, GNAT domain protein
 [Actinomyces sp. oral taxon 171 str. F0337]
 gb|EFW26116.1| toxin-antitoxin system, toxin component, GNAT domain protein
 [Actinomyces sp. oral taxon 171 str. F0337]
 Length = 430

Score = 87.0 bits (214), Expect = 9e-16, Method: Compositional matrix adjust.
 Identities = 60/166 (36%), Positives = 83/166 (50%), Gaps = 3/166 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV- 67
 +IRPAT D A+ I N + S + + Q P L + R LVA V G
 Sbjct: 20 QIRPATMEDSPAIRQIRNAAVRESLAIWTSIEQDPARAETWLAPMVQRTALVAHVSGKP 79

Query: 68 --VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VAV 125
 V G A AGPW + Y TVE ++Y+S Q GLG+ L T L+++ G ++++A+
 Sbjct: 80 HDVIGFAVAGPWHSYEGYTRTVEDSIIYLSPTAQGKGLGARLLTALIEASRQAGDRTMIAL 139

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELP 171
 I N SV LHE G+T GT+ AG KHG D+ R + P
 Sbjct: 140 IEASNATSVHLHERYGFTTVGTVPQAGEKHGQILDLTLSRCLKGP 185

>ref|YP_003638540.1| Phosphinothricin acetyltransferase [Cellulomonas flavigena DSM
 20109]
 gb|ADG76341.1| Phosphinothricin acetyltransferase [Cellulomonas flavigena DSM
 20109]
 Length = 193

Score = 87.0 bits (214), Expect = 9e-16, Method: Compositional matrix adjust.
 Identities = 69/174 (39%), Positives = 92/174 (52%), Gaps = 6/174 (3%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 ++P PV +R AT AD AA + Y+ +TV+F EP T + D + + WL
 Sbjct: 6 LTPADLPVRVRDATVADAAACAAVYAPYVRD TTVSFEAEPPTTAQMADRITASLATHAWL 65

Query: 61 VAEV-----EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 VAE+ G V G AYA P+ AR AY W ++VY+ +R G G LYT LL+ +
 Sbjct: 66 VAE LPTGSPGAGRVVGYAYAAPYAARAAYRWACGTSVYLEPGRRTGAGRALYTALLERL 125

Query: 115 EAQGFKS VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 A G++ VA PN S LH +LG+ GTLR G+KHG W DV QR
 Sbjct: 126 AALGYRQAVAGYTEPNPASAGLHASLGFVVGTLRGVGHKGAWRDVTLVQRPL 179

>ref|YP_001235019.1| GCN5-related N-acetyltransferase [Acidiphilium cryptum JF-5]
 ref|YP_004284371.1| putative acetyltransferase [Acidiphilium multivorum AIU301]
 gb|ABQ31100.1| GCN5-related N-acetyltransferase [Acidiphilium cryptum JF-5]
 dbj|BAJ81489.1| putative acetyltransferase [Acidiphilium multivorum AIU301]
 Length = 167

Score = 87.0 bits (214), Expect = 9e-16, Method: Compositional matrix adjust.
Identities = 59/168 (35%), Positives = 83/168 (49%), Gaps = 16/168 (9%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-----PW 59
          ++IRPA  D+ A  I  H++  T  F  P  +          LE L  R+          W
Sbjct: 1   MDIRPAAPEDLPACQAIYAHHVLEGTGTTFDEVPPS-----LEALTARFREVTGAGRAW 53

Query: 60  LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
          +VA      + G AY  ++AR+AY +T E +VYV      +  G+G  L  LL  A GF
Sbjct: 54  VVAADATGILGFAYFDQYRARSAYRFTAEDSVYVREDVRGQGVGKALVARLLDEARAAGF 113

Query: 120  KSVVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
          + ++AVIG  N  S+ +H +LG+  GTLR  G+K G W DV  QR
Sbjct: 114  REMLAVIGDSENVGSIGVHASLGFQRVGTLRDVGFKFGRWIDVVIMQR 161
```

>ref|ZP_02382636.1| putative antibiotic resistance (acetyltransferase) protein
[Burkholderia ubonensis Bu]
Length = 182

Score = 87.0 bits (214), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 62/182 (34%), Positives = 88/182 (48%), Gaps = 9/182 (4%)

```
Query: 1   MSPERRPVEIR---PATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQ 54
          MSP  ++R  + A  AA+ DI+N  I  ST  +  P+PQ  W  +R
Sbjct: 1   MSPTEHHDDVRFVDCSEAEHAAAILDILNEAIVNSTALYDYAPRPPQAMATWFA-TKRAG 59

Query: 55  DRYPWLVA-EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
          D +P + A +  G + G A  G ++A  AY +TVE +VYV H  +  GLG  L  L++
Sbjct: 60  D-FPVVGAIDASGRLLGFASWGTFRAFPAKYTVEHSVYVHHEQGRGLGERLLRELVR 118

Query: 114  MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAP 173
          +V  I  N  S+RLH  LG+T  GTL  G+K G W D  F+Q  + P
Sbjct: 119  ARDAQVHVLVGCIDASNAGSIRLHTRLGFTHAGTLAQVGFKFGRWLDAAFYQLTLDTPDQ 178

Query: 174  PR 175
          P+
Sbjct: 179  PQ 180
```

>ref|YP_987554.1| GCN5-related N-acetyltransferase [Acidovorax sp. JS42]
gb|ABM43478.1| GCN5-related N-acetyltransferase [Acidovorax sp. JS42]
Length = 173

Score = 87.0 bits (214), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 53/159 (33%), Positives = 82/159 (51%), Gaps = 2/159 (1%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
          IR +  D+AA+  I  H++  T  F  +P T  +          + L  P+LVAE  G V
Sbjct: 4   IRASRDEDVAAITAIYTHHVLHGTGTTFEIDPPTALDMAARRADVLAKGLPYLVAAEEAGQV 63

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
          G AY  +K R AY ++ E ++Y++  +  GLG  L  L  EA G + ++AVIG
Sbjct: 64  LGFAYCNWFKPRPAYRFSIEDSIYIADAARGRLGRQLLEALAVQAEAGVRKLLAVIGD 123

Query: 128  LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
          N  S+ +H A G+T  G +R+ G+K G W D+  ++
Sbjct: 124  SANAGSIGVHRAAGFTDVGVMRSGWKFGAWRDIVLMEK 162
```

>ref|ZP_03699912.1| GCN5-related N-acetyltransferase [Lutella nitroferum 2002]
gb|EEG07215.1| GCN5-related N-acetyltransferase [Lutella nitroferum 2002]
Length = 170

Score = 87.0 bits (214), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 62/171 (36%), Positives = 84/171 (49%), Gaps = 5/171 (2%)

```
Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEV 64
      + IR A AD+ + I N I TST + P T +E W + R YP LVAE
Sbjct: 1  MHIRDARLADLPILAIYNDVIATSTAVYCDLPSTLEERQAWFEG--RRAQGYPVLVAEY 58

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
      V G A G ++A + +TVE +V++ H+ G+G L LL A G +V
Sbjct: 59  GDEVVGFAFGDFRAFPGFRTVEHSVHIHRDHRGRGIGEHLALLPRALALGKHMVG 118

Query: 125  VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175
      + N+ SVR HE LG+T G + GYK G W D+ F QR + P PR
Sbjct: 119  GVDAANEGSVRFHERLGFTQVGHMPQVGKFGRWLDLVFLQRYLDAPDSR 169
```

>ref|ZP_07675196.1| toxin-antitoxin system, toxin component, GNAT family [Ralstonia sp.

5_7_47FAA]

gb|EFP66423.1| toxin-antitoxin system, toxin component, GNAT family [Ralstonia sp.

5_7_47FAA]

Length = 171

Score = 87.0 bits (214), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 60/169 (35%), Positives = 83/169 (49%), Gaps = 5/169 (2%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66
      +R AT AD+ A+ I N I S + P T ++ W+ R YP LVA+ +G
Sbjct: 3  LRDATQADLPAILAIYNDVIANSNAIYETPTVLTEDRTTWL--ALRATQGYPVLVADDDG 60

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 126
      VAG+A G ++ + TVE +V++ + GLGS L L + A G +V I
Sbjct: 61  QVAGVASFGDFRPYPGFRTTVEHSVHIHRDWRGKGLGSRLVEALCERAAALGKHLMVGA 120

Query: 127  GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175
      N S+RLHE LG+ G + A KHG W D+ F QR E P R
Sbjct: 121  DGANAGSIRLHEKLGFKFVGRMPEAAIKHGQWLDLVFMQRWLEAPGTVR 169
```

>ref|YP_003470746.1| Phosphinothricin N-acetyltransferase [Staphylococcus lugdunensis HKU09-01]

gb|ADC86619.1| Phosphinothricin N-acetyltransferase [Staphylococcus lugdunensis HKU09-01]

Length = 164

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
Identities = 52/160 (32%), Positives = 85/160 (53%), Gaps = 1/160 (0%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
      IR A D+ A+ I N I +T + E QT +E + ER + P LV E V
Sbjct: 2  IRHAERQDLPAILSIYNDAIINTTAVYSYESQTIEEREEREFERKVIAGEPILVFEQHQQV 61

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 128
      G A G ++ AY +++E ++YV ++ G+ S L + L++ + +G+++VA I
Sbjct: 62  VGFATYGSFRDWPAYLYSIEHSIYVDSAYRGHGSIASQLLSQLMQIAKDEGYRTMVAGIDA 121

Query: 129  PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
      N+ S+ LHE +G+ GT+ GYK W D+ F+Q D
Sbjct: 122  SNEVSIHLHEKIGFIHAGTINNVGYKFNRWLDLAFYQIDL 161
```

>ref|YP_766974.1| phosphinothricin N-acetyltransferase [Rhizobium leguminosarum bv.

viciae 3841]
 emb|CAK06865.1| putative phosphinothricin N-acetyltransferase [Rhizobium
 leguminosarum bv. viciae 3841]
 Length = 183

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 57/166 (34%), Positives = 77/166 (46%), Gaps = 21/166 (12%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPW----- 59
 V +R AT AD++A+ DI NH +E T W D L L++R W
 Sbjct: 16 AVLLRDATEADLSAIRDIYNHAVE-----HTTAIWNDTLVDLENRLWFRARKAR 65

Query: 60 ----LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
 +VAE+ G VAG A G W+ + Y TVE +VYV + G+G L L+
 Sbjct: 66 GFPVIVAEMSGKVAGYASYGDWRPFDGYRHTVEHSVYVDKDCRGAGIGERLMRELIARAA 125

Query: 116 AQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 A ++A I N S+RLHE LG+ G G K G W D+
 Sbjct: 126 AGNIHVMIAGIEAENTASIRLHEKLGFRLAGRFSEVGTKFGRWLDL 171

>ref|YP_001710475.1| putative acetyltransferase [Clavibacter michiganensis subsp.
 sepedonicus]
 emb|CAQ01871.1| putative acetyltransferase [Clavibacter michiganensis subsp.
 sepedonicus]
 Length = 194

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 56/152 (36%), Positives = 76/152 (50%), Gaps = 5/152 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEV 64
 + IRPA D+ + +I NH I T T + EP E W + D P LVAEV
 Sbjct: 17 MRIRPAEPRDIDDLLEIRNHAILTGTALWTEEPVDRAEREAWFRETTEAGD--PILVAEV 74

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +G AG GPW+ + Y ++VE +VYV Q G+G L ++ A G ++V A
 Sbjct: 75 DGAFAGYGTYPWRMSGYRFSVEDSVYVRDGFQGRGIGRALVEAVVAHARAAGKRAVFA 134

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHG 156
 I N S+RLHE LG+ G L G+K G
 Sbjct: 135 DIEAGNTGSIRLHERLGRQVGLLPGIGWKFG 166

>ref|ZP_07912391.1| acetyltransferase [Staphylococcus lugdunensis M23590]
 gb|EFU83597.1| acetyltransferase [Staphylococcus lugdunensis M23590]
 Length = 164

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 52/160 (32%), Positives = 85/160 (53%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
 IR A D+ A+ I N I +T + E QT +E + ER + P LV E V
 Sbjct: 2 IRHAERQDLPAILSIYNDAIINTTAVYSYESQTIEEREWFERKVIAGEPILVFEQHQVQV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A G ++ AY +++E ++YV ++ G+ S L + L++ + +G++++VA I
 Sbjct: 62 VGFATYGSFRDWPAYLYSIEHSIYVDSAYRGHGSIQLLSQLMQIAKDEGYRTMVAGIDA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF 168
 N+ S+ LHE +G+ GT+ GYK W D+ F+Q D
 Sbjct: 122 SNEVSIHLHEKIGFIHAGTINNVGYKFNRLDLAFYQIDL 161

>ref|ZP_06690604.1| conserved hypothetical protein [Acinetobacter sp. SH024]
 gb|EFF87236.1| conserved hypothetical protein [Acinetobacter sp. SH024]
 Length = 181

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 50/178 (28%), Positives = 86/178 (48%), Gaps = 8/178 (4%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWDLLERLQDRY 57
 ++P R ++ AT A A+ DI+N I ST + P++ + W + ++ +
 Sbjct: 5 LNPRLRLIDCHEATHAK--AILDILNEAIINSTALYDYLPRSEDSMKNWFG--VKRENGF 60

Query: 58 PWL-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
 P + + + + G A G ++A AY +TVE ++Y+ H H+ GL L L+K +
 Sbjct: 61 PVIGIVDETNNKLLGFASWGTFRAFPAKYTVEHSIYIHHEHRGGGLSKILMQELIKRAQE 120

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 ++ I N S+ LHE +G+ GT + G+K G W D F+Q + P P
 Sbjct: 121 ADLHVLIGCIDATNQASIGLHEKMGFIHAGTFKQVGFKGQWLDAAFYQLNLNTPHTP 178

>ref|ZP_03523576.1| probable phosphinothricin acetyltransferase (antibiotic resistance)

protein [Rhizobium etli GR56]
 Length = 171

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 59/171 (34%), Positives = 85/171 (49%), Gaps = 7/171 (4%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWDLLERLQDRYPWLVAE 63
 V +R AT AD+ A+ +I NH +E +T + + + +EW++ R +P +VAE
 Sbjct: 4 AVLLRDATEADLLAIREIYNHAVEHTTAIWNETLVDLENRREWLN--ARKARGFPVIVAE 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + G VAG A G W+A Y TVE +VYV + G+G L L+ A ++
 Sbjct: 62 MSGKVAGYASYGDWRAFEGRYRHTVEHSVYVDKDCRGAGIGEALMRALIARAAAADIHVMI 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 A I N S+RLHE LG+ G G K G W D+ + LPA P
 Sbjct: 122 AGIEAENAASIRLHEKLGFRAGRFEVGTGFRWLDLTCME--LRLPAKP 170

>ref|YP_199234.1| phosphinothricin acetyltransferase [Xanthomonas oryzae pv. oryzae KACC10331]
 gb|AAW73849.1| phosphinothricin acetyltransferase [Xanthomonas oryzae pv. oryzae KACC10331]
 Length = 201

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 58/171 (33%), Positives = 89/171 (52%), Gaps = 3/171 (1%)

Query: 7 PVEIRPATAADMA-AVCDIVNHYIETSTVNFRTEPQTPQEWDLLERLQ-DRYPWL-VAE 63
 P+ I + A A A+ DI N I TS + P+ P+ + Q +P + V +
 Sbjct: 28 PMHIVDCSQARHASAILDIFNEAIATSNALYDYRPRPPESMVGWGFATKQAGGFVIGVED 87

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 +G + G A G ++A A+ ++VE ++YV H+ GLG L L+ + +A+G +V
 Sbjct: 88 ADGTLMGFASYGTFRAPAFKYSVEHSIYVHCDHRGKGLGRLLQLALIAAAQARGVHVILV 147

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+ LHE G+T GT+R AG+K G W D+ F+QR PA P
 Sbjct: 148 GGIDASNQASIALHEQFGFTHAGTVREAGFKFGRWLDLAFYQRILATPADP 198

>ref|YP_192775.1| putative acetyltransferase (antibiotic resistance) protein
 [Gluconobacter oxydans 621H]
 gb|AAW62119.1| Putative acetyltransferase (Antibiotic resistance) protein
 [Gluconobacter oxydans 621H]
 Length = 173

Score = 86.7 bits (213), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 60/158 (37%), Positives = 80/158 (50%), Gaps = 6/158 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVA-EVE 65
 IR A AD+ A+ I N IE + + T P T ++ W +D RL YP LVA +
 Sbjct: 2 IREAGPADLPAILRITNDAIENTDALWITPFTLEQRRQWFED--RLAQGYPVVLVAVDTA 59

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G VAG G +++ Y TVE +VYV+ HQR G+G +L L+ GF +VA
 Sbjct: 60 GEVAGYGSYGSFRSYEGYARTVEHSVYVAPSHQRRGVGRSLHLALINHARDAGFHIMVAG 119

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF 163
 I N SV +H G+ GTL G K G W D+ F
 Sbjct: 120 ITADNAASVAMHHEFGFRNCGTLPQVGRKRGRWLDLLF 157

>ref|XP_645686.1| hypothetical protein DDB_G0271268 [Dictyostelium discoideum AX4]
 gb|EAL71764.1| hypothetical protein DDB_G0271268 [Dictyostelium discoideum AX4]
 Length = 186

Score = 86.3 bits (212), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 51/175 (29%), Positives = 87/175 (49%), Gaps = 22/175 (12%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAE--- 63
 ++IR D+ + +I HY+ F E + +E + D+ +P++VA
 Sbjct: 4 IKIRNVNENDIKEITNIYKHYVLNEVCTFEEEVPSSEEMNKRRSIIVDKNFPYIVATTTT 63

Query: 64 -----VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110
 + +V G AYA ++ R AY +TVE ++Y+ +Q+LG+GS L L
 Sbjct: 64 TTTTIKDGANDITKEIVIGYAYASSFRPRAAYRFTVEDSIYIDINYQKLGVGSILLKEL 123

Query: 111 LKSMEAQGFKSVVAVI--GLPND---PSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 + + +GFK ++AVI G PN S++LH+ G+ + TL+ GYK + D
 Sbjct: 124 ISQCKEKGFKETIIAVIAAGGPNQVGGSSIKLHKKFGFDNQHTLKNVGYKFNQFLD 178

>ref|YP_003744261.1| antibiotic resistance protein (acetyltransferase) [Ralstonia
 solanacearum CFBP2957]
 emb|CBJ41614.1| putative antibiotic resistance protein (Acetyltransferase)
 [Ralstonia solanacearum CFBP2957]
 Length = 182

Score = 86.3 bits (212), Expect = 1e-15, Method: Compositional matrix adjust.
 Identities = 57/169 (33%), Positives = 81/169 (47%), Gaps = 6/169 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVA-EVE 65
 I + A AA+ DI+N I ST + P+ PQ W + +P + A +
 Sbjct: 13 IDCSEAHEAAAILDILNEAIVNSTALYDYTPRPPQAMATWF--AAKRAGGFVVGAVDAS 70

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + G A G ++A AY +TVE +VYV H + GLG L +++ +V
 Sbjct: 71 GKLLGFASWGTFRAFPAYKYTVEHSVYVHHACRGRGLGERLLREVIRRAREQLHVLVGC 130

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPP 174
 I N S LH LG+ GT+R AG+K G W D F+Q + E PA P
 Sbjct: 131 IDAANSASAGLHTRLGFVHAGTIREAGFKFGRWLDAAFYQLNLETPAQP 179

>ref|YP_003109023.1| GCN5-related N-acetyltransferase [Acidimicrobium ferrooxidans DSM 10331]
gb|ACU53350.1| GCN5-related N-acetyltransferase [Acidimicrobium ferrooxidans DSM 10331]
Length = 166

Score = 86.3 bits (212), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 55/160 (34%), Positives = 77/160 (48%), Gaps = 6/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
+RP +D A I NH + T+T EP+TP E W+DD + Y LVAE+ G
Sbjct: 8 LRPLVPSDAEATRRIYNHAVLTTTATLDIEPRTPEHERWDDHLGI---YVCLVAELNG 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A P++ R Y TVE ++Y+ Q G+G+ L T L+ + GF + +A I
Sbjct: 65 DVVGFASISPYRPRAGYASTVEDSIYLDPTAQGRGIGTRLLTSLVDTAADLGFHACIAHI 124

Query: 127 GLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+ S LH G+ G R G K W D+ QR
Sbjct: 125 VADHHVSRSLHARAGFELVGIQREIGRKFSSRWIDLAVMQR 164

>dbj|BAI77991.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
Length = 199

Score = 86.3 bits (212), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 58/171 (33%), Positives = 80/171 (46%), Gaps = 7/171 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
+R A DM V I ++ +F EP + E E L P+ VAE G V
Sbjct: 27 LRDARDDDDMPMHAIYAEHVLEGISSEFEPPSLAEMRRRRRAEVLAKGLPYRVAERLGEV 86

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
G Y P++ R Y +TVE +VYV LG+G L L++ G++ ++A+IG
Sbjct: 87 VGYGYVTPYRPRPGYRFTVEDSVYVSRMGGLGIGQALLGELVEHCVEGGWRQMIAIIGN 146

Query: 128 LPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR-----DFELPAP 173
N S+RLHE LG+ G + G+KHG W D QR LP P
Sbjct: 147 SENTASIRLHERLGFHRVGVFESVGFKHGRWVDTVLMQALGDGSLSLPEP 197

>ref|YP_002550431.1| acetyltransferase [Agrobacterium vitis S4]
gb|ACM37420.1| acetyltransferase [Agrobacterium vitis S4]
Length = 180

Score = 86.3 bits (212), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 54/164 (32%), Positives = 83/164 (50%), Gaps = 7/164 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQD----RYPWLVAEV 64
IRP+ AD+ A+ I +I + TP+ DDL ER ++ R+P +VA +
Sbjct: 3 IRPSRDADVEAMLAIYRRHIRRGLDEGVDDSDTPEP--DDLRRERKNLKSFRPHIVATI 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+G V G AY ++ R AY +TV+ ++YV H H +GS L L+ + A GF+ ++
Sbjct: 61 DGTVVGYAYVFLFRKRPAYRYTVKHSIYVHHDHIGKRVGSQLLRGLIDACAAAGFRQIIG 120

Query: 125 VIGLPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF 168
I N S+ LH+ + G L A Y++G W D QR
Sbjct: 121 YIDADNAASLALHDFRNFVRVGLLPVAVARYGRWADSVMVQRSL 164

>ref|YP_001336218.1| acetyltransferase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
ref|YP_002920431.1| hypothetical acetyltransferase [Klebsiella pneumoniae NTUH-K2044]
ref|ZP_06013401.1| GNAT family toxin-antitoxin system [Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884]
gb|ABR77988.1| hypothetical acetyltransferase [Klebsiella pneumoniae subsp. pneumoniae MGH 78578]
dbj|BAH64364.1| hypothetical acetyltransferase [Klebsiella pneumoniae subsp. pneumoniae NTUH-K2044]
gb|EEW43519.1| GNAT family toxin-antitoxin system [Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884]
Length = 184

Score = 86.3 bits (212), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 55/172 (31%), Positives = 86/172 (50%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
+EIR A D A+ + ++ +F P T E ++ ++D PWLVA G
Sbjct: 12 LEIREALPDDAHAIAALYVWHVLNGRASFEIIPPTVDEMRKRIQTVRDNGLPWLVALWRG 71

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
+ G YA ++ R AY +T+E ++YV G+GS L + L+ E ++ ++A+I
Sbjct: 72 AIVGYCYATFYRPRPAYRYTLEESIYVESGMGGRGIGSALLSRLIAECEKGPWRQMLAI 131

Query: 127 --GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ----DFELP 171
G N S+ +H+ G+T G LR+ GYK G W D QR D+ LP
Sbjct: 132 GDGHNNAGSLAIHKKFGFTVAGQLRSVGYKMGDWRDTLIMQALGDGDWTL 183

>ref|YP_003992355.1| GCN5-like N-acetyltransferase [Caldicellulosiruptor hydrothermalis 108]
gb|ADQ06986.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor hydrothermalis 108]
Length = 161

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 44/158 (27%), Positives = 80/158 (50%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR AT +D+ + I N+ + ST F P+T ++++ + ++YP VAE
Sbjct: 1 MNIRKATISDIPDLLYIYNYEVLNSTSTFDIHPKTTEDFLKLFDSHGKYPYVAEENSA 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G Y P+ + AY TVE ++Y+ ++ G+G + L++ + G +++A +
Sbjct: 61 ILGYGYLSPFSEKEAYSITVEDSIYIHPYRGRGIGKQILKFLIERAKDTGAANIIAKVC 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
N S+ LH++ G+ G L G K G + DV Q
Sbjct: 121 AENYISLHLHKSFGFVEVGKLTKEVSKFGRFLDVIIILQ 158

>ref|ZP_07182496.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 69-1]
gb|EFJ83489.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 69-1]
Length = 193

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 57/174 (32%), Positives = 82/174 (47%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63
R + IR A AD AA+ +I NH + + + I E R YP LV+E

Sbjct: 19 RPDMSIRFARKADCAIAIEIYNHAVLYTAAIWNQTVADNRIAWFEARTLAGYPVLVSE 78

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 +GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V

Sbjct: 79 EDGVTGYASFQDWRSDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDGCKHVMV 138

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 A I N S+ LH++LG+ + G K G W D+ F Q + P +

Sbjct: 139 AGIESQNQASLHLHQSLGFVVTAQMPQVGTGFRWLDLTFMQLQLDERTEPDAI 192

>ref|YP_00122281.1| putative N-acetyltransferase [Clavibacter michiganensis subsp.
 michiganensis NCPPB 382]
 emb|CAN01586.1| putative N-acetyltransferase [Clavibacter michiganensis subsp.
 michiganensis NCPPB 382]
 Length = 177

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 55/152 (36%), Positives = 77/152 (50%), Gaps = 5/152 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEV 64
 + IRPA D+ + +I NH I T T + EP E W + D P LVAEV

Sbjct: 1 MRIRPAEPRDIDDLLEIRNHAILTGALTWTEEPVDRAEREAWFRETTEAGD--PILVAEV 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 +G AG GPW+ + Y ++VE +VYV Q G+G L +++ + G ++V A

Sbjct: 59 DGAFAAGYGTYPWRMSGYRFSVEDSVYVRDGFQGGIGIGALVEAVVEHARSAGKRAVFA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHG 156
 I N S+RLHE LG+ G L G+K G

Sbjct: 119 DIEAGNRGSIRLHERLGRQVGLLPGIGWKFG 150

>ref|YP_001395681.1| acetyltransferase [Clostridium kluyveri DSM 555]
 ref|YP_002472485.1| hypothetical protein CKR_2020 [Clostridium kluyveri NBRC 12016]
 gb|EDK34310.1| Predicted acetyltransferase [Clostridium kluyveri DSM 555]
 dbj|BAH07071.1| hypothetical protein [Clostridium kluyveri NBRC 12016]
 Length = 161

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 82/161 (50%), Gaps = 9/161 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE----WIDDLERLQDRYPWLVAEVE 65
 IR A D+ + DI N I T F EP+T ++ + D +E +P LV E

Sbjct: 2 IRKAAEQDIPFLLDIYNEAILNGTATFDLEPKTLEDKQWIFYDHIET----HPLLVCCKY 57

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSVVA 124
 A ++ + AYD +VE ++Y+ ++ +G+G L +L + E G ++++

Sbjct: 58 EKAIAYASLSTYREKKAYDGSVELSIYIHKDYRGIGIGKQLMEAILNLAKEIDGIHTIIS 117

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 +I N+ S RLHE G+T G ++ AGYK G + D+ +Q

Sbjct: 118 IITAGNEVSDDLHEKFGFTYCGKIKEAGYKFGQYCDINVYQ 158

>ref|YP_002237448.1| putative phosphinothricin N-acetyltransferase [Klebsiella
 pneumoniae 342]
 ref|YP_003438431.1| phosphinothricin acetyltransferase [Klebsiella variicola At-22]
 ref|ZP_06547948.1| acetyltransferase [Klebsiella sp. 1_1_55]
 gb|ACI07463.1| putative phosphinothricin N-acetyltransferase [Klebsiella
 pneumoniae 342]
 gb|ADC57419.1| Phosphinothricin acetyltransferase [Klebsiella variicola At-22]
 gb|EFD85968.1| acetyltransferase [Klebsiella sp. 1_1_55]

Length = 184

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 55/172 (31%), Positives = 86/172 (50%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 +EIR A D A+ + ++ +F P T E ++ ++D PWLVA G
 Sbjct: 12 LEIREALPDDAHAIAALYVWHVLNGRASFEIIPPTVDEMRRKRIKTVRDNGLPWLVALWRG 71

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 + G YA ++ R AY +T+E ++YV G+GS L + L+ E ++ ++A+I
 Sbjct: 72 AIVGYCYATFYRPRPAYRYTLEESIYVESGMGGRGIGSALLSRLIAECEKGPWRQMLAII 131

Query: 127 --GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ----DFELP 171
 G N S+ +H+ G+T G LR+ GYK G W D QR D+ LP
 Sbjct: 132 GDGHNNAGSLAIHKKFGFTVAGQLRSVGYKMGDWRDRLIMQALGDGDWTLTP 183

>ref|YP_001296551.1| phosphinothricin N-acetyltransferase YncA [Flavobacterium
 psychrophilum JIP02/86]
 emb|CAL43744.1| Probable phosphinothricin N-acetyltransferase YncA [Flavobacterium
 psychrophilum JIP02/86]
 Length = 165

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 50/163 (30%), Positives = 77/163 (47%), Gaps = 1/163 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
 +EIRP D A+ I+N+ I ST + P+ I LE + +P +VA
 Sbjct: 3 IEIRPFQIEDTQAILAIINYNILNSTALYDYNPRNLATQIAILEEKTTKGFPPIIVATENK 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 +V G Y ++ R AY +TVE ++YV G+G L L+ +AQ +++ VI
 Sbjct: 63 MVTGFGYYSEFRFREAYKFTVEHSIYVHKDFHNGIGKLLLELISLAKAQLHTMIGVI 122

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFE 169
 N S+ HE G+ G ++ +G+K W D F Q E
 Sbjct: 123 DAENKSSITFHEKFGFKNVGIIKESGFKFNRWLDVFMQLILE 165

>ref|YP_002382603.1| acyl-CoA N-acyltransferase [Escherichia fergusonii ATCC 35469]
 emb|CAQ88971.1| putative acyl-CoA N-acyltransferase [Escherichia fergusonii ATCC
 35469]
 Length = 249

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 57/174 (32%), Positives = 83/174 (47%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63
 R + IR A AD AA+ +I NH + + + + I E R YP LV+E
 Sbjct: 76 RPDMSIRFARKADCAIAIEIYNHAVLYTAAIWNDQTVADANRIAWFEARTIAGYPVLVSE 135

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 123
 +GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
 Sbjct: 136 EDGVVTGYASFQDWRSDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHVMV 195

Query: 124 AVIGLPNDPVRRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRPV 177
 A I N S+ LH++LG+ + G K G W D+ F Q + + P +
 Sbjct: 196 AGIESQNQASLHLHQSLGFVITAQMPQVGTGFRWLDLTFMQLQLDERSEPDAI 249

>ref|ZP_03000532.1| acetyltransferase, GNAT family [Escherichia coli 53638]
 ref|ZP_07133860.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia

coli MS 115-1]
gb|EDU63564.1| acetyltransferase, GNAT family [Escherichia coli 53638]
gb|EFJ98863.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 115-1]
Length = 193

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 57/174 (32%), Positives = 82/174 (47%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAE 63
R + IR A AD AA+ +I NH + + + I E R YP LV+E
Sbjct: 19 RPDMSIRFARKADCAIAIEIYNHAVLYTAAIWNQTVADNRIAWFEARTLAGYPVLVSE 78

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
+GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
Sbjct: 79 EDGVVTGYASFWDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHVMV 138

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFELPAPPRPV 177
A I N S+ LH++LG+ + G K G W D+ F Q + P +
Sbjct: 139 AGIESQNQASLHLHQSLGFVVTAQMPQVGTGKFRWLDLTFMQLQLDERTEPDAI 192

>gb|EGC95077.1| acyl-CoA N-acyltransferase [Escherichia fergusonii ECD227]
Length = 171

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 56/171 (32%), Positives = 82/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
+ IR A AD AA+ +I NH + + + I E R YP LV+E +G
Sbjct: 1 MSIRFARKADCAIAIEIYNHAVLYTAAIWNQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAVI 126
VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASFWDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFELPAPPRPV 177
N S+ LH++LG+ + G K G W D+ F Q + + P +
Sbjct: 121 ESQNQASLHLHQSLGFVVTAQMPQVGTGKFRWLDLTFMQLQLDERSKPDIAI 171

>ref|YP_003377320.1| N-acetyltransferase [Xanthomonas albilineans GPE PC73]
emb|CBA17326.1| putative n-acetyltransferase protein [Xanthomonas albilineans]
Length = 173

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 55/160 (34%), Positives = 83/160 (51%), Gaps = 6/160 (3%)

Query: 20 AVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVE-GVVAGIAYAG 75
A+ +I N I ST + P+ P+ W + P L E E G + G A G
Sbjct: 14 AILEIFNEVIVHSTALYDYRPRPPESMSAWFA--AKHAGALPVLGLEDEVGTLLGFATYG 71

Query: 76 PWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAVIGLPNDPSVR 135
P++A A+ ++VE +VYV H+ G+G L L+ + +A+G +V I N S+
Sbjct: 72 PFRWPAFKYSVEHSVYVHCGHRGKGVGRRLQLALIDTAKARGVHVLVGGIDASNAGSIA 131

Query: 136 LHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFELPAPPR 175
LHE LG+ GT+R AG+K G W D+ F+QR + P P+
Sbjct: 132 LHEQLGFVHAGTVREAGFKFGRWLDLAFYQRILDGPVDPQ 171

>ref|ZP_02799324.2| acetyltransferase, GNAT family [Escherichia coli O157:H7 str. EC4196]

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ref|ZP_02773971.2| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4113]
ref|ZP_03006293.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4076]
ref|ZP_03006647.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4401]
ref|ZP_02794024.2| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4486]
ref|ZP_02786465.2| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4501]
ref|ZP_02813501.2| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC869]
ref|ZP_02824428.2| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC508]
ref|ZP_03064149.1| acetyltransferase, GNAT family [Shigella dysenteriae 1012]
ref|ZP_03252986.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4206]
ref|ZP_03256924.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4045]
ref|ZP_03261912.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4042]
ref|YP_002270455.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    EC4115]
ref|ZP_03445143.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
                    TW14588]
ref|YP_003499369.1| acetyltransferase, GNAT family [Escherichia coli O55:H7 str.
                    CB9615]
gb|EDU33853.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4196]
gb|EDU54780.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4113]
gb|EDU69864.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4076]
gb|EDU75157.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4401]
gb|EDU80364.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4486]
gb|EDU86528.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4501]
gb|EDU90140.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC869]
gb|EDU96606.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC508]
gb|EDX35846.1| acetyltransferase, GNAT family [Shigella dysenteriae 1012]
gb|EDZ74367.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4206]
gb|EDZ81081.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4045]
gb|EDZ89397.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4042]
gb|ACI36491.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               EC4115]
gb|EEC25930.1| acetyltransferase, GNAT family [Escherichia coli O157:H7 str.
               TW14588]
gb|ADD56385.1| Acetyltransferase, GNAT family [Escherichia coli O55:H7 str.
               CB9615]
gb|EFW64747.1| Putative acetyltransferase [Escherichia coli O157:H7 str. EC1212]
gb|EGD64476.1| Putative acetyltransferase [Escherichia coli O157:H7 str. 1044]
gb|EGD64723.1| Putative acetyltransferase [Escherichia coli O157:H7 str. 1125]
Length = 193

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Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 57/174 (32%), Positives = 82/174 (47%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAE 63
 R + IR A AD AA+ +I NH + + + + I E R YP LV+E
 Sbjct: 19 RPDMSIRFARKADCAAIAEINHAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSE 78

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 +GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
 Sbjct: 79 EDGVVTGYASFQDWSFDGFRHTVEHSVYVHPDHQKGLGRKLLSRLIDEARDCGKHVMV 138

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 A I N S+ LH++LG+ + G K G W D+ F Q + P +
 Sbjct: 139 AGIESQNQASLHLHQLSLGFVVTQAQMPQVGTGKFRWLDLTFMQLQLDERTEPDAI 192

>ref|YP_002386887.1| putative acyl-CoA N-acyltransferase [Escherichia coli IAI1]
 ref|YP_002402657.1| putative acyl-CoA N-acyltransferase [Escherichia coli 55989]
 emb|CAU97437.1| putative acyl-CoA N-acyltransferase [Escherichia coli 55989]
 emb|CAQ98303.1| putative acyl-CoA N-acyltransferase [Escherichia coli IAI1]
 Length = 250

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 57/175 (32%), Positives = 82/175 (46%), Gaps = 1/175 (0%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVA 62
 R + IR A AD AA+ +I NH + + + + I E R YP LV+
 Sbjct: 75 SRPDMSIRFARKADCAAIAEINHAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVS 134

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 E +GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +
 Sbjct: 135 EEDGVVTGYASFQDWSFDGFRHTVEHSVYVHPDHQKGLGRKLLSRLIDEARDCGKHVM 194

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 VA I N S+ LH++LG+ + G K G W D+ F Q + P +
 Sbjct: 195 VAGIESQNQASLHLHQLSLGFVVTQAQMPQVGTGKFRWLDLTFMQLQLDERTEPDAI 249

>ref|ZP_05119263.1| phosphinothricin N-acetyltransferase [Vibrio parahaemolyticus 16]
 gb|EED26824.1| phosphinothricin N-acetyltransferase [Vibrio parahaemolyticus 16]
 Length = 164

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 48/153 (31%), Positives = 77/153 (50%), Gaps = 2/153 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL--QDRYPWLVAEVE 65
 +EIR D+AA+ DI N YIE + F T + ++ + ++ VA
 Sbjct: 1 MEIRVGKLGDIAAITDIFNFYIEHTNARFEDRALTQENRLNWFSQFSYNSKHQLFVAIEN 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + G A + P++ +A++ T E TVY++ + G+GS LY+ L S+ G V++
 Sbjct: 61 GKLLGFACSQPYRDISAFEDTAETVYLAETARGKGVGSKLYSKLFSSISDYGVHRVLSG 120

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
 I LPND SV LH+ G+ G K+G +
 Sbjct: 121 IALPNDASVALHKRFGFREVGVFNEYAKKNGKY 153

>ref|ZP_07477230.1| acetyltransferase [Brucella sp. B01]
 gb|EFM56587.1| acetyltransferase [Brucella sp. B01]
 Length = 202

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
 Identities = 52/162 (32%), Positives = 86/162 (53%), Gaps = 5/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT AD+AA+ I N +E + + + +W+++ R +D +P LVAE EG
 Sbjct: 43 IRHATEADLAALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 100

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
 Sbjct: 101 QVVGYASYGPFPRPFEGFRHSSELSVYVASNARGGGIGRTLLAELVEEARERKVVHVLIAI 160

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRDF 168
 N S+ LH++ G+ GTL+ G K G W D+ F Q+
 Sbjct: 161 EAGNAASIALHKSQGFEECGTLKQVGQKFGRWLDLTFMQKTL 202

>ref|NP_753773.1| acetyltransferase yncA [Escherichia coli CFT073]
 ref|YP_540677.1| acetyltransferase YncA [Escherichia coli UTI89]
 ref|YP_001462722.1| acetyltransferase [Escherichia coli E24377A]
 ref|ZP_03034408.1| acetyltransferase, GNAT family [Escherichia coli F11]
 ref|ZP_04003970.1| acetyltransferase yncA [Escherichia coli 83972]
 ref|ZP_04535910.1| acetyltransferase yncA [Escherichia sp. 3_2_53FAA]
 ref|ZP_07137943.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 182-1]
 ref|ZP_07172966.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 200-1]
 ref|ZP_07173458.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 45-1]
 ref|ZP_07193866.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 185-1]
 ref|ZP_07219438.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 78-1]
 gb|AAN80335.1|AE016760_194 Hypothetical acetyltransferase yncA [Escherichia coli CFT073]
 gb|ABE07146.1| hypothetical acetyltransferase YncA [Escherichia coli UTI89]
 gb|ABV21162.1| acetyltransferase, GNAT family [Escherichia coli E24377A]
 gb|EDV66481.1| acetyltransferase, GNAT family [Escherichia coli F11]
 gb|EEH86445.1| acetyltransferase yncA [Escherichia sp. 3_2_53FAA]
 gb|EEJ47296.1| acetyltransferase yncA [Escherichia coli 83972]
 gb|ADE89376.1| acetyltransferase, GNAT family [Escherichia coli IHE3034]
 gb|EFJ57690.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 185-1]
 gb|EFJ63238.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 200-1]
 gb|EFJ93585.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 45-1]
 gb|EFK05118.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 182-1]
 gb|EFK75001.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 78-1]
 gb|EFU49145.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 110-3]
 gb|EFU50028.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 153-1]
 gb|EFU57819.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 16-3]
 gb|EFW70217.1| Putative acetyltransferase [Escherichia coli WV_060327]
 gb|EGB79170.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 57-2]
 gb|EGB84389.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 60-1]
 gb|EGB90253.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 117-3]
 Length = 193

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.

Identities = 57/174 (32%), Positives = 82/174 (47%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAE 63
R + IR A AD AA+ +I NH + + + I E R YP LV+E
Sbjct: 19 RPDMSIRFARKADCAIAIEIYNHAVLYTAAIWNQTVADNRIAWFEARTIAGYPVLVSE 78

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
+GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
Sbjct: 79 EDGVVTGYASFQDWSFDFGRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHVMV 138

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
A I N S+ LH++LG+ + G K G W D+ F Q + P +
Sbjct: 139 AGIESQNQASLHLHQSLGFVVTAQMPQVGTGKGRWLDLTFMQLQLDERTEPDAI 192

>ref|YP_001566360.1| GCN5-like N-acetyltransferase [Delftia acidovorans SPH-1]
gb|ABX37975.1| GCN5-related N-acetyltransferase [Delftia acidovorans SPH-1]
Length = 174

Score = 85.9 bits (211), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 55/160 (34%), Positives = 84/160 (52%), Gaps = 3/160 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVA-EVEGV 67
IR + D+AA+ I H++ T F T+P + + L P+LVA + +G
Sbjct: 4 IRSSLDGDLAAITSIYRHHVLHGTGTFTDPPAESDMATRRADVLAAGLPYLVAVDEQGG 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAVIG 127
V G AYA +K R AY ++ E ++YV + GLG L L + EA G + ++AVIG
Sbjct: 64 VLGFAIANWFKPRPAYRFSAEISYVHDAARGQGLGRLLLDALSRECEAAGVRKLLAVIG 123

Query: 128 -LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+ +H A G+T GTL + G+K G W D+ ++
Sbjct: 124 DSAAGSIGVHRAAGFTPAGTLSSMGWKFGRWLDIVLMEK 163

>ref|YP_449585.1| phosphinothricin acetyltransferase [Xanthomonas oryzae pv. oryzae
MAFF 311018]
ref|YP_001911873.1| N-acetyltransferase [Xanthomonas oryzae pv. oryzae PX099A]
dbj|BAE67311.1| phosphinothricin acetyltransferase [Xanthomonas oryzae pv. oryzae
MAFF 311018]
gb|ACD57341.1| N-acetyltransferase [Xanthomonas oryzae pv. oryzae PX099A]
Length = 173

Score = 85.5 bits (210), Expect = 2e-15, Method: Compositional matrix adjust.
Identities = 54/158 (34%), Positives = 84/158 (53%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
+A+ DI N I TS + P+ P+ + Q +P + V + +G + G A G
Sbjct: 13 SAILDIFNEAIATSNALYDYRPPPEMVGWFATKQAGGFPVIGVEDADGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAVIGLPNDPSVRL 136
++A A+ ++VE ++YV H+ GLG L L+ + +A+G +V I N S+ L
Sbjct: 73 FRAWPAFKYSVEHSIYVHCDHRGKGLGRLLQLALIAAAQARGVHVLVGGIDASNQASIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE G+T GT+R AG+K G W D+ F+QR PA P
Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRIATPADP 170

>ref|YP_002893339.1| GCN5-related N-acetyltransferase [Tolomonas auensis DSM 9187]
gb|ACQ93753.1| GCN5-related N-acetyltransferase [Tolomonas auensis DSM 9187]
Length = 173

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 52/163 (31%), Positives = 83/163 (50%), Gaps = 8/163 (4%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWL-VAEVEGVVAGIAYA 74
AA+ I N I ST + + +T + W + E YP + + +G + G A
Sbjct: 13 AAILAIFNDAILHSTALYDYQARTMENMVTWFKNKE--TGNYPVIGIENAQGELMGFASY 70

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSV 134
G ++A A +T+E +VYV+ H+ G+ + L L+ + Q + +++ I N S+
Sbjct: 71 GSFRAYPANKYTLHSVYVAKAHRGKGIANILMLRLVALAKEQNYHTLIGSIDASNQASI 130

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
LHE LG+ GT+R AG+K G W D+ F+Q LP P PV
Sbjct: 131 ALHEKLGFBHAGTIRHAGFKFGDWLDLAFYQ--LLLPTPAHPV 171

>ref|ZP_07827503.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella
sp. oral taxon 158 str. F0412]
gb|EFR59927.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella
sp. oral taxon 158 str. F0412]
Length = 166

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 51/153 (33%), Positives = 78/153 (50%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IRP T D+AA DI N+ + EP+T EW E Q + V ++ VV
Sbjct: 6 IRPITQDDIAACLDIYNYEVVNGVATLDLEPRTLPEWQAWYEAHQTSCHCIFVGIMDDVV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSVAVIG 127
G A P++ ++A+ TVE ++Y+ ++ G+ S L H+L+ + E + +VV+VI
Sbjct: 66 VGYASLSPYRTKDAFKSTVELSIYIHQFYRGKGVASKLMAHILEYAKETETLHTVVSIVT 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
N S LHE G+T G G+KHG + D
Sbjct: 126 AGNAASTALHERFGFTYCGLTQVGFKHGKYQD 158

>ref|ZP_06703884.1| N-acetyltransferase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 11122]
ref|ZP_06731508.1| N-acetyltransferase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 10535]
gb|EFF44569.1| N-acetyltransferase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 11122]
gb|EFF47366.1| N-acetyltransferase [Xanthomonas fuscans subsp. aurantifolii str.
ICPB 10535]
Length = 173

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 55/158 (34%), Positives = 83/158 (52%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
A+ DI N I ST + P+ P+ + Q +P + V + +G + G A G
Sbjct: 13 GAILDIFNEAIANSTALYDYRPRPPESMVGWFATKQAGGFPVIGVEDADGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRL 136
++A A+ ++VE ++YV H+ GLG L L+ + EA+G +V I N S+ L
Sbjct: 73 FRAWPAFKYSVEHSIYVHRDHRGKGLGRLLQLALIAAAEARGVHVVLVGIDASNQASIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE G+T GT+R AG+K G W D+ F+QR PA P
Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILATPADP 170

>gb|EGC07342.1| acetyltransferase [Escherichia fergusonii B253]
 Length = 171

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 82/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHMVAGI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH++LG+ + G K G W D+ F Q + + P +
 Sbjct: 121 ESQNQASLHLHQSLGFVITAQMPQVGTGKFGRWLDLTFMQLQLDERSKPDAI 171

>ref|ZP_07823528.1| acetyltransferase, GNAT family [Streptococcus pseudoporcinus SPIN
 20026]
 gb|EFR44833.1| acetyltransferase, GNAT family [Streptococcus pseudoporcinus SPIN
 20026]
 Length = 190

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 55/184 (29%), Positives = 81/184 (44%), Gaps = 11/184 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR A +D + I Y+E + + F T ++ ++ +Q YP+LV E EG +
 Sbjct: 2 IRFAHPSDAKQLVAIYQPYVEKAAITFDHVSPTVGQFQQRMQHIQAFYPYLVYEEGRLL 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 AYA R AY W+ E ++YV + G+G LY L + + A G + A I
 Sbjct: 62 AYAYASHLNTAAAYAWSCEVSIYVDQHSRGKIGRCLYQALERYLAAMGIINCNAIATS 121

Query: 130 NDPSVRL-----HEALGYTARGTLRAAGYKHGGWHDVGFQWQDF----ELPAPPRPVR 178
 PS L H+ LGY GT GYK W DV + ++ PPR +
 Sbjct: 122 KIPSSYLPLASHMFHQKLGYLGVGTGFKVGYKFDQWFDVTWMEKALGHHTRGQKPPRSIH 181

Query: 179 PVTQ 182
 V +
 Sbjct: 182 EVLK 185

>ref|YP_001743779.1| acetyltransferase [Escherichia coli SMS-3-5]
 gb|ACB16203.1| acetyltransferase, GNAT family [Escherichia coli SMS-3-5]
 Length = 172

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 55/171 (32%), Positives = 82/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADNRIAWFEARTLAGYPVLVSEQDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VV G A G W++ + + TVE ++YV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSIYVHPDHQKGKGLGRKLLSRLIDEARDCGKHMVAGI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH++LG+ + G K G W D+ F Q + + P +

Sbjct: 121 ESQNQASLHLHQSLGFVVTAQMPQVGTKFGRWLDLTFMQLQLDERSEPDAI 171

>ref|NP_890464.1| hypothetical protein BB3930 [Bordetella bronchiseptica RB50]
 emb|CAE35903.1| conserved hypothetical protein [Bordetella bronchiseptica RB50]
 Length = 184

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 58/163 (35%), Positives = 83/163 (50%), Gaps = 8/163 (4%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQ---TPQEWIDDLERLQDRYPWLVAE-VEGVVAGIAYA 74
 AA+ DI N I TST + +P+ + + W + Q +P + E GV+ G A

Sbjct: 24 AAILDIFNDAILTSTALYDYQPRALASMEAWFQ--AKRQGGFPVVGFEAAGVLMGFASY 81

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 134
 G ++A AY ++VE +VYV R++ GLG L L++ Q +V I N SV

Sbjct: 82 GTFRAWPAYKYSVEHSVYVDRRYRGRGLGEALLRALIERARLQQVHVLVGGIDATNAGSV 141

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 LH LG+ GT+ AG+K G W D+ F+Q L P RPV

Sbjct: 142 ALHRKLGFBHAGTITQAGFKFGRWLDLAFYQ--LTLDTPLRPV 182

>ref|ZP_07623784.1| putative acyl-CoA N-acyltransferase [Escherichia coli H299]
 Length = 171

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 82/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + I E R YP LV+E +G

Sbjct: 1 MSIRFARKADCAAIAEINYHAYLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I

Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQGGKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH++LG+ + G K G W D+ F Q + + P +

Sbjct: 121 ESQNQASLHLHQSLGFVVTAQMPQVGTKFGRWLDLTFMQLQLDERSEPDAI 171

>ref|YP_003820657.1| Phosphinothricin acetyltransferase [Clostridium saccharolyticum
 WM1]

gb|ADL03034.1| Phosphinothricin acetyltransferase [Clostridium saccharolyticum
 WM1]

Length = 163

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 53/160 (33%), Positives = 82/160 (51%), Gaps = 6/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A DM + DI N+ +E F P+T ++ W E +P +VAE +G

Sbjct: 3 IRTAEKDMPELLDIYNYEVEHGLATFDLNPKTMEQRLAWFR--EHNNGNHPLIVAEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSVVAV 125
 G A ++ + AY TVE +VY+ ++R G+ L + +LK + E +V++V

Sbjct: 61 KAVGYASLSSYRPKEAYAATVELSVYIHKDYRRRGVAGDLTSAILKIAKERDDIHTVISV 120

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 I N+ S+RLHE LG+ GT+R G K G D+ +Q

Sbjct: 121 ITGENEASIRLHERLGFHCGTIREVGEKFGKMLDIENYQ 160

>ref|ZP_07463894.1| Phosphinothricin N-acetyltransferase [Streptococcus gallolyticus
subsp. gallolyticus TX20005]
gb|EFM30185.1| Phosphinothricin N-acetyltransferase [Streptococcus gallolyticus
subsp. gallolyticus TX20005]
Length = 212

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 55/183 (30%), Positives = 85/183 (46%), Gaps = 9/183 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGV 67
V I R A D + I +Y+E + + F E + +E+ + + + YP+LVAE G
Sbjct: 25 VIIRLARLEDAKDLLAIYRYVEKTAITFEYEVPSLEEFQERMRSIMAFYPYLVAEEAGQ 84

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI- 126
+ G AYA + R AY W+ E+TVY+ + G+G +Y L + + G ++ A I
Sbjct: 85 ILGYAYASSFHPRAAYAWSAEATVYLDKAARGKGVGRQIYRALEEYLIKMGILNLNACIA 144

Query: 127 -----GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
+ S + H ALGY G +GYK W+D+ W L V+PV
Sbjct: 145 STETEDAYLTNGSEKFHRALGYQLVGKFHQSGYKFNHWYDM-IWMEKM-LGEHDNHVKPV 202

Query: 181 TQI 183
I
Sbjct: 203 KSI 205

>ref|YP_003429952.1| acetyltransferase (GNAT) family [Streptococcus gallolyticus
UCN34]
emb|CBI13008.1| putative acetyltransferase (GNAT) family [Streptococcus
gallolyticus UCN34]
Length = 190

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 55/183 (30%), Positives = 85/183 (46%), Gaps = 9/183 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGV 67
V I R A D + I +Y+E + + F E + +E+ + + + YP+LVAE G
Sbjct: 3 VIIRLARLEDAKDLLAIYRYVEKTAITFEYEVPSLEEFQERMRSIMAFYPYLVAEEAGQ 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI- 126
+ G AYA + R AY W+ E+TVY+ + G+G +Y L + + G ++ A I
Sbjct: 63 ILGYAYASSFHPRAAYAWSAEATVYLDKAARGKGVGRQIYRALEEYLIKMGILNLNACIA 122

Query: 127 -----GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
+ S + H ALGY G +GYK W+D+ W L V+PV
Sbjct: 123 STETEDAYLTNGSEKFHRALGYQLVGKFHQSGYKFNHWYDM-IWMEKM-LGEHDNHVKPV 180

Query: 181 TQI 183
I
Sbjct: 181 KSI 183

>ref|YP_001880295.1| acetyltransferase, GNAT family [Shigella boydii CDC 3083-94]
ref|ZP_03048002.1| acetyltransferase, GNAT family [Escherichia coli E110019]
ref|ZP_03068754.1| acetyltransferase, GNAT family [Escherichia coli 101-1]
ref|ZP_07144470.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia
coli MS 187-1]
gb|ACD07274.1| acetyltransferase, GNAT family [Shigella boydii CDC 3083-94]
gb|EDV90057.1| acetyltransferase, GNAT family [Escherichia coli E110019]
gb|EDX40671.1| acetyltransferase, GNAT family [Escherichia coli 101-1]
gb|EFK26527.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia
coli MS 187-1]

Length = 193

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 57/174 (32%), Positives = 81/174 (46%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAE 63
R + IR A AD AA+ +I NH + + + + I E R YP LV+E
Sbjct: 19 RPDMSIRFARKADCAAIAEINYHNAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSE 78

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 123
+GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
Sbjct: 79 EDGVVTGYASFQDWRSDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDSGKHVMV 138

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
A I N S+ LH +LG+ + G K G W D+ F Q + P +
Sbjct: 139 AGIESQNQASLHLHSLGFVVTQAQMPQVGTGKFRWLDLTFMQLQLDERTEPDAI 192

>ref|YP_002919687.1| hypothetical acetyltransferase [Klebsiella pneumoniae NTUH-K2044]
dbj|BAH63620.1| hypothetical acetyltransferase [Klebsiella pneumoniae subsp.
pneumoniae NTUH-K2044]
Length = 180

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 58/173 (33%), Positives = 83/173 (47%), Gaps = 5/173 (2%)

Query: 5 RRPVEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWL 61
R + IRPA D AA+ +I NH + T+ + N +T + W + R +P LV
Sbjct: 6 RFAMSIRPAIKDDCAAIAEINYHNAVHTAAIWNDKTVTDNRIAWFE--ARQLAGFPVLV 63

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
+E +GV+ G + G W+A + + TVE +VYV HQ GLG L L+
Sbjct: 64 SEEDGVITGYSSFGDWRAFQDGRHTVEHSVYVHPEHQKGLGRKLLVALIAEARLNKHV 123

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
+VA I N S+ LHE LG+ G + G K G W D+ F Q + P
Sbjct: 124 MVAGIESQNHASLHLHETLGFITTGQMPQVGTGKFRWLDLTFMQLQLDARQDP 176

>gb|EGB59486.1| acetyltransferase [Escherichia coli M863]
gb|EGB71999.1| acetyltransferase [Escherichia coli TW10509]
Length = 171

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 56/171 (32%), Positives = 82/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
+ IR A AD AA+ +I NH + + + + I E R YP LV+E +G
Sbjct: 1 MSIRFARKADCAAIAEINYHNAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 126
VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASFQDWRSDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH++LG+ + G K G W D+ F Q + + P +
Sbjct: 121 ESQNQASLHLHSLGFVITAQMPQVGTGKFRWLDLTFMQLQLDERSEPDAI 171

>ref|ZP_07618583.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
[Escherichia coli TA280]
Length = 171

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 56/171 (32%), Positives = 81/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
+ IR A AD AA+ +I NH + + + + I E R YP LV+E G
Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADNRIAWFEARTLAGYPVLVSEENG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASFWDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH++LG+ + G K G W D+ F Q + + P +
Sbjct: 121 ESQNQASLHLHQSLGFVVTAQMPQVGTGFGRWLDLTFMQLQLDERSEPDAI 171

>ref|ZP_07162231.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 116-1]
ref|ZP_07170365.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 175-1]
ref|ZP_07192310.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 196-1]
ref|ZP_07245334.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 146-1]
gb|EFI86093.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 196-1]
gb|EFJ64876.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 175-1]
gb|EFK15960.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 116-1]
gb|EFK91150.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 146-1]
Length = 193

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 57/174 (32%), Positives = 81/174 (46%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAE 63
R + IR A AD AA+ +I NH + + + + I E R YP LV+E
Sbjct: 19 RPDMSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADNRIAWFEARTLAGYPVLVSE 78

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
Sbjct: 79 ENGVTGYASFWDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHVMV 138

Query: 124 AVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
A I N S+ LH++LG+ + G K G W D+ F Q + P +
Sbjct: 139 AGIESQNQASLHLHQSLGFVVTAQMPQVGTGFGRWLDLTFMQLQLDERTEPDAI 192

>ref|ZP_06486378.1| phosphinothricin acetyltransferase [Xanthomonas campestris pv. vasculorum NCPPB702]
Length = 173

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 54/158 (34%), Positives = 84/158 (53%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
+A+ DI N I ST + P+ P+ + Q +P + V + +G + G A G
Sbjct: 13 SAILDIFNEAIANSTALYDYPRPPEMVGWGFATKQAGGFPVIGVEDADGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSPVRL 136
++A A+ ++VE ++YV H+ GLG L L+ + +A+G +V I N S+ L

Sbjct: 73 FRAWPAFKYSVEHSIYVHRDHRGKGLGRLLLQALIAAAQARGVHVLVGGIDANNQVSIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 HE G+T GT+R AG+K G W D+ F+QR PA P

Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILATPADP 170

>ref|ZP_08029282.1| acetyltransferase, GNAT family [Solobacterium moorei F0204]
 gb|EFW24030.1| acetyltransferase, GNAT family [Solobacterium moorei F0204]
 Length = 163

Score = 85.5 bits (210), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 44/160 (27%), Positives = 73/160 (45%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR D+ + D N YI S F TE + + + + + YPW++ E

Sbjct: 2 IRKIEEKDIPVILDWYNWYISNSIATFETEEISLEGFKQRFVAFITEKYPWVILEENDKPV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AY + R AY TV+ +Y+ G G TL ++ G+K+++++

Sbjct: 62 GYAYYSDFNHRQAYACTVDLAIYLDPNACHHGYGKTLMKEMIDIARKSGYKNIISLVTAG 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N S +LHE G+ + T GYKH W V ++ E

Sbjct: 122 NIASEKLHERFGFMKKATFEDIGYKHNQWLAVSYYLQLE 161

>emb|CAZ87971.1| Phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
 (Phosphinothricin-resistance protein) [Thiomonas sp.
 3As]
 Length = 175

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 54/156 (34%), Positives = 78/156 (50%), Gaps = 2/156 (1%)

Query: 24 IVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVVAGIAYAGPWKARNA 82
 I H++ T F T E + L+ +Q R PWLVA + G AYA ++AR A

Sbjct: 20 IYGHVHLHGTGTFETLAPDEAEMLHRLQEVQSRGLPWVAVRGQEIIIGYAYANWFRARE 79

Query: 83 YDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG-LPNDPSVRLHEALG 141
 + +TVE ++Y++ R G+G L L+ S G + ++AVIG N S+ LH A G

Sbjct: 80 FRFTVEDSIYIAPNGLRQGVGGQLLDALIDSCTRSGMRQMLAVIGDSANAGSIGLHRARG 139

Query: 142 YTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 + G + A G+K W DV F QR A P+

Sbjct: 140 FEELGRMSAVGWKFDRWLDVFMQALGAGAETSPI 175

>ref|ZP_08187501.1| sortase-like acyltransferase [Xanthomonas perforans 91-118]
 gb|EGD14907.1| sortase-like acyltransferase [Xanthomonas perforans 91-118]
 Length = 173

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
 Identities = 53/158 (33%), Positives = 83/158 (52%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
 +A+ DI N I ST + P+ P+ + Q +P + V +G + G A G

Sbjct: 13 SAILDIFNEAIA NSTALYDYRPPPEMSVGFATKQAGGFVIGVEHDDGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
 ++A A+ ++VE ++YV H+ GLG L L+ + + +G +V I N S+ L

Sbjct: 73 FRAWPAFKYSVEHSIYVHRDHRGKGLGRLLLQALIAAAQVRGVHVLVGGIDASNQASIAL 132

Query: 137 HEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE G+T GT+R AG+K G W D+ F+QR + PA P
Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILDTPADP 170

>gb|EFW57438.1| Putative acetyltransferase [Shigella boydii ATCC 9905]
Length = 193

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 57/174 (32%), Positives = 82/174 (47%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR---YPWLVAE 63
R + IR A AD AA+ +I NH + + + I E R YP LV+E
Sbjct: 19 RPDMSIRFARKADCAIAEINHAVLYTAAIWNQTVADNRIAWFEARSAGYPVLVSE 78

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 123
+GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
Sbjct: 79 EDGVTGYASFQDWRSDGFRHTVEHSVYVPHDQHGKGLGRKLLSRLIDEARDGCKHVMV 138

Query: 124 AVIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPP 177
A I N S+ LH++LG+ + G K G W D+ F Q + P +
Sbjct: 139 AGIESQNQASLHLHQLSLGFVVTAQMPQVGTGFRWLDLTFMQLQLDERTEPDAI 192

>ref|YP_299321.1| GCN5-related N-acetyltransferase [Ralstonia eutropha JMP134]
gb|AAZ64477.1| GCN5-related N-acetyltransferase [Ralstonia eutropha JMP134]
Length = 175

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 63/173 (36%), Positives = 84/173 (48%), Gaps = 10/173 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR---YPWLVAE 63
+ IR A DM AV I N +ET+T + +TP + + LE L R YP LVA
Sbjct: 1 MNIRDAGPDDMPAVTVIYNEAVETTTAIWN---ETPVDTANRLEWLAARRKAGYPVLVA- 56

Query: 64 VEGVVAGIAYA--GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
V+G + YA G W+A + Y TVE +VYV +R G+ L L+ G
Sbjct: 57 VDGDAVGVGYSFQDWRADFGRHTVEHSVYVRSQRRKGIAEALMVALIDRARELGKHV 116

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPP 174
+VA I N S+RLHE LG+ G L G K G W D+ F Q + + P
Sbjct: 117 MVAAIEAQNASSIRLHEKLGFRQVGLLPEVGTGFGKWLDAFLQIQLDQRSDP 169

>ref|NP_644097.1| phosphinothricin acetyltransferase [Xanthomonas axonopodis pv.
citri str. 306]
gb|AAM38633.1| phosphinothricin acetyltransferase [Xanthomonas axonopodis pv.
citri str. 306]
Length = 173

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 54/158 (34%), Positives = 84/158 (53%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
+A+ DI N I ST + P+ P+ + Q +P + V +G + G A G
Sbjct: 13 SAILDIFNEAIANSTALYDYRPRPPESMVGFATKQTGGFPVIGVEHDDGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 136
++A A+ ++VE ++YV H+ GLG L L+ + +A+G +V I N S+ L
Sbjct: 73 FRAWPAFKYSVEHSIYVHRDHRGKGLGRLLQLALIAAAQARGVHVVLGGIDASNQASIAL 132

Query: 137 HEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE G+T GT+R AG+K G W D+ F+QR + PA P

Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILDTPADP 170

>ref|ZP_06488940.1| phosphinothricin acetyltransferase [Xanthomonas campestris pv. musacearum NCPPB4381]
Length = 173

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 54/158 (34%), Positives = 84/158 (53%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
+A+ DI N I ST + P+ P+ + Q +P + V + +G + G A G

Sbjct: 13 SAILDIFNEAIANSTALYDYRPRPPESMVGFATKQVGGFPVIGVEDADGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++A A+ ++VE ++YV H+ GLG L L+ + +A+G +V I N S+ L

Sbjct: 73 FRAWPAFKYSVEHSIYVHRDHRGKGLGRLLLQALIAAAQARGVHVLVGGIDANNQVSIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE G+T GT+R AG+K G W D+ F+QR PA P

Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILATPADP 170

>ref|YP_002546043.1| phosphinothricin N-acetyltransferase (antibiotic resistance)
protein [Agrobacterium radiobacter K84]
gb|ACM28110.1| phosphinothricin N-acetyltransferase (antibiotic resistance)
protein [Agrobacterium radiobacter K84]
Length = 185

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 53/159 (33%), Positives = 83/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAE-VEGV 67
+R A D+ + I + T ++ P E + + + D+ YP++VAE G

Sbjct: 5 LRQAAPNDLPRITAIYRDAVLNGTASYELIPPDEAEMANRFQAILDKGYPIVAEDGSGK 64

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA ++ R AY W VE ++Y++ + GLG L L+++ EA GF+ ++AVIG

Sbjct: 65 ILGYAYASAFRTRPAYRWMVEDSIYIAPEARGRGLGKLLAKLVETCEALGFRQMIAVIG 124

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
S+ LH A G+ G L+ GYKHG W D Q+

Sbjct: 125 GAAPASIALHRAAGFAETGLLKGTGYKHGRWLDTMLMQK 163

>ref|YP_365646.1| N-acetyltransferase [Xanthomonas campestris pv. vesicatoria str. 85-10]
emb|CAJ25646.1| N-acetyltransferase [Xanthomonas campestris pv. vesicatoria str. 85-10]
Length = 173

Score = 85.1 bits (209), Expect = 3e-15, Method: Compositional matrix adjust.
Identities = 54/158 (34%), Positives = 84/158 (53%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
+A+ DI N I ST + P+ P+ + Q +P + V +G + G A G

Sbjct: 13 SAILDIFNEAIANSTALYDYRPRPPESMVGFATKQAGGFPVIGVEHDDGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++A A+ ++VE ++YV H+ GLG L L+ + +A+G +V I N S+ L

Sbjct: 73 FRAWPAFKYSVEHSIYVHRDHRGKGLGRLLLQALIAAAQARGVHVLVGGIDASNQASIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174

HE G+T GT+R AG+K G W D+ F+QR + PA P
 Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILDTPADP 170

>ref|ZP_06352816.1| toxin-antitoxin system, toxin component, GNAT family [Citrobacter
 youngae ATCC 29220]
 gb|EFE08802.1| toxin-antitoxin system, toxin component, GNAT family [Citrobacter
 youngae ATCC 29220]
 Length = 172

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 58/172 (33%), Positives = 80/172 (46%), Gaps = 1/172 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEG 66
 + IR A+ AD AA+ +I NH + + + + + I E Q YP LV+E G
 Sbjct: 1 MSIRFASKADCAAIAEIYNHAVLHTAAIWNDQTVDAENRIAWYEARQLMSYPVLVSEENG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV G A G W+ + + TVE +VYV HQ GLG L L++ A G +VA I
 Sbjct: 61 VVTGYASFWDWRNFDGFRHTVEHSVYVHPEHQGKGLGRALLGRLLIEEARACGKHVMVAGI 120

Query: 127 GLPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRPVR 178
 N S+ LH LG+ + G K G W D+ F Q + P R
 Sbjct: 121 ESQNQASLHLHSTLGFKTTAQMPQVGTGKFGRWLDLTFMQLQLDDRLEPDASR 172

>ref|NP_837412.1| putative resistance protein [Shigella flexneri 2a str. 2457T]
 ref|NP_707633.2| putative resistance protein [Shigella flexneri 2a str. 301]
 gb|AAP17221.1| putative resistance protein [Shigella flexneri 2a str. 2457T]
 gb|AAN43340.2| putative resistance protein [Shigella flexneri 2a str. 301]
 gb|EFS14940.1| acetyltransferase family protein [Shigella flexneri 2a str. 2457T]
 Length = 172

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 81/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFWDWRSFDGFRHTVEHSVYVHPDHQGKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRPV 177
 N S+ LH++LG+ + G K G W D+ F Q + P +
 Sbjct: 121 ESQNQASLHLHQLSLGFVVTAQMPQVGTGKFGHWLDLTFMQLQLDERTEPDAI 171

>ref|ZP_07825890.1| acetyltransferase, GNAT family [Dialister microaerophilus UPII
 345-E]
 gb|EFR42634.1| acetyltransferase, GNAT family [Dialister microaerophilus UPII
 345-E]
 Length = 192

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 46/168 (27%), Positives = 83/168 (49%), Gaps = 11/168 (6%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWI--DDLRLQDRYPWLVAEVE 65
 + +R D + DI ++Y+E + + TE P E+ +E++ +YP++VAE +
 Sbjct: 2 INLRYVEPEDSEILRDIYSYVENTCIT--TECTLPDEYAFQKRVEKISSKYPYIVAERD 59

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125

G + G YA P R A + V+ ++YV H R G+G +Y + + G ++ A
 Sbjct: 60 GHIVGYIYASPLVEREAINHCVQISIIYVRHGLGRSGVGKRMRYAIESVLSRMGITNMYAR 119

Query: 126 IGLPN-----DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 + +P S++ HE +G+T G L +GYK W D+ ++

Sbjct: 120 VAVPKIENEHLTRNSLQFHEYMGFTKVGFLKSGYKFNQWFDLAIMEK 167

>ref|ZP_01734503.1| hypothetical protein FBBAL38_09159 [Flavobacteria bacterium BAL38]
 gb|EAZ95145.1| hypothetical protein FBBAL38_09159 [Flavobacteria bacterium BAL38]
 Length = 164

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 48/154 (31%), Positives = 78/154 (50%), Gaps = 3/154 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQT--PQEWIDDLERLQDRYPWLVAEV 64
 ++IR AD A+ I+N I ST + +T QE I + E+LQ +P +VAE+

Sbjct: 2 EIKIRDYQTDPCAILAIINDAILHSTALYDYNERTLAAQEMIFE-EKLQKGFPPVIVAEM 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 V G Y ++ R AY +TVE +VY + G+G L T L++ + Q +++

Sbjct: 61 NNEVVGFGYGYSEFRFREAYKFTVEHSVYANKNAIGKGIGKLLLTIELIERAKQNLHTMIG 120

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
 VI N S+ H+ G+ G ++ +G+K W

Sbjct: 121 VIDSENTNSIDFHKRFGFEEVGFIKESGFKFDRW 154

>ref|NP_287713.1| putative resistance protein [Escherichia coli O157:H7 EDL933]
 ref|NP_310079.1| resistance protein [Escherichia coli O157:H7 str. Sakai]
 ref|YP_403336.1| putative resistance protein [Shigella dysenteriae Sdl97]
 ref|YP_669358.1| acetyltransferase YncA [Escherichia coli 536]
 ref|YP_852603.1| acyltransferase [Escherichia coli APEC 01]
 ref|ZP_03082321.1| acyltransferase [Escherichia coli O157:H7 str. EC4024]
 ref|YP_002292806.1| putative acetyltransferase [Escherichia coli SE11]
 ref|YP_002329115.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli O127:H6 str. E2348/69]
 ref|YP_002391291.1| acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli S88]
 ref|YP_002397588.1| putative acyl-CoA N-acyltransferase domain-containing
 acyltransferase [Escherichia coli ED1a]
 ref|YP_002412436.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli UMN026]
 ref|YP_003077830.1| putative acyl-CoA N-acyltransferase domain-containing
 acyltransferase [Escherichia coli O157:H7 str. TW14359]
 ref|ZP_05432198.1| putative acyl-CoA N-acyltransferase [Shigella sp. D9]
 ref|YP_003229064.1| putative acyltransferase [Escherichia coli O26:H11 str. 11368]
 ref|YP_003234295.1| putative acyltransferase [Escherichia coli O111:H- str. 11128]
 ref|ZP_05938675.1| putative acyl-CoA N-acyltransferase [Escherichia coli O157:H7 str.
 FRIK2000]
 ref|ZP_05949884.1| putative acyl-CoA N-acyltransferase [Escherichia coli O157:H7 str.
 FRIK966]
 ref|ZP_06648919.1| acetyltransferase [Escherichia coli FVEC1412]
 ref|ZP_06653364.1| conserved hypothetical protein [Escherichia coli B354]
 ref|ZP_06657434.1| acetyltransferase [Escherichia coli B185]
 ref|ZP_06662258.1| acetyltransferase [Escherichia coli B088]
 ref|ZP_06990170.1| acetyltransferase [Escherichia coli FVEC1302]
 ref|ZP_07118247.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia
 coli MS 198-1]
 ref|ZP_07447764.1| putative acyl-CoA N-acyltransferase [Escherichia coli NC101]
 ref|ZP_07501944.1| putative acyl-CoA N-acyltransferase [Escherichia coli M605]
 ref|ZP_07512113.1| putative acyl-CoA N-acyltransferase [Escherichia coli TA206]

ref|ZP_07517341.1| putative acyl-CoA N-acyltransferase [Escherichia coli TA143]
 ref|ZP_07683172.1| acetyltransferase, GNAT family [Shigella dysenteriae 1617]
 ref|ZP_07783449.1| acetyltransferase, GNAT family [Escherichia coli 2362-75]
 gb|AAG56327.1|AE005361_8 putative resistance protein [Escherichia coli O157:H7 str. EDL933]
 dbj|BAB35475.1| putative resistance protein [Escherichia coli O157:H7 str. Sakai]
 gb|ABB61845.1| putative resistance protein [Shigella dysenteriae Sd197]
 gb|ABG69457.1| hypothetical acetyltransferase YncA [Escherichia coli 536]
 gb|ABJ00889.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain [Escherichia coli APEC 01]
 gb|ACI83756.1| putative resistance protein [Escherichia coli]
 gb|ACI83757.1| putative resistance protein [Escherichia coli]
 gb|ACI83758.1| putative resistance protein [Escherichia coli]
 gb|ACI83759.1| putative resistance protein [Escherichia coli]
 gb|ACI83760.1| putative resistance protein [Escherichia coli]
 dbj|BAG77055.1| putative acetyltransferase [Escherichia coli SE11]
 emb|CAS09137.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain [Escherichia coli O127:H6 str. E2348/69]
 emb|CAR02859.1| putative acyltransferase with acyl-CoA N-acyltransferase domain [Escherichia coli S88]
 emb|CAR07800.2| putative acyltransferase with acyl-CoA N-acyltransferase domain [Escherichia coli ED1a]
 emb|CAR12899.1| putative acyltransferase with acyl-CoA N-acyltransferase domain [Escherichia coli UMN026]
 emb|CAP75936.1| Uncharacterized acetyltransferase yncA [Escherichia coli LF82]
 gb|ACT71754.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain [Escherichia coli O157:H7 str. TW14359]
 dbj|BAI25324.1| predicted acyltransferase [Escherichia coli O26:H11 str. 11368]
 dbj|BAI35744.1| predicted acyltransferase [Escherichia coli O111:H- str. 11128]
 dbj|BAI54912.1| putative acetyltransferase [Escherichia coli SE15]
 emb|CBG34402.1| putative acetyltransferase [Escherichia coli 042]
 gb|EFE64071.1| acetyltransferase [Escherichia coli B088]
 gb|EFF00162.1| acetyltransferase [Escherichia coli FVEC1412]
 gb|EFF07816.1| acetyltransferase [Escherichia coli B185]
 gb|EFF12740.1| conserved hypothetical protein [Escherichia coli B354]
 gb|EFI19527.1| acetyltransferase [Escherichia coli FVEC1302]
 gb|EFJ72268.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 198-1]
 gb|EFM53472.1| putative acyl-CoA N-acyltransferase [Escherichia coli NC101]
 gb|ADN46231.1| acetyltransferase [Escherichia coli ABU 83972]
 gb|ADN71338.1| putative acyl-CoA N-acyltransferase [Escherichia coli UM146]
 gb|EFP69102.1| acetyltransferase, GNAT family [Shigella dysenteriae 1617]
 gb|EFR14046.1| acetyltransferase, GNAT family [Escherichia coli 2362-75]
 gb|ADR26857.1| putative acyl-CoA N-acyltransferase [Escherichia coli O83:H1 str. NRG 857C]
 gb|EFV00153.1| acetyltransferase family protein [Escherichia coli 3431]
 gb|EFX06907.1| putative acyl-CoA N-acyltransferase [Escherichia coli O157:H7 str. G5101]
 gb|EFX11699.1| putative acyl-CoA N-acyltransferase [Escherichia coli O157:H- str. 493-89]
 gb|EFX16514.1| putative acyl-CoA N-acyltransferase [Escherichia coli O157:H- str. H 2687]
 gb|EFX21513.1| putative acyl-CoA N-acyltransferase [Escherichia coli O55:H7 str. 3256-97 TW 07815]
 gb|EFX26664.1| putative acyl-CoA N-acyltransferase [Escherichia coli O55:H7 str. USDA 5905]
 gb|EFX31104.1| putative acyl-CoA N-acyltransferase [Escherichia coli O157:H7 str. LSU-61]
 gb|EFZ43489.1| acetyltransferase family protein [Escherichia coli EPECa14]
 gb|EFZ63649.1| acetyltransferase family protein [Escherichia coli 1180]
 gb|EFZ72612.1| acetyltransferase family protein [Escherichia coli RN587/1]
 gb|EGB43774.1| acetyltransferase [Escherichia coli H120]
 gb|EGB48538.1| acetyltransferase [Escherichia coli H252]

gb|EGB52591.1| acetyltransferase [Escherichia coli H263]
 gb|EGC11556.1| acetyltransferase [Escherichia coli E1167]
 Length = 172

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 81/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHMVAGI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH++LG+ + G K G W D+ F Q + P +
 Sbjct: 121 ESQNQASLHLHQSLGFVVTAQMPQVGTGKGRWLDLTFMQLQLDERTEPDAI 171

>ref|NP_385668.1| putative acetyltransferase (antibiotic resistance) protein
 [Sinorhizobium meliloti 1021]
 ref|ZP_07587666.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti BL225C]
 ref|ZP_07596613.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti AK83]
 emb|CAC46141.1| N-acetyltransferase [Sinorhizobium meliloti 1021]
 gb|EFN28005.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti AK83]
 gb|EFN32160.1| Phosphinothricin acetyltransferase [Sinorhizobium meliloti BL225C]
 Length = 169

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 57/178 (32%), Positives = 81/178 (45%), Gaps = 22/178 (12%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA----- 62
 +EIR A D+ A+C I N + +T W + L + +R WL A
 Sbjct: 1 MEIRDAAETDLPAICAIYNDAVANTTAI-----WNETLVDVANRKTWLKARNAAG 50

Query: 63 -----EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
 ++G V G A G W+A + Y TVE +VYV + G+G L L+ E
 Sbjct: 51 FPVLAALSLDGEVVGYSFGEWRAFDGYRHTVEHSVYVRADQRGGGIGRALMLELIDRAE 110

Query: 116 AQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAP 173
 A G ++A I N PS+RLHE LG+ G ++ G K G W D+ F Q +P
 Sbjct: 111 ALGKHVMIAGIESGNLPSIRLHEQLGFRETGHMKEVGTGKGRWLDLTFMQLILRTGSP 168

>gb|EFW74048.1| Putative acetyltransferase [Escherichia coli EC4100B]
 Length = 172

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHTVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDCGKHMVAGI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH +LG+ + G K G W D+ F Q + P +
 Sbjct: 121 ESQNQASLHLHSLGFVVTAQMPQVGTGKGRWLDLTFMQLQLDERTEPDAI 171

>gb|EFW52005.1| putative acetyltransferase [Shigella dysenteriae CDC 74-1112]
 gb|EFW59651.1| Putative acetyltransferase [Shigella flexneri CDC 796-83]
 gb|EGB57967.1| acetyltransferase [Escherichia coli H489]
 gb|EGB68817.1| acetyltransferase [Escherichia coli TA007]
 Length = 172

Score = 85.1 bits (209), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDSGKHVMVAGI 120

Query: 127 GLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH +LG+ + G K G W D+ F Q + P +
 Sbjct: 121 ESQNQASLHLHSLGFVVTAQMPQVGTGKFGRWLDLTFMQLQLDERTEPDAI 171

>ref|ZP_05077427.1| phosphinothricin acetyltransferase [Rhodobacterales bacterium Y4I]
 gb|EDZ45406.1| phosphinothricin acetyltransferase [Rhodobacterales bacterium Y4I]
 Length = 173

Score = 84.7 bits (208), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 56/172 (32%), Positives = 80/172 (46%), Gaps = 4/172 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRPATAAD AVC I N I + F T +TP++ + Y LVAE +G +
 Sbjct: 3 IRPATAADAEAVCAIANWVIRDTLATFNTVEKTPEQVRGQIAASNGAY--LVAEQDGSIL 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G A+ P+++ Y +T E T+++ Q G G L L G ++A +
 Sbjct: 61 GHAHYFPPRSGPGYRFTAETHIHLPAAGQGAGRALMQALEARAREAGLHVLIASVSSA 120

Query: 130 NDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE--LPAPPRPVRP 179
 N ++ H ALGY + G K+G W D F Q+ +PAP V P
 Sbjct: 121 NPGAIAFHAAALGYVETARMPGLGCKNGLWLDTVFMQKILTPGIPAPDSAVNP 172

>gb|AAT96234.1| phosphinothricin N-acetyltransferase [Pseudomonas viridiflava]
 Length = 199

Score = 84.7 bits (208), Expect = 4e-15, Method: Compositional matrix adjust.
 Identities = 57/170 (33%), Positives = 82/170 (48%), Gaps = 2/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
 +R A DM + I ++ +F EP + +E I L++ P+ VAE G V
 Sbjct: 26 LRDAREDDMPVIQAIYADHVLHGISSFELEPPSVEELIRRRALVLENGLPYRVAEHAGEV 85

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
 G YA P++ R AY +T E +VYV +G+G L L+ E G++ +VAVIG
 Sbjct: 86 VGYGYATPYRPRPAYRFTAEDSVYVRDGMGGMGIGRALLGDLIWHCEQGGWRQMVAVIGN 145

Query: 128 LPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LHE+ G+ G + G+KHG W D Q A PV
 Sbjct: 146 SENAASIGLHESFGFRRVGVFESVGFKHGRWVDTVLMQCALGDGASTLPV 195

>emb|CBJ36480.1| putative antibiotic resistance protein (Acetyltransferase)

[*Ralstonia solanacearum* CMR15]
Length = 182

Score = 84.7 bits (208), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 58/172 (33%), Positives = 86/172 (50%), Gaps = 7/172 (4%)

Query: 8 VEIRPATAADMA-AVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVA- 62
V + T A+ A A+ +I+N I ST + P+ PQ W + +P + A
Sbjct: 10 VRLIDCTEAHAPAILEILNEAIVNSTALYDYVPRPPQAMATWF--AAKRAGGFVVGAV 67

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
+ G + G A G ++A AY +TVE +VYV H + LG L L++ +A +
Sbjct: 68 DASGKLLGFASWGTFRAFPAKYKTVESVYVHHACGRRLGERLLRELIRRAQAAQVHVL 127

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
V I N S+ LH LG+ GT+R AG+K G W D F+Q + E+PA P
Sbjct: 128 VGCIDAANGASIGLHTRLGFVHAGTIREAGFKFGRWLDAAFYQLNLEMPAQF 179

>ref|ZP_05626426.1| phosphinothricin N-acetyltransferase [*Campylobacter gracilis*
RM3268]
gb|EEV16503.1| phosphinothricin N-acetyltransferase [*Campylobacter gracilis*
RM3268]
Length = 256

Score = 84.7 bits (208), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 41/104 (39%), Positives = 58/104 (55%), Gaps = 5/104 (4%)

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA +K R AYDW+ ES+VYVS + LG+G LY L ++++AQ + A I
Sbjct: 123 ILGYAYASAFKERAAYDWSAESSVYVSQNVRLGIGRLLYEALQALKAQNIADMNACIA 182

Query: 128 LP-----NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
ND SVR HE +G+ G YK G W+D+ + Q+
Sbjct: 183 CGDDEYLNDASVRFHERMGFRFVGKFERCAYKFGRWYDMAWMQK 226

>ref|YP_001458245.1| acetyltransferase [*Escherichia coli* HS]
ref|ZP_07103356.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 119-7]
ref|ZP_07119897.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 84-1]
ref|ZP_07212292.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 124-1]
ref|ZP_07688576.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 145-7]
gb|ABV05862.1| acetyltransferase, GNAT family [*Escherichia coli* HS]
gb|EFJ89612.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 84-1]
gb|EFK45257.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 119-7]
gb|EFK66282.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 124-1]
gb|EFO59319.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 145-7]
gb|EFU33452.1| toxin-antitoxin system, toxin component, GNAT family [*Escherichia coli* MS 85-1]
Length = 193

Score = 84.7 bits (208), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 57/174 (32%), Positives = 81/174 (46%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAE 63

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      R + IR A AD AA+ +I NH + + + + I E R YP LV+E
Sbjct: 19 RPDMSIRFARKADCAIAIEIYNHAVLYTAAIWNDQTVADADNRIAWFEARTIAGYPVLVSE 78

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
      +GVV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
Sbjct: 79 EDGVVTGYASF GDWRSFDGFRHTVEHSVYVHPDHQ GKGLGRKLLSRLIDEARDCGKHMV 138

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
      A I N S+ LH +LG+ + G K G W D+ F Q + P +
Sbjct: 139 AGIESQNQASLHLHSLGFFVTAQMPQVGTGKGRWLDLTFMQLQLDERTEPDAI 192

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>ref|YP_004287364.1| phosphinothricin acetyltransferase [Streptococcus gallolyticus
      subsp. gallolyticus ATCC BAA-2069]
emb|CBZ47620.1| phosphinothricin acetyltransferase [Streptococcus gallolyticus
      subsp. gallolyticus ATCC BAA-2069]
      Length = 190

```

Score = 84.7 bits (208), Expect = 4e-15, Method: Compositional matrix adjust.
Identities = 55/183 (30%), Positives = 85/183 (46%), Gaps = 9/183 (4%)

```

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
      V IR A D + I +Y+E + + F E + +E+ + + + YP+LVAE G
Sbjct: 3 VIIRLARLEDAKDLLAIYRYVEKTAITFEYEVPSLEEFQERMCSIMAFYPYLVAEEAGQ 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI- 126
      + G AYA + R AY W+ E+TVY+ + G+G +Y L + + G ++ A I
Sbjct: 63 ILGYAYASSFHPRAAYAWSAEATVYLDKAARGKGVGRQIYRALEEYLIKMGILNLNACIA 122

Query: 127 -----GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 180
      + S + H ALGY G +GYK W+D+ W L V+PV
Sbjct: 123 STETEDAYLTNGSEKFHRLGYQLVGKFHQSGYKFNHWYDM-IWMEKM-LGEHDNHVKPV 180

Query: 181 TQI 183
      I
Sbjct: 181 KSI 183

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>ref|YP_408038.1| resistance protein [Shigella boydii Sb227]
gb|ABB66210.1| putative resistance protein [Shigella boydii Sb227]
      Length = 172

```

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 56/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

```

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
      + IR A AD AA+ +I NH + + + + I E R YP LV+E +G
Sbjct: 1 MSIRFARKADCAIAIEIYNHAVLYTAAIWNDQTVADADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
      VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASF GDWRSFDGFRHTVEHSVYVHPDHQ GKGLGRKLLSRLIDEARDCGKHMVAGI 120

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
      N S+ LH +LG+ + G K G W D+ F Q + P +
Sbjct: 121 ESQNQASLHLHSLGFFVTAQMPQVGTGSGRWLDLTFMQLQLDERTEPDAI 171

```

```

>ref|ZP_04562062.1| conserved hypothetical protein [Citrobacter sp. 30_2]
gb|EEH93038.1| conserved hypothetical protein [Citrobacter sp. 30_2]
      Length = 172

```

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.

Identities = 57/172 (33%), Positives = 80/172 (46%), Gaps = 1/172 (0%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
          + IR A+ D AA+ +I NH + + + + + I E Q YP LV+E G
Sbjct: 1   MSIRFASKEDCAAIAEINYHAYLHTAAIWNDQTIDAENRISWYEARQLMGYPVLVSEENG 60

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          VV G A G W+ + + TVE +VYV HQ GLG L + L+ A G +VA I
Sbjct: 61  VVTGYASFGDWRNFDGFRHTVEHSVYVHPEHQGKGLGRALLSRLIDEARACGKHMVAVI 120

Query: 127  GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
          N S+ LH LG+ + G K G W D+ F Q + P +R
Sbjct: 121 ESQNQASLHLHSLGFKTTAQMPOVGTKFGRWLDLTFMQLQLDDRREPDALR 172
```

>ref|ZP_05639427.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv. tabaci ATCC 11528]
Length = 130

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 48/115 (41%), Positives = 66/115 (57%), Gaps = 1/115 (0%)

```
Query: 53  LQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112
          L + P+LVAE+ G V G YA P++ R AY +TVE +VY+ G+G L L++
Sbjct: 2   LVNGLPYLVAELAGEVVGYGATPYRPRPAYRFTVEDSVYIRDGMGGRGIGLALLGELVQ 61

Query: 113  SMEAQGFKSVVAVIG-LPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 166
          E G++ +VAVIG N S+RLHE LG+ G + G+KHG W D QR
Sbjct: 62  RCEQGGWRQMVAVIGNSENIASRLRHERLGFRRVGVFESVGFKHGRWVDTVLMQR 116
```

>ref|ZP_05056656.1| acetyltransferase, GNAT family [Verrucomicrobiae bacterium DG1235]
gb|EDY81796.1| acetyltransferase, GNAT family [Verrucomicrobiae bacterium DG1235]
Length = 165

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 51/150 (34%), Positives = 78/150 (52%), Gaps = 6/150 (4%)

```
Query: 20  AVCDIVNHYIETSTVNFRTPEQTP---QEWDLLERLQDRYPWLVAEVE-GVVAGIAYAG 75
          ++ I NH I TST + +P+T Q+W E+ +P + E E G + G A G
Sbjct: 14  SILQIFNHAIATSTSLYDQPRTEKSMQDWFATKEK--GNFPVIGIEAENGELMGFASYG 71

Query: 76  PWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVR 135
          ++ AY +TVE ++YV ++ GLG L + +++ Q ++ VI N SV
Sbjct: 72  IFRPHAAYQYTVESLYVHSNYRGNGLGKLLSEIIERARRQNLHLMIGVIDSTNTTSVH 131

Query: 136  LHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165
          LH++LG+T GTL GYK W D F+Q
Sbjct: 132 LHKSLGFTYAGTLNQVGKFERWLDADFYQ 161
```

>sp|P31668.1|PAT_ALCFA RecName: Full=Phosphinothricin N-acetyltransferase; Short=PPT
N-acetyltransferase; AltName:
Full=Phosphinothricin-resistance protein
Length = 197

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.
Identities = 52/164 (31%), Positives = 83/164 (50%), Gaps = 2/164 (1%)

```
Query: 5   RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAE 63
          R +R D+ A+ I H++ T T +F P E ++ D P+LVAE
Sbjct: 23  RCACTVRVVRDDDLPAITAIYAAHVRTGTASFEEVPPDDTEMRARCAKVLDAGLPYLVAE 82
```


Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 +G + G AYA ++ R+AY +T+E +VY++ G+G TL L+ E ++ ++
 Sbjct: 83 RDGKLLGYAYATHYRPRSAYRFTLEDSVYIAPDAIGQGVGRTLTLTLIARCEGGPWRQLI 142

Query: 124 AVIGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 A +G N S+ LH A G+ G L++ G+K G W D QR
 Sbjct: 143 ANVGDSGNTASLGLHAACGFVQAGVLKSVGFKFGRWIDTVLMQR 186

>ref|NP_415965.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 ref|AP_002071.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. W3110]
 ref|YP_001730442.1| acyltransferase [Escherichia coli str. K-12 substr. DH10B]
 ref|YP_002926471.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BW2952]
 ref|ZP_05436740.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia sp. 4_1_40B]
 ref|ZP_07497456.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli H736]
 ref|ZP_07785790.1| acetyltransferase family protein [Escherichia coli 1827-70]
 sp|P76112.1|YNCA_ECOLI RecName: Full=Uncharacterized N-acetyltransferase YncA
 gb|AAC74530.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. MG1655]
 dbj|BAA15080.2| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K12 substr. W3110]
 gb|ACB02664.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli str. K-12 substr. DH10B]
 gb|ACR64123.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BW2952]
 gb|ACX39848.1| GCN5-related N-acetyltransferase [Escherichia coli DH1]
 gb|EFQ01412.1| acetyltransferase family protein [Escherichia coli 1827-70]
 dbj|BAJ43247.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli DH1]
 gb|EGB38378.1| acetyltransferase [Escherichia coli E482]
 Length = 172

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNQTVADNRIAWFEARTLAGYPVLVSEENG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRPV 177
 N S+ LH++LG+ + G K G W D+ F Q + P +
 Sbjct: 121 ESQNQASLHLHQSGLGFVVTQMPQVGTGKFRWLDLTFMQLQLDERTEPDAI 171

>ref|YP_003648553.1| GCN5-related N-acetyltransferase [Tsukamurella paurometabola DSM
 20162]
 gb|ADG80214.1| GCN5-related N-acetyltransferase [Tsukamurella paurometabola DSM
 20162]
 Length = 165

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.
 Identities = 55/162 (33%), Positives = 81/162 (50%), Gaps = 5/162 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64

+EIR A +D+ A+ I N ++ ST + E E W+ ER +P LVA V
 Sbjct: 4 MEIRDAQPSDLPAILVIHNDVNDSTAIWSEEKADLAERTAWL--AERRAGGFVPLVAIV 61
 Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +G + G A GP++++ Y +TVE++VYV+ R G+ L L++ + VVA
 Sbjct: 62 DGELGGYASYGPFRTGYRYTVENSIVYVADGFYRRGIAEALMNALIERAQQSDVHVVA 121
 Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
 I N SV LH LG+ G + G K G W D+ QR
 Sbjct: 122 AIEESNHASVALHRKLGFRVTGQMPQVGKIFGRWLDLVLQM 163

>ref|YP_003801878.1| GCN5-related N-acetyltransferase [Spirochaeta smaragdinae DSM
 11293]
 gb|ADK79284.1| GCN5-related N-acetyltransferase [Spirochaeta smaragdinae DSM
 11293]
 Length = 173

Score = 84.7 bits (208), Expect = 5e-15, Method: Compositional matrix adjust.
 Identities = 49/166 (29%), Positives = 85/166 (51%), Gaps = 8/166 (4%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWL-VAEVEGVVAGIAYA 74
 +++ DI N I ST + +P+T + W DD E+ +P + + + + G
 Sbjct: 12 SSILDIYNEAIIHSTALYDYKPRTIESMGTFWDDKEK--KGFPFIIGLVDDKNRLIGFGTY 69
 Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSV 134
 G ++AR AY +TVE ++Y+ ++ G G L ++ Q + ++A I N S+
 Sbjct: 70 GNFRARPAYHYTVEHSIYIQKEYRGCGYGELLREIIAKAAEQDYHCLIAIDSENAASI 129
 Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 180
 LH+ LG++ G L+ GYK G W ++ F+Q LP P P R +
 Sbjct: 130 HLHKKLGFSLGELKQVGYKFGRWLNLVFYQ--LILPTPQEPQREI 173

>ref|YP_003036408.1| GCN5-related N-acetyltransferase [Escherichia coli
 BL21-Gold(DE3)pLysS AG]
 ref|YP_003044614.1| putative acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli B str. REL606]
 emb|CAQ31933.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BL21(DE3)]
 gb|ACT29223.1| GCN5-related N-acetyltransferase [Escherichia coli
 'BL21-Gold(DE3)pLysS AG']
 gb|ACT39078.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli B str. REL606]
 gb|ACT43288.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
 [Escherichia coli BL21(DE3)]
 Length = 172

Score = 84.3 bits (207), Expect = 6e-15, Method: Compositional matrix adjust.
 Identities = 56/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNQTVADNRIAWFEARTIAGYPVLVSEEDG 60
 Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVYPDHQKGKGLGRKLLSRLIDEARDSGKHVMVAGI 120
 Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH +LG+ + G K G W D+ F Q + P +
 Sbjct: 121 ESQNQASLHLHSLGFVVTAQMPQVGTGKFGRWLDLTFMQLQLDERTEPDAI 171

>ref|YP_001991332.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris TIE-1]
gb|ACF00857.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris TIE-1]
Length = 180

Score = 84.3 bits (207), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 58/176 (32%), Positives = 83/176 (47%), Gaps = 7/176 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQD---RYPWL 61
P+ IR + D+ A+ DI +YI + TPQ DDL ER ++ R+P LV
Sbjct: 6 PILIRSSHDGDVEAMLDIYRYIIRGLDEGIDDHGTPQP--DDLKERRKNLRNRRFPHLV 63

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 121
A V G AY ++ R AY +TV+ ++YV H G+G L L+ + A GF+
Sbjct: 64 AIRGETVVGAYAVVLFKRKPAYRYTVKHSIYVHPDHLGSGIGRLLMRELIDACAAAGFRQ 123

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
++ I N S+ LH G+ G L Y++G W D QR A PV
Sbjct: 124 MIGYIDADNAASLGLHHGFGFATVGRLPGVAYRYGRWADTMVQVQSLGAGATTPPV 179

>ref|ZP_06934756.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
[Escherichia coli OP50]
Length = 172

Score = 84.3 bits (207), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 56/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
+ IR A AD AA+ +I NH + + + I E R YP LV+E +G
Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVI 126
VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVYPDHQKGLGRKLLSRLIDEARDSGKHVMVAGI 120

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH +LG+ + G K G W D+ F Q + P +
Sbjct: 121 ESQNQASLHLHSLGFVVTAQIPQVGTGKGRWLDLTFMQLQLDERTEPDAI 171

>ref|ZP_04661553.1| Acetyltransferase (GNAT) family protein [Acinetobacter baumannii AB900]
Length = 181

Score = 84.3 bits (207), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 50/180 (27%), Positives = 88/180 (48%), Gaps = 12/180 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE----RLQD 55
+ R ++ A A A+ +I+N I ST + P++ +D ++ + ++
Sbjct: 5 LDSNFRLLIDCNEAEHA--VAILEILNDIVNSTALYDYVPRS----LDSMKTWFSVKREN 58

Query: 56 RYPWL-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
+P + V + G + G A G ++A AY +TVE ++Y+ H H+ GL L L++
Sbjct: 59 GFPVIGVDESGLKLGFAWGTFRAFPAKYTVESHSIYHHEHRGCGLSKVLMQALIQRA 118

Query: 115 EAQGFKS VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
+ F ++ I N S+ LHE +G+T GT + G+K G W D F+Q + P P
Sbjct: 119 QQAQFHVLIQCIDATNQASIGLHEKMGFTAGTFKQVGFKFGQWLDAAFYQLVLDTPFEP 178

>ref|YP_002544927.1| phosphinothricin acetyltransferase (antibiotic resistance)
protein

[Agrobacterium radiobacter K84]
gb|ACM26997.1| phosphinothricin acetyltransferase (antibiotic resistance) protein
[Agrobacterium radiobacter K84]
Length = 183

Score = 84.3 bits (207), Expect = 6e-15, Method: Compositional matrix adjust.
Identities = 58/161 (36%), Positives = 82/161 (50%), Gaps = 8/161 (4%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTV--NFRTEPQTPQEWIDDLERLQDRYPW 59
P+ P+ IR A A D+ + I N + + + + +EW+ D RL+ YP
Sbjct: 4 PKEEPMRIRDAEATDIDGITAIYNDAVANTAAIWNEKQVDADNRREWLRLD--RLKLGYPV 61

Query: 60 LVA--EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
LVA + E VV G A G W+A + Y TVE +VYV + +R G+G L L+ +A
Sbjct: 62 LVAIDREDVV--GYASFGDWRAFDGYRHTVEHSVYVRNDQRRNGVGKGLMIELIGRAKAI 120

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
G ++VA I N S+RLHE LG+ G L G K G W
Sbjct: 121 GKHAMVAGIEAGNTGSIRLHEKLGFKQVGLLPEVGTGKFRGW 161

>ref|YP_001335576.1| acetyltransferase [Klebsiella pneumoniae subsp. pneumoniae MGH
78578]
ref|ZP_06017603.1| GNAT family toxin-antitoxin system [Klebsiella pneumoniae subsp.
rhinoscleromatis ATCC 13884]
gb|ABR77346.1| hypothetical acetyltransferase [Klebsiella pneumoniae subsp.
pneumoniae MGH 78578]
gb|EEW39306.1| GNAT family toxin-antitoxin system [Klebsiella pneumoniae subsp.
rhinoscleromatis ATCC 13884]
Length = 172

Score = 84.3 bits (207), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 57/170 (33%), Positives = 82/170 (48%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
+ IRPA D AA+ +I NH + T+ + N +T + W + R +P LV+E
Sbjct: 1 MSIRPAIKDDCAAIAEINYHNAVHTAAIWNDKTVDTDNRIAWFE--ARQLAGFPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+GV+ G + G W+A + + TVE +VYV HQ GLG L L+ +VA
Sbjct: 59 DGVITGYSSFGDWRAFDGFRHTVEHSVYVHPHQKGLGRKLLVALIAEARRLNKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
I N S+ LHE LG+ G + G K G W D+ F Q + P
Sbjct: 119 GIESQNHASLHLHETLGFITGQMPQVGTGKFRWLDTFMQLQLDARQDP 168

>ref|YP_001453059.1| hypothetical protein CKO_01490 [Citrobacter koseri ATCC BAA-895]
gb|ABV12623.1| hypothetical protein CKO_01490 [Citrobacter koseri ATCC BAA-895]
Length = 172

Score = 84.3 bits (207), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 59/170 (34%), Positives = 82/170 (48%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
+ IR A D A + +I NH + T+ + N +T + W D R YP LV+E
Sbjct: 1 MSIRFAGKEDCATIAEINYHNAVHTAAIWNDQTVDDVDNRIAWFD--ARQLSGYPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
GVV G A G W+ + + TVE +VYV HQ GLG L + L++ A G +VA
Sbjct: 59 NGVVTGYASFGDWRFNFDGFRHTVEHSVYVHPDHQKGLGRALLSRLIEEARACGKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174

I N S+ LHE LG++ + G K G W D+ F Q + P
Sbjct: 119 GIESQNQASLHLHETLGFSTIAQMPQVGTGKFGRWLDLTFMQLQLDDRCDP 168

>ref|YP_004109757.1| GCN5-like N-acetyltransferase [Rhodopseudomonas palustris DX-1]
gb|ADU45024.1| GCN5-related N-acetyltransferase [Rhodopseudomonas palustris DX-1]
Length = 180

Score = 84.0 bits (206), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 55/167 (32%), Positives = 81/167 (48%), Gaps = 7/167 (4%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDL-ERLQD---RYPWL 61
P+ IR + D+ A+ DI +YI + PQ DDL ER ++ R+P LV
Sbjct: 6 PILIRSSHGDVEAMLDIYRYIIRGLDEGIDDNMGMPQP--DDLKERRKNLRNRRFPHLV 63

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
A VAG AY ++ R AY +TV+ ++YV H G+G L L+ + A GF+
Sbjct: 64 ALRGEAVAGYAYVVLFRKRPAYRYTVKHSIYVHPDHLGCGIGRLLMHLEIDACAAAGFRQ 123

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
++ I N S+ LH + G+ G L Y++G W D QR
Sbjct: 124 MIGYIDADNTASLALHHSFGFATVGRPLPGVAYRYGRWADTVMVQRSL 170

>ref|YP_310616.1| putative resistance protein [Shigella sonnei Ss046]
ref|YP_001725176.1| GCN5-related N-acetyltransferase [Escherichia coli ATCC 8739]
ref|ZP_03026820.1| acetyltransferase, GNAT family [Escherichia coli B7A]
ref|ZP_07521998.1| GCN5-related N-acetyltransferase [Escherichia coli TA271]
ref|ZP_07589419.1| GCN5-related N-acetyltransferase [Escherichia coli W]
ref|ZP_07613275.1| GCN5-related N-acetyltransferase [Escherichia coli H591]
gb|AAZ88381.1| putative resistance protein [Shigella sonnei Ss046]
gb|ACA77849.1| GCN5-related N-acetyltransferase [Escherichia coli ATCC 8739]
gb|EDV64453.1| acetyltransferase, GNAT family [Escherichia coli B7A]
gb|EFN39981.1| GCN5-related N-acetyltransferase [Escherichia coli W]
gb|ADT75053.1| predicted acyltransferase with acyl-CoA N-acyltransferase domain
[Escherichia coli W]
gb|EFZ55306.1| acetyltransferase family protein [Shigella sonnei 53G]
gb|ADX50976.1| Phosphinothricin acetyltransferase [Escherichia coli K011]
Length = 172

Score = 84.0 bits (206), Expect = 7e-15, Method: Compositional matrix adjust.
Identities = 56/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDL-RLQDRYPWLVAEVEG 66
+ IR A AD AA+ +I NH + + + + I E R YP LV+E +G
Sbjct: 1 MSIRFARKADCAAI AEIYNHAVLYTAAIWNQTVADNR IAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVI 126
VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQGKGLGRKLLSRLIDEARDCGKHMVAGI 120

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH +LG+ + G K G W D+ F Q + P +
Sbjct: 121 ESQNQASLHLHSLGFVVTAQMPQVGTGKFGRWLDLTFMQLQLDERTEPDAI 171

>gb|AAT96250.1| phosphinothricin N-acetyltransferase [Pseudomonas viridiflava]
Length = 199

Score = 84.0 bits (206), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 53/158 (33%), Positives = 79/158 (50%), Gaps = 2/158 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
 +R A DM + I ++ +F EP + +E + L++ P+ VAE G V
 Sbjct: 26 LRDAREDDMPVIQAIYADHVLHGIISSFELEPPSVEELMRRRALVLENGLPYRVAEHAGEV 85

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
 G YA P++ R AY +T E +VYV +G+G L L+ E G++ +VAVIG
 Sbjct: 86 VGYGYATPYRPRPAYRFTAEDSVYVRDGMGGMIGRALLGDLIWHCEQGGWRQMVAVIGN 145

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 N S+ LHE+ G+ G + G+KHG W D Q
 Sbjct: 146 SENAASIGLHESFGFRRVGVFESVGFKHGRWVDTVLMQ 183

>gb|AAT96331.1| phosphinothricin N-acetyltransferase [Pseudomonas viridiflava]
 Length = 199

Score = 84.0 bits (206), Expect = 8e-15, Method: Compositional matrix adjust.
 Identities = 55/163 (33%), Positives = 81/163 (49%), Gaps = 10/163 (6%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-----LQDRYPWLVAE 63
 +R A DM + I ++ +F EP + + +L R L+ P+ VAE
 Sbjct: 25 NLRDAREDDMPVIQAIYADHVLHGIISSFELEPPS----VGELARRRALVLESGLPYRVAE 80

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMV 123
 G V G YA P++ R AY +TVE +VYV + +G+G L L+ E G++ +V
 Sbjct: 81 HAGEVVGYYATPYRPRPAYRFTVEDSVYVRNGMGMIGRALLGDLIWHCEQGGWRQMV 140

Query: 124 AVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 AVIG N S+ LHE+ G+ G + G+KHG W D Q
 Sbjct: 141 AVIGNSENAASIGLHESFGFRRVGVFESVGFKHGRWVDTVLMQ 183

>gb|AAT96291.1| phosphinothricin N-acetyltransferase [Pseudomonas viridiflava]
 Length = 199

Score = 84.0 bits (206), Expect = 8e-15, Method: Compositional matrix adjust.
 Identities = 56/170 (32%), Positives = 82/170 (48%), Gaps = 2/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
 +R A DM + I ++ +F EP + +E + L++ P+ VAE G V
 Sbjct: 26 LRDAREDDMPVIQAIYADHVLHGIISSFELEPPSVEELMRRRALVLENGLPYRVAEHAGEV 85

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG- 127
 G YA P++ R AY +T E +VYV +G+G L L+ E G++ +VAVIG
 Sbjct: 86 VGYGYATPYRPRPAYRFTAEDSVYVRDGMGGMIGRALLGDLIWHCEQGGWRQMVAVIGN 145

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LHE+ G+ G + G+KHG W D Q A PV
 Sbjct: 146 SENAASIGLHESFGFRRVGVFESVGFKHGRWVDTVLMQCALGDGASTLPV 195

>ref|NP_947397.1| putative phosphinothricin N-acetyltransferase [Rhodopseudomonas
 palustris CGA009]
 emb|CAE27493.1| putative phosphinothricin N-acetyltransferase [Rhodopseudomonas
 palustris CGA009]
 Length = 203

Score = 84.0 bits (206), Expect = 8e-15, Method: Compositional matrix adjust.
 Identities = 58/176 (32%), Positives = 84/176 (47%), Gaps = 7/176 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDL-ERLQD----RYPWL 61
 P+ IR + D+ A+ DI +YI + TPQ DDL ER ++ R+P LV

Sbjct: 29 PILIRSSHDGDVEAMLDIYRYIIRGLDEGIDDHGTPQP--DDLKERRKNLRNRRFPHLV 86

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
A V G AY ++ R AY +TV+ ++YV H G+G L L+ + A GF+

Sbjct: 87 AIRGETVIGYAYVVLFRKRPAYRYTVKHSIYVHPDHLGSGIGRLLMHOLIDACAAAGFRQ 146

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQPDFELPAPPRPV 177
++ I N S+ LH + G+ G L Y++G W D QR A PV

Sbjct: 147 MIGYIDADNAASLGLHHSFGFATVGRLPGVAYRYGRWADTMVQVQSLGAGATTPPV 202

>ref|ZP_07153818.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 21-1]
gb|EFK19464.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 21-1]
Length = 214

Score = 84.0 bits (206), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 56/174 (32%), Positives = 81/174 (46%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLE-RLQDRYPWLVAE 63
R + IR A AD AA+ +I NH + + + + I E R YP LV+E

Sbjct: 40 RPNMSIRFARKADCAIAIEYNHAVLYTAAIWNQTVADNRIAWFEARTLAGYPVLVSE 99

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
+GVV G G W++ + + TVE +VYV HQ GLG L + L+ G +V

Sbjct: 100 QDGVVTGYVSFGDWRSFDFGRHTVEHSVYVHPDHQKGLGRKLLSRLIDEARDCGKHMV 159

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQPDFELPAPPRPV 177
A I N S+ LH++LG+ + G K G W D+ F Q + P +

Sbjct: 160 AGIESQNQASLHLHQSLGFVITAQMPQVGTGFRWLDLTFMQLQLDERTEPDAI 213

>ref|YP_001630169.1| acetyltransferase [Bordetella petrii DSM 12804]
emb|CAP41900.1| acetyltransferase [Bordetella petrii]
Length = 186

Score = 84.0 bits (206), Expect = 8e-15, Method: Compositional matrix adjust.
Identities = 58/171 (33%), Positives = 83/171 (48%), Gaps = 8/171 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAE- 63
VE A AD A+ I N I TST + P+TP + W + + +P + E

Sbjct: 17 VECTHARHAD--AILAIFNDAILTSTALYEYRPRTPATMRAWFE--AKQAGGFVIGFEN 72

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
G + G A G ++A A +TVE +VY+ R + GL L L+ + +V

Sbjct: 73 AGGELMGFASYGAFRAYPANKYTVEHSVIDARFRGRGLAEALMRTLARARERQLHVLV 132

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQPDFELPAPP 174
I N S+RLHE LG+ GT+R AG+K G W D+ F+Q + PA P

Sbjct: 133 GGIDAANTASIRLHEKLGFEHAGTIRHAGFKFGRWLDLAFYQLTLDTPAEP 183

>ref|YP_003365162.1| putative acetyltransferase [Citrobacter rodentium ICC168]
emb|CBG88346.1| putative acetyltransferase [Citrobacter rodentium ICC168]
Length = 172

Score = 84.0 bits (206), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 60/174 (34%), Positives = 84/174 (48%), Gaps = 5/174 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
+ IR A D AA+ +I NH + T+ + N +T + + W + + L YP LV+E

Sbjct: 1 MSIRFACKEDCAAIAIEYNHAVLHTAAIWNQTVDAENRIAWYEARQLLG--YPVLVSEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
G V G A G W+ + + TVE +VYV HQ GLG L + L+ A G +VA
Sbjct: 59 NGTVTGYASFGDWRNFDGFRHTVEHSVYVHPDHQGKGLGRQLLSRLIDEARACGKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
I N S+ LHE LG+T + G K G W D+ F Q + P R
Sbjct: 119 GIESQNHASLHLHETLGFTLTAQMPQVGTGFRWLDLTFMQLQLDDRLEPDARR 172

>ref|YP_004214190.1| GCN5-related N-acetyltransferase [Rahnella sp. Y9602]
gb|ADW75063.1| GCN5-related N-acetyltransferase [Rahnella sp. Y9602]
Length = 173

Score = 84.0 bits (206), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 47/159 (29%), Positives = 82/159 (51%), Gaps = 6/159 (3%)

Query: 20 AVCDIVNHYIETSTVNFRTPEQ---TPQEWIDDLERLQDRYPWL-VAEVEGVVAGIAYAG 75
A+ DI N I TST + +P+ + W +L +P + + + +G + G A G
Sbjct: 14 AILDIFNDAILTSTALYDYKPRHIDSMTSWFA--TKLTHNFPVIGLEDAQGTLLGFASYG 71

Query: 76 PWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVR 135
++A AY ++VE ++Y+ H+ GLG L + L+++ +G +++ I N S+
Sbjct: 72 TFRAPPAYKYSVEHSIYIHKDHRGKGLKILLSALVEAARERGVHTLIGAIDAANSGSIA 131

Query: 136 LHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
LHE G+ GT++ A +K W D+ F+Q E P P
Sbjct: 132 LHEKNGFIHTGTIKQAQAFKFRWLDLAFYQMIETPLKP 170

>ref|ZP_02244935.1| phosphinothricin acetyltransferase [Xanthomonas oryzae pv.
oryzicola BLS256]
Length = 173

Score = 84.0 bits (206), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 53/158 (33%), Positives = 83/158 (52%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL-VAEVEGVVAGIAYAGP 76
+A+ DI N I S + P+ P+ + Q +P + V + +G + G A G
Sbjct: 13 SAILDIFNEAIANSNALYDYRPRPPESMVGFATKQAGGFPVIGVEDADGTLMGFASYGT 72

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++A A+ ++VE ++YV H+ GLG L L+ + +A+G +V I N S+ L
Sbjct: 73 FRAWPAFKYSVEHSIYVHCDHRGKGLGRLLLQALIAAAQARGVHVLVGGIDASNQASIAL 132

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE G+T GT+R AG+K G W D+ F+QR PA P
Sbjct: 133 HEQFGFTHAGTVREAGFKFGRWLDLAFYQRILATPADP 170

>ref|YP_002983106.1| GCN5-like N-acetyltransferase [Ralstonia pickettii 12D]
gb|ACS64434.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12D]
Length = 171

Score = 84.0 bits (206), Expect = 9e-15, Method: Compositional matrix adjust.
Identities = 59/169 (34%), Positives = 82/169 (48%), Gaps = 5/169 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
+R AT AD+ A+ I N I S + P T ++ W+ R YP LVA+ +
Sbjct: 3 LRDATQADLPAILAIYNDVIANSNAIYETPTVLTEDRTAWL--ALRATQGYPVLVADDDR 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VAG+A G ++ + TVE +V++ + GLGS L L + A G +V I

Sbjct: 61 QVAGVASFGDFRPHPGFRTTVEHSVHIHRDWRGQGLGSRLVEALCERAAALGKHLMVGAI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFELPAPPR 175

N S+RLHE LG+ G + A KHG W D+ F QR E P R

Sbjct: 121 DGGNAGSIRLHEKLGFKFVGRMPEAAIKHGQWLDLVFMQRWLEAPGTVR 169

>ref|ZP_04600234.1| hypothetical protein VEIDISOL_01683 [Veillonella dispar ATCC 17748]

gb|EEP64622.1| hypothetical protein VEIDISOL_01683 [Veillonella dispar ATCC 17748]

Length = 166

Score = 83.6 bits (205), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 50/153 (32%), Positives = 76/153 (49%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68

IRP T D+AA DI N+ + E +T EW + E Q + V ++ VV

Sbjct: 6 IRPITKDDIAACLDIYNYEVVNGVATLDLEARTLLEWQEWYEAHQTSSEHCIFVGLIDDVV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSVAIVIG 127

G A P++ ++A+ TVE ++Y+ ++ G+ S L H+L + E +VV+VI

Sbjct: 66 VGYASLSPYRTKDAFKSTVELSIYIHQFYRGRGVASKLMAHILDHAKETDTLHTTVSVIT 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

N S LHE G+T G G+KHG + D

Sbjct: 126 AGNAASTALHERFGFTYCGLTPQVGFKHGKYQD 158

>gb|ADY81488.1| putative antibiotic resistance (acetyltransferase) protein

[Acinetobacter calcoaceticus PHEA-2]

Length = 181

Score = 83.6 bits (205), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 48/176 (27%), Positives = 85/176 (48%), Gaps = 4/176 (2%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPW 59

++ R ++ AT A A+ DI+N I ST + P++ + + ++ +P

Sbjct: 5 LNSNLRLLIDCHEATHAK--AILDILNEAIINSTALYDYLPRSEESMKNWFAVKRENGFPV 62

Query: 60 L-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118

+ + + + G A G ++A AY +TVE ++Y+ H H+ GL L L+K +

Sbjct: 63 IGIIDETNKLGLFASWGTFRAPFAYKYTVEHSIYIHHEHRGGGLSKILMQELIKRAQEAD 122

Query: 119 FKSVAIVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFELPAPP 174

++ I N S+ LHE +G+ GT + G+K G W D F+Q + P P

Sbjct: 123 LHVLIIGCIDATNQASIGLHEKMGFIHAGTFKQVGFKFGQWLDAAFYQLNLNTPHTP 178

>ref|YP_001622888.1| hypothetical protein BSUIS_B1127 [Brucella suis ATCC 23445]

gb|ABY40066.1| Hypothetical protein, conserved [Brucella suis ATCC 23445]

Length = 164

Score = 83.6 bits (205), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 52/160 (32%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66

IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG

Sbjct: 5 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAIVI 126

V G A GP++ + + E +VYV+ + G+G TL L+K + ++A I

Sbjct: 63 QVVGYASYGPFRRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIKEARERKRVHVLIAIGI 122

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

N S+ LH + G+ GTL+ G K G W D+ F Q+

Sbjct: 123 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 162

>ref|YP_001270028.1| GCN5-related N-acetyltransferase [Pseudomonas putida F1]

gb|ABQ80844.1| GCN5-related N-acetyltransferase [Pseudomonas putida F1]

Length = 171

Score = 83.6 bits (205), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 59/169 (34%), Positives = 76/169 (44%), Gaps = 5/169 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEP---QTPQEWIDDLERLQDRYPWLVAEVE 65

EIR A D+ + DI N + +T + P Q W + R Q YP LVA E

Sbjct: 4 EIRDARPTDVPGILDIYNDAVLNTTAIWNETPVDLGNRQAWFE--ARAQQGYPIVLATDE 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125

V G A G W+ + TVE +VYV + GLG L L++ + G +VA

Sbjct: 62 TGVLYGASFGDWRPFEGFRILTVEHSVYVRGDQRGKGLGPVLMALIERAKGCGKHMVA 121

Query: 126 IGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPAPP 174

I N SVRLHE LG+ G + G K G W D+ F Q A P

Sbjct: 122 IESGNAASVRLHERLGFVVTGQMPQVGKFGRWLDLTFMQLVLNPGAEP 170

>emb|CBJ01023.1| putative acetyltransferase [Escherichia coli ETEC H10407]

gb|EGB33769.1| acetyltransferase [Escherichia coli E1520]

Length = 172

Score = 83.6 bits (205), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 55/171 (32%), Positives = 81/171 (47%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVAEVEG 66

+ IR A AD AA+ +I NH + + + + I E R YP LV+E +G

Sbjct: 1 MSIRFARKADCAAIAEIIYNHAVLYTAAIWNQTVADNRIAWFEARTLAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126

VV G A G W++ + + TVE +VYV HQ GLG L + ++ G +VA I

Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQKGLGRKLLSRVIDEARDGKHMVAVI 120

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPAPPRPV 177

N S+ LH++LG+ + G K G W D+ F Q + P +

Sbjct: 121 ESQNQASLHLHQSLGFVITAQMPQVGTKFGRWLDLTFMQLQLDERTEPDAI 171

>ref|YP_001893348.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12J]

ref|YP_002983691.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12D]

gb|ACD29921.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12J]

gb|ACS65019.1| GCN5-related N-acetyltransferase [Ralstonia pickettii 12D]

Length = 182

Score = 83.6 bits (205), Expect = 1e-14, Method: Compositional matrix adjust.

Identities = 54/160 (33%), Positives = 79/160 (49%), Gaps = 6/160 (3%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEPQTPQE---WIDDLERLQDRYPWLVA-EVEGVVAGIAYA 74

+A+ DI+N I ST + P+ PQ W + +P + A + G + G A

Sbjct: 22 SAILDILNEAIVNSTALYDYVPRPPQAMQVWF--AAKRAGGFVVGAVDASGRLLGFASW 79

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPSV 134

G ++A AY +TVE +VYV H + GLG L L++ +A +V I N SV

Sbjct: 80 GTFRAFPAYKYTVEHSVYVHSSRGRGLGERLLQELIRRAQAAQVHVLVGCIDAANAGSV 139

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPAPP 174

LH LG+ GT++ AG+K G W D F+Q + P P
 Sbjct: 140 ALHTRLGVHAGTIKEAGFKFGRWLDAAFYQLNLATPEHP 179

>ref|ZP_03043698.1| acetyltransferase, GNAT family [Escherichia coli E22]
 ref|ZP_07096562.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 107-1]
 gb|EDV84326.1| acetyltransferase, GNAT family [Escherichia coli E22]
 gb|EFK52092.1| toxin-antitoxin system, toxin component, GNAT family [Escherichia coli MS 107-1]
 Length = 194

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
 Identities = 56/174 (32%), Positives = 81/174 (46%), Gaps = 1/174 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAE 63
 R + IR A AD AA+ +I NH + + + + I E R YP LV+E
 Sbjct: 20 RPDMSIRFARKADCAIAIEIYNHAVLYTAAIWNQTVADADNRIAWFEARTIAGYPVLVSE 79
 Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +V
 Sbjct: 80 EDSVVTGYASFQDWRSDGFRHTVEHSVYVHPDHQKGKGLGRKLLSRLIDEARDGKHMV 139
 Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRPV 177
 A I N S+ LH++LG+ + G K G W D+ F Q + P +
 Sbjct: 140 AGIESQNQASLHLHQSLGFVVTAQMPQVGTGKFRWLDLTFMQLQLDERTEPDAI 193

>ref|ZP_07466039.1| phosphinothricin N-acetyltransferase [Streptococcus bovis ATCC 700338]
 gb|EFM27940.1| phosphinothricin N-acetyltransferase [Streptococcus bovis ATCC 700338]
 Length = 212

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
 Identities = 55/183 (30%), Positives = 84/183 (45%), Gaps = 9/183 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGV 67
 V IR A D + I +Y+E + + F E + +E+ + + YP+LVAE G
 Sbjct: 25 VIIRLARLEDAKDLLAIYRYVEKTAITFEYEVPSLEEFGKRMCSIMAFYPYLVAEEAGQ 84
 Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI- 126
 + G AYA + R AY W+ E+TVY+ + G+G +Y L + + G ++ A I
 Sbjct: 85 ILGYAYASSFHPRAAYAWSAEATVYLDKAVRGKGVGRQIYRALEEYLIKMGILNLNACIA 144
 Query: 127 -----GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPRPVRPV 180
 + S + H ALGY G +GYK W+D+ W L V+PV
 Sbjct: 145 STETEDAYLTNGSEKFHRALGYQLVGKFHQSGYKFNHWYDM-IWMEKM-LGEHDNHVKPV 202
 Query: 181 TQI 183
 I
 Sbjct: 203 KSI 205

>ref|ZP_00049330.1| COG1247: Sortase and related acyltransferases [Magnetospirillum magnetotacticum MS-1]
 Length = 206

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
 Identities = 62/174 (35%), Positives = 87/174 (50%), Gaps = 13/174 (7%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEEVG 66
 V +RPAT D+ V +I ++ + V F E W L+ + R P+LVAEV+

Sbjct: 33 VTVRPATVHDLPRVAEIAAPFVRDTCVTFEEVWDVPAWHRKLDLDDVTARGLPFLVAEVD 92

Query: 67 -----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
VVAG AYA W+ + AY T E T+Y+ H G+G+ L LLK++ A

Sbjct: 93 PGGPSSPTGAVVAGYAYASAWRPKPAYRHTAEDTIYLDPAHAGRGVGTALLAALLKAVAA 152

Query: 117 QGFKSVVAVIG-LPNDP-SVRLHEALGYTARGLRAAGYKHGGWHDVGFWRD 168
G + VV+V+ +P S+ LH G+ G L A G+KHG W D QR

Sbjct: 153 AGVRQVSVVADVPEAAGSLPLHRRFGFVEAGRLTAVGFKHGRWVDTILLQRTL 206

>ref|ZP_03629351.1| GCN5-related N-acetyltransferase [bacterium Ellin514]
gb|EEF60255.1| GCN5-related N-acetyltransferase [bacterium Ellin514]
Length = 172

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 48/161 (29%), Positives = 81/161 (50%), Gaps = 8/161 (4%)

Query: 21 VCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWL-VAEVEGVVAGIAYAGP 76
+ +I N I ST + +P+T + W D + + +P + + G + G G

Sbjct: 14 ILNIFNDAILNSTALYDYKPRITLENMATWFD--LKTGNFVIGLVTDAGELMGFGTYGT 71

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++ Y +TVE ++YV + + GLG L ++ + +AQ + ++ V+ N S+ L

Sbjct: 72 FRGFAGYKYTVEHSIYVDAKFRGQGLGKRLLQEIIISAAQAQDYHVLIGVVDANSASIAL 131

Query: 137 HEALGYTARGLRAAGYKHGGWHDVGFWRDFFELPAPPRPV 177
H+ G+T GT+R AG+K W DV F+Q LP P PV

Sbjct: 132 HKKFGFTHAGTIRQAGFKFNRWLDVDFYQ--LVLPTPGIPV 170

>ref|ZP_02691607.1| Phosphinothricin N-acetyltransferase [Epulopiscium sp. 'N.t.
morphotype B']
Length = 182

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 47/167 (28%), Positives = 84/167 (50%), Gaps = 3/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR D+ + I ++Y+ + + E + +E+ + + + + ++V E+EG +

Sbjct: 2 IRFVKDITDIERYIKIYSYVYTYTGASLEIELPSLEEFKNRVNTIAKTHSYIVYELEGDII 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G AYA + R Y ++V +++Y+ G+G LY LL ++ QGF + A+I

Sbjct: 62 GFAYATKFMDRREGYKYSVTTSIYLDPSFVEQIGIGEYLYKALLALLKVQGFYTAYAIITSS 121

Query: 130 NDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFWRQ---RDFELPAP 173
N S++ HE LG+T T+ GYK W D ++ +D E PA

Sbjct: 122 NKKSMKFHEKLGFTLVATMEKIGYKFDEWLDTAYYVYPIKDIEEPAK 168

>ref|YP_001239152.1| putative phosphinothricin N-acetyltransferase [Bradyrhizobium sp.
BTai1]
gb|ABQ35246.1| putative phosphinothricin N-acetyltransferase [Bradyrhizobium sp.
BTai1]
Length = 190

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 50/167 (29%), Positives = 79/167 (47%), Gaps = 7/167 (4%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQD-----RYPWL 61
PV +RP+ D+ A+ I +I + +P+ DDL++ + R P LV

Sbjct: 13 PVLVRPSRDEDVEAMLAIYRRHIRRGVEDSAANS GSPEP--DDLQRRKNLRNHLPLV 70

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 A G V G AY ++ R AY + V+ ++YV H H G+G L L+ + A G++
 Sbjct: 71 ATFRGEVVGAYVYVQFRKRPAYRFAVKHSIYVHHEHLGRGVGRLLMQALIDASAAAGYRQ 130

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 ++ I N S+ +HE G+ G L Y++G W D QR
 Sbjct: 131 MIGYIDADNTASLGIHERFGFVRVGLLPGVAYRYGRWSDTVMVQVRS 177

>ref|ZP_05827462.1| sortase [Acinetobacter baumannii ATCC 19606]
 gb|EEX05080.1| sortase [Acinetobacter baumannii ATCC 19606]
 Length = 181

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
 Identities = 50/180 (27%), Positives = 87/180 (48%), Gaps = 12/180 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-----RLQD 55
 + R ++ A A AA+ +I+N I ST + P++ +D ++ + ++
 Sbjct: 5 LDSNFLIDCNEAEHA--AAILEILNDAIVNSTALYDYVPRS---LDSMKTWFSVKREN 58

Query: 56 RYPWL-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 +P + V + G + G A G ++A AY +TVE ++Y+ H H+ GL L L++
 Sbjct: 59 GFPVIGVVDSESKLLGFASWGTFRAFPAYKYTVEHSIYIHHEHRGCGLSKVLMLQALIQRA 118

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 + ++ I N S+ LHE +G+T GT + G+K G W D F+Q P P
 Sbjct: 119 QQAQLHVLIGCIDATNQASIGLHEKMGFTHAGTFKQVGFKFGQWLDAAFYQLILNTPFEP 178

>ref|NP_881122.1| hypothetical protein BP2495 [Bordetella pertussis Tohama I]
 emb|CAE42767.1| conserved hypothetical protein [Bordetella pertussis Tohama I]
 Length = 180

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
 Identities = 57/163 (34%), Positives = 82/163 (50%), Gaps = 8/163 (4%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQ---TPQEWIDDLERLQDRYPWLVAE-VEGVVAGIAYA 74
 AA+ DI N I TST + +P+ + + W + Q +P + E GV+ G A
 Sbjct: 20 AAILDIFNDAILTSTALYDYQPRALASMEAWFQ--AKRQGGFPVVGFEAAGVLMGFASY 77

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 134
 G ++A AY ++VE +VYV R++ GLG L L++ Q +V I N SV
 Sbjct: 78 GTFRAWPAYKYSVEHSVYVDRRYRGRGLGEALLRALIERARLQOVHVLVGGIDATNAGSV 137

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 LH LG+ GT+ AG+K G W D+ F+Q L RPV
 Sbjct: 138 ALHRKLGFBHAGTITQAGFKFGRWLDLAFYQ--LTLDTSLRPV 178

>ref|ZP_07507612.1| putative acyl-CoA N-acyltransferase [Escherichia coli M718]
 Length = 172

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
 Identities = 55/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR A AD A+ +I NH + + + + I E R YP LV+E +G
 Sbjct: 1 MSIRFARKADCVAIAEIYNHAVLYTAAIWNQTVADADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFWDWRSFDGFRHTVEHSVYVHPDHQKGKLGKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH++LG+ + G K G W D+ F Q + P +
Sbjct: 121 ESQNQASLHLHQLSLGFVITAQMPQVGTGKGRWLDLTFMQLQLDERTEPDAI 171

>ref|YP_003635502.1| Phosphinothricin acetyltransferase [Cellulomonas flavigena DSM
20109]
gb|ADG73303.1| Phosphinothricin acetyltransferase [Cellulomonas flavigena DSM
20109]
Length = 173

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 59/163 (36%), Positives = 83/163 (50%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
V++R A D+AAV I +HY+ TST F EP W L+ L +P+ VA ++G
Sbjct: 3 VQVRAAADGDVA AVARIYDHYVATSTATFELEPPGEPVWRGRLDTLTAAGWPFQVAVLDG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VAG AY GPW+ R AY TVE T+Y+ G+G+ L T +L + A G + V+AV+
Sbjct: 63 QVAGFAYVGPWRPRPAYAHTVEDTIYLDPAATGRGVGTRLLTSVLDAAAGAGAREVIAVV 122

Query: 127 GLPND-PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
+ S+ LH G+ G L G K W Q+
Sbjct: 123 ADGDTAASLALHRRAGFHTAGRLERVGRKFRWLGTTLQKTL 165

>ref|NP_746951.1| GCN5-related N-acetyltransferase [Pseudomonas putida KT2440]
gb|AAN70415.1|AE016683_6 phosphinothricin N-acetyltransferase, putative [Pseudomonas
putida
KT2440]
Length = 171

Score = 83.2 bits (204), Expect = 1e-14, Method: Compositional matrix adjust.
Identities = 59/169 (34%), Positives = 75/169 (44%), Gaps = 5/169 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVE 65
EIR A D+ + DI N + +T + P Q W + R Q YP LVA E
Sbjct: 4 EIRDALHTDVPGLDIYNDVAVLNTTAIWNETPVDLDNRQAWFE--ARAQQGYPIVLVAVDE 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
V G A G W+ + TVE +VYV + GLG L L++ G +VA
Sbjct: 62 TGVGLYASFQDWRPFEGFRLTVEHSVYVRSQDQRGKGLGPVLMALVERARGCGKHMVMAA 121

Query: 126 IGLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
I N SVRLHE LG+ G + G K G W D+ F Q A P
Sbjct: 122 IERGNAASVRLHERLGFVVTGMPQVGVKGRWLDLTFMQLVLNPGAEP 170

>ref|YP_003612366.1| GCN5-related N-acetyltransferase [Enterobacter cloacae subsp.
cloacae ATCC 13047]
gb|ADF61417.1| GCN5-related N-acetyltransferase [Enterobacter cloacae subsp.
cloacae ATCC 13047]
Length = 172

Score = 83.2 bits (204), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 55/172 (31%), Positives = 81/172 (47%), Gaps = 5/172 (2%)

Query: 10 IRPATAADMAAVCDIVNH-YIETSTVNFRTEPQTPQE--WIDDLERLQDRYPWLVAEVEG 66
+R A D AA+ +I NH + T+ + T T W + R YP LV+E G
Sbjct: 3 VRHACKEDCAAIGEIYNHAVLHTAAIWNDDTTVDNRIAWFE--ARTLAGYPVLVSEENG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 ++ G A G W+A + + TVE +VYV HQ G+G L L+ G +VA I
 Sbjct: 61 IITGYASFGDWRAFDGFRHTVEHSVYVHPDHQKGIGRMLMKALIIIEARDIGKHMVAVI 120

Query: 127 GLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 N S+ LH+ LG+ G + G K G W D+ F Q + + P ++
 Sbjct: 121 EAQNHASIHLHQTLGFVTTGQMPQVGTGKFGRWLDLTFMQLQLDERSDPDAIK 172

>ref|YP_003882401.1| GCN5-related N-acetyltransferase [Dickeya dadantii 3937]
 gb|ADM97844.1| GCN5-related N-acetyltransferase [Dickeya dadantii 3937]
 Length = 170

Score = 83.2 bits (204), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 58/158 (36%), Positives = 77/158 (48%), Gaps = 6/158 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVA-EVE 65
 IR A + D+ V DI NH + +T F + W+ D RL YP LVA +
 Sbjct: 3 IRDAKSDDLETVADIYNHAVLNTTAIFNDTTVDVANRAIWLADRTLGL--YPVLVALSDD 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G A G W+A + Y TVE +VYV H+ G+ L L++ A G S+VA
 Sbjct: 61 GSVMGYASFGDWRAFDGYRHTVEHSVYVHIDHRGKGIAEALMKALIERARAIGKHSVMAG 120

Query: 126 IGLPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGF 163
 I N S+RLHE LG+ + G K G W D+ F
 Sbjct: 121 IESKNAASIRLHEKLGFRVDPIPVGMKFGQWLDLTF 158

>gb|AAT96242.1| phosphinothricin N-acetyltransferase [Pseudomonas viridiflava]
 Length = 199

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 55/170 (32%), Positives = 82/170 (48%), Gaps = 2/170 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68
 +R A DM + I ++ +F EP + +E + +++ P+ VAE G V
 Sbjct: 26 LRDAREDDMPVIQAIYADHVLHGISSFELEPPSVEELMRRRALVIENGLPYRVAEHAGEV 85

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG- 127
 G YA P++ R AY +T E +VYV +G+G L L+ E G++ +VAVIG
 Sbjct: 86 VGYGYATPYRPRPAYRFTAEDSVYVRDGMGMGIGRALLGDLIWHCEQGGWRQMVAVIGN 145

Query: 128 LPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LHE+ G+ G + G+KHG W D Q A PV
 Sbjct: 146 SENAASIGLHESFGFRRVGVFESVGFKHGRWVDTVLMQCALGDGASTLPV 195

>ref|YP_001671123.1| GCN5-related N-acetyltransferase [Pseudomonas putida GB-1]
 gb|ABZ00788.1| GCN5-related N-acetyltransferase [Pseudomonas putida GB-1]
 Length = 171

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 58/169 (34%), Positives = 75/169 (44%), Gaps = 5/169 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVE 65
 EIR A D+ + DI N + +T + P Q W + R Q YP LVA E
 Sbjct: 4 EIRDALPTDVP GILDIYNDAVRNTTAIWNETPVDLANRQAWFE--ARAQQGYPIILVAVDE 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 V G A G W+ + TVE +VY+ + GLG L L++ G +VA
 Sbjct: 62 TGVGLGYASFGDWRPFEGFRLTVEHSVYIRGDQRGKGLGPVLMALVERARGCGKHMVAA 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQPDFLPAPP 174
 I N SVRLHE LG+ G + G K G W D+ F Q A P
 Sbjct: 122 IESGNAASVRLHERLGFVVTGQMPQVGKFGRWLDLTFMQLVLNPGAEP 170

>ref|ZP_03786255.1| acetyltransferase [Brucella ceti str. Cudo]
 ref|ZP_06791581.1| acetyltransferase [Brucella sp. NVSL 07-0026]
 gb|EEH13115.1| acetyltransferase [Brucella ceti str. Cudo]
 gb|EFG38544.1| acetyltransferase [Brucella sp. NVSL 07-0026]
 Length = 208

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
 Sbjct: 49 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 106

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
 Sbjct: 107 QVVGYASYGPFPRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIAGI 166

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 N S+ LH + G+ GTL+ G K G W D+ F Q+
 Sbjct: 167 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 206

>ref|YP_001259507.1| acetyltransferase [Brucella ovis ATCC 25840]
 gb|ABQ60154.1| acetyltransferase, GNAT family [Brucella ovis ATCC 25840]
 Length = 202

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
 Sbjct: 43 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 100

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
 Sbjct: 101 QVVGYASYGPFPRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIAGI 160

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 N S+ LH + G+ GTL+ G K G W D+ F Q+
 Sbjct: 161 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 200

>gb|ADZ87583.1| GCN5-related N-acetyltransferase [Brucella melitensis M5-90]
 Length = 196

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
 Sbjct: 37 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 94

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
 Sbjct: 95 QVVGYASYGPFPRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIAGI 154

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 N S+ LH + G+ GTL+ G K G W D+ F Q+

Sbjct: 155 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 194

>ref|ZP_01816180.1| toxin resistance protein [Vibrionales bacterium SWAT-3]
gb|EDK26445.1| toxin resistance protein [Vibrionales bacterium SWAT-3]
Length = 172

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 45/154 (29%), Positives = 78/154 (50%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV 64
++IR A +D+AA+ I N YIE + F + + Q+W +Y VA
Sbjct: 1 MKIRTAELSDIAAITYIFNFYIEHTNARFEEDKFTLENRQQWFSQFSS-DSKYQLYVATE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+ G A + P++A +A++ T E T+Y++ + G+GS LY+ L S+ G V++
Sbjct: 60 NDSLLGFACSQPYRATSAFEDTAEVTTIYLAEDAKGKGIGSKLYSQLFASIIDFGVHRVLS 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
+ LPN+ S+ LH+ G+ G K+G +
Sbjct: 120 GVALPNEASIALHXYFGFREVGVFNEYAKKNGKY 153

>ref|YP_368499.1| GCN5-related N-acetyltransferase [Burkholderia sp. 383]
gb|ABB07855.1| GCN5-related N-acetyltransferase [Burkholderia sp. 383]
Length = 182

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 60/178 (33%), Positives = 91/178 (51%), Gaps = 6/178 (3%)

Query: 2 SPERRP-VEIRPATAADMA-AVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYP 58
SP++R V + + A+ A A+ +I+N I TST + +P+ P+ + + +P
Sbjct: 3 SPKQRDDVRLIDCSEAEHAPAILIILNDIAIATSTALYDYKPRPPEAMVAFAAKRAGGFP 62

Query: 59 WLVA-EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
+ A + G + G A G ++A AY +TVE +VYV HR QR GLG L +++
Sbjct: 63 VIGAVDASGTLGLGFASWGTFRAFPAKYTVEHSVYV-HRDQRGRGLGEVLLREVVRRAHE 121

Query: 117 QGFKSVAIVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPP 174
VV I N S+ LH LG+ GT+ AG+K G W D F+Q + PA P
Sbjct: 122 AQVHVVGICIDATNAGSIALHTKLGFVHSGTITQAGFKFGRWLDAAFYQLTLDTPAQP 179

>gb|ADZ66726.1| GCN5-related N-acetyltransferase [Brucella melitensis M28]
Length = 195

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR AT AD+ A+ I N +E + + + ++W+++ R +D +P LVAE EG
Sbjct: 36 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 93

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAIVI 126
V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
Sbjct: 94 QVVGASYGPFRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIAI 153

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166
N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 154 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 193

>ref|YP_003221537.1| putative acyltransferase [Escherichia coli O103:H2 str. 12009]

dbj|BAI30403.1| predicted acyltransferase [Escherichia coli O103:H2 str. 12009]
 gb|EFZ49427.1| acetyltransferase family protein [Escherichia coli E128010]
 Length = 172

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 55/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLRLQDRYPWLVAEVEG 66
 + IR A AD AA+ +I NH + + + + I E R YP LV+E +
 Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNDQTVADNRNIAWFEARTIAGYPVLVSEEDS 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
 Sbjct: 61 VVTGYASFGDWRSDGFRHTVEHSVYVHPDHQKGLGRKLLSRLIDEARDCGKHMVAVAGI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
 N S+ LH++LG+ + G K G W D+ F Q + P +
 Sbjct: 121 ESQNQASLHLHQSLGFVVTAQMPQVGTGKFGRWLDLTFMQLQLDERTEPDAI 171

>ref|NP_539296.1| phosphinothricin N-acetyltransferase [Brucella melitensis bv. 1 str. 16M]
 ref|ZP_05836325.1| conserved hypothetical protein [Brucella melitensis bv. 1 str. 16M]
 gb|AAL51560.1| phosphinothricin n-acetyltransferase [Brucella melitensis bv. 1 str. 16M]
 gb|EEW86310.1| conserved hypothetical protein [Brucella melitensis bv. 1 str. 16M]
 Length = 164

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLRLQDRYPWLVAEVEG 66
 IR AT AD+ A+ I N +E + + + + ++W+++ R +D +P LVAE EG
 Sbjct: 5 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
 Sbjct: 63 QVVGYSYGFPRFPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIASI 122

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ LH + G+ GTL+ G K G W D+ F Q+
 Sbjct: 123 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 162

>ref|YP_001221862.1| putative acetyltransferase [Clavibacter michiganensis subsp. michiganensis NCPPB 382]
 emb|CAN01164.1| putative acetyltransferase [Clavibacter michiganensis subsp. michiganensis NCPPB 382]
 Length = 229

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 56/155 (36%), Positives = 76/155 (49%), Gaps = 7/155 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEW---IDDLRLQDRYPWLVA-EV 64
 EIR ATA D+ + ++ NHY+ STV F T W LER+ P+LVA
 Sbjct: 29 EIRRATADDLPDIREVYNHYVMNSTVTFDETRMTLARWRGRFGQLERMG--MPFLVAVSP 86

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G V G A P R + TVE ++Y+ GLG L L+ + G + V+A
 Sbjct: 87 SGQVLGYALVEPVGNRRSSRTTVEDSIYLGAASTGKGLGRALLEALVDACREAGIREVIA 146

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGW 158

VI D S+RLH +LG+T G + G+K G W
 Sbjct: 147 VIADQGADASIRLHASLGFTESGRMGRVGVKFGRW 181

>ref|YP_001713984.1| putative antibiotic resistance (phosphinothricin
 N-acetyltransferase) [Acinetobacter baumannii AYE]
 ref|YP_002319120.1| phosphinothricin acetyltransferase [Acinetobacter baumannii
 AB0057]
 ref|YP_002325866.1| Acetyltransferase (GNAT) family protein [Acinetobacter baumannii
 AB307-0294]
 ref|ZP_06781135.1| Acetyltransferase (GNAT) family protein [Acinetobacter sp.
 6013113]
 ref|ZP_06796061.1| Acetyltransferase (GNAT) family protein [Acinetobacter sp.
 6013150]
 ref|ZP_07228364.1| Acetyltransferase (GNAT) family protein [Acinetobacter baumannii
 AB056]
 ref|ZP_07235545.1| Acetyltransferase (GNAT) family protein [Acinetobacter baumannii
 AB058]
 ref|ZP_07241878.1| Acetyltransferase (GNAT) family protein [Acinetobacter baumannii
 AB059]
 emb|CAM86995.1| putative antibiotic resistance (phosphinothricin
 N-acetyltransferase) [Acinetobacter baumannii AYE]
 gb|ACJ41137.1| phosphinothricin acetyltransferase [Acinetobacter baumannii AB0057]
 gb|ACJ56797.1| Acetyltransferase (GNAT) family protein [Acinetobacter baumannii
 AB307-0294]
 Length = 181

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 50/180 (27%), Positives = 88/180 (48%), Gaps = 12/180 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLE-----RLQD 55
 + R ++ A A AA+ +I+N I ST + P++ +D ++ + ++
 Sbjct: 5 LDSNFLIDCNEAEHA--AAILEILNDAIVNSTALYDYVPRS----LDSMKTWFSVKREN 58

Query: 56 RYPWL-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 +P + V + G + G A G ++A AY +TVE ++Y+ H H+ GL L L++
 Sbjct: 59 GFPVIGVDELGKLLGFASWGTFRAPPAYKYTVEHSIYIHHEHRGCGLSKVLMQALIQRA 118

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 + ++ I N S+ LHE +G+T GT + G+K G W D F+Q + P P
 Sbjct: 119 QQAQLHVLIGCIDATNQASIGLHEKMGFTAGTFKQVGFQWLDAAFYQLVLDTPFEP 178

>ref|YP_359127.1| putative phosphinothricin N-acetyltransferase [Carboxydothermus
 hydrogenoformans Z-2901]
 gb|ABB13647.1| putative phosphinothricin N-acetyltransferase [Carboxydothermus
 hydrogenoformans Z-2901]
 Length = 168

Score = 82.8 bits (203), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 52/158 (32%), Positives = 78/158 (49%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 E + V IR A D+ + I N + F TEP ++ + L + R+P LV E
 Sbjct: 3 ETKDVIIREAKVEDLKEIFAINEEVLHGIATFDTEPLEGEDQLTWLLKRGARHPVLVGE 62

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 VEG +A P+ R AYD T +VYV + G G + LL+ +G +++
 Sbjct: 63 VEGRIAVWGSNLPYSPRKAYDLTATESVYVHKDFRGRGYGEKMLMALLEEARNRGLRALL 122

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 A+I N+ S+RLH G+ G L+ G+K G W DV
 Sbjct: 123 ALIAAENEASLRLHAKCGFQKVGELKKVGFKFGRWLDV 160

>ref|ZP_05824268.1| sortase [Acinetobacter sp. RUH2624]
 gb|EEX00288.1| sortase [Acinetobacter sp. RUH2624]
 Length = 181

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 52/180 (28%), Positives = 86/180 (47%), Gaps = 12/180 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE----RLQD 55
 + R ++ A A AA+ +I+N I ST + P++ +D ++ + +
 Sbjct: 5 LDSNFRLIDCNEAEHA--AAILEILNEAIVNSTALYDYVPRS----LDSMKTWFSVKTGN 58

Query: 56 RYPWLVAEVE-GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 +P + A E G + G A G ++A AY +TVE ++Y+ H H+ GL L L++
 Sbjct: 59 SFPVIGAVDESGKLLGFASWGAFRAFPAYKYTVEHSIYIHHEHRGCGLSKVLQALIQRA 118

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 + ++ I N S+ LHE LG+T GT + G+K G W D F+Q P P
 Sbjct: 119 QEAQIHVLIGCIDATNQASIGLHEKLGFTHAGTFKQVGFKFGQWLDAAFYQLILNTPFEP 178

>ref|YP_003751039.1| antibiotic resistance protein (acetyltransferase) [Ralstonia
 solanacearum PSI07]
 emb|CBJ49725.1| putative antibiotic resistance protein(Acetyltransferase)
 [Ralstonia solanacearum PSI07]
 Length = 182

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 55/169 (32%), Positives = 80/169 (47%), Gaps = 6/169 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVA-EVE 65
 I A A+ +I+N I ST + P+ PQ W + +P + A +
 Sbjct: 13 IDCTEAHACAILLEILNEAILNSTALYDYAPRPPQAMATWFA--AKRAGGFVVGAVDAS 70

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + G A G ++A AY +TVE +VYV H + LG L L++ +V
 Sbjct: 71 GKLLGFASWGTFRAFPAYKYTVEHSVYVHHACRGRRLGEHLLRELIRRAHEAQVHVLVGC 130

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+ LH LG+ GT+R AG+K G W D F+Q + E+PA P
 Sbjct: 131 IDAANSASIGLHMRLGFVHAGTIREAGFKFGRWLDAAFYQLNLEMPAQP 179

>ref|ZP_01984684.1| phosphinothricin N-acetyltransferase [Vibrio harveyi HY01]
 gb|EDL70838.1| phosphinothricin N-acetyltransferase [Vibrio harveyi HY01]
 Length = 164

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
 Identities = 48/154 (31%), Positives = 76/154 (49%), Gaps = 4/154 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
 +EIR +D+A + DI N YIE + F + T + W ++ VA
 Sbjct: 1 MEIRVGKLSDVATITDIFNFYIEHTNARFEEQAFTQENRLNWFSQFS-CNSKHQLYVAIE 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G + G A + P++ +A++ T E TVY++ + G+GS LY+ L S+ G V++
 Sbjct: 60 SGELLGFACSQPYRDISAFEDTAEVTVYLAAPTAKGKGVGSKLYSKLFSSISGYGVHRVLS 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
 I LPND SV LH+ G+ G K+G +
 Sbjct: 120 GIALPNDASVALHKRFGFREIGVFNEYAKNGEY 153

>gb|ADR62194.1| GCN5-related N-acetyltransferase [*Pseudomonas putida* BIRD-1]
Length = 171

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 57/160 (35%), Positives = 73/160 (45%), Gaps = 5/160 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVE 65
EIR A D+ + DI N + +T + P Q W + R Q YP LVA E
Sbjct: 4 EIRDALPTDVPGLDIYNDAVLNTTAIWNETPVDLGNRQAWFE--ARAQQGYPILVAVDE 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
V G A G W+ + TVE +VYV + GLG L L++ G +VA
Sbjct: 62 TGVGLGYASFQDWRPFEGFRLTVEHSVYVRSDQRGKGLPELMAALVERARGCGKHMVMAA 121

Query: 126 IGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
I N SVRLHE LG+ G + G K G W D+ F Q
Sbjct: 122 IERGNAAASVRLHERLGFVVTGOMPQVGKFGRWLDLTFMQ 161

>ref|ZP_08178282.1| sortase-like acyltransferase [*Xanthomonas vesicatoria* ATCC 35937]
gb|EGD09502.1| sortase-like acyltransferase [*Xanthomonas vesicatoria* ATCC 35937]
Length = 175

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 57/163 (34%), Positives = 80/163 (49%), Gaps = 1/163 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
PVE+R AD+ A+ I I T P + + + + YP+LVAE G
Sbjct: 2 PVELRAVREADIPAITAIYAEQIAGFNTYETAPSSAEMYARMRAIVDAGYPYLVAEHAG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G AYA ++AR Y WTVE+++Y++ Q G+G L L+ E +G + ++AVI
Sbjct: 62 AVVGAYAYASAYRARAGYRWTVENSIYLAADMQGRGIGKALLGELIARCEQRGDRQMIAVI 121

Query: 127 G-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
G N S+RLHE G+ G G K G W D QR
Sbjct: 122 GDASNQASRLHERFGFRTVGVFTGIGRKQGRWLDGVQMQRQL 164

>ref|YP_001792179.1| GCN5-like N-acetyltransferase [*Leptothrix cholodnii* SP-6]
gb|ACB35414.1| GCN5-related N-acetyltransferase [*Leptothrix cholodnii* SP-6]
Length = 198

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 50/159 (31%), Positives = 80/159 (50%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+++RPA D AA+ I+NHYI +T F TEP + + + +P VAE +GV
Sbjct: 28 LQLRPAQLHDAAAIAAILNHYIVFTTATFMTEPVSVDSRRAFIVERKPEHPIWVAERDGV 87

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
G A + R+AY T+E+++Y+ H G+G+ L + L+ + +GF S++A
Sbjct: 88 AIGWAALAQHQPR SAYGHTLENSIYLHPGHVGRGIGITLLMSQLVADAQRRGFHSLIAGAC 147

Query: 128 LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
S+ LHE +GY K W DV + +R
Sbjct: 148 SEQAGSLALHERMGYRRC AHFHEVARKFDRWLDVVYLER 186

>ref|ZP_04595027.1| GCN5-related N-acetyltransferase [*Brucella abortus* str. 2308 A]
gb|EEP62906.1| GCN5-related N-acetyltransferase [*Brucella abortus* str. 2308 A]
Length = 208

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 83/160 (51%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
Sbjct: 49 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRHQWLEN--RNRDGFVPVLVAEREG 106

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
Sbjct: 107 QVVGYASYGPFPRPFEGFRHSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIAGI 166

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 167 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 206

>ref|ZP_05967781.1| toxin-antitoxin system, toxin component, GNAT family
[Enterobacter
cancerogenus ATCC 35316]
gb|EFC56775.1| toxin-antitoxin system, toxin component, GNAT family [Enterobacter
cancerogenus ATCC 35316]
Length = 172

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 54/166 (32%), Positives = 75/166 (45%), Gaps = 1/166 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLE-RLQDRYPWLVAEVEGVV 68
+R A D AA+ DI NH + + + + I E R +P LV+E G V
Sbjct: 3 VRHACKEDCAAIGDIYNHAVLHTAAIWNKDITVDVDNRIAWFEARTLAGFPVLVSEENGTV 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A G W+A + TVE +VYV HQ G+G L L+ G +VA I
Sbjct: 63 TGYASFGDWRAFEGFRHTVEHSVYVHPDHQKGIGRVLNMLALIDEARKMGKHMVAGIET 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
N S+ LH+ LG+ G + G K G W D+ F Q + + P
Sbjct: 123 QNHASIHLDITLGFITTGQMPQVGTGKFGRWLDLTFMQLQLDERSDP 168

>ref|YP_001176830.1| GCN5-related N-acetyltransferase [Enterobacter sp. 638]
gb|ABP60779.1| GCN5-related N-acetyltransferase [Enterobacter sp. 638]
Length = 171

Score = 82.4 bits (202), Expect = 2e-14, Method: Compositional matrix adjust.
Identities = 58/171 (33%), Positives = 80/171 (46%), Gaps = 5/171 (2%)

Query: 10 IRPATAADMAAVCDIVNH-YIETSTVNFRTEPQTPQE--WIDDLERLQDRYPWLVAEVEG 66
IR A+ D AA+ +I NH + T+ + T T W + R YP LV+E G
Sbjct: 3 IRHASKEDCAAIGEIYNHAVVHTAAIWNDDTTVDTENRIAWFE--ARTLMGYPPVLVSEENG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VV G A G W+A + + TVE +VYV HQ G+G L L+ G +VA I
Sbjct: 61 VVTGYASFGDWRAFDGFRHTVEHSVYVHPDHQKGIGRELKALIGERNIGKHMVAGI 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH+ LG+ G + G K G W D+ F Q + P +
Sbjct: 121 EAQNHGSIHLHKTGLGFVITGQMPQVGTGKFGRWLDLTFMQLQLDERIDPDAI 171

>ref|YP_001935515.1| GCN5-related N-acetyltransferase [Brucella abortus S19]
ref|ZP_06932635.1| acetyltransferase [Brucella abortus bv. 5 str. B3196]
gb|ACD73041.1| GCN5-related N-acetyltransferase [Brucella abortus S19]

gb|EFH33417.1| acetyltransferase [Brucella abortus bv. 5 str. B3196]
Length = 202

Score = 82.4 bits (202), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 83/160 (51%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
Sbjct: 43 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRHQWLEN--RNRDGFVPVLVAEREG 100

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
Sbjct: 101 QVVGYASYGPFRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIAGI 160

Query: 127 GLPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 161 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 200

>ref|YP_001707430.1| putative antibiotic resistance (phosphinothricin
N-acetyltransferase) [Acinetobacter baumannii SDF]
emb|CAP01454.1| putative antibiotic resistance (phosphinothricin
N-acetyltransferase) [Acinetobacter baumannii]
Length = 181

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 50/180 (27%), Positives = 87/180 (48%), Gaps = 12/180 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER----RLQD 55
+ R ++ A A AA+ +I+N I ST + P++ +D ++ + ++
Sbjct: 5 LDSNFRLIDCNEAEHA--AAILEILNDAIVNSTALYDYVPRS---LDSMKTWFSVKREN 58

Query: 56 RYPWL-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
+P + V + G + G A G ++A AY +TVE ++Y+ H H+ GL L L++
Sbjct: 59 GFPVIGVVDLGLKLLGFASWGTFRAFPAYKYTVEHSIYIHHEHRGCGLSKVLMLQALIQRA 118

Query: 115 EAQGFKSVVAVIGLPNDPVSRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPP 174
+ ++ I N S+ LHE +G+T GT + G+K G W D F+Q P P
Sbjct: 119 QQAQLHVLIGCIDATNQASIGLHEKMGFTAGTFKQVGFKFGQWLDAAFYQLILNTPFEP 178

>ref|ZP_02188651.1| phosphinothricin N-acetyltransferase [alpha proteobacterium
BAL199]
gb|EDP64479.1| phosphinothricin N-acetyltransferase [alpha proteobacterium BAL199]
Length = 172

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 54/162 (33%), Positives = 84/162 (51%), Gaps = 10/162 (6%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER----LQDRYPWLVAEVE 65
R + AD+ A+ I ++ +F P + I++L R L+ P LVAE++
Sbjct: 8 RDSREADLDAIQIYAFHVLHGLASFEEPPPS----IEELGRRRQDVLRSDLPVLVAELD 63

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
V G +YA P++ + AY T+E++VYV + G+G L L+ E ++ +VAV
Sbjct: 64 DAVVGYSYASPYRQQPAYCRTIENSVYVRNGFHGHGIGRVLLAALIARCELGPWRQMVAV 123

Query: 126 IG-LPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
IG N S+ LH A G+ GT+R+ G+K G W D QR
Sbjct: 124 IGDENRASIGLHAAFGFQHAGTVRSVGFKFGRWVDSVLMQR 165

>ref|ZP_06487360.1| putative phosphinothricin N-acetyltransferase [Xanthomonas

campestris pv. vasculorum NCPB702]
Length = 145

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 49/143 (34%), Positives = 74/143 (51%), Gaps = 1/143 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
PVE+R AD+ A+ I I + P + + +P+LVAE++G
Sbjct: 2 PVELRAVRDADIPAITAIYADQICGVNTYEYSAPSLDEMRRARVSAIVDAGHPYLVAELDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VAG AY ++AR Y WTVE+++Y++ Q G+G L L+ E +GF+ ++AVI
Sbjct: 62 AVAGYAYVSAFRARAGYRWTVENSIYLAAAMQGRGIGKALLGELIAVCEQRGFRQMIAVI 121

Query: 127 G-LPNDPSVRLHEALGYTARGTL 148
G N S +LHE G+ G L
Sbjct: 122 GDAGNLASRQLHERFGFRTVGVL 144

>ref|ZP_08117889.1| GCN5-related N-acetyltransferase [Thermoanaerobacterium
xylanolyticum LX-11]
gb|EGB24160.1| GCN5-related N-acetyltransferase [Thermoanaerobacterium
xylanolyticum LX-11]
Length = 161

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 47/159 (29%), Positives = 74/159 (46%), Gaps = 6/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEG 66
IR A D+ + DI N + +T TEP + ++W E DRY VA +
Sbjct: 3 IRKANIDDIKRINDIYNQAVLNTTATIDTEPRPLEYHKKW---FEAHNDRYAVFVAIEDD 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+V G A W + Y E ++Y+ ++ G+G L +++ + F ++VA I
Sbjct: 60 IVVGWASLSIWSEKCGYRAVAEDSIYIDKSYKGRGIGDKLIKKIIEHAKENEFHTIVARI 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHHGGWHDVGVFWQ 165
ND S+ LHE G+ GTL+ GYK + D+ Q
Sbjct: 120 SEGNDVSIHLHEKYGFKIVGTLKELGYKFNRYLDIHILQ 158

>ref|YP_002733348.1| GCN5-related N-acetyltransferase [Brucella melitensis ATCC 23457]
ref|ZP_05156143.1| hypothetical protein Babob3T_06580 [Brucella abortus bv. 3 str.
Tulya]
ref|ZP_05170308.1| hypothetical protein BpinM_16375 [Brucella pinnipedialis
M163/99/10]
ref|ZP_05170480.1| hypothetical protein BpinB_00119 [Brucella pinnipedialis B2/94]
ref|ZP_05176327.1| hypothetical protein BcetM6_14495 [Brucella ceti M644/93/1]
ref|ZP_05179225.1| hypothetical protein BcetM_13624 [Brucella ceti M13/05/1]
ref|ZP_05443809.1| hypothetical protein BpinM2_06039 [Brucella pinnipedialis
M292/94/1]
ref|ZP_05448159.1| hypothetical protein Bmelb1R_12287 [Brucella melitensis bv. 1 str.
Rev.1]
ref|ZP_05454969.1| hypothetical protein Bmelb3E_15503 [Brucella melitensis bv. 3 str.
Ether]
ref|ZP_05458059.1| hypothetical protein BcetM4_15287 [Brucella ceti M490/95/1]
ref|ZP_05461113.1| hypothetical protein BcetB_15111 [Brucella ceti B1/94]
ref|ZP_05465929.1| conserved hypothetical protein [Brucella melitensis bv. 2 str.
63/9]
ref|YP_003107572.1| acetyltransferase, GNAT family [Brucella microti CCM 4915]
ref|ZP_05754683.1| hypothetical protein BruF5_05780 [Brucella sp. F5/99]
ref|ZP_05928902.1| N-acetyltransferase [Brucella abortus bv. 3 str. Tulya]
ref|ZP_05933525.1| N-acetyltransferase [Brucella ceti M13/05/1]


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ref|ZP_05937061.1| N-acetyltransferase [Brucella ceti B1/94]
ref|ZP_05955175.1| N-acetyltransferase [Brucella pinnipedialis M163/99/10]
ref|ZP_05955356.1| N-acetyltransferase [Brucella pinnipedialis B2/94]
ref|ZP_05961502.1| N-acetyltransferase [Brucella ceti M644/93/1]
ref|ZP_06001018.1| conserved hypothetical protein [Brucella sp. F5/99]
ref|ZP_06099780.1| N-acetyltransferase [Brucella pinnipedialis M292/94/1]
ref|ZP_06104247.1| N-acetyltransferase [Brucella melitensis bv. 1 str. Rev.1]
ref|ZP_06108084.1| N-acetyltransferase [Brucella melitensis bv. 3 str. Ether]
ref|ZP_06111295.1| N-acetyltransferase [Brucella ceti M490/95/1]
gb|ACO01394.1| GCN5-related N-acetyltransferase [Brucella melitensis ATCC 23457]
gb|ACU48623.1| acetyltransferase, GNAT family [Brucella microti CCM 4915]
gb|EEX83089.1| N-acetyltransferase [Brucella abortus bv. 3 str. Tulya]
gb|EEX88017.1| N-acetyltransferase [Brucella ceti B1/94]
gb|EEX90901.1| N-acetyltransferase [Brucella ceti M13/05/1]
gb|EEX98491.1| N-acetyltransferase [Brucella ceti M644/93/1]
gb|EEX98878.1| N-acetyltransferase [Brucella pinnipedialis B2/94]
gb|EEY08501.1| N-acetyltransferase [Brucella pinnipedialis M163/99/10]
gb|EEY25289.1| conserved hypothetical protein [Brucella sp. F5/99]
gb|EEZ09196.1| N-acetyltransferase [Brucella ceti M490/95/1]
gb|EEZ12429.1| N-acetyltransferase [Brucella melitensis bv. 3 str. Ether]
gb|EEZ15049.1| N-acetyltransferase [Brucella melitensis bv. 1 str. Rev.1]
gb|EEZ17463.1| conserved hypothetical protein [Brucella melitensis bv. 2 str.
63/9]
gb|EEZ29681.1| N-acetyltransferase [Brucella pinnipedialis M292/94/1]
Length = 164

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Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

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Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
Sbjct: 5  IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 62

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
Sbjct: 63  QVVGYASYGPFRPFEGFRHSSELSVYVASNARGGGIGRTLLAELIEEARERKVVHVLIAI 122

Query: 127  GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 123  EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 162

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>ref|YP_001580341.1| GCN5-related N-acetyltransferase [Burkholderia multivorans ATCC
17616]
ref|YP_001945562.1| acetyltransferase [Burkholderia multivorans ATCC 17616]
gb|ABX15844.1| GCN5-related N-acetyltransferase [Burkholderia multivorans ATCC
17616]
dbj|BAG43026.1| acetyltransferase [Burkholderia multivorans ATCC 17616]
Length = 184

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Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 58/180 (32%), Positives = 87/180 (48%), Gaps = 9/180 (5%)

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Query: 3  PERRPVEIRPATAADMA-AVCDIVNHYIETSTVNFRTEPQTPQE--WIDDLERLQDRYP 58
P+R V + T A+ A A+ +I+N I ST + +P+ P+ W + +P
Sbjct: 7  PQRDDVRLIDCTEAHAPAILIILNDAIVNSTALYDYKPRPPEAMAAWF--ATKRASGFP 64

Query: 59  WLVA-EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
+ A G + G A G ++A A+ +TVE +VYV H+ GLG L L++
Sbjct: 65  VVGAVNAAGTLLGFASWGTFRAFPAYKYTVEHSVYVHRDHRGRGLGEWLLRELIRRAHDA 124

Query: 118  GFKSVVAVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPPRPV 177
+V I N S+ LH LG+ GT++ AG+K G W D F+Q L P RPV

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Sbjct: 125 DVHLLVGCIDATNAGSIALHTRLGFVHSGTIKEAGFKFGRWLDAAFYQ--LRLDTPSRPV 182

>gb|EFZ55752.1| acetyltransferase family protein [Escherichia coli LT-68]
Length = 172

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 55/171 (32%), Positives = 80/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
+ IR A AD AA+ +I NH + + + + I E R YP LV+E +G
Sbjct: 1 MSIRFARKADCAAIAEINYHNAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQGKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDPSPVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH++L + + G K G W D+ F Q + P +
Sbjct: 121 ESQNQASLHLHQSLEFVVTAQMPQVGTFKGRWLDLTFMQLQLDERTEPDAI 171

>ref|ZP_07773233.1| acetyltransferase [Pseudomonas fluorescens WH6]
gb|EFQ65817.1| acetyltransferase [Pseudomonas fluorescens WH6]
Length = 170

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 55/168 (32%), Positives = 78/168 (46%), Gaps = 5/168 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVAEVEG 66
IR AT D+ A+ DI N + +T + +P W + + L YP LVA
Sbjct: 2 IRDATEKDLPAIRDIYNDAVRNTTAIWNEQPVDLANRLAWFNARQALG--YPILVAVEND 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A G W+ + ++VE +VYV + + GLG L L++ + G +VA I
Sbjct: 60 AVTGYASFGDWRPFEGFRYSVEHSVYVRNDQRGKGLGPRMLQVLIERARSGGKYVMVAAI 119

Query: 127 GLPNDPSPVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPP 174
N S+RLHE LG+ G + G K G W D+ F Q A P
Sbjct: 120 ESGNQASIRLHERLGFITTGQMPQVGIFKGRWLDLTFMQLALNPGAEP 167

>gb|EFZ70777.1| acetyltransferase family protein [Escherichia coli 1357]
Length = 172

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
Identities = 55/171 (32%), Positives = 79/171 (46%), Gaps = 1/171 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
+ IR A AD AA+ +I NH + + + + I E R YP LV+E +
Sbjct: 1 MSIRFARKADCAAIAEINYHNAVLYTAAIWNDQTVADNRIAWFEARTIAGYPVLVSEEDS 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHRQLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I
Sbjct: 61 VVTGYASFGDWRSFDGFRHTVEHSVYVHPDHQGKGLGRKLLSRLIDEARDCGKHVMVAGI 120

Query: 127 GLPNDPSPVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
N S+ LH +LG+ + G K G W D+ F Q + P +
Sbjct: 121 ESQNQASLHLHSLGFVVTAQMPQVGTFKGRWLDLTFMQLQLDERTEPDAI 171

>ref|NP_521254.1| putative antibiotic resistance (acetyltransferase) protein
[Ralstonia solanacearum GMI1000]

emb|CAD16842.1| putative antibiotic resistance (acetyltransferase) protein
 [Ralstonia solanacearum GMI1000]
 Length = 182

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
 Identities = 54/169 (31%), Positives = 81/169 (47%), Gaps = 6/169 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVA-EVE 65
 I A +A+ +I+N I ST + P+ PQ W + +P + A +
 Sbjct: 13 IDCTEAEHASAILLEILNEAIVNSTALYDYVPRPPQAMATWF--AAKRAGGFPVVGAVDAS 70

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 125
 G + G G ++A AY +TVE +VYV H + LG L L++ + +V
 Sbjct: 71 GKLLGFGSWGTFRAFPAYKYTVEHSVYVHHECRGRRLLGERLLRELIRRAQEAQVHVLVGC 130

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+ LH LG+ GT+R AG+K G W D F+Q + E+PA P
 Sbjct: 131 IDAANAASIGLHTRLGFVHAGTIREAGFKFGRWLDAAFYQLNLEMPAQ 179

>ref|ZP_06348055.1| toxin-antitoxin system, toxin component, GNAT family [Clostridium
 sp. M62/1]
 gb|EFE10730.1| toxin-antitoxin system, toxin component, GNAT family [Clostridium
 sp. M62/1]
 Length = 163

Score = 82.0 bits (201), Expect = 3e-14, Method: Compositional matrix adjust.
 Identities = 51/159 (32%), Positives = 85/159 (53%), Gaps = 8/159 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ---DRYPWLVAE 63
 ++IR A D+ + +I N+ + ST +F + +T + D LE +P +VAE
 Sbjct: 1 MKIRSALEQDVREMEIFNYEVRNSTASFAIQEKT---YEDRLEWFHAHGTGNHPLIVAE 57

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKS 122
 +G VAG A ++ AY TVE +VYVS ++ G+G L +++ + E + ++V
 Sbjct: 58 EDGRVAGYACLSQYRPHEAYKKTVELSVYVSPDFRKRGVGEALMQEIIRLAREDRNTRTV 117

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 ++VI N S+RLHE LG++ G + G K G D+
 Sbjct: 118 ISVITAENQASIRLHEKLGFSFCGKMHEVGEKFGRM LDI 156

>ref|YP_001710167.1| putative toxin resistance acetyltransferase [Clavibacter
 michiganensis subsp. sepedonicus]
 emb|CAQ01551.1| putative acetyltransferase protein (toxin resistance) [Clavibacter
 michiganensis subsp. sepedonicus]
 Length = 229

Score = 81.6 bits (200), Expect = 4e-14, Method: Compositional matrix adjust.
 Identities = 55/155 (35%), Positives = 75/155 (48%), Gaps = 7/155 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEW---IDDLERLQDRYPWLVA-EV 64
 EIRPA +D+ + +I NHY+ STV F T W LER+ P+LVA
 Sbjct: 29 EIRPAVTSDDLPIREIYNHYVMNSTVTFTDETRMTLARWRGRFGQLERMG--MPFLVAVSP 86

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 G V G A P R + TVE ++Y+ GLG L L+ + +V+A
 Sbjct: 87 SGQVLGYALVEPVGNRRSSRTTVEDSIYLGAASTGKGLGRALLVALVDACREARIREVIA 146

Query: 125 VIGLPN-DPSVRLHEALGYTARGTLRAAGYKHGGW 158
 VI D S+RLH +LG+T G + G+K G W
 Sbjct: 147 VIADQGADASIRLHASLGFTESGRMGRVGVKFGRW 181

>ref|ZP_06548680.1| acetyltransferase [Klebsiella sp. 1_1_55]
 gb|EFD86700.1| acetyltransferase [Klebsiella sp. 1_1_55]
 Length = 172

Score = 81.6 bits (200), Expect = 4e-14, Method: Compositional matrix adjust.
 Identities = 57/170 (33%), Positives = 80/170 (47%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IRPA D AA+ +I NH + T+ + N +T + W + R +P LV E
 Sbjct: 1 MSIRPAIKDDCAAIAEIYNHAVVHTAAIWNDKTVDTDNRIAWFE--ARQLAGFPVLVNEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 GV+ G + G W+A + + TVE +VYV HQ GLG L L+ +VA
 Sbjct: 59 NGVITGYSSFGDWRAFDGFRHTVEHSVYVHPDHQKGKGLGRKLLVALIAEARRLNKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+ LHE LG+ G + G K G W D+ F Q + P
 Sbjct: 119 GIESQNHASLHLHETLGFITTGQMPQVGTKFGRWLDLTFMQLQLDERQAP 168

>ref|YP_002997301.1| phosphinothricin N-acetyltransferase [Streptococcus dysgalactiae
 subsp. equisimilis GGS_124]
 dbj|BAH82087.1| phosphinothricin N-acetyltransferase [Streptococcus dysgalactiae
 subsp. equisimilis GGS_124]
 Length = 206

Score = 81.6 bits (200), Expect = 4e-14, Method: Compositional matrix adjust.
 Identities = 50/163 (30%), Positives = 75/163 (46%), Gaps = 9/163 (5%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEVG 66
 V +R AT D A+ I Y+ + V F E + + + ++ YP+LVAE G
 Sbjct: 14 SVSVRLATLEDAEALLAIYAPYVTDTAFTDYEVDPLEAFKKRMIQIMAFYPYLVAEEAG 73

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 126
 + G AYA + AR AY W+ E T+Y++ ++ G G+ LY L + + G + A I
 Sbjct: 74 SILGYAYASAFHARAAYAWSAEVTIYLAMENKGGFGTKLYQALERYLTKMGILNCNACI 133

Query: 127 G-----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 L N + HE +GY G GYK W D+
 Sbjct: 134 ASTACESPCLANHSQL-FHEKMGYQLVGKFHQVGYKFDQWFDM 175

>ref|ZP_03543324.1| GCN5-related N-acetyltransferase [Comamonas testosteroni KF-1]
 gb|EED67610.1| GCN5-related N-acetyltransferase [Comamonas testosteroni KF-1]
 Length = 177

Score = 81.6 bits (200), Expect = 4e-14, Method: Compositional matrix adjust.
 Identities = 51/159 (32%), Positives = 80/159 (50%), Gaps = 3/159 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWL-VAEEGVVAGIAYAGP 76
 AA+ DI N I ST + +P+T Q + E + +P + + + +G + G G
 Sbjct: 16 AAILDIFNDAIVNSTALYDYQPRTAQNMVSWFEAKRAGGFPVIGIEDAQGRLLGFCSWG 75

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG-FKSVVAVIGLPNDPSVR 135
 ++A AY +TVE +VYV H+ LGLG L L+ +G +V I N S+
 Sbjct: 76 FRAYPAYKYTVEHSVYVHPEHRGLGLGQQQLMDLLIAEARQRGDVHVLVGIDAANAGSIA 135

Query: 136 LHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 LH+ LG+ + G + G+K G W D+ F+Q + P P
 Sbjct: 136 LHKRLGFESVGLMPQVGFKFGRWLDLAFYQLTLQTPLNP 174

>ref|YP_002238268.1| acetyltransferase, GNAT family [Klebsiella pneumoniae 342]
ref|YP_003439315.1| GCN5-related N-acetyltransferase [Klebsiella variicola At-22]
gb|ACI09389.1| acetyltransferase, GNAT family [Klebsiella pneumoniae 342]
gb|ADC58283.1| GCN5-related N-acetyltransferase [Klebsiella variicola At-22]
Length = 172

Score = 81.6 bits (200), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 57/170 (33%), Positives = 80/170 (47%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
+ IRPA D AA+ +I NH + T+ + N +T + W + R +P LV E
Sbjct: 1 MSIRPAIKDDCAAIAEIYNHAVVHTAAIWNDKTVDTDNRIAWFE--ARQLAGFPVLVNEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
GV+ G + G W+A + + TVE +VYV HQ GLG L L+ +VA
Sbjct: 59 NGVITGYSSFGDWRAFDGFRHTVEHSVYVHPDHQKGKGLGRKLLVALIAEARRLNKHMVMA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
I N S+ LHE LG+ G + G K G W D+ F Q + P
Sbjct: 119 GIESQNHASLHLHETLGFITTGQMPQVGTKFGRWLDLTFMQLQLDERQDP 168

>ref|YP_002140771.1| GNAT family acetyltransferase [Geobacter bemidjensis Bem]
gb|ACH40975.1| acetyltransferase, GNAT family [Geobacter bemidjensis Bem]
Length = 178

Score = 81.6 bits (200), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 52/157 (33%), Positives = 77/157 (49%), Gaps = 2/157 (1%)

Query: 20 AVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWL-VAEVEGVVAGIAYAGPW 77
A+ +I N I ST + +P+T Q +D + +P + + + GV+ G G +
Sbjct: 19 AILEIFNDAILHSTALYDYKPRTLQAMVDWFAAKRAGGFPVIGIEDSNGVLLGFGSYGTF 78

Query: 78 KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLH 137
+ AY +TVE +VYV H+ GLG + LL +VV I N S+ LH
Sbjct: 79 RGWPAYKYTVEHSVYVHKDHRGHGLGQAVMRELLAVARENDVHAVVGAIDAANTGSIALH 138

Query: 138 EALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
E LG+ GTL G+K G W D+ F+Q + PA P
Sbjct: 139 ERLGFKHVGTLPQVGFKFGRWLDLAFYQLLLDTPAHP 175

>ref|YP_222318.1| acetyltransferase [Brucella abortus bv. 1 str. 9-941]
ref|YP_415015.1| GCN5-related N-acetyltransferase [Brucella melitensis biovar
Abortus 2308]
ref|ZP_05153077.1| GCN5-related N-acetyltransferase [Brucella abortus bv. 6 str. 870]
ref|ZP_05159799.1| GCN5-related N-acetyltransferase [Brucella abortus bv. 2 str.
86/8/59]
ref|ZP_05189435.1| GCN5-related N-acetyltransferase [Brucella abortus bv. 4 str. 292]
ref|ZP_05463612.1| GCN5-related N-acetyltransferase [Brucella abortus bv. 9 str. C68]
ref|ZP_05822965.1| N-acetyltransferase [Brucella abortus NCTC 8038]
ref|ZP_05867702.1| N-acetyltransferase [Brucella abortus bv. 6 str. 870]
ref|ZP_05870924.1| N-acetyltransferase [Brucella abortus bv. 4 str. 292]
ref|ZP_05874745.1| N-acetyltransferase [Brucella abortus bv. 2 str. 86/8/59]
ref|ZP_05895984.1| N-acetyltransferase [Brucella abortus bv. 9 str. C68]
gb|AAx74957.1| acetyltransferase, GNAT family [Brucella abortus bv. 1 str. 9-941]
emb|CAJ11620.1| GCN5-related N-acetyltransferase [Brucella melitensis biovar
Abortus 2308]
gb|EEW79470.1| N-acetyltransferase [Brucella abortus NCTC 8038]
gb|EEX55834.1| N-acetyltransferase [Brucella abortus bv. 4 str. 292]
gb|EEX59655.1| N-acetyltransferase [Brucella abortus bv. 2 str. 86/8/59]
gb|EEX62283.1| N-acetyltransferase [Brucella abortus bv. 6 str. 870]
gb|EEX80967.1| N-acetyltransferase [Brucella abortus bv. 9 str. C68]

Length = 164

Score = 81.6 bits (200), Expect = 4e-14, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 83/160 (51%), Gaps = 5/160 (3%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
          IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
Sbjct: 5   IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRHQWLEN--RNRDGFVPVLVAEREG 62

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
Sbjct: 63  QVVGYASYGPFPRPFEGFRHSSELSVYVASNARGGGIGRTLAEELIEEARERKVVHVLIAGI 122

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
          N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 123 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 162
```

>gb|EFA85320.1| hypothetical protein PPL_02321 [Polysphondylium pallidum PN500]
Length = 176

Score = 81.6 bits (200), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 43/170 (25%), Positives = 85/170 (50%), Gaps = 6/170 (3%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER--LQDRYPWLVAEVE 65
          + IR A +D+AA+ DI N+ I F + E E +++++P++VA
Sbjct: 6   INIRYAKYSDIAAITDIYNYSIRHEISTFEEVEISVDEMKARYEEVVIKEKHPYIVATTR 65

Query: 66  G----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
          G +V G Y ++AR+ Y +T ++Y+ H H+ +GS L +++ + + +
Sbjct: 66  GKDGEIVIGYCYLLRYRARSGRYRTSTDYIYIHHEHRGKRVGSLLEIRIIEIAKEMNYYN 125

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRFELP 171
          ++ V ND S++LH+ G+ ++ G K W + ++Q +F+L
Sbjct: 126 MIGVASGGNDVSIKHLKRFGRFLCSMENVGLKFNQWINTDYFQLNFQLT 175
```

>gb|EFY03230.1| acetyltransferase (GNAT) family protein [Streptococcus dysgalactiae
subsp. dysgalactiae ATCC 27957]
Length = 325

Score = 81.3 bits (199), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 50/162 (30%), Positives = 75/162 (46%), Gaps = 9/162 (5%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
          V IR AT D + I Y+ + V F E + + + ++ YP+LVAE G
Sbjct: 3   VSIRLATLEDAETLLAIYAPYVTDTAFTDYEVNLEAFKKCMVQIMAFYPYLVAEEAGS 62

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
          + G AYA + AR AY W+ E T+Y++ ++ G+G+ LY L + + G + A I
Sbjct: 63  ILGYAYASAFHARAAYAWSAEVTIYLAMENKKGKGVGKLYQALERYLTKMGILNCNACIA 122

Query: 128 -----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
          L N + HE +GY G GYK W D+
Sbjct: 123 STACESPYLANHSQL-FHEKMGYQLAGKFHQVGKFDQWFDM 163
```

>ref|YP_001527618.1| putative acetyltransferase protein [Azorhizobium caulinodans ORS
571]
dbj|BAF90700.1| putative acetyltransferase protein [Azorhizobium caulinodans ORS
571]
Length = 171

Score = 81.3 bits (199), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 59/171 (34%), Positives = 82/171 (47%), Gaps = 6/171 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVA-E 63
++IR ATAAD+ + I N + +T + + W+ R + YP LVA +
Sbjct: 1 MDIRDATAADIDGILAIYNDAVAHTTAIWNETLVDRDNRLAWL--TARTEAGYPVLVAVD 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
G V G A G W+A + Y TVE +VYV + G+G L L+ A G +V
Sbjct: 59 SAGAVLGYASFQDWRADFQYRHTVEHSVYVRADARGGGIGRALMEALIARARALGKHMV 118

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
A I N S++LH ALG+ A G L G K G W D+ F Q + P P
Sbjct: 119 AGIDAENAASLKLHAALGFKAVGHLPEVGKFGRWLDLAFQLILDPPGTP 169

>ref|NP_698636.1| acetyltransferase [Brucella suis 1330]
ref|YP_001593471.1| phosphinothricin N-acetyltransferase [Brucella canis ATCC 23365]
ref|ZP_05165263.1| phosphinothricin N-acetyltransferase [Brucella suis bv. 3 str. 686]
ref|ZP_05839212.1| N-acetyltransferase [Brucella suis bv. 4 str. 40]
ref|ZP_05997773.1| N-acetyltransferase [Brucella suis bv. 3 str. 686]
gb|AAN30551.1| acetyltransferase, GNAT family [Brucella suis 1330]
gb|ABX62700.1| Phosphinothricin N-acetyltransferase [Brucella canis ATCC 23365]
gb|EEW89210.1| N-acetyltransferase [Brucella suis bv. 4 str. 40]
gb|EEY31743.1| N-acetyltransferase [Brucella suis bv. 3 str. 686]
Length = 164

Score = 81.3 bits (199), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
Sbjct: 5 IRHATEADLPALLAIYNDAVENTLAIWNETLVLDLENRRQWLEN--RNRDGFVPLVAEREG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
Sbjct: 63 QVVGYASYGFRPFEGFRHSELSVYVASNARGGGIGRTLAEELIEERERKQVHVLIAGI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 166
N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 123 EPGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 162

>ref|YP_003977234.1| GNAT family acetyltransferase 4 [Achromobacter xylosoxidans A8]
gb|ADP14519.1| acetyltransferase, GNAT family protein 4 [Achromobacter xylosoxidans A8]
Length = 185

Score = 81.3 bits (199), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 52/158 (32%), Positives = 78/158 (49%), Gaps = 6/158 (3%)

Query: 21 VCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAE-VEGVVAGIAYAGP 76
+ I+N I ST + +P + Q W + Q +P + E G + A G
Sbjct: 27 ILAILNEAIVNSTALYDYKPRPREAMQGWQFQ--AKQQGGFPVVGYENAAAGELMAFASYGT 84

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++A A+ ++VE +VYV R + LGLG L L++ A +V I N S+RL
Sbjct: 85 FRAWPAFKYSVEHSVYVDGRFRGLGLGEALMQVLIQRARANQVHVLVGGIDASNQGSIRL 144

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE LG+ GT+R AG+K G W D+ F+Q + P P
Sbjct: 145 HEKLGFKHAGTIREAGFKFGRWLDLAFYQLTLDTPEQP 182

>ref|ZP_08127446.1| hypothetical protein AoriK_13175 [Actinomyces oris K20]
Length = 427

Score = 81.3 bits (199), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 60/168 (35%), Positives = 84/168 (50%), Gaps = 9/168 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQT---PQEWIDDLERLQDRYPWLVAEVEG 66
IRPAT AD A+ I N + S + + Q + W L + R LVA V G
Sbjct: 20 IRPATMADSPAIRIRNAAVRESLAIWTSIEQDHAGAEAW---LAPMVQRTALVAHVSG 76

Query: 67 V---VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
V G A AGPW + Y TVE ++Y+S Q GLG+ L L+++ G ++++
Sbjct: 77 EPHDVVGFAVAGPWHSYEGYARTVEDSIYLSPPAAQKGKGLGARLLAALIEASRRAGDRTMI 136

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELP 171
A+I + SVRLHE G+T GT+ AG KHG D+ R + P
Sbjct: 137 ALIEAGHATSVRLHERYGFTTVGTVPQAGEKHGQILDLTLMRCLKGP 184

>ref|YP_003271604.1| GCN5-like N-acetyltransferase [Gordonia bronchialis DSM 43247]
gb|ACY19711.1| GCN5-related N-acetyltransferase [Gordonia bronchialis DSM 43247]
Length = 172

Score = 81.3 bits (199), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 53/170 (31%), Positives = 84/170 (49%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTV--NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
++IR A AD+ A+ I N +E +T N R + + + W+ ++R YP LVA+
Sbjct: 1 MDIRDALQADLDAITAIYNDAVENTTAIWNERVVDVENRRAWM--VDRRAAGYPVLVADD 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+G + G A G ++ + Y TVE +VYV + +G +L L++ ++A
Sbjct: 59 DGDIVGYATFGDYRPFQGYRHTVEHSVYVRFDQGRQVWVSLMVELIERARQLDKHVMIA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPP 174
+ N S+RLHE LG+ G LR G K G W D+ F Q + P
Sbjct: 119 AVDAENSGSIRLHEKLGFPAGELRQVGTKFGRWLDLAFQLTLDDRVPD 168

>ref|YP_001206849.1| putative phosphinothricin N-acetyltransferase [Bradyrhizobium sp.
ORS278]
emb|CAL78632.1| putative phosphinothricin N-acetyltransferase [Bradyrhizobium sp.
ORS278]
Length = 190

Score = 81.3 bits (199), Expect = 5e-14, Method: Compositional matrix adjust.
Identities = 53/177 (29%), Positives = 81/177 (45%), Gaps = 12/177 (6%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTTPQEWIDDLERLQD-----RYPWLVA 62
V +RP+ D+ A+ I +I + P+ DDL++ + R P LVA
Sbjct: 14 VLVRPSRDEVEAMLAIYRRHIRRGVEDSAANTGAPEP---DDLKQRRKNLRNHLRPLVA 71

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
G V G AY ++ R AY + V+ ++YV H H G+G L L+ + A G++ +
Sbjct: 72 TFRGEVVGAYVYVQFRKRPAYRFAVKHSIYVHHEHLGRGVGRLLMQALIDASAAAGYRQM 131

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF-----ELPAPP 174
+ I N S+ +HE G+ G L Y++G W D QR E P A P
Sbjct: 132 IGYIDADNTASLGIHERFGFVRVGLLPVAYRYGRWSDTVMVQSLGPGAAEAPATP 188

>ref|ZP_06911259.1| phosphinothricin N-acetyltransferase [Streptomyces
pristinaespiralis ATCC 25486]
gb|EDY64129.1| phosphinothricin N-acetyltransferase [Streptomyces
pristinaespiralis ATCC 25486]
Length = 182

Score = 81.3 bits (199), Expect = 6e-14, Method: Compositional matrix adjust.
Identities = 53/181 (29%), Positives = 90/181 (49%), Gaps = 16/181 (8%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP--WLV 61
E V++R AD+ A+ DI NHY+ +++ F T TP++ L + P LV
Sbjct: 3 EHAEVQVRAGAEADLKALTDIYNHYVRETSITFDTTVFTPEQRRSWLHSHPEDGPHRLLV 62

Query: 62 AE-----VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYT 108
A+ +G++ G A + P++ + AY +VE +VY + + G+G+ LY
Sbjct: 63 AQDVRFAGPDPSPKHPADGIL-GYATSSPFRPKAAYSTSVEVSVYCAPQAAGGGIGTLLYK 121

Query: 109 HLLKSMEAQGFKSVMVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
L +++ + A + LPND SVRLH G+ GT G K G + DV ++++
Sbjct: 122 ALFEALADEDVHAYAGVALPNDASVRLHTRFGFRHVGTYGEVGRKFGRYWDVAWYEKRL 181

Query: 169 E 169
+
Sbjct: 182 D 182

>ref|NP_662156.1| acetyltransferase [Chlorobium tepidum TLS]
gb|AAM72498.1| acetyltransferase GNAT family [Chlorobium tepidum TLS]
Length = 164

Score = 81.3 bits (199), Expect = 6e-14, Method: Compositional matrix adjust.
Identities = 46/163 (28%), Positives = 80/163 (49%), Gaps = 2/163 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-EVE 65
P+E+ P A D+ + I N+Y+E + + P + + ++ L YP VA + +
Sbjct: 3 PIELLPVCADDLDEMAGIFNYVEHTLATYTETPVSVVERFVS-LMCFSPGYPAFVARDSD 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
G +AG P+ A+D T E T ++S + G+GS + L G +++VA
Sbjct: 62 GALAGFGLLRPYSPIPAFDRTAELTCFLSKGNTGRGIGSAILQALESEAVELGIETIVAT 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
+ N+ S+R H A G+ +G L G ++G DV + Q+ F
Sbjct: 122 VSSLNEESLRFHLARGFVEQGRLVGIGSRNGRCFDVIYQLKTF 164

>ref|ZP_01229015.1| phosphinothricin N-acetyltransferase [Aurantimonas manganoxydans
SI85-9A1]
gb|EAS48385.1| phosphinothricin N-acetyltransferase [Aurantimonas manganoxydans
SI85-9A1]
Length = 182

Score = 80.9 bits (198), Expect = 7e-14, Method: Compositional matrix adjust.
Identities = 51/159 (32%), Positives = 82/159 (51%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAE-VEGV 67
IR A AD+ A+ I + T +F P E + + +P++VAE +G
Sbjct: 6 IRLAVLADVLPALTAIYEDAVLHGTASFELVPPDQAEMEAFNAITGQCFPYIVAEDSDGT 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
V G AYA ++ R AY + VE +VY++ + +G+ L + L++ +GF+ ++AVIG
Sbjct: 66 VLGAYAYANAFRTRPAYRFAVEDSVYLAPEAKGRRIGTDLLSRLVELSAERGFQMIAVIG 125

Query: 128 LPN-DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165

+ PS+RLHE G+ G +G+K G W D Q

Sbjct: 126 GSDHTPSIRLHERAGFRMIGVFENSGFKFGRWIDTVLMQ 164

>ref|YP_001846218.1| sortase [Acinetobacter baumannii ACICU]
 ref|ZP_06785718.1| sortase [Acinetobacter sp. 6014059]
 gb|ACC56871.1| Sortase [Acinetobacter baumannii ACICU]
 gb|ACU00284.1| sortase [Acinetobacter baumannii]
 gb|ADX03651.1| sortase [Acinetobacter baumannii 1656-2]
 gb|ADX91665.1| sortase [Acinetobacter baumannii TCDC-AB0715]
 gb|ADX92177.1| sortase [Acinetobacter baumannii TCDC-AB0715]
 Length = 181

Score = 80.9 bits (198), Expect = 8e-14, Method: Compositional matrix adjust.
 Identities = 49/180 (27%), Positives = 86/180 (47%), Gaps = 12/180 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLE-----RLQD 55
 + R ++ A A A+ +I+N I ST + P++ +D ++ + ++
 Sbjct: 5 LDSNFLIDCNEAEHA--VAILEILNDAIVNSTALYDYVPRS----LDSMKTWFSVKREN 58

Query: 56 RYPWL-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 +P + V + G + G A G ++A AY +TVE ++Y+ H H+ GL L L++
 Sbjct: 59 GFPVIGVDELGKLLGFASWGTFRAFPAYKYTVEHSIYIHHEHRGCGLSKVLQMQLIQRA 118

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 + ++ I N S+ LHE +G+T GT + G+K G W D F+Q P P
 Sbjct: 119 QQAQLHVLIGCIDATNQASIGLHEKMGFTHAGTFKQVGFKFGQWLDAAFYQLILNTPFEP 178

>ref|YP_001751487.1| GCN5-related N-acetyltransferase [Pseudomonas putida W619]
 gb|ACA75118.1| GCN5-related N-acetyltransferase [Pseudomonas putida W619]
 Length = 171

Score = 80.5 bits (197), Expect = 8e-14, Method: Compositional matrix adjust.
 Identities = 57/169 (33%), Positives = 75/169 (44%), Gaps = 5/169 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVE 65
 EIR A AD+ + DI N + +T + P W + R Q YP LVA
 Sbjct: 4 EIRDALPADVPGLDIYNDAVRNTTAINWDTVPDLGNRHAWFE--ARAQQGYPIVAVDH 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 V G A G W+ + TVE +VY+ + GLG L L++ G +VA
 Sbjct: 62 SGVLGYASFQDWRPFEGFRNTVEHSVYIRGDQRGKGLGPQLMAALIERARGCGKHMVMAA 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N SVRLHE LG+ G + G K G W D+ F Q + A P
 Sbjct: 122 IESGNAASVRLHERLGFVVTGQMPQVGKFGRWLDLTFMQLVLDPGAEP 170

>ref|YP_003642748.1| Phosphinothricin acetyltransferase [Thiomonas intermedia K12]
 gb|ADG30418.1| Phosphinothricin acetyltransferase [Thiomonas intermedia K12]
 Length = 175

Score = 80.5 bits (197), Expect = 8e-14, Method: Compositional matrix adjust.
 Identities = 52/156 (33%), Positives = 77/156 (49%), Gaps = 2/156 (1%)

Query: 24 IVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVVAGIAYAGPWKARNA 82
 I H++ T F T E + L+ +Q R PWLVA + G AYA ++AR A
 Sbjct: 20 IYGHVHLHGTGTFTLAPDEAEMLRRLQEVQSRGLPWLVAVRGQEIIGYAYANWFRAREA 79

Query: 83 YDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG-LPNDPSVRLHEALG 141
 + +TVE ++Y++ R G+G L L+ + G + ++AVIG N S+ LH A G

Sbjct: 80 FRFTVEDSIYIAPNGLRQGVGGQLLDALIDTCTQSGARQMLAVIGDSANAGSIGLHRARG 139

Query: 142 YTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRPV 177

+ G + G+K W DV F QR A P+

Sbjct: 140 FEELGRMPTVGWKFDRWLDVVFMRALGAGAETSPI 175

>ref|YP_003732477.1| putative antibiotic resistance (phosphinothricin
N-acetyltransferase) [Acinetobacter sp. DR1]
gb|ADI91104.1| putative antibiotic resistance (phosphinothricin
N-acetyltransferase) [Acinetobacter sp. DR1]
Length = 181

Score = 80.5 bits (197), Expect = 9e-14, Method: Compositional matrix adjust.
Identities = 43/158 (27%), Positives = 77/158 (48%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWL-VAEVEGVVAGIAYAGP 76

A+ +I+N I ST + P++ + + + ++ +P + + + + G A G

Sbjct: 21 GAILEILNEAIINSTALYDYLPRSEESMKNWFSVKRENGFPVIGIIDETNKLGFASWGT 80

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRL 136

++A AY +TVE ++Y+ H H+ GL L L+K + ++ I N S+ L

Sbjct: 81 FRAFPAYKYTVEHSIYIHHEHRGCGLSKILMQELIKRAQEAEHLVLIGCIDATNQASIGL 140

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPP 174

HE +G+ GT + G+K G W D F+Q + P P

Sbjct: 141 HEKMGFIHAGTFKQVGFKFGQWLDAAFYQLNLNTPQQP 178

>gb|ACR54770.1| sortase [Acinetobacter genomosp. 13TU]
Length = 181

Score = 80.5 bits (197), Expect = 9e-14, Method: Compositional matrix adjust.
Identities = 49/180 (27%), Positives = 86/180 (47%), Gaps = 12/180 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE----RLQD 55

+ R ++ A A A+ +I+N I ST + P++ +D ++ + ++

Sbjct: 5 LDSNIRLIDCNEAEHA--VAILEILNDAIVNSTALYDYVPRS----LDSMKTWFSVKREN 58

Query: 56 RYPWL-VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114

+P + V + G + G A G ++A AY +TVE ++Y+ H H+ GL L L++

Sbjct: 59 GFPVIGVDELGKLLGFASWGTFRAPPAYKYTVEHSIYIHHEHRGCGLSKVLMQALIQRA 118

Query: 115 EAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPP 174

+ ++ I N S+ LHE +G+T GT + G+K G W D F+Q P P

Sbjct: 119 QQAQLHVLIGCIDATNQASIGLHEKMGFTAGTFKQVGFKFGQWLDAAFYQLILNTPFEP 178

>ref|YP_522665.1| GCN5-related N-acetyltransferase [Rhodoferax ferrireducens T118]
gb|ABD69134.1| GCN5-related N-acetyltransferase [Rhodoferax ferrireducens T118]
Length = 174

Score = 80.5 bits (197), Expect = 9e-14, Method: Compositional matrix adjust.
Identities = 50/169 (29%), Positives = 81/169 (47%), Gaps = 2/169 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68

IRP+ D+ A+ I ++ T F +P +P + ++ L P+LVA V

Sbjct: 4 IRPSQTEDIPAIAAIYARHVLHGTGTFTDPPSPDDMAQRRVDVLAKGLPYLVAAGDQV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127

G AY +K R AY ++ E ++Y++ GLG L L+ E G + ++AVIG

Sbjct: 64 MGFAYCNWFKPRPAYRFSAEYSIYLADEAIGQGLGRALLAELMAQAEKAGVRKLIIVIGD 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQPDFELPAPPRP 176
 N S+ +H + G++ G L++ G+K W DV + L A P
 Sbjct: 124 SANHGSIGVHRSAGFSMVGVLKSCGWKFDQWLDVVMMDKALGLGATRAP 172

>ref|YP_004278147.1| GCN5-related N-acetyltransferase [Agrobacterium sp. H13-3]
 gb|ADY63827.1| GCN5-related N-acetyltransferase [Agrobacterium sp. H13-3]
 Length = 165

Score = 80.5 bits (197), Expect = 9e-14, Method: Compositional matrix adjust.
 Identities = 49/158 (31%), Positives = 76/158 (48%), Gaps = 5/158 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 +E+R AT D++ + +I N + +T + + +EW R +P +VA
 Sbjct: 2 SLELRDATVEDLSGIMEIYNDAVLNTTAIWNEVLVDLENRKEWFS--ARKSRDFPVIVAI 59

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 ++G VAG A G W+A + Y T E +VYV + G+G L L+ ++
 Sbjct: 60 LDGKVAGYASYGDWRAFDGYRHTREHSVYVHKDARGHGIGKRLMQALIDHASGNDVHVLI 119

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 A I N S+RLHE+LG+T G G K G W D+
 Sbjct: 120 AAIESENAASIRLHESLGF+TVAGRFSEVGTKFGRWLDL 157

>ref|ZP_07471113.1| acetyltransferase [Brucella sp. NF 2653]
 gb|EFM62873.1| acetyltransferase [Brucella sp. NF 2653]
 Length = 202

Score = 80.5 bits (197), Expect = 1e-13, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 83/160 (51%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
 Sbjct: 43 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGF+VVLVAEREG 100

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A GP++ + + E +VYV+ + G+G L L++ + ++A I
 Sbjct: 101 QVVGYASYGPF+RPFEGFRHSSELSVYVASNARGGGIGRALLAELVEEARERK+VHVLIAGI 160

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
 N S+ LH + G+ GTL+ G K G W D+ F Q+
 Sbjct: 161 EAGNAASIALHRSQGFECEGTLKQVGQKFGRWLDLLFMQK 200

>ref|ZP_06808016.1| phosphinothricin acetyltransferase [Aerococcus viridans ATCC 11563]
 gb|EFG49489.1| phosphinothricin acetyltransferase [Aerococcus viridans ATCC 11563]
 Length = 186

Score = 80.5 bits (197), Expect = 1e-13, Method: Compositional matrix adjust.
 Identities = 56/170 (32%), Positives = 86/170 (50%), Gaps = 10/170 (5%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWL 60
 E V IRPA AD A + I N+YI+ +T++FR T+ ++ I ER+ P+L
 Sbjct: 16 ENDQVLIRPAELADAAQLTAIYNYIQTNTTISFRIALTDVSLKEQI--TERIGIN-PFL 72

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG-- 118
 VA+ EG V G AY A Y + E ++Y+ + G+GS LY L + +
 Sbjct: 73 VADYEGQVIGFAYTSDAGAYEGYRPSKEISIYLD+HVAKGIGSRLYQALEQEVIDNYPD 132

Query: 119 -FKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRD 167
 +K V V G N+ S++ H+ G+ G + GYK W DV + ++D

Sbjct: 133 IYKLVSQVTG-TNESSLKFKHKKHGFEGVCKNMGYKFDQWLDVVYLEKD 181

>ref|YP_003308692.1| phosphinothricin acetyltransferase [Sebaldella termitidis ATCC 33386]

gb|ACZ08761.1| Phosphinothricin acetyltransferase [Sebaldella termitidis ATCC 33386]

Length = 165

Score = 80.5 bits (197), Expect = 1e-13, Method: Compositional matrix adjust.

Identities = 51/157 (32%), Positives = 83/157 (52%), Gaps = 1/157 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER-LQDRYPWLVAEVEGVV 68

IR +D A+ I N+Y++ +TV F TE E +++ L+ YP++V E EG+V

Sbjct: 2 IRSVRLSDAEIAIAKIYNYVVKETTTFETEIDITEMEKRIKKTLEYGYPFIVHEEEGIV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128

G AY W+ R +Y+ T+E+++YV + G G LY L++ + G ++ V+

Sbjct: 62 TGYAYVRKWRERISYNNLTETSIYVDKDKTKGTGKKLYNSLIEKCKKSGVHVLIGVLSH 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165

N S +LH+ G+ G + A K G + DV FW

Sbjct: 122 TNTASKKLHKNTGFECTGHFKEAANKFGKFIDVEFW 158

>ref|YP_046305.1| putative phosphinothricin N-acetyltransferase [Acinetobacter sp. ADP1]

pdb|2JLM|A Chain A, Structure Of A Putative Acetyltransferase (Aciad1637) From Acinetobacter Baylyi Adp1

pdb|2JLM|B Chain B, Structure Of A Putative Acetyltransferase (Aciad1637) From Acinetobacter Baylyi Adp1

pdb|2JLM|C Chain C, Structure Of A Putative Acetyltransferase (Aciad1637) From Acinetobacter Baylyi Adp1

pdb|2JLM|D Chain D, Structure Of A Putative Acetyltransferase (Aciad1637) From Acinetobacter Baylyi Adp1

pdb|2JLM|E Chain E, Structure Of A Putative Acetyltransferase (Aciad1637) From Acinetobacter Baylyi Adp1

pdb|2JLM|F Chain F, Structure Of A Putative Acetyltransferase (Aciad1637) From Acinetobacter Baylyi Adp1

emb|CAG68483.1| putative antibiotic resistance (phosphinothricin N-acetyltransferase) [Acinetobacter sp. ADP1]

Length = 182

Score = 80.5 bits (197), Expect = 1e-13, Method: Compositional matrix adjust.

Identities = 49/159 (30%), Positives = 81/159 (50%), Gaps = 6/159 (3%)

Query: 21 VCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVE-GVVAGIAYAGP 76

+ +I+N I ST + +P+++ + W + Q+ +P + A E G + G A G

Sbjct: 24 ILEILNDAIINSTALYDYKPRSKESMAAWF--ATKQNNFPIIGAVNEVGQLGFASWGS 81

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPSVRL 136

++A AY +TVE +VY+ ++ LGL L L+K +V I N S++L

Sbjct: 82 FRAFPAYKYTVEHSVYIHKDYRGLGLSKHLMNELIKRAVESEVHVMVGCIDATNVAISIQL 141

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175

H+ LG+ GT++ AG+K G W D F+Q + P P+

Sbjct: 142 HQKLGFIHSGTIQQAGFKFGRWLDAAFYQLTLDTPHPQ 180

>ref|ZP_04681054.1| acetyltransferase [Ochrobactrum intermedium LMG 3301]

gb|EEQ96560.1| acetyltransferase [Ochrobactrum intermedium LMG 3301]

Length = 198

Score = 80.1 bits (196), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 82/160 (51%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR AT AD+ A+ I N +E + + + +EW+ R +D +P LVAE +G
Sbjct: 39 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRREWLG--ARNRDGFPVLVAERDG 96

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+ G A GP++ + + E ++YV+ + G+G L L++ + +VA I
Sbjct: 97 AILGYASYGPFPRPFEGFRHSSSELSIYVASNARGGGIGRALLAELVEEARERKVVHVLVAGI 156

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N SV LH++ G+ GTLR G K G W D+ F Q+
Sbjct: 157 EAGNAASVALHKSQGFEDCGTLRQVGQKFGRWLDLTFMQK 196

>ref|ZP_06686178.1| acetyltransferase [Achromobacter piechaudii ATCC 43553]
gb|EFF76894.1| acetyltransferase [Achromobacter piechaudii ATCC 43553]
Length = 185

Score = 80.1 bits (196), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 57/181 (31%), Positives = 84/181 (46%), Gaps = 15/181 (8%)

Query: 7 PVEIRPATAADMA-----AVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQ 54
P EIR A + + I N I ST + +P+P Q W + Q
Sbjct: 4 PAEIRAPQGATLVDCTHARHADQILAIFNDAIVNSTALYDYKPRPPEAMQGWFG--AKQQ 61

Query: 55 DRYPWLVAEVE-GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
+P + E E G + A G ++A A+ ++VE +VYV R + GLG + L++
Sbjct: 62 GGFPPVVGFEAGELMAFASYGTFRAPAFKYSVEHSVYVDARFRGQGLGIAMMQVLIER 121

Query: 114 MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAP 173
A +V I N S+ LHE LG+T GT+R AG+K G W D+ F+Q + P
Sbjct: 122 ARANQVHVLVGGIDASNTGSIHLHEKLGFTHAGTIRQAGFKFGRWLDLAFYQLTLDTPEQ 181

Query: 174 P 174
P
Sbjct: 182 P 182

>ref|YP_003807359.1| GCN5-related N-acetyltransferase [Desulfarculus baarsii DSM 2075]
gb|ADK84765.1| GCN5-related N-acetyltransferase [Desulfarculus baarsii DSM 2075]
Length = 365

Score = 80.1 bits (196), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 49/159 (30%), Positives = 76/159 (47%), Gaps = 1/159 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ +RPA A D AV I NHY+ S + P PQ + L D ++VAE +G
Sbjct: 206 IVLRPADAQDGPVMAIFNHYVANSFAAYPETPHPPQAFEHLLNICLDG-SFVVAEEDGQ 264

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G+ + P+ T + T +++ H GLG L L+ S +G +++A +
Sbjct: 265 VIGLGLTLPFLPAETLRRTAQVTYFIAPEHTGKGLGRLLQLSLVASARQGVDTLLAHVS 324

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+R H+ G+ RG L+ G KHG V + Q+
Sbjct: 325 SLNQGSIRFHQQNGFERRGELQVRGRKHGQDFGVVYLQK 363

>gb|ADX25103.1| acetyltransferase (GNAT) family protein [Streptococcus dysgalactiae
subsp. equisimilis ATCC 12394]
Length = 194

Score = 80.1 bits (196), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 49/163 (30%), Positives = 74/163 (45%), Gaps = 9/163 (5%)

```
Query: 7   PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
          V +R AT  D  A+  I   Y+  + V F  E   +  +  + ++  YP+LVAE  G
Sbjct: 2   SVSVRLATLEDAEALLAIYAPYVTDTAFTDYEVDPLEAFKKRMIQIMAFYPYLVAEEAG 61

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
          + G AYA  + AR AY W+ E T+Y++ ++  G G+ LY  L + +  G  +  I
Sbjct: 62  SILGYAYASAFHARAAYAWSAEVTIYLAMENKGGFGTKLYQALERYLTKMGILNCNVC I 121

Query: 127 G-----LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
          L N  +  HE +GY  G      GYK  W D+
Sbjct: 122 ASTACESPYLANHSQL-FHEKMGYQLVGKFHQVGYKFDQWFDM 163
```

>ref|YP_001326928.1| GCN5-related N-acetyltransferase [Sinorhizobium medicae WSM419]
gb|ABR60093.1| GCN5-related N-acetyltransferase [Sinorhizobium medicae WSM419]
Length = 169

Score = 80.1 bits (196), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 56/170 (32%), Positives = 79/170 (46%), Gaps = 6/170 (3%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVA-E 63
          ++IR A   D+ A+C I N  +  +T  +      +      W+D  R      P LVA
Sbjct: 1   MKIRDAIETDLPAICAIYNDAVANTTAIWNETLVDVANRATWLD--ARNSAGLPVLVALS 58

Query: 64  VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VV 123
          G V G A  G W+A + Y  TVE +VYV  +  G+G L  L+  E  G  ++
Sbjct: 59  GTGEVVGYSFGEWRAFDGYRHTVEHSVYVRLDQRRGGGIGRALMLELIGRAEGLGKHVMI 118

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAP 173
          A I   N PS+RLHE LG+  G ++  G K G W D+ F Q      +P
Sbjct: 119 AGIESGNLPSIRLHEQLGFRQTGHMKEVGTKFGRWLDLTFMQLILSSGSP 168
```

>emb|CBK87879.1| Sortase and related acyltransferases [Eubacterium cylindroides
T2-87]
Length = 182

Score = 80.1 bits (196), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 44/159 (27%), Positives = 77/159 (48%), Gaps = 1/159 (0%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          IR   + D+ ++ DI  +Y++ ST  F   P   +  +  +  +  +  YP+ VAE +G  +
Sbjct: 4   IRLFDSMDVESIYDIYAYYVKNSTAIFDLAPMDKEVFNKMLDTSEEYPPFYVAEHDGELI 63

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
          G AY      + AY + VE ++Y  +  G+  L  + ++  +G+K ++A I
Sbjct: 64  GYAYVHKAPTKEAYRFCVELSIYFK-KGNHYGMADALVKKVEEACIQGYKWIIACITDT 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
          N S+  H  GY  G+L+  GYK  WH V +  +D
Sbjct: 123 NTTSINFHLKHGYVKTGSLQNCGYKWNQWHGVNWLCKDL 161
```

>gb|ABB77438.1| acetyl- or acyltransferase [Mitsuokella multacida]
Length = 148

Score = 79.7 bits (195), Expect = 1e-13, Method: Compositional matrix adjust.
Identities = 48/142 (33%), Positives = 73/142 (51%), Gaps = 9/142 (6%)

Query: 51 ERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110
 +++ + YP+LVAE G V G YA + R AY W+VE+++YV+ + G G LY L
 Sbjct: 6 KKIFEHYPYLVAEQGGRVLGYIYAHEFYGRAAYAWSVEASIIYVASDARGQGFRKLYAAL 65

Query: 111 LKSMEAQGFKSQVAVIGLP---NDP-----SVRLHEALGYTARGTLRAAGYKHGGWHDVG 162
 ++ G ++ I +P +DP S+ H+ LGY G +GYK G W+DV
 Sbjct: 66 EDALRGMGVLNINVCIAVPRAADDPYLTVGSI AFHKRLGYQMVGIFHQSGYKFGRWYDVA 125

Query: 163 FWQRDF-ELPAPPRPVRPVTQI 183
 + ++ E PP VR I
 Sbjct: 126 WMEKMLGEHEEPPAAVRDFHGI 147

>ref|ZP_01158185.1| phosphinothricin N-acetyltransferase, putative [Oceanicola
 granulosus HTCC2516]
 gb|EAR49680.1| phosphinothricin N-acetyltransferase, putative [Oceanicola
 granulosus HTCC2516]
 Length = 156

Score = 79.7 bits (195), Expect = 1e-13, Method: Compositional matrix adjust.
 Identities = 54/157 (34%), Positives = 75/157 (47%), Gaps = 4/157 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR A D A+ + N IET+TV F +EP++ + + L P LVAE G VA
 Sbjct: 2 IRAARTQDATAIAAVWNGIIEITTTVTFASEPKS---VAAVTELIAERPVLVAERAGAVA 57

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSQVAVIGLP 129
 G A GP++ + Y T E TV+++ + GLG L L QG +VA I
 Sbjct: 58 GFATFGPFRGGSGYRHTAELTVHLTEAARGQGLGRRLVAALEAEAAAGQGVHVLVAAISAE 117

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N ++ H LG+ G L G K G W D+ Q+
 Sbjct: 118 NAGALAFHARLGFEEAGRLAEVGRKFGRWLDLVLMOQ 154

>ref|ZP_06113675.1| toxin-antitoxin system, toxin component, GNAT family [Clostridium
 hathewayi DSM 13479]
 gb|EFC99939.1| toxin-antitoxin system, toxin component, GNAT family [Clostridium
 hathewayi DSM 13479]
 Length = 163

Score = 79.7 bits (195), Expect = 1e-13, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 81/160 (50%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWLVAEVEG 66
 +EIR A D+ + DI N+ + F P+T E +D +P +VA +G
 Sbjct: 1 MEIRIAQEEDVPYLLDIYNYEVLHGEATFDINPRTLSERLDWYYAHNISHPLIVAVEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSQVAV 125
 G A P++ + AY TVE +VYV +++ G+ L H+L + E + +V++V
 Sbjct: 61 HAVGYASLSPYRVKEAYAATVELSVYVHRDYRKRGIAKRLTLHILNMAREDERIHTVISV 120

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 I N S+ LHE LG+ GT++ G K G + D+ +Q
 Sbjct: 121 ITGGNQASIHLEELGFLHCGTIKEVGKFGKYLDIENYQ 160

>ref|ZP_05181470.1| hypothetical protein Bru83_08976 [Brucella sp. 83/13]
 ref|ZP_06097408.1| conserved hypothetical protein [Brucella sp. 83/13]
 gb|EEZ33526.1| conserved hypothetical protein [Brucella sp. 83/13]
 Length = 164

Score = 79.7 bits (195), Expect = 1e-13, Method: Compositional matrix adjust.

Identities = 50/160 (31%), Positives = 83/160 (51%), Gaps = 5/160 (3%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
          IR AT AD+ A+ I N +E + + + +W+++ R +D +P LVAE EG
Sbjct: 5   IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPVLVAEREG 62

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          V G A GP++ + + E +VYV+ + G+G L L++ + ++A I
Sbjct: 63  QVVGYASYGPFPRPFEGFRHSSELSVYVASNARGGGIGRALLAELVEEARERKVHVLIAGI 122

Query: 127  GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
          N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 123  EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 162
```

>ref|ZP_07474073.1| acetyltransferase [Brucella sp. B02]
 gb|EFM59904.1| acetyltransferase [Brucella sp. B02]
 Length = 164

Score = 79.7 bits (195), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 83/160 (51%), Gaps = 5/160 (3%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
          IR AT D+ A+ I N +E + + + +W+++ R +D +P LVAE EG
Sbjct: 5   IRHATETDLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPVLVAEREG 62

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          VAG A GP++ + + E +VYV+ + G+G L L++ + ++A I
Sbjct: 63  QVAGYASYGPFPRPFEGFRHSSELSVYVASNARGGGIGRALLAELVEEARERKVHVLIAGI 122

Query: 127  GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
          N S+ LH + G+ GTL+ G K G W D+ F Q+
Sbjct: 123  EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 162
```

>ref|YP_001764419.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia MC0-3]
 ref|ZP_04939211.1| Sortase [Burkholderia cenocepacia PC184]
 gb|EAY62382.1| Sortase [Burkholderia cenocepacia PC184]
 gb|ACA90297.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia MC0-3]
 Length = 184

Score = 79.7 bits (195), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 52/167 (31%), Positives = 78/167 (46%), Gaps = 2/167 (1%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWLVA-EVEGV 67
          I + A AA+ I+N I ST + P+ P+ + + +P A + G
Sbjct: 15  IDCSEAEHAAAAILAILNDAIVNSTALYDYRPRPPEAMVTFATKRAAGFPVFGAVDAAGT 74

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
          + G A G ++A A+ +TVE +VYV H + GLG L +++ +V I
Sbjct: 75  LLGFASWGTFRAFPAPFKYTVEHSVYVRHDQGRGLGELLLREVVRRAEAQVHVLVGCID 134

Query: 128  LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPAPP 174
          N S+ LH LG+ GT+ AG+K G W D F+Q E PA P
Sbjct: 135  ATNTGSIALHTKLGFVHSGTVAEAGFKFGRWLDAAFYQLKLETPAQP 181
```

>ref|YP_744013.1| phosphinothricin N-acetyltransferase [Granulibacter bethedensis
 CGDNIH1]
 gb|ABI61090.1| phosphinothricin N-acetyltransferase [Granulibacter bethedensis
 CGDNIH1]
 Length = 183

Score = 79.7 bits (195), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 55/164 (33%), Positives = 81/164 (49%), Gaps = 10/164 (6%)

```
Query: 9  EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-----QDRYPWLVAE 63
          + RPA  D A +  I  H++  T  F  P  T  ++ +ERL  + +P++VAE
Sbjct: 7  DFRPAQREDSAFIQSIYAHHVHLHGTGTFEETPPT----VEQMERLVHTIKSEAWPFIVAE 62

Query: 64  VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
          + G AYA  ++ R+AY +  E +VYV  +  G+G  L  T  LL  GF+ +V
Sbjct: 63  DRTGIIGYAYAAQFRDRSAYRYCAEDSVYVREDVRGQGVGKALLTLLLHESARAGFRQM 122

Query: 124  AVIG-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
          A+IG  N  S+ +H  LG+ + G LR  G  K  DV  QR
Sbjct: 123  ALIGDAENIGSIGVHATLGFKSVGRLREVGKLERLDVVLQMQR 166
```

```
>ref|NP_253553.1| hypothetical protein PA4866 [Pseudomonas aeruginosa PAO1]
ref|YP_793333.1| hypothetical protein PA14_64360 [Pseudomonas aeruginosa UCBPP-PA14]
ref|YP_002442830.1| putative phosphinothricin N-acetyltransferase [Pseudomonas
aeruginosa LESB58]
gb|AAG08251.1|AE004900_5 conserved hypothetical protein [Pseudomonas aeruginosa PAO1]
gb|ABJ14250.1| putative phosphinothricin N-acetyltransferase [Pseudomonas
aeruginosa UCBPP-PA14]
emb|CAW30006.1| putative phosphinothricin N-acetyltransferase [Pseudomonas
aeruginosa LESB58]
Length = 172
```

Score = 79.7 bits (195), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 55/165 (33%), Positives = 75/165 (45%), Gaps = 6/165 (3%)

```
Query: 9  EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EV 64
          IR A  AD+  +  I N  +  +T  +  P  Q  W  D  R  +  YP  LVA  +
Sbjct: 4  SIRDAGVADLPGILAIYNDAVGNTTAIWNETPVDLANRQAWFD--TRARQGYPILVASDA 61

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
          G V G A  G W+  +  TVE +VYV  +  GLG  L  L++  AQG  +VA
Sbjct: 62  AGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVMVA 121

Query: 125  VIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQORDFE 169
          I  N  S+ LH  LG+  G  +  G  K  G  W  D+ F  Q  +  +
Sbjct: 122  AIESGNAASIGLHRRLGFEISGQMPQVGQKFGRWLDLTFMQLNLD 166
```

```
>ref|YP_002908175.1| GCN5-related N-acetyltransferase [Burkholderia glumae BGR1]
gb|ACR30940.1| GCN5-related N-acetyltransferase [Burkholderia glumae BGR1]
Length = 174
```

Score = 79.7 bits (195), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 60/176 (34%), Positives = 83/176 (47%), Gaps = 6/176 (3%)

```
Query: 8  VEIRPATAADMAAVCDIVNHYI-ETSTVNFRTEPQTPQE--WIDDLERLQDRYPWLVA-E 63
          +EIR A  D+A +  I N  +  T  +  T  T  W+ D  R  +  YP  LVA  +
Sbjct: 1  MEIRDAREQDVAGITAIYNDAVMNTLAIWNETAVDLTANRTAWLAD--RGRAGYPVLVAVD 58

Query: 64  VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
          V G A  G W+  +  +  TVE ++YV  +  G+G  L  L++  A G  +V
Sbjct: 59  AAQQVLGYASFQDWRPFDFGRATVEHSIYVRADQRGNGIGRQLMVALIERARAIGKHMV 118

Query: 124  AVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQORDFELPAPPRPVRP 179
          A I  N  S+RLHE LG+  GTLR  G  K  G  W  D+ F  Q  +  A  P+  P
Sbjct: 119  AGIEANNAGSIRLHETLGRDGTGTLRQVGMKFGQWLDLTFMQLTLDTRATPQAKLP 174
```

>ref|ZP_04931736.1| conserved hypothetical protein [Pseudomonas aeruginosa C3719]
 ref|ZP_04937560.1| conserved hypothetical protein [Pseudomonas aeruginosa 2192]
 gb|EAZ55855.1| conserved hypothetical protein [Pseudomonas aeruginosa C3719]
 gb|EAZ61679.1| conserved hypothetical protein [Pseudomonas aeruginosa 2192]
 Length = 172

Score = 79.7 bits (195), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 55/165 (33%), Positives = 75/165 (45%), Gaps = 6/165 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EV 64
 IR A AD+ + I N + +T + P Q W D R + YP LVA +
 Sbjct: 4 SIRDAGVADLPGILAIYNDAVGNTTAIWNETPVDLANRQAWFD--TRARQGYPILVASDA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 G V G A G W+ + TVE +VYV + GLG L L++ AQG +VA
 Sbjct: 62 AGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQQLLALIERARAQGLHVMVA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 I N S+ LH LG+ G + G K G W D+ F Q + +
 Sbjct: 122 AIESGNAASIGLHRRLLGFEISGQMPQVGQKFGRWLDLTFMQLNLD 166

>ref|ZP_01367883.1| hypothetical protein PaerPA_01005037 [Pseudomonas aeruginosa PACS2]
 ref|ZP_07795793.1| putative phosphinothricin N-acetyltransferase [Pseudomonas aeruginosa 39016]
 gb|EFQ40889.1| putative phosphinothricin N-acetyltransferase [Pseudomonas aeruginosa 39016]
 Length = 172

Score = 79.7 bits (195), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 55/165 (33%), Positives = 75/165 (45%), Gaps = 6/165 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EV 64
 IR A AD+ + I N + +T + P Q W D R + YP LVA +
 Sbjct: 4 SIRDAGVADLPGILAIYNDAVGNTTAIWNETPVDLANRQAWFD--TRARQGYPILVASDA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 G V G A G W+ + TVE +VYV + GLG L L++ AQG +VA
 Sbjct: 62 AGEVLGYAAYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQQLQALIERARAQGLHVMVA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 I N S+ LH LG+ G + G K G W D+ F Q + +
 Sbjct: 122 AIESGNAASIGLHRRLLGFEISGQMPQVGQKFGRWLDLTFMQLNLD 166

>ref|YP_001350908.1| hypothetical protein PSPA7_5587 [Pseudomonas aeruginosa PA7]
 pdb|2J8M|A Chain A, Structure Of P. Aeruginosa Acetyltransferase Pa4866
 pdb|2J8M|B Chain B, Structure Of P. Aeruginosa Acetyltransferase Pa4866
 pdb|2J8N|A Chain A, Structure Of P. Aeruginosa Acetyltransferase Pa4866 Solved
 At Room Temperature
 pdb|2J8N|B Chain B, Structure Of P. Aeruginosa Acetyltransferase Pa4866 Solved
 At Room Temperature
 pdb|2J8R|A Chain A, Structure Of P. Aeruginosa Acetyltransferase Pa4866 Solved
 In Complex With L-Methionine Sulfoximine
 pdb|2J8R|B Chain B, Structure Of P. Aeruginosa Acetyltransferase Pa4866 Solved
 In Complex With L-Methionine Sulfoximine
 gb|ABR81107.1| conserved hypothetical protein [Pseudomonas aeruginosa PA7]
 Length = 172

Score = 79.3 bits (194), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 55/165 (33%), Positives = 75/165 (45%), Gaps = 6/165 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EV 64
 IR A AD+ + I N + +T + P Q W D R + YP LVA +
 Sbjct: 4 SIRDAGVADLPGILAIYNDAVGNTTAIWNETPVDLANRQAWFD--ARARQGYPILVASDA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G V G A G W+ + TVE +VYV + GLG L L++ AQG +VA
 Sbjct: 62 AGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVMVA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFE 169
 I N S+ LH LG+ G + G K G W D+ F Q + +
 Sbjct: 122 AIESGNAASIGLHRRLGFEISGQMPQVGQKFGRWLDLTFMQLNLD 166

>ref|ZP_01442088.1| phosphinothricin N-acetyltransferase, putative [Pelagibaca bermudensis HTCC2601]
 gb|EAU47570.1| phosphinothricin N-acetyltransferase, putative [Roseovarius sp. HTCC2601]
 Length = 159

Score = 79.3 bits (194), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 51/157 (32%), Positives = 75/157 (47%), Gaps = 2/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEEGVVA 69
 IRPA A D A + + N +IET+ + F T +TP+ D+ D + LVAE +G +
 Sbjct: 3 IRPAHATDAAPLAALWNPWIETTAITFSTALKTPEGLATDIAARGDAF--LVAEADGALL 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A P++ Y T E TV ++ + G G L L + +Q S+ A +
 Sbjct: 61 GFATFFPFRRGGPGYARTKEHTVILAPEARGRGAGRALMNALAEVARSQQVHSLFAGVSAE 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 N V H A+G+T L GYK G W D+ Q+
 Sbjct: 121 NPAGVAFHAAIGFTETARLPQVGKFGRWMDLVLMQK 157

>ref|ZP_06881175.1| putative phosphinothricin N-acetyltransferase [Pseudomonas aeruginosa PAb1]
 Length = 172

Score = 79.3 bits (194), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 55/165 (33%), Positives = 75/165 (45%), Gaps = 6/165 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EV 64
 IR A AD+ + I N + +T + P Q W D R + YP LVA +
 Sbjct: 4 SIRDAGVADLPGILAIYNDAVGNTTAIWNETPVDLANRQAWFD--TRARQGYPILVASDA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G V G A G W+ + TVE +VYV + GLG L L++ AQG +VA
 Sbjct: 62 AGEVLGYASYGDWRPFEGFRSTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVMVA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFE 169
 I N S+ LH LG+ G + G K G W D+ F Q + +
 Sbjct: 122 AIESGNAASIGLHRRLGFEISGQMPQVGQKFGRWLDLTFMQLNLD 166

>ref|NP_294906.1| phosphinothricin acetyltransferase [Deinococcus radiodurans R1]
 gb|AAF10750.1|AE001967_3 phosphinothricin acetyltransferase [Deinococcus radiodurans R1]
 Length = 174

Score = 79.3 bits (194), Expect = 2e-13, Method: Compositional matrix adjust.
 Identities = 53/167 (31%), Positives = 78/167 (46%), Gaps = 6/167 (3%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRY 57
M+ RP IR AT AD+ + +I N + +T ++ EP T Q EW +R +
Sbjct: 1 MTSVIRPAVIRLATPADLPGILEIYNDAVLNTTASYDLEPATLQSREEWFAARQRAG--F 58

Query: 58 PWLVAEVEG-VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
P VA+ EG V G A G ++ + Y+ TVE +VY+ + GLG L L+ A
Sbjct: 59 PVFVAQGEAGTGLGFASYGTFREKPGYNGTVEHSVYIRDGQRGAGLGLALMERLIAEARA 118

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF 163
Q ++ + N S+ HE LG+ G K G W D+ F
Sbjct: 119 QHLHVMLGSVDADNAGSIAFHERLGRQVAHFHQVGRKFGRWLDVMF 165

>ref|XP_002536396.1| conserved hypothetical protein [Ricinus communis]
gb|EEF25987.1| conserved hypothetical protein [Ricinus communis]
Length = 458

Score = 79.3 bits (194), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 47/159 (29%), Positives = 80/159 (50%), Gaps = 6/159 (3%)

Query: 20 AVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWL-VAEVEGVVAGIAYAG 75
A+ DI N I ST + +P+T + W + + +P + + + +G + G G
Sbjct: 299 AILDIFNDAILNSTALYEQPRTLEVMTTWFE--TKRNGGFPVIGIEDDKGALLGFGSYG 356

Query: 76 PWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVR 135
++A A+ +TVE +VY+ H+ G+G L L+ + A +++ I N S++
Sbjct: 357 TFRAFPAFKYTVEHSVYIHKDHRGQGIGKALMHELIAAARAANLHAMMGIDAANAGSIK 416

Query: 136 LHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
LHE LG+ GTL G+K G W D+ F+Q + P P
Sbjct: 417 LHEGLGFKHVGTLPQVGFKFGHWLDLAFYQLILDTPPEQP 455

>ref|ZP_06825188.1| phosphinothricin N-acetyltransferase [Streptomyces sp. SPB74]
gb|EDY45167.1| phosphinothricin N-acetyltransferase [Streptomyces sp. SPB74]
Length = 177

Score = 79.3 bits (194), Expect = 2e-13, Method: Compositional matrix adjust.
Identities = 53/175 (30%), Positives = 80/175 (45%), Gaps = 7/175 (4%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-- 58
M V++R D+ + + NHY+ + + F T P TP + +D P
Sbjct: 1 MPESTEKQVRAGCEGDLPLQTLALYNHYVTETPITFDTVPFPTDQRLDWFRAPTGGPHR 60

Query: 59 WLVAEVEGV-----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
LVA G V G A +G ++++ AY +VE +VY GLG+ LYT L
Sbjct: 61 LLVAHAPGRPAGTDVLGYATSGAFRSKPAYATSVEVSVYCRPGEGGNGLGLTRYLTALFAC 120

Query: 114 MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
+ + A I LPN S+ LHE G+ GT G K G + DV ++++D
Sbjct: 121 LADEDVHRAYAGIALPNTASLALHERFGFRHLGTAEVGRKFGRYWDVAWYEKDL 175

>ref|ZP_03520117.1| putative phosphinothricin N-acetyltransferase (antibiotic
resistance) protein [Rhizobium etli GR56]
Length = 164

Score = 79.0 bits (193), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 54/172 (31%), Positives = 77/172 (44%), Gaps = 32/172 (18%)

Query: 1 MSPERRPVEIRPATAA---DMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY 57
M+P R VE+R TA D AA IV +Y
Sbjct: 1 MNPFERHVELRDHTALGRDRAAFAAIVGQ-----QY 32

Query: 58 PWLVA-EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
 P++ A + +G G AYA ++ R AY W VE ++Y++ + G+G L T L+
 Sbjct: 33 PYIAAADDDGNFLGYAYASAFRTRPAYRWMVEDSIYLAPEARGRGIGKALMTTELIDRCIV 92

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 GF+ +VAVIG + S+ LH G+ G ++ GYKHG W D QR
 Sbjct: 93 LGFRQMVAVIGGASPASIALHLKAGFVEVGLMQGTGYKHGRWLDTMLMQRSL 144

>gb|EGD02187.1| GCN5-related N-acetyltransferase [Burkholderia sp. TJI49]
 Length = 182

Score = 78.6 bits (192), Expect = 3e-13, Method: Compositional matrix adjust.
 Identities = 57/175 (32%), Positives = 86/175 (49%), Gaps = 5/175 (2%)

Query: 4 ERRPVEIRPATAADMA-AVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWL 61
 +R V + T A+ A A+ +I+N I ST + P+ P+ + + +P +
 Sbjct: 6 QRDDVRLIDCTEAHAPAILLEILNDAIVNSTALYDYRPRPPEAMVAWFAAKRAGGFPVVG 65

Query: 62 A-EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQR-LGLGSTLYTHLLKSMEAQGF 119
 A + G + G A G ++A A+ +TVE +VYV HR QR GLG L L++
 Sbjct: 66 AVDAAGTLLGFASWGTFRAFPAPFKYTVEHSVYV-HRDQGRGLGEFLLRELIRRAREADV 124

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 +V I N S+ LH LG+ GT+ AG+K G W D F+Q + PA P
 Sbjct: 125 HLLVGCIDATNAGSIALHTRLGFBVHSGTIAEAGFKFGRWLDAAFYQLKLDTPAQP 179

>ref|ZP_06056650.1| sortase [Acinetobacter calcoaceticus RUH2202]
 gb|EEY77949.1| sortase [Acinetobacter calcoaceticus RUH2202]
 Length = 181

Score = 78.6 bits (192), Expect = 3e-13, Method: Compositional matrix adjust.
 Identities = 45/167 (26%), Positives = 79/167 (47%), Gaps = 2/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWL-VAEVEGV 67
 I A A+ +I+N I ST + P++ + + + Q+ +P + + +
 Sbjct: 12 IDCNEAEHSVAILEILNEAIINSTALYDYFRSEESMKNWFSVKRQNGFPVIGIVDETDK 71

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G G ++A AY +TVE ++Y+ H H+ GL L L++ + ++ I
 Sbjct: 72 LLGFTSWGTFRAFPAYKYTVEHSIYIHHEHRGSGLSKILMQELIQRAQEAEHLVLIQCID 131

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N S+ LHE +G+T GT + G+K G W D F+Q + P P
 Sbjct: 132 ATNQASIGLHEKMGFTAGTFKQVGFKFGEWLDAAFYQLNLSTPFHP 178

>ref|ZP_05341911.1| acetyltransferase, gnat family [Thalassiosira sp. R2A62]
 gb|EET47578.1| acetyltransferase, gnat family [Thalassiosira sp. R2A62]
 Length = 161

Score = 78.6 bits (192), Expect = 3e-13, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 75/160 (46%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A+ D + +C I N I S+V F + +TP + I D + R+ VA+++G
 Sbjct: 2 IRAASIDDASEICGIWNPIIRDSSVTFNISIKKTPSDVAAMIRDKQGANQRF--CVAQLDG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V G A G ++ Y TVE ++ + Q G+G L L + A G S+ A +
 Sbjct: 60 AVVGAFATYQFRGGIGYQHTVEHSIILDPAAQGGVGRLLMDDLFEHARANGMHSMFAGV 119

Query: 127 GLPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166

N V H ALG+ G L G+K G W D+ Q+

Sbjct: 120 SGENPAGVAFHAALGFETIGRLPEVGFKFGRWFDLVLMOQ 159

>ref|YP_003850803.1| GCN5-related N-acetyltransferase [Thermoanaerobacterium
thermosaccharolyticum DSM 571]

gb|ADL67719.1| GCN5-related N-acetyltransferase [Thermoanaerobacterium
thermosaccharolyticum DSM 571]

Length = 161

Score = 78.6 bits (192), Expect = 3e-13, Method: Compositional matrix adjust.

Identities = 46/159 (28%), Positives = 73/159 (45%), Gaps = 6/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEG 66

IR A D+ + I N + +T TEP + ++W E DRY VA +

Sbjct: 3 IRKANIDDIERINGIYNQAVLNTTATIDTEPRPLEYHKKW---FEAHNDRYAVFVAIEDD 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126

+V G A W + Y E ++YV ++ G+G L +++ + F +++A I

Sbjct: 60 IVVGWASLSIWSEKCGYRAVAEDSIYVDESYKGRGIGDKLIKKIIEHAKENEFHTIIARI 119

Query: 127 GLPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165

ND S+ LHE G+ GTL+ GYK + D+ Q

Sbjct: 120 SEGNDVSIHLHEKYGFKIVGTLKELGYKFNRYLDIHILQ 158

>ref|XP_001617616.1| hypothetical protein NEMVEDRAFT_vlg225937 [Nematostella
vectensis]

gb|EDO25516.1| predicted protein [Nematostella vectensis]

Length = 170

Score = 78.6 bits (192), Expect = 3e-13, Method: Compositional matrix adjust.

Identities = 54/160 (33%), Positives = 77/160 (48%), Gaps = 6/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVA-EVE 65

I+ ATA D+ A+ I N + +T + + Q W+ ER +P LVA +

Sbjct: 3 IQDATADDLPAILAIYNDAVLNTTAIWNETQVDLANRQAWLS--ERNAAGFPVVLVAHDAA 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125

G V G + G W+A + TVE +VYV + GLG L L++ + G +VA

Sbjct: 61 GEVVGYSYSGTWRAIEGFRHTVEHSVYVRSRQGRQGLGPRLMQALIERAQTAGLHVMAA 120

Query: 126 IGLPNDPVSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165

I N S+RLHE LG+ G + G K G W D+ F Q

Sbjct: 121 IESGNSASIRLHERLGFVTTGQMPQVGRKFGRWLDLTFMQ 160

>ref|YP_001437992.1| hypothetical protein ESA_01902 [Cronobacter sakazakii ATCC BAA-
894]

gb|ABU77156.1| hypothetical protein ESA_01902 [Cronobacter sakazakii ATCC BAA-894]

Length = 172

Score = 78.6 bits (192), Expect = 3e-13, Method: Compositional matrix adjust.

Identities = 57/171 (33%), Positives = 80/171 (46%), Gaps = 5/171 (2%)

Query: 10 IRPATAADMAAVCDIVNHYI-ETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66

IR ATA D AA+ +I N+ + T+ + + + + W +R YP LVA

Sbjct: 3 IRHATADDCAAIAEINYAVLHTAAIWNATVDTENRLAWF--YQRCNAGYPVVLVAVEGD 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126

V G A G W+A + + TVE +VYV H G+G L T L+ A G +VA I

Sbjct: 61 RVVGYASFGDWRAFDGFRHTVEHSVYVHPEHHGKGIGKALMTRLIVEARAIGKHMVAGI 120

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177

N S+ LHE LG+T + G K G W D+ F Q + P +

Sbjct: 121 ESRNAASIALHEKLGFTTITAQMPQVGTFGRWLDLTFMQLQLDNRTPEDAI 171

>ref|YP_004125851.1| phosphinothricin acetyltransferase [Alicyclophilus denitrificans BC]

gb|ADU98963.1| Phosphinothricin acetyltransferase [Alicyclophilus denitrificans BC]

Length = 175

Score = 78.6 bits (192), Expect = 3e-13, Method: Compositional matrix adjust.
Identities = 53/159 (33%), Positives = 84/159 (52%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68

IR + D+AA+ I H++ T F +P Q+ + R P+LVAE +G V

Sbjct: 6 IRASRDDLAAITAIYAHVHLHGTGTFEIDPPGIQDMAARRADVLARGLPYLVAEEDGRV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG- 127

G AY +K R AY ++ E ++YV+ + GLG L L + +A G + ++AVIG

Sbjct: 66 TGFAYCNWFKPRPAYRYSAEDSIYVADHARGRGLGRLLLLDALAEHAQAAGVRKLLAVIGD 125

Query: 128 LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

N S+ +H A G+T G +R+ G+K G W D+ ++

Sbjct: 126 SANAGSIAVHRAAGFTEVGVMRSVGWKFAGWRDIVLMEK 164

>ref|YP_003278266.1| GCN5-related N-acetyltransferase [Comamonas testosteroni CNB-2]

ref|ZP_07045593.1| GCN5-related N-acetyltransferase [Comamonas testosteroni S44]

gb|ACY32970.1| GCN5-related N-acetyltransferase [Comamonas testosteroni CNB-2]

gb|EFI60824.1| GCN5-related N-acetyltransferase [Comamonas testosteroni S44]

Length = 177

Score = 78.6 bits (192), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 50/159 (31%), Positives = 80/159 (50%), Gaps = 3/159 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL-VAEVEGVVAGIAYAGP 76

AA+ DI N I ST + +P+T Q + E + +P + + + +G + G G

Sbjct: 16 AAILDIFNDAIVNSTALYDYQPRTTQNMVSWFEAKRAGGFPVIGIEDAQGRLLGFCSWGG 75

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG-FKSVAVIGLPNDPSPV 135

++A AY +TVE +VYV +H+ GLG L L+ +G +V I N S+

Sbjct: 76 FRAYPAYKYTVEHSVYVHPQHRGRGLGQQLMELLIAEARQRGDVHVLVGIDAANAGSIA 135

Query: 136 LHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174

LH+ LG+ + G + G+K G W D+ F+Q + P P

Sbjct: 136 LHKRLGFESVGLMPQVGFKFGRWLDLAFYQLTLQTPEHP 174

>ref|ZP_01547046.1| phosphinothricin N-acetyltransferase, putative [Stappia aggregata IAM 12614]

gb|EAV44363.1| phosphinothricin N-acetyltransferase, putative [Stappia aggregata IAM 12614]

Length = 171

Score = 78.2 bits (191), Expect = 4e-13, Method: Compositional matrix adjust.
Identities = 54/156 (34%), Positives = 75/156 (48%), Gaps = 2/156 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-GV 67

IR A D+ A+ N + +T + + +T E + E R++ P LVA E

Sbjct: 3 IRNAEPKDVPAILARYNQAVRETTAAWTSREETLDERLTWFEGRMKQDLPLVAVDETDA 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G A GP++ R Y T E +VYV QR G+G L L++ A+ +V VI
 Sbjct: 63 VLGFASFGPFRPREGYRLTAEHSVYVDPAAQRRGIGRALLERLMEIANAKNLHVLVGVID 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF 163
 N S+ LHE LG+ G L AG K G W D+ F
 Sbjct: 123 GGNAASIALHEKLG FHVAGRLPEAGTKFGCWL DLVF 158

>ref|YP_257776.1| acetyltransferase [Pseudomonas fluorescens Pf-5]
 gb|AA96041.1| acetyltransferase, GNAT family [Pseudomonas fluorescens Pf-5]
 Length = 177

Score = 78.2 bits (191), Expect = 4e-13, Method: Compositional matrix adjust.
 Identities = 61/172 (35%), Positives = 78/172 (45%), Gaps = 7/172 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
 IR A AD+ A+ DI N + +T + +P Q W R YP LV E
 Sbjct: 5 IRDALHADLPAIRDIYNDAVLNTTAIWNEQPVDLGNRQAWFS--ARQAQGYPIILVIINAE 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 V G A G W+ + + TVE +VYV + GLG L LL+ G +VA
 Sbjct: 63 EQVLGYASFQDWRPFDFGRHTVEHSVYVRSQDQGNGLGPQLMAVLLERARGCGKHMVMAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPA-PPRP 176
 I N SVRLHE LG+ + G + G K G W D+ F Q A PP P
 Sbjct: 123 IESGNSASVRLHERLGFISTGQMPQVGTGFRWLDLTFMQLILNPGAQPPAP 174

>ref|ZP_03127829.1| GCN5-related N-acetyltransferase [Chthoniobacter flavus Ellin428]
 gb|EDY21748.1| GCN5-related N-acetyltransferase [Chthoniobacter flavus Ellin428]
 Length = 168

Score = 78.2 bits (191), Expect = 5e-13, Method: Compositional matrix adjust.
 Identities = 56/163 (34%), Positives = 83/163 (50%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA 62
 P +P +R A D AA+ I N I T+T F TE ++ ++ L+ +R+P LVA
 Sbjct: 2 PSHQPAIVRAEINDAAAIAGIYNEAILTTTATFDTETKSVEDRAQWLQAHDERHPVLVA 61

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 V+G V G A W R AYD T E++ YV H+ G+G L ++ G+ ++
 Sbjct: 62 VVDGHVVGWASLTSWSERRAYDATAETSFYVHSTHRGRGIGRRLKEAIIAEARQLGYHTL 121

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 +A I + SV L+E+ G+ GTL+ G K G DV Q
 Sbjct: 122 IARIAEGSHESVHLNESAGFVHVGTLEKVGKFGRRLDVHIMQ 164

>ref|ZP_02153326.1| phosphinothricin N-acetyltransferase, putative [Oceanibulbus
 indolifex HEL-45]
 gb|EDQ05122.1| phosphinothricin N-acetyltransferase, putative [Oceanibulbus
 indolifex HEL-45]
 Length = 174

Score = 78.2 bits (191), Expect = 5e-13, Method: Compositional matrix adjust.
 Identities = 55/159 (34%), Positives = 74/159 (46%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRPA D AA+ D+ N I S F T+ +T E + D + WL AE G V
 Sbjct: 15 IRPAEPRDAAALADLWNGMIRDSLSTFTTDEKTQAEITALIATRDAF-WL-AEAAGEVL 72

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G G ++ Y TVE ++ +S Q GLG L T ++ AQG +VA I
Sbjct: 73 GFVTYGSFRGGPGYAATVEHSIVLSAAAQGRGLGRGLMTRAEEAAAAQGRHVMVAAISSA 132

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF 168
N +V HE LG+ G + G KHG W D+ Q+
Sbjct: 133 NPGAVIFHEKLGFAQVGRMPEVGRKHGQWLDLILMQKTL 171

>ref|ZP_07975671.1| phosphinothricin N-acetyltransferase [Streptomyces sp. SA3_actG]
Length = 177

Score = 78.2 bits (191), Expect = 5e-13, Method: Compositional matrix adjust.
Identities = 53/175 (30%), Positives = 81/175 (46%), Gaps = 7/175 (4%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP-- 58
M V++R D+ + +I NHY+ + + F T P T + +D P
Sbjct: 1 MPESTEKVVQVRAGREGDLPQLTEIYNHYVTETPITFDTVPFTADQRMDFRAHPTGGPHR 60

Query: 59 WLVAEEVEGV-----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
LVA G V G A +G ++++ AY +VE +VY GLG+ LYT L S
Sbjct: 61 LLVAHAPGRPAGADVLYATSGAFRSKPAYATSVEVSVYCRPGEAGHGLGTRLYTALFAS 120

Query: 114 MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF 168
+ + A I LPN S+ LH+ G+ GT G K G + DV ++++D
Sbjct: 121 LAGEDVHRAYAGIALPNPASLALHDFRFGFRHLGTYAEVGRKFGRYWDVAWYEKDL 175

>gb|EFV82779.1| acetyltransferase [Achromobacter xylosoxidans C54]
Length = 185

Score = 78.2 bits (191), Expect = 5e-13, Method: Compositional matrix adjust.
Identities = 49/156 (31%), Positives = 78/156 (50%), Gaps = 2/156 (1%)

Query: 21 VCDIVNHYIETSTVNFRTEPQTPQEWIDDLE-RLQDRYPWLVAE-VEGVVAGIAYAGPWK 78
+ I N I TST + +P+ + + + + +P + E G + A G ++
Sbjct: 27 ILAIFNEAIATSTALYDYKPRPREAMLGWFAQAKAAGGFPVVGFFENAAGELMAFASYGTFR 86

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHE 138
A AY ++VE +VYV R + GLG L L++ A ++ I N S++LHE
Sbjct: 87 AWPAYKYSVEHSVYVDGRFRGRGLGEALMRVLIERARANQVHLMIGGIDAANQGSIKLHE 146

Query: 139 ALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPP 174
LG+ GT+R AG+K G W D+ F+Q + PA P
Sbjct: 147 KLGFBVHAGTIREAGFKFGRWLDLAFYQLTLDTPAQP 182

>ref|ZP_05162143.1| hypothetical protein Bsuib55_05592 [Brucella suis bv. 5 str. 513]
ref|ZP_05994518.1| N-acetyltransferase [Brucella suis bv. 5 str. 513]
gb|EEY28488.1| N-acetyltransferase [Brucella suis bv. 5 str. 513]
Length = 161

Score = 78.2 bits (191), Expect = 5e-13, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 84/160 (52%), Gaps = 8/160 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEEVG 66
IR AT AD+ A+ I N +E + + + + +W+++ R +D +P LVAE EG
Sbjct: 5 IRHATEADLPALLAIYNDAVENTLAIWNETLVDLENRRQWLEN--RNRDGFVPLVAEREG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A GP++ + + E +VYV+ + G+G TL L++ + ++A I
Sbjct: 63 QVVGYASYGPFEG---FRHSSELSVYVASNARGGGIGRTLLAELIEEARERKRVHVLIAGI 119

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

N S+ LH + G+ GTL+ G K G W D+ F Q+

Sbjct: 120 EAGNAASIALHRSQGFEECGTLKQVGQKFGRWLDLLFMQK 159

>ref|YP_002870251.1| putative acetyltransferase [Pseudomonas fluorescens SBW25]

emb|CAY46852.1| putative acetyltransferase [Pseudomonas fluorescens SBW25]

Length = 170

Score = 77.8 bits (190), Expect = 5e-13, Method: Compositional matrix adjust.

Identities = 54/168 (32%), Positives = 75/168 (44%), Gaps = 5/168 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEG 66

IR AT D+ A+ DI N + +T + +P Q W R YP LV+

Sbjct: 2 IRDATQNDLPAIRDIYNDAVLNTTAIWNEQPVDLGNRQAWFS--ARHAQGYPIILVSVENA 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126

V G A G W+ + ++VE +VYV + + GLG L L++ G +VA I

Sbjct: 60 EVTGYASFQDWRPFEGFRYSVEHSVYVRNDQRGKGLGPLLMQALIERARTCGKHVMVAAI 119

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDFELPAPP 174

N S+RLHE G+ G + G K G W D+ F Q A P

Sbjct: 120 ESGNQASIRLHERQGFITTGQMPRVGIKFGRWLDLTFMQLALNPGAEP 167

>ref|YP_004211929.1| Phosphinothricin acetyltransferase [Rahnella sp. Y9602]

gb|ADW72802.1| Phosphinothricin acetyltransferase [Rahnella sp. Y9602]

Length = 175

Score = 77.8 bits (190), Expect = 5e-13, Method: Compositional matrix adjust.

Identities = 48/160 (30%), Positives = 79/160 (49%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66

+EI A + A+ I ++ T +F T+P +E L+++++ WLWV E

Sbjct: 1 MEIIEAGEQHIPAIQKIYAWHVLHGTASFETQPPDEREMAGRLKKIKEAGLLWLVLVHED 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126

V G Y G ++ R AY T+E ++Y+ Q+ G G L + E G++ ++ +

Sbjct: 61 EVKGYCYLGHYRERYAYRHTLEDSIYIDPAFQKRGAGKALLRRAIDWAETHGYRQLIGNV 120

Query: 127 G-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 165

G N S+ LH A + +GTL + G+KHG W D F Q

Sbjct: 121 GDSSENKASIGLHLAARFQMKGTLHSGVGFKHGRWLDTVFMQ 160

>ref|YP_002230172.1| acetyltransferase (GNAT) family protein [Burkholderia cenocepacia

J2315]

ref|YP_002231952.1| acetyltransferase (GNAT) family protein [Burkholderia cenocepacia

J2315]

emb|CAR51326.1| acetyltransferase (GNAT) family protein [Burkholderia cenocepacia

J2315]

emb|CAR53150.1| acetyltransferase (GNAT) family protein [Burkholderia cenocepacia

J2315]

Length = 182

Score = 77.4 bits (189), Expect = 9e-13, Method: Compositional matrix adjust.

Identities = 51/167 (30%), Positives = 79/167 (47%), Gaps = 2/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWLVA-EVEGV 67

I + A AA+ +I+N I ST + P+ P+ + + +P A + G

Sbjct: 13 IDCSEAEHAAAILEILNDAIVNSTALYDYRPRPPEAMVTFATKRAGGFPVFGAVDAAGE 72

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A G ++A A+ +TVE +VYV + + GLG L +++ +V I
 Sbjct: 73 LLGFASWGTFRAFPAPFKYTVEHSVYVRNDQGRGLGERLLREVVRREAAQVHVLVGCID 132

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N S+ LH LG+ GT+ AG+K G W D F+Q E PA P
 Sbjct: 133 ATNAGSIALHTKLGFBVHAGTIAEAGFKFGRWLDAAFYQLKLETPAQ 179

>ref|YP_620550.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia AU 1054]
 ref|YP_834791.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia HI2424]
 gb|ABF75577.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia AU 1054]
 gb|ABK07898.1| GCN5-related N-acetyltransferase [Burkholderia cenocepacia HI2424]
 Length = 182

Score = 77.0 bits (188), Expect = 9e-13, Method: Compositional matrix adjust.
 Identities = 50/167 (29%), Positives = 78/167 (46%), Gaps = 2/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWLVA-EVEGV 67
 I + A AA+ +I+N I ST + P+ P+ + + +P A + G
 Sbjct: 13 IDCSEAEHAAAILEILNDAIANSTALYDYRPRPPEAMVTWTFATKRAGGFVFGAVDSAGT 72

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A G ++A A+ +TVE +VYV + + GLG L +++ +V I
 Sbjct: 73 LLGFASWGTFRAFPAPFKYTVEHSVYVRNDQGRGLGELLREVVRREAAQVHVLVGCID 132

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N S+ LH LG+ GT+ AG+K G W D F+Q E P P
 Sbjct: 133 ATNAGSIALHTKLGFBVHSGTIAEAGFKFGRWLDAAFYQLKLETPVQP 179

>ref|ZP_06833815.1| putative acetyltransferase (antibiotic resistance) protein
 [Gluconacetobacter hansenii ATCC 23769]
 gb|EFG85012.1| putative acetyltransferase (antibiotic resistance) protein
 [Gluconacetobacter hansenii ATCC 23769]
 Length = 173

Score = 77.0 bits (188), Expect = 9e-13, Method: Compositional matrix adjust.
 Identities = 55/170 (32%), Positives = 77/170 (45%), Gaps = 6/170 (3%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWDLERLQDRY 57
 MS + IRPAT D+ A+ DI+N I ST + T T +W+ D +
 Sbjct: 1 MSDPDPAIHIRPATPDIPAIVDIINDAIRNSTTLWETRETTVPVRLDWLRDSN--AQGF 58

Query: 58 PWLVAEV-EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
 P LVA EG VAG ++ + Y TVE ++Y++ +R G+GS L HL
 Sbjct: 59 PILVAVTPEGTVAGYCSWKTFRPFSGYAHTVEHSIYIAPAFKRRGIGSLLLGHLCTLARN 118

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 +VA I N S LHE + G + G K G W D+ F +
 Sbjct: 119 SDVHVMVAAITASNTASRLHERFDFQPGMIPQCGTKFGRWMDLMFLYK 168

>ref|YP_001369814.1| GCN5-like N-acetyltransferase [Ochrobactrum anthropi ATCC 49188]
 gb|ABS13985.1| GCN5-related N-acetyltransferase [Ochrobactrum anthropi ATCC 49188]
 Length = 164

Score = 77.0 bits (188), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 49/160 (30%), Positives = 81/160 (50%), Gaps = 5/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDLERLQDRYPWLVAEVEG 66
 IR AT D+ A+ I N ++ + + + +EW+ R +D +P LVAE EG

Sbjct: 5 IRHATETDLPALLAIYNDAVQNTLAIWNETLVDLENRREWLKG--RNRDGFVPLVAEREG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A GP++ + + E ++YV+ + G+G L T L+ + ++A I

Sbjct: 63 QVVGYASYGPFPRPFEGFRHSSELSIYVASDARGGGIGRALLTELVDPEARERKVHVLIAGI 122

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+ LH++ G+ GTL+ G K G W D+ F Q+

Sbjct: 123 EAGNAASIALHKSQGFEDCGTLKQVGQKFGRWLDLTFMQK 162

>ref|YP_003938516.1| Phosphinothricin N-acetyltransferase [Bifidobacterium bifidum S17]

gb|AD052942.1| Phosphinothricin N-acetyltransferase [Bifidobacterium bifidum S17]
Length = 184

Score = 77.0 bits (188), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 53/162 (32%), Positives = 78/162 (48%), Gaps = 6/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEP---QTPQEWIDDLERLQDRYPWLVAEV-E 65
IR A AD+ A+ DI N + + EP ++ + W+D R + +YP +V E E

Sbjct: 9 IRAAVDADVPAIADIYNEAVIRGGASADLEFVSLESRRRAWVDS-HRPRAKYPVVVIEGPE 67

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G + R YD E + Y++ HQR GLG+ + L+ + +GF V A+

Sbjct: 68 GAVVGFSGSLSKFHQRAGYDGAELSYIADHDHQRQGLGTMVRLIDAAAERGFTHTVTAI 127

Query: 126 IGLPNDPSPVRLHEALGYTARGTLRAA-GYKHGGWHDVGFQWQR 166
I N SV L G+ G L AA G G HD+ +W +

Sbjct: 128 IYADNAGSVALMRRFGFIRFGLLPAAVGALDGLKLDMSYVVK 169

>ref|ZP_03129084.1| GCN5-related N-acetyltransferase [Chthoniobacter flavus Ellin428]
gb|EDY20325.1| GCN5-related N-acetyltransferase [Chthoniobacter flavus Ellin428]
Length = 177

Score = 77.0 bits (188), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 57/175 (32%), Positives = 92/175 (52%), Gaps = 6/175 (3%)

Query: 4 ERRPVEI-RPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQ---EWIDDLERLQDRYPW 59
++R V+I R + + I N I ST + +P+T + W + +++ YP

Sbjct: 2 DKRSVKIIRCSERHAEPILAIFNEAIVNSTALYDYKPRTKEMMESWFE--AKVRGNYPV 59

Query: 60 LVAEEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
+ E EG + G A GP++A AY +TVE ++YV R +R G+G L ++++ Q +

Sbjct: 60 IGLEEEGELLGFASYGPFRAFPAYKYTVEHSIYVDTRFRRRGVGRVLLEQVIEAARGQDY 119

Query: 120 KSVVAVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
++V I N S+ LHE LG+ GT+R AG+K G W D+ F+Q P P

Sbjct: 120 HALVGGIDSTNHASIVLHEKLGFAHCGTIRQAGFKFGRWLDLAFYQLMLSTPLHP 174

>ref|ZP_07272181.1| phosphinothricin N-acetyltransferase [Streptomyces sp. SPB78]
gb|EFL00550.1| phosphinothricin N-acetyltransferase [Streptomyces sp. SPB78]
Length = 177

Score = 77.0 bits (188), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 52/175 (29%), Positives = 81/175 (46%), Gaps = 7/175 (4%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYP-- 58
M V++R D+ + +I NHY+ + + F T P T + ++ P

Sbjct: 1 MPESTEKVQVRAGREGDLPQLTEIYNHYVTETPITFDTPFTADQREVFRAHPTGGPHR 60

Query: 59 WLVAEVEGV-----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
 LVA G V G A +G ++++ AY +VE +VY GLG+ LYT L S
 Sbjct: 61 LLVAHAPGRPAGADVLGYATSGAFRSKPAYATSVEVSVYCRPGEGGHGLGTLTYTALFAS 120

Query: 114 MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 + + A I LPN S+ LH+ G+ GT G K G + DV ++++D
 Sbjct: 121 LAGEDVHRAYAGIALPNPASLALHDFRFGFRHLGTYAEVGRKFGRYWDVAWYEKDL 175

>ref|ZP_04744486.1| toxin-antitoxin system, toxin component, GNAT family [Roseburia
 intestinalis L1-82]
 gb|EEV00318.1| toxin-antitoxin system, toxin component, GNAT family [Roseburia
 intestinalis L1-82]
 emb|CBL08536.1| Sortase and related acyltransferases [Roseburia intestinalis M50/1]
 emb|CBL11042.1| Sortase and related acyltransferases [Roseburia intestinalis XB6B4]
 Length = 170

Score = 77.0 bits (188), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 49/150 (32%), Positives = 78/150 (52%), Gaps = 1/150 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A D+ AV DI N I +T F TE + ++ + + +Y V E G
 Sbjct: 4 IMIRKAELKDIPAVMDIYNDAILHTTATFDEIKDYEDRLAWFQAHTGQYVIFVYEEAGT 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSVVAVI 126
 VAG A ++ R A+D VE ++Y+ ++ G+G +L L+ + E +VV++I
 Sbjct: 64 VAGYASLSRYRERKAFDPAVEISIIYIHAGYRGRGIGRSLMEKTLQYAKECPQIGTVVSLI 123

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHG 156
 N+ S+RLHE G++ G +R AG K G
 Sbjct: 124 TSENEVSIRLHERFGFSYCGQIRQAGVKFG 153

>pdb|2BL1|A Chain A, Crystal Structure Of A Putative Phosphinothricin
 Acetyltransferase (Pa4866) From Pseudomonas Aeruginosa
 Pac1
 Length = 172

Score = 77.0 bits (188), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 55/165 (33%), Positives = 73/165 (44%), Gaps = 6/165 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EV 64
 IR A AD+ + I N + +T + P Q W D R + YP LVA +
 Sbjct: 4 SIRDAGVADLPGILAIYNDVGNNTAIWNETPVDLANRQAWFD--ARARQGYPILVASDA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G V G A G W+ + TVE +VYV + GLG L L++ AQG VA
 Sbjct: 62 AGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVXVA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 I N S+ LH LG+ G G K G W D+ F Q + +
 Sbjct: 122 AIESGNAASIGLHRRLGFEISGQXPQVGQKFGRWLDLTFXQLNLD 166

>ref|ZP_07316760.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella
 atypica ACS-134-V-Col7a]
 gb|EFL57320.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella
 atypica ACS-134-V-Col7a]
 Length = 166

Score = 77.0 bits (188), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 45/153 (29%), Positives = 77/153 (50%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
 IR D+ A I N+ +E EP+T +EW + D + P +V ++ VV
 Sbjct: 6 IRLIAKDDVFACLSIYNYEVEYGVATLDLEPRTLEEWHEWYNAHSDEHHPPIIVGTIDDVV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSVVAVIG 127
 G A P++ ++A+ TVE ++Y+ ++ G+ + L +L+ + E +VV+VI
 Sbjct: 66 VGYASLSPYRLKDAFKSTVELSIYIHQDYRGQGVATRLMERILEIAKEDTMLHNVVSVIT 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 N+ S +LH G+T G G+KHG + D
 Sbjct: 126 AGNEESTKLHNRFGFTYCGLTPEVGFKGKGYQD 158

>pdb|1YVO|A Chain A, Hypothetical Acetyltransferase From P.Aeruginosa Pa01
 pdb|1YVO|B Chain B, Hypothetical Acetyltransferase From P.Aeruginosa Pa01
 Length = 172

Score = 76.6 bits (187), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 55/165 (33%), Positives = 73/165 (44%), Gaps = 6/165 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EV 64
 IR A AD+ + I N + +T + P Q W D R + YP LVA +
 Sbjct: 4 SIRDAGVADLPGILAIYNDAVGNTTAIWNETPVDLANRQAWFD--TRARQGYPILVASDA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G V G A G W+ + TVE +VYV + GLG L L++ AQG VA
 Sbjct: 62 AGEVLGYASYGDWRPFEGFRGTVEHSVYVRDDQRGKGLGVQLLQALIERARAQGLHVXVA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFE 169
 I N S+ LH LG+ G G K G W D+ F Q + +
 Sbjct: 122 AIESGNAASIGLHRRLGFEISGQXPQVGQKFGRWLDLTFXQLNLD 166

>ref|ZP_07986020.1| phosphinothricin N-acetyltransferase [Streptomyces sp. SA3_actF]
 Length = 170

Score = 76.6 bits (187), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 51/168 (30%), Positives = 80/168 (47%), Gaps = 7/168 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP--WLVAEVE 65
 +++R D+ + +I NHY+ + + F T P T + +D P LVA
 Sbjct: 1 MQVRAGREGDLPQLTEIYNHYVTETPITFDTPFTADQRMDFRAHPTGGPHRLLVAHAP 60

Query: 66 GV-----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 G V G A +G ++++ AY +VE +VY GLG+ LYT L S+ +
 Sbjct: 61 GRPAGADVLGYATSGAFRSKPAYATSVESVYCRPGEKGHGLGTRLYTALFASLAGEDVH 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF 168
 A I LPN S+ LH+ G+ GT G K G + DV ++++D
 Sbjct: 121 RAYAGIALPNPASLALHDFRHLGTAEVGRKFGRYWDVAWYEKDL 168

>ref|ZP_06898706.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC
 49957]
 gb|EFH09589.1| phosphinothricin acetyltransferase [Roseomonas cervicalis ATCC
 49957]
 Length = 168

Score = 76.6 bits (187), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 57/156 (36%), Positives = 71/156 (45%), Gaps = 1/156 (0%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGV 67
 EIR A AD+ + I N I S + TE T + D L + Q R P LVA G

Sbjct: 8 EIRDAGEADLPGILAI FNQAIRESLAVWHEETTTLEARRDWLAQRQGRGLPVLVAVRGGE 67

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G A G ++ + TVE +VYV Q GLG L L+ A G +VA I

Sbjct: 68 VLGFASYGDFRPFAGFAATVEHSVYVDPAAQGGGLGRALLAALIDRARAAGLHVMVAGIE 127

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF 163
N S+ LH G+ G LR G K G W D+ F

Sbjct: 128 AGNTASIALHAKAGFEEAGLLREVGRKFGRWLDLRF 163

>ref|ZP_05087661.1| phosphinothricin N-acetyltransferase, putative [Pseudovibrio sp.
JE062]
gb|EEA91855.1| phosphinothricin N-acetyltransferase, putative [Pseudovibrio sp.
JE062]
Length = 175

Score = 76.6 bits (187), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 51/166 (30%), Positives = 81/166 (48%), Gaps = 22/166 (13%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR----- 56
+++R AT +D+ + +I N ++T W D LE L+DR

Sbjct: 1 MKLRHATKSDLPILLEIHNDVKT-----LAAIWTDTLETLEDRESWFEEKRIAGG 50

Query: 57 YPWLVAEVE-GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
+P +VAE E G V G GP++ ++ Y+ TVE +VYV+ + + G GS L L+ +

Sbjct: 51 FPIIVAEDENGDLVGYGSYGPFRKESGYNKTVEHSVYVTPQSRGRGAGSVLLEKLIDLAK 110

Query: 116 AQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
++ I N S+RLHE +G+ G L G+K G W D+

Sbjct: 111 QDDRHLVLAIDSENKGSIRLHERIGFKITGELPQVGFKFGRWLDL 156

>ref|YP_003970832.1| phosphinothricin N-acetyltransferase [Bifidobacterium bifidum
PRL2010]
gb|ADP35795.1| Phosphinothricin N-acetyltransferase [Bifidobacterium bifidum
PRL2010]
Length = 180

Score = 76.6 bits (187), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 53/162 (32%), Positives = 78/162 (48%), Gaps = 6/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV-E 65
IR A AD+ A+ DI N + + EP ++ + W+D R + +YP +V E E

Sbjct: 5 IRAAVDADVPAIADIYNEAVIRGRASADLEPVSLERRAWVDS-HRPRAKYPVVVIEGPE 63

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G + R YD E + Y++ HQR GLG+ + L+ + +GF V A+

Sbjct: 64 GAVVGFGSLSKFHQRAGYDGAELSYIAGDHQRQGLGTMVRLIDAAAERGFTHTVTAI 123

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAA-GYKHGGWHDVGFWR 166
I N SV L G+ G L AA G G HD+ +W +

Sbjct: 124 IYADNAGSVALMRRFGFIRFGLLPAAVGALDGLHDMSYWK 165

>ref|NP_353926.1| phosphinothricin acetyltransferase [Agrobacterium tumefaciens str.
C58]
gb|AAK86711.1| Phosphinothricin acetyltransferase [Agrobacterium tumefaciens str.
C58]
Length = 165

Score = 76.6 bits (187), Expect = 1e-12, Method: Compositional matrix adjust.
Identities = 48/158 (30%), Positives = 76/158 (48%), Gaps = 5/158 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAE 63
 VE+R AT D++ + +I N + +T + + + +W R +P +VA
 Sbjct: 2 SVELRDATVDDLSGIMEIYNDAVVNTTAIWNEVVVDLENRKDF--AARTSRGFPVIVAI 59

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
 ++G VAG A G W+A + Y T E +VYV + G+G L L+ ++
 Sbjct: 60 LDGKVAGYASYGDWRAFDGYRHTREHSVYVHKDARGHGIGKRLMQALIDHAGGNDVHVL 119

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 A I N S+RLHE+LG+ G G K G W D+
 Sbjct: 120 AAIEAENTASIRLHESLGFRVVGFRFSEVGTKFGRWLDL 157

>ref|ZP_01755850.1| phosphinothricin N-acetyltransferase, putative [Roseobacter sp.
 SK209-2-6]
 gb|EBA15329.1| phosphinothricin N-acetyltransferase, putative [Roseobacter sp.
 SK209-2-6]
 Length = 161

Score = 76.6 bits (187), Expect = 1e-12, Method: Compositional matrix adjust.
 Identities = 51/159 (32%), Positives = 73/159 (45%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRPA D+AA+ I+N I + V F T + E + D +LVAE G V
 Sbjct: 5 IRPANKDDVAAITGILNEAIRKTLVTFTTTEKIESEIAASIN--ADDTHYLVAEQAGCVV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJVAVIGLP 129
 G A GP++ Y T E T++++ + GLG L L + A+ +VA I
 Sbjct: 63 GYASYGPFQPGYKHTKEHTIHLAPTARGSGGLGRALIEQLAEERAENVHVLVAGISSA 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 N +V H ALG+ G + G K G W D+ Q+
 Sbjct: 123 NPEAVSFHAALGFINIGRMPETGRKWGWQWLDLILMQKTL 161

>ref|YP_001862480.1| GCN5-related N-acetyltransferase [Burkholderia phymatum STM815]
 gb|ACC75434.1| GCN5-related N-acetyltransferase [Burkholderia phymatum STM815]
 Length = 175

Score = 76.3 bits (186), Expect = 2e-12, Method: Compositional matrix adjust.
 Identities = 57/173 (32%), Positives = 83/173 (47%), Gaps = 8/173 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVA-E 63
 ++IR A + + I N + +T + + W+ D R + YP LVA +
 Sbjct: 1 MQIRDAGPEHIEGITAIYNDAVAHTTAIWNDQVVDHANRTAWLAD--RQKAGYPVLVAVD 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
 +G V G A G W+A + Y TVE +VYV + GLG +L L+ ++ G +V
 Sbjct: 59 DQGAVLGYASFQDWRAFDGYRHTVEHSVYVRGDQRGKGLGRSLMQALIGRAQSIGKHVMV 118

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 A I N S+RLHE LG+ G L+ G K G W D+ F Q +L P P
 Sbjct: 119 AGIEANNANSIRLHEQLGFHVHGLKEVGMKFGTWLDLAFMQ--LKLDDRPTP 169

>ref|YP_003579438.1| GNAT family acetyltransferase [Rhodobacter capsulatus SB 1003]
 gb|ADE87031.1| acetyltransferase, GNAT family [Rhodobacter capsulatus SB 1003]
 Length = 167

Score = 76.3 bits (186), Expect = 2e-12, Method: Compositional matrix adjust.
 Identities = 53/150 (35%), Positives = 73/150 (48%), Gaps = 1/150 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEGVV 68
 IR AT D A+ I N + T+T + T +D + R Q +P LV E V
 Sbjct: 2 IRDATPEDAQAIATIYNDVVRTTTTAIWNEVEVTALNRVDWIAARQQAGFPVLVLEEGAKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
 G A GP++A + Y TVE +VYV + G G L + L+ A Q G +VA I
 Sbjct: 62 VGYASYGPFRAFDDGYRGTVESVYVRTDLRGGRGRALLSALILRARAQGLHVMVAAIEA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
 N+ S+ LH+ LG+ A G + G K G W
 Sbjct: 122 ENNASIILHQRLGFAAVGLMPQVGQKFGRW 151

>ref|ZP_08184514.1| sortase-like acyltransferase [Xanthomonas gardneri ATCC 19865]
 gb|EGD17850.1| sortase-like acyltransferase [Xanthomonas gardneri ATCC 19865]
 Length = 175

Score = 76.3 bits (186), Expect = 2e-12, Method: Compositional matrix adjust.
 Identities = 56/161 (34%), Positives = 81/161 (50%), Gaps = 1/161 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 PVE+R AD+ A+ I + + P + + + YP+LVAE +
 Sbjct: 2 PVEVREVCEADIPAITAIYAEQVAGVNSYSEYSAPSSDEMRTVRATVDAGYPYLVAERDA 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 V G AYAG ++AR Y WTVE+++Y++ Q G+G L L+ E +G++ ++AVI
 Sbjct: 62 AVVGAYAGAYRARAGYRWTVENSIYLASDMQGRGIGKALLGELIARCEQRGYRQMIAVI 121

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 G N S RLHE G+ G G KHG W D QR
 Sbjct: 122 GDAENQASRRLHERFGFRTVGVFTGIGRKHGRWLDGLQMQR 162

>ref|ZP_04817732.1| possible Phosphinothricin acetyltransferase [Staphylococcus
 epidermidis M23864:W1]
 gb|EES41698.1| possible Phosphinothricin acetyltransferase [Staphylococcus
 epidermidis M23864:W1]
 Length = 163

Score = 76.3 bits (186), Expect = 2e-12, Method: Compositional matrix adjust.
 Identities = 45/161 (27%), Positives = 84/161 (52%), Gaps = 3/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER--LQDRYPWLVAEVEGV 67
 IR A D+ +I N I +T + +P+ +E + E + D W+ + +
 Sbjct: 2 IRFARKEDLPDILNIYNDAIINTTAIYTYDPKELEERVQWFEAKAMADEPIWVYVKDNI 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
 V G A G ++ AY +++E ++YV +++ G+ S L T L++ + +++VA I
 Sbjct: 62 V-GYATYGSFRDWPAYLYSIEHSIYVDPKYRGQGIASQLLTTLIQHAKDNNYRTIVAGID 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 N+ S++LH+ +T GT+ GYK W D+ F+Q D
 Sbjct: 121 ASNEGSIQLHKKFNFTHAGTITNVGYKFERWLDLAFYQLDL 161

>ref|ZP_05117294.1| acetyltransferase, GNAT family [Labrenzia alexandrii DFL-11]
 gb|EEE47893.1| acetyltransferase, GNAT family [Labrenzia alexandrii DFL-11]
 Length = 189

Score = 76.3 bits (186), Expect = 2e-12, Method: Compositional matrix adjust.
 Identities = 51/168 (30%), Positives = 82/168 (48%), Gaps = 2/168 (1%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPW 59

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      + + R + +R A   D+ A+ + N + +T + ++ +T E I   E Q+ +P
Sbjct: 11 LQKDDRFMPLRDAEPGDIPAILALYNQAVRETTAAWTSQEETLDERITWFETRQAGWPV 70

Query: 60 LVAEV-EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
      +VA E + G A G ++ R Y T+E TVYV Q G+G+ L L+ +AQ
Sbjct: 71 IVATSPEDKLIGFASYGAFRPREGYRKTLEHTVYVDPDFQGGIGAKLLQQLIDKAQAQE 130

Query: 119 FKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
      +V V+ N S+ LH+ LG+ G L AG K G W D+ F +
Sbjct: 131 VHVLVGVVDGDNATASIALHKKLGFELIAGRLPEAGTKFGRWLDLVFLTK 178

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>gb|ADZ72147.1| Phosphinothricin N-acetyltransferase, putative [Polymorphum gilvum
      SL003B-26A1]
      Length = 172

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Score = 76.3 bits (186), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 52/166 (31%), Positives = 76/166 (45%), Gaps = 22/166 (13%)

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Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR----- 56
      + +R ATAAD+ A+ I N + T W D E L+DR
Sbjct: 1 MHLRDATAADLPALLAIHNDVVRT-----LKAIWTDKTETLEDRTWFDRRAAG 50

Query: 57 YPWLVAE-VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
      +P +VAE G V G GP++A++ Y T+E +VYV Q G+G L L++
Sbjct: 51 FPVIVAEDAAGRNVGYGSYGPFRKADGYRLTLEHSVYVDPATQGRGVGKALLKRLIELAR 110

Query: 116 AQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
      A G+ +V I N+ S+ LH G+ G + G K G W D+
Sbjct: 111 ADGYHVLVGAIIDGENETSIALHRQFGFETVGRMPQVGKFGQWLDL 156

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>pdb|1YR0|A Chain A, Crystal Structure Of Phosphinothricin Acetyltransferase
      From Agrobacterium Tumefaciens
pdb|1YR0|B Chain B, Crystal Structure Of Phosphinothricin Acetyltransferase
      From Agrobacterium Tumefaciens
pdb|1YR0|C Chain C, Crystal Structure Of Phosphinothricin Acetyltransferase
      From Agrobacterium Tumefaciens
pdb|1YR0|D Chain D, Crystal Structure Of Phosphinothricin Acetyltransferase
      From Agrobacterium Tumefaciens
      Length = 175

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Score = 75.9 bits (185), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 48/158 (30%), Positives = 76/158 (48%), Gaps = 5/158 (3%)

```

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAE 63
      VE+R AT D++ + +I N + +T + + + ++W R +P +VA
Sbjct: 4 SVELRDATVDDLSGIXEYNDVNTTAIWNEVVVDLENRKDWF--AARTSRGFPVIVAI 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
      ++G VAG A G W+A + Y T E +VYV + G+G L L+ ++
Sbjct: 62 LDGKVAGYASYGDWRAFDGYRHTREHSVYVHKDARGHGIGKRLXQALIDHAGGNDVHVLI 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
      A I N S+RLHE+LG+ G G K G W D+
Sbjct: 122 AAIEAENTASIRLHESLGFRVVGFRFSEVGTKFGRWLDL 159

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>ref|YP_587199.1| putative GNAT family acetyltransferase [Cupriavidus metallidurans
      CH34]
gb|ABF11930.1| putative acetyltransferase, GNAT family [Cupriavidus metallidurans
      CH34]
      Length = 164

```

Score = 75.9 bits (185), Expect = 2e-12, Method: Compositional matrix adjust.
Identities = 48/161 (29%), Positives = 77/161 (47%), Gaps = 6/161 (3%)

Query: 18 MAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-GVVAGIAY 73
M AVC I N + +T + + ++W+ R + +P LVA+ E G V G A
Sbjct: 1 MEAVCAIYNDAVANTTAIWNDVLVDVNRKDWL--AARRKAGFPVLVAQDEAGAVVGyas 58

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133
G W+A + Y TVE +VY+ + + G+ + L++ +V I N S
Sbjct: 59 FGDWRAFDGYRHTVEHSVYIRNDQGRGIAGLMMKALIERARDLNKHIMVGAIEAGNASS 118

Query: 134 VRLHEALGYTARGTLRAAGYKHGGWHDVGFWQDRDFELPAPP 174
+RLHE LG+ G ++ G K G W D+ F Q + + + P
Sbjct: 119 IRLHEKLGFEQVGLMKEVGMKFGKWLDLVMQLNIDHRSTP 159

>ref|YP_610326.1| acetyltransferase [Pseudomonas entomophila L48]
emb|CAK17543.1| putative acetyltransferase, GNAT family [Pseudomonas entomophila L48]
Length = 174

Score = 75.5 bits (184), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 52/158 (32%), Positives = 73/158 (46%), Gaps = 1/158 (0%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+IR A D+ + DI N + +T + P ++ E R Q YP LVA +
Sbjct: 4 QIRDALIDDPGILDIYNDAVANTTAIWNETPVDLGNRLNWFEEARAQQGYPIILVAVDDSG 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G A G W+ + TVE +VYV + GLG L L++ +VA I
Sbjct: 64 VLGYASFWDWRPFEGFRHTVEHSVYVRGDQRGKGLGPVLM DALIERARHCDKHVMVAAIE 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQ 165
N S+RLHE LG++ G + G K G W D+ F Q
Sbjct: 124 SGNAASIRLHERLGFSTGMPQVGVKFGRWLDLTFMQ 161

>ref|YP_002434888.1| GCN5-related N-acetyltransferase [Desulfovibrio vulgaris str. 'Miyazaki F']
gb|ACL07420.1| GCN5-related N-acetyltransferase [Desulfovibrio vulgaris str. 'Miyazaki F']
Length = 178

Score = 75.1 bits (183), Expect = 3e-12, Method: Compositional matrix adjust.
Identities = 58/178 (32%), Positives = 81/178 (45%), Gaps = 11/178 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
IR A + D+ + I N + +T + T+ W+ D R +P LVA G
Sbjct: 3 IRDAESGDIEGIVAIYNDAVCNTTAIWNESVTDAAGRAAWLAD--RRAAGHPVLVAVEAG 60

Query: 67 -----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
VV G A G W+A + Y TVE +VYV + GLG+ L L+ G
Sbjct: 61 RNGGPVVLGYATFGDWRAWDGYRHTVEHSVYVHKDTRGRGLGAALLHALIGRARDMGKHV 120

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQDRDFELPAPPRPVRP 179
+VA + N+ S+ LH +G+T G LR G K G W D+ F Q + P P RP
Sbjct: 121 MVAGVEAGNEASMLHRKMGFTEVGMLREVGCCKFGRWLDLAFLLQLTLTDARETP-PARP 177

>ref|ZP_06067059.1| predicted protein [Acinetobacter junii SH205]
gb|EEY92620.1| predicted protein [Acinetobacter junii SH205]
Length = 181

Score = 75.1 bits (183), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 49/158 (31%), Positives = 78/158 (49%), Gaps = 3/158 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVE 65
P +IR AT D+ + I NH I T T N+ + +++ + +Q + +P +V E +
Sbjct: 15 PYQIRFATLNDLEQILTIYNHEILTGTANWNDQAVALEQYQQRFDQMQQQFPMIVVEDQ 74

Query: 66 --GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
VAG AY +++ + Y ++E +V+V + R GLG L L+ Q +V
Sbjct: 75 HHNKVAGYAYYAAFRSISGYRQSIHESVFDPSYARQGLGKALMQQLIHLAIQQNMHIMV 134

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
A I N S+ LHE LG+ G + G K G W D+
Sbjct: 135 AAIDSENMGSIVLHEQLGFVQTGYMPQVGQKFGQWRDL 172

>ref|NP_633926.1| hypothetical protein MM_1902 [Methanosarcina mazei Gol]
gb|AAM31598.1| hypothetical protein MM_1902 [Methanosarcina mazei Gol]
Length = 163

Score = 75.1 bits (183), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 45/159 (28%), Positives = 73/159 (45%), Gaps = 2/159 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV- 67
+ P ++ D AV D N+YIE S + E + P E+ + ++ YP V E
Sbjct: 4 KFSPISSEDREAVIDTFNYYIENSFAAY-PETRVPEYEFEEFFLQVTSGYPNNAVVRDENKN 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
G P+ +A+ T E + ++ G GS + HLL +G S++A I
Sbjct: 63 FVGFCMLRPYSPMSAFSGTAEISYFIRPEFTGKGTGSLMLEHLLSGAREKGLHSILASIS 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVWQR 166
N+ S+R H G++ G R AG K+G + D + Q+
Sbjct: 123 SLNEGSIRFHHGFSECGRFREAGKKNKFFDTVWMQK 161

>ref|ZP_02081461.1| hypothetical protein CLOLEP_02937 [Clostridium leptum DSM 753]
gb|EDO60119.1| hypothetical protein CLOLEP_02937 [Clostridium leptum DSM 753]
Length = 129

Score = 75.1 bits (183), Expect = 4e-12, Method: Compositional matrix adjust.
Identities = 41/127 (32%), Positives = 64/127 (50%), Gaps = 1/127 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+++R A D+ + I YI+T + F T Q++ + L YP+LV E +G
Sbjct: 3 IKVRLAGTGDVPQLLKIYEQYIDTP-ITFEYTLPTQDFTKRILSLTKDYPYLVCEKQGR 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G AYA R AY W E ++Y+ + G+G LY L++ +E QG K+V +
Sbjct: 62 LVGYAYAHRHMERAYQWNAELSIYLGRPYTSQGIGKRLYCALIELLEKQGVKNVYGGVT 121

Query: 128 LPNDPSV 134
LPN S
Sbjct: 122 LPNVKSC 128

>ref|ZP_05780450.1| acetyltransferase, gnat family [Citricella sp. SE45]
gb|EEX14214.1| acetyltransferase, gnat family [Citricella sp. SE45]
Length = 172

Score = 74.7 bits (182), Expect = 6e-12, Method: Compositional matrix adjust.
Identities = 47/122 (38%), Positives = 60/122 (49%)

Query: 57 YPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
 YP LVA VAG A G W+A + Y TVE +VYV + GL L L++ A
 Sbjct: 51 YPVLVARDGDFVAGYASFGDWRAFDGYRHTVEHSVYVHPDARGRGLAGALMAALVERARA 110

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
 G +VA I N PS+RLHE +G+ G + G K G W D+ F Q + A P
 Sbjct: 111 MGKHMMVAGIESGNLPSIRLHERMGFRITGEMPQVGCKFGRWLDLTFMQLSLDDRAAPED 170

Query: 177 VR 178
 R
 Sbjct: 171 AR 172

>ref|ZP_01056746.1| phosphinothricin N-acetyltransferase, putative [Roseobacter sp.
 MED193]
 gb|EAQ45398.1| phosphinothricin N-acetyltransferase, putative [Roseobacter sp.
 MED193]
 Length = 161

Score = 74.3 bits (181), Expect = 6e-12, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 74/160 (46%), Gaps = 2/160 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 PVEIR A D + I N I + F T+ + P+E L +D P+LVAE++G
 Sbjct: 2 PVEIRQAQPRDATGIARIANSMIRETLFTFTTQERRPEEIALRLR--EDPRPFLVAELDG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G A G ++ Y T E ++ + Q GLG L L + A+ +VA I
 Sbjct: 60 RLLGFATYGDFTGPGYRHTQEHSIQLLPDAQGHGLGRALMAKLEDAARAREVHVLVAGI 119

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N +V H A+G+T G + G K W D+ Q+
 Sbjct: 120 SSANPKAVGFHSAIGFTQTGLMPQVGRKWDQWLDLILMQK 159

>ref|ZP_04704159.1| phosphinothricin N-acetyltransferase [Streptomyces albus J1074]
 ref|ZP_06592888.1| phosphinothricin N-acetyltransferase [Streptomyces albus J1074]
 gb|EFE83349.1| phosphinothricin N-acetyltransferase [Streptomyces albus J1074]
 Length = 181

Score = 74.3 bits (181), Expect = 6e-12, Method: Compositional matrix adjust.
 Identities = 48/168 (28%), Positives = 81/168 (48%), Gaps = 9/168 (5%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWI----DDLRLQDRYPWL 60
 ++RP A D+ + ++ NHY+ + + F T P TP+ +W D RL
 Sbjct: 10 QVRPGIAEDLTGLTNLYNHVLRTPITFDITVPLTPEGRMQWFLSHPKDGPRLMVATKPA 69

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 + E ++ G A + P + + AY +VE +VY + G+G+ LYT L ++ +
 Sbjct: 70 PSGPERLL-GYATSSPLRPKAAAYATSVESVYCAPDAAGRGVGTALYTALFDALSGEDLH 128

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 A + PND S RLH G+ GT G K G + DV +++++
 Sbjct: 129 RAYAGVTQPNDASHRLHTRFGFRPIGTYGQVGRKFGRYWDVVRWYEKEL 176

>ref|YP_001789720.1| GCN5-like N-acetyltransferase [Leptothrix cholodnii SP-6]
 gb|ACB32955.1| GCN5-related N-acetyltransferase [Leptothrix cholodnii SP-6]
 Length = 186

Score = 74.3 bits (181), Expect = 6e-12, Method: Compositional matrix adjust.
 Identities = 61/165 (36%), Positives = 83/165 (50%), Gaps = 6/165 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWI---DDLRLQDRYPWLVAEVEG 66
 IRP AAD+ A+ DI +E T F E + E DD+ L PVLVA+
 Sbjct: 6 IRPGVAADLPAITDIYAWNVEHGTGTFELEAPSQAEMAHRDDV--LSKGLPWLVAQRGD 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
 V G AYA ++ R A+ + +E +VY++ Q GLG+ L LL A G + + AVI
 Sbjct: 64 QVLGYAYANHFRPRPAFRFALEDSVYLAPAAQGGGLGTLALLAELLARCTAIGARQMFVAI 123

Query: 127 G-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFEL 170
 G N S+ +H G+ G +RAAG+K W DV QR L
 Sbjct: 124 GDSANAGSIGVHRRCGFAEVGMRAAGWKFDRLDVMIMQRSLSGL 168

>ref|YP_682326.1| acetyltransferase, putative [Roseobacter denitrificans OCh 114]
 gb|ABG31640.1| acetyltransferase, putative [Roseobacter denitrificans OCh 114]
 Length = 158

Score = 74.3 bits (181), Expect = 6e-12, Method: Compositional matrix adjust.
 Identities = 47/159 (29%), Positives = 72/159 (45%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLRLQDRYPWLVAEVEGVVA 69
 IRPA+ D AA+ + N I + F T P+T E + ++ +AE +G+
 Sbjct: 2 IRPASPDASAAIAALWNWMIRDTLATFTTVPKTSAEVAARITSAPTQFH--IAENKGIFV 59

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G GP++ Y TVE T+ + + G+G L + A G K ++ I
 Sbjct: 60 GFVTFGPFPRPGPGYAATVEHTILIDPQAHGRGIGRALMAQAETAARAAGKKVMIGAISSH 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168
 N ++R HE L Y G L GYK G W D+ Q++
 Sbjct: 120 NRGAIRFHERLAYIQVGHLPVGVGYKQGWLDLILMQKNL 158

>ref|ZP_05091057.1| phosphinothricin acetyltransferase [Ruegeria sp. R11]
 gb|EEB72749.1| phosphinothricin acetyltransferase [Ruegeria sp. R11]
 Length = 174

Score = 74.3 bits (181), Expect = 7e-12, Method: Compositional matrix adjust.
 Identities = 48/157 (30%), Positives = 72/157 (45%), Gaps = 2/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLRLQDRYPWLVAEVEGVVA 69
 +R AT+AD A+ +I N I + + F T+ +TP E D+ R VAE G +
 Sbjct: 3 VRQATSADAPAAIEITNQIIRDTLITFTTDEKTPAEVAADIGSKGARLQ--VAEEAGEIL 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G G ++ Y T E +Y++ + G G L T + A+G +VA I
 Sbjct: 61 GYINLGGFRTGPGYARTCEHAIYLAETARGRGAGRALMTAIEDVARAEGVHVLVAGISAA 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 N V H A+G+ G + GYK G W D+ Q+
 Sbjct: 121 NPGGVAFHAAVGFSAEVGRMPEVGYKWGWLDLVLMQK 157

>ref|YP_346316.1| GCN5-related N-acetyltransferase [Pseudomonas fluorescens Pf0-1]
 gb|ABA72327.1| putative acetyltransferase [Pseudomonas fluorescens Pf0-1]
 Length = 177

Score = 73.9 bits (180), Expect = 8e-12, Method: Compositional matrix adjust.
 Identities = 55/171 (32%), Positives = 75/171 (43%), Gaps = 6/171 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLRLQDRYPWLVAEVE 65
 IR A AD+ A+ DI N + +T + P Q W R YP LV + +

Sbjct: 5 IRDALHADLPAIRDIYNDAVLNTTAIWNESPVDLGNRQAWFS--ARQAQGYPILVIVDAD 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G A G W+ + + TVE +VYV + GLG L T L++ + +VA

Sbjct: 63 NTTLGYASFQDWRPFDFGRHTVEHSVYVRSQDQNGNLGPQLMTALIERAKTCDKHKVMVAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
I N S+RLHE G+ G + G K G W D+ F Q A P P

Sbjct: 123 IESGNAASIRLHERAGFITTGQMPQVGTGFRWLDLTFMQLTLNPGAEPPE 173

>ref|YP_926367.1| N-acetyltransferase [Shewanella amazonensis SB2B]
gb|ABL98697.1| N-acetyltransferase [Shewanella amazonensis SB2B]
Length = 165

Score = 73.9 bits (180), Expect = 9e-12, Method: Compositional matrix adjust.
Identities = 46/148 (31%), Positives = 74/148 (50%), Gaps = 1/148 (0%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-EVEGVVAGIAYAGPW 77
A + I NH I +T + EP+ + + YP L A + +G + G A GP+

Sbjct: 13 AIIQHIFNHAIAANTTALYEYEPDMARIAAWFAQKEGLYPVLGAFDEKGDLMGFASYGPF 72

Query: 78 KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLH 137
+ A ++VE +VYV H+ G+ L L+++ + G +V I N+ S+ LH

Sbjct: 73 RGFPANLYSVEHSVYVHSDHRGKGVALKLMQALIQAAKDAGLHMMVGGIDASNNASIALH 132

Query: 138 EALGYTARGTLRAAGYKHGGWHDVGFQW 165
+ LG+ GTL+ GYK W D+ F+Q

Sbjct: 133 KKLGFEGHAGTLKEVGYKFNRLDLAFYQ 160

>ref|ZP_06070386.1| conserved hypothetical protein [Acinetobacter lwoffii SH145]
gb|EEY89037.1| conserved hypothetical protein [Acinetobacter lwoffii SH145]
Length = 170

Score = 73.9 bits (180), Expect = 9e-12, Method: Compositional matrix adjust.
Identities = 48/166 (28%), Positives = 80/166 (48%), Gaps = 7/166 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNF-RT--EPQTPQEWIDDLERLQDRYPWLVAE-- 63
+IRPAT D+ + +I N + T + RT + + W L+ +P V E

Sbjct: 5 DIRPATEHDLTILEIYNQEVLYGTATWNRTAFDLNFKIWFQKLN--QNFPVFVVEDT 62

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
VVAG A +++ + TVE +++++ + GLGS L +L++ + Q +V

Sbjct: 63 QNQVVAGYACYDQFRSIQGFQQTVEHSIFLNPDYAGQGLGSKLLQYLIEQAQVQKLHIMV 122

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
A I N+ S+RLHE LG+ + G K G W D+ Q + +

Sbjct: 123 AAIDSENNSSIRLHEKLGTVQAYMPQVGQKFGQWRDLVLLQLNLD 168

>ref|YP_004246656.1| GCN5-related N-acetyltransferase [Spirochaeta sp. Buddy]
gb|ADY12462.1| GCN5-related N-acetyltransferase [Spirochaeta sp. Buddy]
Length = 172

Score = 73.9 bits (180), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 51/163 (31%), Positives = 82/163 (50%), Gaps = 10/163 (6%)

Query: 21 VCDIVNHYIETSTVNFRTPEQTPQE----WIDDLERLQDRYP--WLVAEVEGVVAGIAYA 74
+ I N I T+T + + PQE W D E Q YP LV + + ++A Y

Sbjct: 14 ILAIYNDAILTTTAMYEY-VKRPQESMLSWFDAKE--QGGYPVIGLVDDNDKLLAFGTY- 69

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 134

GP++ R AY +T+E +VYV ++ GLG + + L+K Q + +++A I N S+
Sbjct: 70 GPFRT RPAYHYTIEHSVYVHKDYRGKGLGQIILSLLIKKAIEQQYHTIIAAIDSSNIA SI 129

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177

LHE G+ G ++ GYK G + + F Q P+ P+ +
Sbjct: 130 HLHEKAGFEHCGVVKEVG YKFG LFRSLVFMQLLLPTPSEPKEI 172

>ref|ZP_06729221.1| phosphinothricin acetyltransferase [Acinetobacter haemolyticus ATCC

19194]
gb|EFF81078.1| phosphinothricin acetyltransferase [Acinetobacter haemolyticus ATCC
19194]
Length = 182

Score = 73.6 bits (179), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 49/166 (29%), Positives = 81/166 (48%), Gaps = 3/166 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGV 67

+IR AT D+ + I NH I T N+ + + ++ + LQ + +P +V E + +
Sbjct: 17 KIRLATIHDLKQILAIYNHEIITGAANWNDQAVSLTDYQQRFDLQQQQQFPMIVVEDQQL 76

Query: 68 --VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125

+AG AY +++ + Y +VE +V+++ + R GLG L L+ Q +VA
Sbjct: 77 DRIAGYAYYSAFRSISGYRHSVEHSVFINPSYARQGLGKALMQQLIHLATQQHMMHMAA 136

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELP 171

I N S+ LHE LG+ G + G K G W D+ Q + P
Sbjct: 137 IDSENRGSIVLHEQLGFIQTGYMPQIGQKFGQWRDLVLMQLQLKTP 182

>ref|YP_003576977.1| GNAT family acetyltransferase [Rhodobacter capsulatus SB 1003]

gb|ADE84570.1| acetyltransferase, GNAT family [Rhodobacter capsulatus SB 1003]
Length = 161

Score = 73.6 bits (179), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 52/159 (32%), Positives = 76/159 (47%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ--DRYPWLVAEVEGV 67

IRPAT AD+ AV N IET+TV F P T + + Q DR +LVAE G
Sbjct: 2 IRPATPADVPVAVLAFWNPLIETATVGFSPPTHTLESALTALIASRQAEDR-AFLVAETAGA 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

V G A ++ Y ++E T+ ++ + + G+G L + +G +VA +
Sbjct: 61 VLGFASYDQFRKGLGYARSMEHTIILAAQARGQGVGRALMAAIEDHARTRG AHLMVAGVS 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

N + H ALGY G + AGYK G + D+ Q+
Sbjct: 121 AENPAGLAFHSALGYVEAGRIAQAGYKFGRFIDLVLQMOK 159

>ref|ZP_03612639.1| acetyltransferase, gnat family [Staphylococcus capitis SK14]

gb|EEE50349.1| acetyltransferase, gnat family [Staphylococcus capitis SK14]
Length = 163

Score = 73.6 bits (179), Expect = 1e-11, Method: Compositional matrix adjust.
Identities = 44/161 (27%), Positives = 84/161 (52%), Gaps = 3/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID--DLERLQDRYPWLVAEVEGV 67

IR A D+ + +I N I +T + +P+ +E + + + + + W+ + V
Sbjct: 2 IRHARKEDLPDILEIYNDAIINTTAVYTYDPKELEERLQWFETKSIAEPIWVYVKDHHV 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

V G A G ++ AY +++E ++YV ++ G+ S L L++ +A+ ++++VA I
 Sbjct: 62 V-GYATYGSFRNWPAYLYSIEHSIYVDPDYRGQGIASKLLETLIQDAKAKNYRTIVAGID 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168

N S+ LH+ +T GT++ GYK W D+ F+Q D
 Sbjct: 121 ASNVGSIELHKKFNFTHAGTIKNVGYKFERWLDLAFYQLDL 161

>ref|ZP_03646126.1| GCN5-related N-acetyltransferase [Bifidobacterium bifidum NCIMB 41171]

Length = 184

Score = 73.2 bits (178), Expect = 1e-11, Method: Compositional matrix adjust.
 Identities = 51/162 (31%), Positives = 78/162 (48%), Gaps = 6/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV-E 65

IR A AD+ A+ DI N + + EP ++ + W+D + + +YP +V + E
 Sbjct: 9 IRAAVDADVPAIADIYNEAVIRGGASADLEFVSLESRRRAWVDS-HQPRAKYPVVVIKGP 67

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 125

G V G + R YD E + Y++ HQR GLG+ + L+ + +GF V A+
 Sbjct: 68 GAVVGFGLSKFHFQAGYDGAELSYYIAGDHQRQGLGTMVRLIDAAAERGFTHTVTAI 127

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAA-GYKHGGWHDVGFQWQ 166

I N SV L G+ G L AA G G HD+ +W +
 Sbjct: 128 IYADNAGSVALMRRFGFIRFGLLPAAVGALDGLHDMSYVVK 169

>ref|ZP_07802156.1| conserved hypothetical protein [Bifidobacterium bifidum NCIMB 41171]

gb|EFR50090.1| conserved hypothetical protein [Bifidobacterium bifidum NCIMB 41171]

Length = 180

Score = 73.2 bits (178), Expect = 1e-11, Method: Compositional matrix adjust.
 Identities = 51/162 (31%), Positives = 78/162 (48%), Gaps = 6/162 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV-E 65

IR A AD+ A+ DI N + + EP ++ + W+D + + +YP +V + E
 Sbjct: 5 IRAAVDADVPAIADIYNEAVIRGGASADLEFVSLESRRRAWVDS-HQPRAKYPVVVIKGP 63

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 125

G V G + R YD E + Y++ HQR GLG+ + L+ + +GF V A+
 Sbjct: 64 GAVVGFGLSKFHFQAGYDGAELSYYIAGDHQRQGLGTMVRLIDAAAERGFTHTVTAI 123

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAA-GYKHGGWHDVGFQWQ 166

I N SV L G+ G L AA G G HD+ +W +
 Sbjct: 124 IYADNAGSVALMRRFGFIRFGLLPAAVGALDGLHDMSYVVK 165

>ref|ZP_05740840.1| phosphinothricin n-acetyltransferase [Silicibacter sp. TrichCH4B]

gb|EEW60136.1| phosphinothricin n-acetyltransferase [Silicibacter sp. TrichCH4B]

Length = 181

Score = 73.2 bits (178), Expect = 2e-11, Method: Compositional matrix adjust.
 Identities = 54/168 (32%), Positives = 78/168 (46%), Gaps = 5/168 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAE-VEGVV 68

IRPA D A+ + H ++T+ + F TE ++ +W DD+ L P LVAE +G
 Sbjct: 9 IRPARDRDTEAITHLQRHIVDTTLMTFATEARSLSWQDDI--LYGDPPIILVAEDTDGEF 66

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 128

G A +++ Y TVE ++Y+S + G G L T L G +VA I

Sbjct: 67 LGYATYTGFRSSEGYRHTVELSIYLSEAARGRTGRKLLTELENRAIEGGIHMVMAAISS 126

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF--ELPAPP 174

N + + H A GYT G L G K W D+ Q+ + APP

Sbjct: 127 ANPTAQQFHAACGYTEVGRPLPQVGRKWDQWLDLVLQMOKILREDGTAPP 174

>ref|ZP_03528901.1| GCN5-related N-acetyltransferase [Rhizobium etli CIAT 894]
Length = 167

Score = 72.8 bits (177), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 47/131 (35%), Positives = 69/131 (52%), Gaps = 4/131 (3%)

Query: 40 PQTPQEWIDDLERLQDR-YPWLVAEVEG-VVAGIAYAGPWKARNAYDWTVESTVYVSHRH 97

PQ P+E + L+DR +P +VA +EG V G AY ++ R AY +TV+ ++YV H H

Sbjct: 23 PQ-PEELRQRRKNLKDRRFPVVA-IEGEKVVGAYVVLFRKRPAYRYTVKHSIYVHHDH 80

Query: 98 QRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGG 157

G+GS L L+ + A GF+ ++ I N S+ LHE G+ G L Y++

Sbjct: 81 IGQGIGSLLMRGLIDACAAAGFRQMIGYIAADNVASLALHERFGFVRVGLLPGVAYRYDR 140

Query: 158 WHDVGFQWQDF 168

W D QR

Sbjct: 141 WADSVMVQRSL 151

>ref|ZP_07841923.1| toxin-antitoxin system, toxin component, GNAT family
[Staphylococcus caprae C87]
gb|EFS16257.1| toxin-antitoxin system, toxin component, GNAT family
[Staphylococcus caprae C87]
Length = 163

Score = 72.8 bits (177), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 44/161 (27%), Positives = 84/161 (52%), Gaps = 3/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID--DLERLQDRYPWLVAEVEGV 67

IR A D+ + +I N I +T + +P+ +E + + + + + W+ + V

Sbjct: 2 IRHARKEDLPDILEIYNDAIINTTAVYTYDPKELEERLQWFETKSIAEPIWVYVKDHHV 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

V G A G ++ AY +++E ++YV ++ G+ S L L++ +A+ ++++VA I

Sbjct: 62 V-GYATYGSFRDWPAYLYSIEHSIYVDPDYRGQGIASKLLETLIQVAKAKNYRTIVAGID 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168

N S+ LH+ +T GT++ GYK W D+ F+Q D

Sbjct: 121 ASNVGSIELHKKFNFTHAGTIKNVGYKFERWLDLAFYQLDL 161

>gb|EFV00086.1| acetyltransferase family protein [Escherichia coli 3431]
Length = 139

Score = 72.4 bits (176), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 48/137 (35%), Positives = 69/137 (50%), Gaps = 1/137 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66

+ IR A AD AA+ +I NH + + + + + I E R YP LV+E +G

Sbjct: 1 MSIRFARKADCAAIAEIYNHAVLYTAAIWNQTVADNRIAWFEARTIAGYPVLVSEEDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126

VV G A G W++ + + TVE +VYV HQ GLG L + L+ G +VA I

Sbjct: 61 VVTGYASFGDWRSDGFRHTVEHSVYVHPDHQKGGLGRKLLSRLIDEARDCGKHMVAGI 120

Query: 127 GLPNDPSVRLHEALGYT 143

N S+ LH++LG+
Sbjct: 121 ESQNQASLHLHQSLGFV 137

>ref|YP_003698513.1| GCN5-like N-acetyltransferase [Bacillus selenitireducens MLS10]
gb|ADH97947.1| GCN5-related N-acetyltransferase [Bacillus selenitireducens MLS10]
Length = 174

Score = 72.4 bits (176), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 49/172 (28%), Positives = 74/172 (43%), Gaps = 4/172 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IRP T + AV I ++T F T + W + L+AE G
Sbjct: 4 ILIRPMTVQEWPAVSAIQAGLDTELATFETVVPVSWDSW---NQAHHETCRLIAEYGGT 59

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+AG A P R AY E ++Y++ LG+G TL L++ E GF ++ + I
Sbjct: 60 IAGWAALAPTSPRYAYRGVAEISIIYIAPGASGLGVGRTLNLALIEDSEKAGFWTIQSAIF 119

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
N S+ LH+ G+ G +HG WHD+ +R + A RP
Sbjct: 120 RENQASIHLLKKCGFRQIGYREQVAERHGVWHDIIILMERRSPIVAASPSARP 171

>ref|ZP_03574401.1| acetyltransferase, gnat family [Burkholderia multivorans CGD2M]
ref|ZP_03581840.1| acetyltransferase, gnat family [Burkholderia multivorans CGD2]
gb|EEE03747.1| acetyltransferase, gnat family [Burkholderia multivorans CGD2]
gb|EEE11038.1| acetyltransferase, gnat family [Burkholderia multivorans CGD2M]
Length = 184

Score = 72.4 bits (176), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 58/180 (32%), Positives = 88/180 (48%), Gaps = 9/180 (5%)

Query: 3 PERRPVEIRPATAADMA-AVCDIVNHYIETSTVNFRTEPQTPQE--WIDDLERLQDRYP 58
P+R V + T A+ A A+ +I+N I ST + +P+ P+ W + +P
Sbjct: 7 PQRDDVRLIDCTEAHAPAILIILNDAIVNSTALYDYKPRPPEAMAAWF--ATKRASGFP 64

Query: 59 WLVA-EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
+ A + G + G A G ++A A+ +TVE +VYV H+ GLG L L++
Sbjct: 65 VVGAVDASGTLGLGFASWGTFRAPPAFKYTVEHSVYVHRDHRGRGLGELLLRELIRRAHDA 124

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
+V I N S+ LH LG+ GT++ AG+K G W D F+Q L P RPV
Sbjct: 125 DVHLLVGCIDATNAGSIALHTRLGTVHSGTIKEAGFKFGRWLDAAFYQ--LRDTPSPRPV 182

>ref|YP_004118309.1| GCN5-related N-acetyltransferase [Pantoea sp. At-9b]
gb|ADU71753.1| GCN5-related N-acetyltransferase [Pantoea sp. At-9b]
Length = 169

Score = 72.4 bits (176), Expect = 2e-11, Method: Compositional matrix adjust.
Identities = 58/172 (33%), Positives = 81/172 (47%), Gaps = 8/172 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTV--NFRTEPQTPQ-EWIDDLERLQDRYPWLVA-- 62
+ IRPA D A + I N + ST N +T + +W+ D R Q +P LVA
Sbjct: 1 MNIRPAVEQDAAVIAAIYNDAVLNSTAIWNDKTVAVANRVQWMD--RQQAGFPVLVAVD 58

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
E +GV+ G A G W+ + Y +TVE +VYV + G G L L+ QG +
Sbjct: 59 EQDGV-LGYASYGDWRPWDGYRFTVEHSVYVLSARGKGAGEALMRALITHATHQGHVM 117

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
VA I N S+ LH LG++ G + G K G W D+ F Q + P

Sbjct: 118 VAGIESENTASIALHHKLGFEAGRVSEVGKFKGRWLDLTFLLQLRLDQRQQP 169

>ref|YP_237501.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae B728a]

gb|AA39463.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae B728a]

Length = 185

Score = 72.4 bits (176), Expect = 3e-11, Method: Compositional matrix adjust.

Identities = 56/180 (31%), Positives = 78/180 (43%), Gaps = 12/180 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65

IR A D+ + DI N + +T + +P Q W R YP LVA +

Sbjct: 5 IRDALPDDLPGILDYNDVAVLNTTAIWNEQPVDLANRQAWY--AARQSQGYPIILVAVDNA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAGGFKSVVAV 125

G V G + G W+ + TVE +VYV + GLG L L++ +VA

Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMAALIERARDCDKHMMVAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAP-----PRPVRP 179

I N S+ LH+ LG+ G + G K G W D+ F Q D AP P+P+ P

Sbjct: 123 IESGNAASIALHDLRGKITGMPQVGTGKFRWLDLTFMQLDLSPGAPAPASQAPKPLSP 182

>ref|ZP_01092054.1| GCN5-related N-acetyltransferase [Blastopirellula marina DSM 3645]

gb|EAQ79584.1| GCN5-related N-acetyltransferase [Blastopirellula marina DSM 3645]

Length = 104

Score = 72.0 bits (175), Expect = 3e-11, Method: Compositional matrix adjust.

Identities = 35/103 (33%), Positives = 53/103 (51%), Gaps = 2/103 (1%)

Query: 75 GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAGGFKSVVAVIGLPNDPSV 134

GP++ + Y +T E ++Y+ + GLG L ++ A+ ++ VI N SV

Sbjct: 2 GPFRPQPGYKYTAHSIYIQQDFRGQGLGGVLLQEMIAQATAKDLHCLIGVIDQANQASV 61

Query: 135 RLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177

LH G+ G +R AG+K GGW D G++Q LP P PV

Sbjct: 62 ALHLKHGFLVLAGVMREAGFKFGWLDAGYYQ--LVLPTPQTPV 102

>ref|ZP_03823828.1| acetyltransferase [Acinetobacter sp. ATCC 27244]

gb|EEH68285.1| acetyltransferase [Acinetobacter sp. ATCC 27244]

Length = 182

Score = 72.0 bits (175), Expect = 3e-11, Method: Compositional matrix adjust.

Identities = 49/166 (29%), Positives = 79/166 (47%), Gaps = 3/166 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGV 67

+IR AT D+ + I NH I T N+ + + ++ + LQ + +P +V E + +

Sbjct: 17 KIRLATIHDLQILAIYNHEIITGAANWNDQAVSLTDYQQRFDLQQQQFPMIVVEDQHL 76

Query: 68 --VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAGGFKSVVAV 125

+AG AY +++ + Y +VE +V++ + R GLG L L+ Q +VA

Sbjct: 77 KKIAGYAYYSAFRSISGYRHSVEHSVFIDPSYARQGLGKALMQQLIHLATQQHMHMMVAA 136

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELP 171

I N S+ LHE LG+ G + G K G W D+ Q P

Sbjct: 137 IDSENRGSIVLHEQLGFIQTGYMPQIGQKFGQWRDLVLMQLQLNTP 182

>ref|ZP_07250854.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas syringae pv. tomato K40]

Length = 180

Score = 72.0 bits (175), Expect = 3e-11, Method: Compositional matrix adjust.
Identities = 55/177 (31%), Positives = 77/177 (43%), Gaps = 10/177 (5%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EVE 65
          IR A A D+ + I N + +T + +P      ++W      R      YP LVA +
Sbjct: 5   IRDALADDLPILAIYNDAVLNTTAIWNEQPVDLANREDWY--TSRQAQAYPVLVAVDSS 62

Query: 66  GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
          G V G + G W+ + TVE +VYV + GLG L L++ A +VA
Sbjct: 63  GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMAELIERARACDKHMMVAA 122

Query: 126  IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQ 182
          I N S+ LHE LG+ G + G K G W D+ F Q D P P +Q
Sbjct: 123  IESGNAASIALHERLGFKTTGQMPQVGTKFGRWLDLTFMQLDLS----PGACAPASQ 175
```

```
>ref|ZP_03972494.1| Phosphinothricin acetyltransferase [Corynebacterium
                    glucuronolyticum ATCC 51866]
gb|EEI62615.1| Phosphinothricin acetyltransferase [Corynebacterium
                    glucuronolyticum ATCC 51866]
                    Length = 161
```

Score = 71.6 bits (174), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 57/165 (34%), Positives = 77/165 (46%), Gaps = 18/165 (10%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL-----VA 62
          IR A A+D A+ I N E ST F P T + +R WL VA
Sbjct: 5   IRLALASDAPALARIRNWAAEESTALFDNTPVT-----VANRTRWLAEEPVVVFA 54

Query: 63  EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKS 121
          +V+G V G A GP++ Y TVE++VYV +Q G+G+ L L+ EA
Sbjct: 55  DVDGEVIGYASYGPFRVLTGYRHTVENSIVYVLPGNQAGIGTGLLQTLIAHAEPDVRH 114

Query: 122  VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
          +V I N+ S+ LH G+ +G L GYK G W DV +R
Sbjct: 115  MVVWISTNEASLALHRRHGFEEKGRLTEVGKCGRWLDVTILER 159
```

```
>ref|ZP_03396120.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
                    tomato T1]
gb|EEB60866.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
                    tomato T1]
                    Length = 180
```

Score = 71.6 bits (174), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 55/177 (31%), Positives = 76/177 (42%), Gaps = 10/177 (5%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVA-EVE 65
          IR A A D+ + I N + +T + +P      + W      R      YP LVA +
Sbjct: 5   IRDALADDLPILAIYNDAVLNTTAIWNEQPVDLANREAWC--TSRQAQAYPVLVAVDSS 62

Query: 66  GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
          G V G + G W+ + TVE +VYV + GLG L L++ A +VA
Sbjct: 63  GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMAELIERARACDKHMMVAA 122

Query: 126  IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQ 182
          I N S+ LHE LG+ G + G K G W D+ F Q D P P +Q
Sbjct: 123  IESGNAASIALHERLGFKTTGQMPQVGTKFGRWLDLTFMQLDLS----PGACAPASQ 175
```

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>ref|ZP_03587049.1| acetyltransferase, gnat family [Burkholderia multivorans CGD1]
```

gb|EED98726.1| acetyltransferase, gnat family [Burkholderia multivorans CGD1]
Length = 184

Score = 71.6 bits (174), Expect = 4e-11, Method: Compositional matrix adjust.
Identities = 58/180 (32%), Positives = 88/180 (48%), Gaps = 9/180 (5%)

Query: 3 PERRPVEIRPATAADMA-AVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYP 58
P+R V + T A+ A A+ +I+N I ST + +P+ P+ W + +P
Sbjct: 7 PQRDDVRLIDCTEAHAPAILLEILNDAIVNSTALYDYKPRPPEAMAAWF--ATKRASGFP 64

Query: 59 WLVA-EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
+ A + G + G A G ++A A+ +TVE +VYV H+ GLG L L++
Sbjct: 65 VVGAVDASGTLGLFASWGTFRAFPAPFKYTVESVYVHRDHRGRGLGELLRELIRRAYDA 124

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPV 177
+V I N S+ LH LG+ GT++ AG+K G W D F+Q L P RPV
Sbjct: 125 DVHLLVGCIDATNAGSIALHTRLGFFVHSGTIKEAGFKFGRWLDAAFYQ--LRDTPSPRPV 182

>sp|Q54225.1|NAT_STRGR RecName: Full=N-acetyltransferase
emb|CAA56304.1| N-acetyltransferase [Streptomyces griseus]
Length = 194

Score = 71.6 bits (174), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 46/169 (27%), Positives = 79/169 (46%), Gaps = 11/169 (6%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAEVE 65
++RP A D+ + ++ NHY+ + + F T P TP+ +W L +D L+ E
Sbjct: 10 QVRPGIAEDLTGLTNLYNHVLRTPITFDTVPLTPEGRMQWF--LSHPKDGPHRLMVAEE 67

Query: 66 GV-----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
+ G A + P + + AY + E +VY + G+G+ LYT L ++ +
Sbjct: 68 PAPSGPERLLGYATSSPLRPKAAAYATSAEVSVCAPDAAGRGVGTALYTALFDALAGEDL 127

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
A + PND S RLH + GT G K G + DV +++++
Sbjct: 128 HRAYAGVTQPNDAASHRLHTRFDFRPIGTYGVGRKFGRYWDVVRWYEKEL 176

>ref|YP_917443.1| GCN5-related N-acetyltransferase [Paracoccus denitrificans PD1222]
gb|ABL71747.1| GCN5-related N-acetyltransferase [Paracoccus denitrificans PD1222]
Length = 162

Score = 71.2 bits (173), Expect = 5e-11, Method: Compositional matrix adjust.
Identities = 46/158 (29%), Positives = 72/158 (45%), Gaps = 1/158 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDRYPWLVAEVEGVV 68
+RP D+ A+ N I +T+ F +E +T + + +R +LVAE V
Sbjct: 3 LRPVAEGDIPAMLAFWNPLIRETTITFSSEERTAEGLARMIADRRAGRAFLVAEEASTV 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G+A ++ N Y +E TV +S +R G+G L L G S++A +
Sbjct: 63 LGLASYDQFRGGNGYAHCMHTVILSPAARRRGVGRALMAALEDHARTAGSHSMIAAVSA 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N+ + H A+GY G L AG K G W D+ Q+
Sbjct: 123 ENEAGIAFHRAIGYVPVGLLPQAGRKFGRWLDLALLQK 160

>ref|NP_691255.1| phosphinothricin N-acetyltransferase [Oceanobacillus iheyensis
HTE831]
dbj|BAC12290.1| phosphinothricin N-acetyltransferase [Oceanobacillus iheyensis
HTE831]

Length = 168

Score = 71.2 bits (173), Expect = 6e-11, Method: Compositional matrix adjust.
Identities = 42/140 (30%), Positives = 72/140 (51%), Gaps = 5/140 (3%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVA 62
+ + R AT D+ + I N I + V TEP T +E W ++ + + R P LVA
Sbjct: 3 KNLTFRNATIEDLPEIVAIYNSTIVSRMTADTEPVTVEERQNWFEHDSV--RRPLLVA 60

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
E+EG + G + R AY+ T E ++Y+ R + GLG L ++++ + G + +
Sbjct: 61 ELEGEICGWISLESFYGRPAYNQTAEVSIYIDERFRGEGLGKKLLNYIEKSPSYGIEIL 120

Query: 123 VAVIGLPNDPSVRLHEALGY 142
+ I N+PS++L E G+
Sbjct: 121 LGFIFAHNEPSIKLFRFGRF 140

>ref|NP_767756.1| phosphinothricin acetyltransferase [Bradyrhizobium japonicum USDA
110]
dbj|BAC46381.1| phosphinothricin acetyltransferase [Bradyrhizobium japonicum USDA
110]
Length = 171

Score = 71.2 bits (173), Expect = 6e-11, Method: Compositional matrix adjust.
Identities = 54/170 (31%), Positives = 76/170 (44%), Gaps = 7/170 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEG 66
+R AT D + I NH +T + P + + WI R + YP LVA
Sbjct: 6 VRDATLEDAEDILAIYNHAAINTTAVWTDGPVLDLSRRRAWIR--ARREAGYPVLVAMKGR 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A G ++ Y TVE++VYV RH R G+G L L++ A ++VA I
Sbjct: 64 DVVGFAFGDFRPWPFGYRHTVENSIVYDERHHRAGIGRGLMVALIERATALNKHTMVAI 123

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRP 176
N S+ LH + G+ G + G K G W D+ Q L + RP
Sbjct: 124 EASNSASIALHASFGFAEVGRMPEVGCKFGRWLDMLMQ--MRLSSGVRP 171

>ref|YP_003210449.1| N-acetyltransferase YncA [Cronobacter turicensis z3032]
emb|CBA30780.1| Uncharacterized N-acetyltransferase yncA [Cronobacter turicensis
z3032]
Length = 156

Score = 70.9 bits (172), Expect = 6e-11, Method: Compositional matrix adjust.
Identities = 45/127 (35%), Positives = 61/127 (48%)

Query: 51 ERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110
+R YP LVA + V G A G W+A + + TVE +VYV H G+G L T L
Sbjct: 29 QRGNAGYPVLVAVLGDTVVGYSFGDWRAFDFGRHTVEHSVYVHPDHHGKGIGKALMTRL 88

Query: 111 LKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170
+ +A G +VA I N S+ LHE LG+T + G K G W D+ F Q +
Sbjct: 89 IVEAQAIGKHVMVAGIESRNAGSIALHEKLGFTITATQMPQVGTFGRWLDLTFMQLQLDN 148

Query: 171 PAPPRPV 177
P +
Sbjct: 149 RNEPDAI 155

>ref|ZP_07232129.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas
syringae pv. tomato Max13]

ref|ZP_07257576.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas syringae pv. tomato NCPPB 1108]
Length = 180

Score = 70.9 bits (172), Expect = 7e-11, Method: Compositional matrix adjust.
Identities = 55/177 (31%), Positives = 76/177 (42%), Gaps = 10/177 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
IR A A D+ + I N + +T + +P + W R YP LVA +
Sbjct: 5 IRDALADDLPGILAIYNDAVLNTTAIWNEQPVDLANREAWY--TSRQAQAYPVLVAVDSS 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
G V G + G W+ + TVE +VYV + GLG L L++ A +VA
Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMAELIERARACDKHMMVAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVPRVPTQ 182
I N S+ LHE LG+ G + G K G W D+ F Q D P P +Q
Sbjct: 123 IESGNAASIALHERLGFKTTGOMPQVGTKFGRWLDLTFMQLDLS----PGACAPASQ 175

>ref|YP_003922093.1| phosphinothricin acetyltransferase [Bacillus amyloliquefaciens DSM

7]
emb|CBI44623.1| putative phosphinothricin acetyltransferase [Bacillus amyloliquefaciens DSM 7]
Length = 165

Score = 70.9 bits (172), Expect = 7e-11, Method: Compositional matrix adjust.
Identities = 51/162 (31%), Positives = 75/162 (46%), Gaps = 1/162 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-G 66
+ +R A + D+ AV I N I + V TE TP++ +D R DR P +VAE E G
Sbjct: 3 LTLRKAVSEDLDAVVAIYNSTIASRMVTADTEEVTPEDRMDWFLRHTDRRPLMVAEDENG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
VA + R AYD T E ++Y+ + G GS L L G ++++A I
Sbjct: 63 KVAAWISFETFYGRPAYDKTAEISIIYHQDCRGKGAGSFLKEALAIAPKIGIRNLMAFI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
N PS++L E G+T G G +D+ R+
Sbjct: 123 FGHNVPSIKLFEKFGFTEWGVFPGIAEMDGKRYDLNILGREL 164

>ref|ZP_05637338.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas syringae pv. tabaci ATCC 11528]
Length = 180

Score = 70.9 bits (172), Expect = 7e-11, Method: Compositional matrix adjust.
Identities = 56/177 (31%), Positives = 79/177 (44%), Gaps = 12/177 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
IR A D+ + +I N + +T + +P Q W + R YP LVA +
Sbjct: 5 IRDALPDDLPGILEIYNDAVLNTTAIWNEQPVDLANRQAWYE--ARQSQAYPILVAVDHA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
G V G + G W+ + TVE +VYV + GLG L L++ +VA
Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPLLMASLIERARDCEKHMMAVAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE--LPAP----PRP 176
I N S+ LHE LG+ G + G K G W D+ F Q D +PAP P+P
Sbjct: 123 IESGNAASIALHERLGFKTTGRMPQVGTKFGRWLDLTFMQLDLSPGVPAPASQAPKP 179

>ref|YP_001998872.1| GCN5-related N-acetyltransferase [Chlorobaculum parvum NCIB 8327]
 gb|ACF11672.1| GCN5-related N-acetyltransferase [Chlorobaculum parvum NCIB 8327]
 Length = 166

Score = 70.9 bits (172), Expect = 7e-11, Method: Compositional matrix adjust.
 Identities = 44/160 (27%), Positives = 73/160 (45%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-EVEG 66
 VE+ P A D+ + I N Y+E S + TE + ++L YP VA +V+G
 Sbjct: 3 VELLPVCADDLEEMAAIFNDYVEHSLATW-TETPVSVDRFEELMCFAPDYPAFVARDVDG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V+AG P+ + A+D E T ++ G+G L L G ++++++
 Sbjct: 62 VMAGFGLLRPYSSIPAFDRATEMTCFKQDFTGQGIGRKLAALESDAAKLGVTTIISML 121

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
 N S+ H G+ RG L G ++G DV +Q+
 Sbjct: 122 SSLNKQSLHFHSRCGFIERGRLVGIGRRNGLDFDVVLFQK 161

>ref|YP_001338537.1| N-acetyltransferase-like protein [Klebsiella pneumoniae subsp.
 pneumoniae MGH 78578]
 gb|ABR80307.1| N-acetyltransferase-like protein [Klebsiella pneumoniae subsp.
 pneumoniae MGH 78578]
 Length = 175

Score = 70.5 bits (171), Expect = 8e-11, Method: Compositional matrix adjust.
 Identities = 56/164 (34%), Positives = 75/164 (45%), Gaps = 6/164 (3%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVA 62
 E + IR D AV +I I T F+T EW + LQD RY VA
 Sbjct: 10 EMAEIIIRKMHEEDWCAVREIYQEGIATGNATFQTAAPWLEWNEG--HLQDCRY---VA 64

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 V+ V G A P+ R+AY E ++YVS Q G G L + L+K E+ GF ++
 Sbjct: 65 TVDNRVVGWAALSPFSRRHAYRGVAELSIYVSTHFQKGAGRALLSGLIKGESAGFWTL 124

Query: 123 VAVIGLPNDPVRLEALGYTARGTLRAAGYKHGGWHDVGFQW 166
 +A I N SV LH + G+ G G +G W DV +R
 Sbjct: 125 LAGIFPENQASVALHRSQGFREVGCRENVGEMNGKWRDVLILR 168

>ref|ZP_06042260.1| GCN5-related N-acetyltransferase [Corynebacterium aurimucosum
 ATCC
 700975]
 Length = 164

Score = 70.5 bits (171), Expect = 8e-11, Method: Compositional matrix adjust.
 Identities = 50/159 (31%), Positives = 82/159 (51%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVA-EVEGV 67
 IR AT AD+ A+ +N I + FR+EP T +E + L +L+ D+ P A E +G
 Sbjct: 3 IREATDADVPAMTATLNWAIRETHFIFRSEPATVEERTEYLHQLRRDKCPCFAAFEDDGT 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSVVAVI 126
 G A P++ + E+T+YV G+G+ L +++ + EA+ +++A+I
 Sbjct: 63 YLGWALYRPYRDPKVWQGCYETTIYVDPTAHGRGVGTRLLDAVVQHAREAEQVHTLLALI 122

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 N S++LHE G+ GTL+ K G W D+ Q
 Sbjct: 123 VADNVASIKLHEKFGFATVGTLEKVSRAKGRWIDLTHLQ 161

>ref|NP_794626.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv. tomato str. DC3000]
gb|AA058321.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas syringae pv. tomato str. DC3000]
Length = 180

Score = 70.5 bits (171), Expect = 9e-11, Method: Compositional matrix adjust.
Identities = 55/177 (31%), Positives = 76/177 (42%), Gaps = 10/177 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVA-EVE 65
IR A A D+ + I N + +T + +P + W R YP LVA +
Sbjct: 5 IRDALADDLPILAIYNDAVLNTTAIWNEQPVDLANREAWY--TSRQAQAYPVLVAVDSA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G + G W+ + TVE +VYV + GLG L L++ A +VA
Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMAELIERARACDKHMMVAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPVTQ 182
I N S+ LHE LG+ G + G K G W D+ F Q D P P +Q
Sbjct: 123 IESGNAASIALHERLGFKTTGQMPQVGTKFGRWDLTFMQLDLS----PGACAPASQ 175

>ref|ZP_07317215.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella atypica ACS-049-V-Sch6]
gb|EFL56974.1| toxin-antitoxin system, toxin component, GNAT family [Veillonella atypica ACS-049-V-Sch6]
Length = 166

Score = 70.5 bits (171), Expect = 9e-11, Method: Compositional matrix adjust.
Identities = 42/153 (27%), Positives = 75/153 (49%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
IR D+ A I N+ +E EP+T +EW + D + P +V ++ VV
Sbjct: 6 IRSIAEDDVFACLSIYNYEVEHGVATLDLEPRTLEEWHEWYNAHSDEHHPPIIVGTMDNVV 65

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG-FKSVVAVIG 127
G A ++ ++A+ TVE ++Y+ ++ G+ + L ++ ++ +VV+VI
Sbjct: 66 VGYASLSLRLKDAFKSTVELSIYIHQDYRGQGVATQLMERIIAMAKSDDTLHNVSIVIT 125

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
N+ S +LH G+T G G+KHG + D
Sbjct: 126 AGNEGSTKLHNRFGFTYCGLTPEVGFKHGYQD 158

>ref|YP_003212788.1| hypothetical protein Ctu_3p00440 [Cronobacter turicensis z3032]
emb|CBA34749.1| hypothetical protein Ctu_3p00440 [Cronobacter turicensis z3032]
Length = 175

Score = 70.5 bits (171), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 56/164 (34%), Positives = 74/164 (45%), Gaps = 6/164 (3%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVA 62
E + IR D AV +I I T F+T EW + LQD RY VA
Sbjct: 10 EMAEIIIRKMHEEDWCAVREIYQEGIAIATNFQTAAPWLEWNEG--HLQDCRY--VA 64

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
V+ V G A P+ R+AY E ++YVS Q G G L + L+K E GF ++
Sbjct: 65 TVDNRVVGWAALSPFSRRHAYRGVAELSIYVSTHFQKGAGRALLSGLIKGSEGAGFWTL 124

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
+A I N SV LH + G+ G G +G W DV +R
Sbjct: 125 LAGIFPENQASVALHRSQGFREVGCREKVGEMNGKWRDVLILR 168

>ref|YP_003559670.1| putative acetyltransferase [Sphingobium japonicum UT26S]
dbj|BAI98938.1| putative acetyltransferase [Sphingobium japonicum UT26S]
Length = 181

Score = 70.5 bits (171), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 50/140 (35%), Positives = 73/140 (52%), Gaps = 1/140 (0%)

Query: 27 HYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVVAGIAYAGPWKARNAYDW 85
H++ T ++ P T E + + R+ R +P+LVA V G YA ++ R AY
Sbjct: 26 HHVLHGTASYEFVPPTVAETVAKIGRVTGRGWPFVLVACDGAEEVVGICYATQFRDRPAYAH 85

Query: 86 TVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTAR 145
E+++YV+H + G+G L LL + EA GF+ +VAVIG SV LH A G+
Sbjct: 86 ACENSIYVAHRRGGGIGRALLEALLDAAEAFGRQMVAVIGGGEPASVALHAACGFRQA 145

Query: 146 GTLRAAGYKHGGWHDVGFQW 165
G L G+K G W D + Q
Sbjct: 146 GRLTGMGWKAGRWLDTVYMQ 165

>ref|YP_001422934.1| YwnH [Bacillus amyloliquefaciens FZB42]
gb|ABS75703.1| YwnH [Bacillus amyloliquefaciens FZB42]
Length = 165

Score = 70.5 bits (171), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 52/162 (32%), Positives = 73/162 (45%), Gaps = 1/162 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-G 66
+ +R A D+ AV I N I + V TE TP + +D R DR P +VAE E G
Sbjct: 3 LTLRKAVLEDLDAVVAIYNSTIASRMVTADTEEVTPADRMDFLRLHTDRRPLMVAEDETG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
VA + R AYD T E ++Y+ + G GS L L G +S++A I
Sbjct: 63 KVAAWISFETFYGRPAYDKTAEISYIYHQDCRGKGAGSFLKEALALAPTIGIRSLMAFI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
N PS++L E G+T G G +D+ R+
Sbjct: 123 FGHNVPSTIKLFKFGFTEWGVFPGIAEMDGKRYDLNILGREL 164

>ref|YP_001762213.1| GCN5-like N-acetyltransferase [Shewanella woodyi ATCC 51908]
gb|ACA88118.1| GCN5-related N-acetyltransferase [Shewanella woodyi ATCC 51908]
Length = 162

Score = 70.5 bits (171), Expect = 1e-10, Method: Compositional matrix adjust.
Identities = 48/159 (30%), Positives = 70/159 (44%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++IR AD AV DI I+ F +P+ EW +R LV E++
Sbjct: 1 MKIREFEFADFKAFTDIYQEGIDGGNATFEKQPKAWPEW----DRAMLAPCRLVIEIDSQ 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G A P R AY VE ++Y+S + G G L T L+K E G ++ + I
Sbjct: 57 LVGWAGLLPTSTREAYAGVVEVSIYISDNAKNGAGYALLTELKQSEEAGCWTLSAIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N S+ LH+ G+ G G +G W DV +R
Sbjct: 117 PENQASINLHQKCGFKILGVRERLGQMNGVWRDVVLMER 155

>ref|ZP_03394589.1| acetyltransferase, gnat family [Corynebacterium amycolatum SK46]
gb|EEB62368.1| acetyltransferase, gnat family [Corynebacterium amycolatum SK46]

Length = 173

Score = 70.1 bits (170), Expect = 1e-10, Method: Compositional matrix adjust.
 Identities = 51/170 (30%), Positives = 80/170 (47%), Gaps = 4/170 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
 IR AT D A+ +I N + + + + + I +E D+ YP VA ++ V
 Sbjct: 3 IRQATREDAEIAIEIYNEAVSNTVAIWNDGTVSAENRIAWMEAHWDKDPVFPVATLDDEV 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 AG A ++ + + +TVE+++YV Q G+G L + + G +VA I
 Sbjct: 63 AGYATFSDFRDFDGFYTVENSIYVHPNFQGRGIGGKLLQVTIDAAREAGKHVLAADIG 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ---RDFELPAPPR 175
 N+ S+ LHE G+ G L G K+G W D+ Q D + PA PR
 Sbjct: 123 SNEGSIALHEKYGFQRVGLLPQVGTKNGRWLDMLLMQVMLTDEQPPAQPR 172

>ref|YP_001807735.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MC40-6]
 gb|ACB63519.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MC40-6]
 Length = 182

Score = 70.1 bits (170), Expect = 1e-10, Method: Compositional matrix adjust.
 Identities = 54/167 (32%), Positives = 81/167 (48%), Gaps = 2/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVE-GV 67
 I + A AA+ +I+N I ST + P+ P+ + + + +P + A E G
 Sbjct: 13 IDCSEAHEHAAAILEILNDAIVNSTALYDYRPRPPEAMVAWFATKRANGFPVVGAVDESGT 72

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 + G A G ++A A+ +TVE +VYV H+ GLG L L++ +V I
 Sbjct: 73 LVGFASWGTFRAPFAFKYTVESVYVHRDHRGRGLGELLLRELIRRAREADVHVLVGCID 132

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPP 174
 N SV LH LG+ GT+ AG+K G W D F+Q + PA P
 Sbjct: 133 ATNGGSVALHTRLGFVHSGTITEAGFKFGRWLDAAFYQLTLDTPAQP 179

>ref|ZP_01910089.1| PHOSPHINOTHRICIN N-ACETYLTRANSFERASE [Plesiocystis pacifica SIR-1]
 gb|EDM76954.1| PHOSPHINOTHRICIN N-ACETYLTRANSFERASE [Plesiocystis pacifica SIR-1]
 Length = 163

Score = 70.1 bits (170), Expect = 1e-10, Method: Compositional matrix adjust.
 Identities = 41/108 (37%), Positives = 58/108 (53%), Gaps = 1/108 (0%)

Query: 60 LVAEVEGV-VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 +VAE EG VA A PW + Y T E + +V+ H+R GLG + L+ EA G
 Sbjct: 54 VVAEREGTTVAAWGRAKPWSFKRGYARTRELSTFVAQAHRRLGLRLVTAALIAEAEASG 113

Query: 119 FKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 +VA I + N+PS+ L+ +LG+ G R G++ G W DV QR
 Sbjct: 114 AHHLVARIFVDNEPSMALYSSLGFELVGIQRQIGWRDGAWVDVALLQR 161

>ref|YP_003941905.1| Phosphinothricin acetyltransferase [Enterobacter cloacae SCF1]
 gb|ADO48621.1| Phosphinothricin acetyltransferase [Enterobacter cloacae SCF1]
 Length = 172

Score = 69.7 bits (169), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 58/170 (34%), Positives = 86/170 (50%), Gaps = 5/170 (2%)

Query: 8 VEIRPATAADMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEV 64
 + IR A D AA+ +I NH + T+ + N +T + W + + L YP LV+E

Sbjct: 1 MTIRYACKDDCAAIAEIIYNHAVVHTAAIWNQTVDTDNRIAWYEARQLLG--YPVLVSED 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
GV+ G A G W+A + + TVE +VYV +HQ GLG L T L+ + G +VA

Sbjct: 59 NGVITGYASFGDWRAFDGFRHTVEHSVYVHPQHQQGKGLGRLLLTRLISEAKRVGKHMVA 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
I N S++LH +LG+ + G K G W D+ F Q + + P

Sbjct: 119 GIESQNAASLKLHASLGFITTAQMPQVGTKFGRWLDLTFMQLQLDNRSEP 168

>ref|YP_613856.1| GCN5-related N-acetyltransferase [Ruegeria sp. TM1040]
gb|ABF64594.1| GCN5-related N-acetyltransferase [Ruegeria sp. TM1040]
Length = 177

Score = 69.7 bits (169), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 51/168 (30%), Positives = 75/168 (44%), Gaps = 5/168 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-GV 68
IR A D A+ + H I+T+ F TE ++ +W DD+ L P LVAE E G

Sbjct: 5 IRAARDGDTEAITHLQRHIIDTTLATFATEGRLSDWQDDI--LYGDPPILVAEAEQGQF 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
G A +++ Y T E ++Y++ + G+G L + L A G +VA I

Sbjct: 63 LGYATYSGFRSSEGYRHTGEHSIYLTEAARGQGVGHKLLSELENRARAAGIHMVMAAIISS 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF--ELPAPP 174
N + R H GY G + G K W D+ Q+ + APP

Sbjct: 123 ANPAAARFHARCGYAEVGRMPQVGRKWDQWLDLILMQKILREQGTAPP 170

>ref|YP_001943206.1| GCN5-related N-acetyltransferase [Chlorobium limicola DSM 245]
gb|ACD90227.1| GCN5-related N-acetyltransferase [Chlorobium limicola DSM 245]
Length = 163

Score = 69.7 bits (169), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 47/160 (29%), Positives = 72/160 (45%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-G 66
+ + P +D V DI N Y + S + +P + + LE L + YP VA E G

Sbjct: 3 IVLEPLAVSDGPEVLDFNFYADRSFAAYSLKPLSDEMAMFLE-LSNGYPAFVARDENG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
G P+ A+ T E T+++ + G+G + HL++ G S++A I

Sbjct: 62 KAVGFGMLRPYSPMPAFAGTAEITLFLRDGYTGQIGKVILDHLVEQAAEMGLVSILASI 121

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N+ S+R H G+ G R AG K G DV + QR

Sbjct: 122 SSLNEGSIRFHLRNGFQECGRFRDAGEKLGRKFDVVCYQR 161

>ref|YP_003688562.1| Acetyltransferase [Propionibacterium freudenreichii subsp.
shermanii CIRM-BIA1]
emb|CBL57137.1| Acetyltransferase [Propionibacterium freudenreichii subsp.
shermanii CIRM-BIA1]
Length = 170

Score = 69.7 bits (169), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 48/155 (30%), Positives = 76/155 (49%), Gaps = 6/155 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP--QEWDLRLQDRYPWLVA-EVE 65
+R A D A+ I N +T ++ P T + W+ + + R+P LVA + +

Sbjct: 7 VRNAVNDDAVALTAIHNAQGVATTASYALTPGTVPDRRAWL--VRQHAARHPVLVAADGQ 64

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + G A +++ YD TVE +VY + H+RLG+G+ L L+ + G ++V V
 Sbjct: 65 GRIVGFADYDRFRSLPGYDLTVEHSVYTAPGHERLGIGAALMDQLIDRARSAGMHAMVG 124

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 I N S+ H+ LG+ GTL G K W D
 Sbjct: 125 IDADNAASIDFHQRLGFRLCGTLPQVGRKFRDRLD 159

>ref|ZP_07050608.1| phosphinothricin N-acetyltransferase [Lysinibacillus fusiformis
 ZC1]
 gb|EFI67774.1| phosphinothricin N-acetyltransferase [Lysinibacillus fusiformis
 ZC1]
 Length = 162

Score = 69.3 bits (168), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 48/161 (29%), Positives = 70/161 (43%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR D+ V I IET F T + Q W D+ R+ VAE V
 Sbjct: 6 IRKMEKKDLKEVLKIYKEGIETGMATFETIVPSKQVW-DERHHAALRF---VAEEHNRRV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G P R Y E VY+S H+ G+ S L+ L+++E +GF ++ + I
 Sbjct: 62 GWISISPVSTRAVYSGVGEVIVYLSSDHKGKGIASRLFKLLIETSEKEGFWTQSSIFAI 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170
 N S++LH+ +G+ GT G WHDV +R +
 Sbjct: 122 NTSSIQLHKKMGFRIVGTREKIAQLDGIWHDVVLMEERLNI 162

>ref|ZP_05964895.1| N-acetyltransferase [Brucella neotomae 5K33]
 gb|EEY05175.1| N-acetyltransferase [Brucella neotomae 5K33]
 Length = 120

Score = 69.3 bits (168), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 40/115 (34%), Positives = 61/115 (53%)

Query: 52 RLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
 R +D +P LVAE EG V G A GP++ + + E +VYV+ + G+G TL L+
 Sbjct: 4 RNRDGFVPLVAEREGQVVGYSYSGPFRPFEGFRHSSELSVYVASNARGGGIGRTLLAELI 63

Query: 112 KSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
 + + ++A I N S+ LH + G+ GTL+ G K G W D+ F Q+
 Sbjct: 64 EEAREKRVHVLIAIEAGNAASIALHRSQGFEECGTLKQVQKQFGRWLDLLFMQK 118

>ref|YP_003825004.1| GCN5-related N-acetyltransferase [Thermosediminibacter oceani
 DSM
 16646]
 gb|ADL07381.1| GCN5-related N-acetyltransferase [Thermosediminibacter oceani DSM
 16646]
 Length = 164

Score = 69.3 bits (168), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 49/161 (30%), Positives = 74/161 (45%), Gaps = 7/161 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVE- 65
 +R AT D+ ++ I N IE T P+T E W+ LER +RY LV E +
 Sbjct: 5 VREATLEDIPSITKIYNQGIEDRIATLETRPTEDEMRKWL--LER-GERYKVLVIEDDA 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125

G V G A + AR Y + ++Y+ + GLG L L+++ QGF +V
 Sbjct: 62 GKVHGWASLNVFNARCCYSGVSDISYIEREMRGKGLGKVLGSLIETARKQGFHKMVL 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166

+ N + L+ +LG+ GT G G W D+ +R
 Sbjct: 122 VFKENRIAKGLYRSLGFREVGTYEKHGLLDGKWVDITIMER 162

>ref|ZP_06538070.1| putative acetyltransferase [Salmonella enterica subsp. enterica
 serovar Typhi str. AG3]
 Length = 144

Score = 69.3 bits (168), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 48/130 (36%), Positives = 69/130 (53%), Gaps = 5/130 (3%)

Query: 17 DMAAVCDIVNH-YIETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAY 73

D AA+ +I N + T+ + N RT + W + + L YP LV+E GVV G A
 Sbjct: 7 DCAAITEIYNRAVLHTAAIWNDRVTDNRLAWYEARQLLG--YPVLVSEENGVTGYAS 64

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPS 133

G W++ + + +TVE +VYV HQ GLG L + L+ G +VA I N S
 Sbjct: 65 FGDWRSFDGFRYTVESVYVHPAHQKGKGLGRKLLSRLIDEARRCGKHMVAGIESQNAAS 124

Query: 134 VRLHEALGYT 143

+RLH +LG+T
 Sbjct: 125 IRLHHSLGFT 134

>ref|ZP_03226282.1| acetyltransferase [Bacillus coahuilensis m4-4]
 Length = 134

Score = 69.3 bits (168), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 39/129 (30%), Positives = 68/129 (52%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR A D+ + +I N I T F T+ ++ +E ++YP +V E +G V
 Sbjct: 2 IRYAEEKDLPDLVEIYNEAIRTLNATFDTKESVEERKAWFSSYGEKYPLIVYEDQGVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129

G A P+ + AY TVE ++Y+S+ ++ G+G+ L +L+ + + F +V++ I
 Sbjct: 62 GYASLSPYNIKPAYRLTVELSIYISNAYRGKGIGNKLIVEILREGKIRAFHTVISGITGG 121

Query: 130 NDPSVRLHE 138

N SV LH+
 Sbjct: 122 NKGSVHLHK 130

>ref|YP_002785791.1| acetyltransferase [Deinococcus deserti VCD115]
 gb|AC046037.1| putative acetyltransferase [Deinococcus deserti VCD115]
 Length = 176

Score = 69.3 bits (168), Expect = 2e-10, Method: Compositional matrix adjust.
 Identities = 54/174 (31%), Positives = 80/174 (45%), Gaps = 5/174 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64

V +R A AD+ A+ +I N + +T ++ P + + W D + Q +P LVAE
 Sbjct: 5 VTVRRADRADVPAILEIYNEAVVNTTASYDLAPVSLESRLTWFD--HKQQAGWPVLVAEQ 62

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124

EG V A GP++ + Y TVE +VYV + G+G L LL + ++
 Sbjct: 63 EGRVVAWATYGPYRDKAGYAGTVEHSVYVHAGGRGGGIGRALMAALLADARERSLHVMLG 122

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPPRPVR 178

VI N S+R HE G+ G L G K W D + Q + AP +R
Sbjct: 123 VIDAENAASIRFHENFGFVVVGRSLSQVGRKFDRWLDTVYMLQLMQTEAPTTSLR 176

>ref|ZP_03697450.1| GCN5-related N-acetyltransferase [Lutiella nitroferrum 2002]
gb|EEG09936.1| GCN5-related N-acetyltransferase [Lutiella nitroferrum 2002]
Length = 176

Score = 68.9 bits (167), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 44/158 (27%), Positives = 78/158 (49%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGP 76
AA+ DI N I ST + +P+ + + E + + +P + V + +G +

Sbjct: 16 AAILDIFNDAIVNSTALYDYKPRPAESMVSWFETKRKGFPVIGVEDSDGQLLAFGSYST 75

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++A A+ ++VE +VYV ++ GLG+T+ L+ + +++ I N S+ L

Sbjct: 76 FRAWPAFKYSVEHSVYVHKDYRGQGLGNTVMKALIAAARQNDVHAMMGIDASNAGSIAL 135

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
HE LG+ TL G+K G W D+ F+Q + P P

Sbjct: 136 HERLGFKHVATLPEVGFKFGRWLDLAFYQLLLDTPHTP 173

>ref|ZP_02906179.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MEX-5]
gb|EDT42716.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria MEX-5]
Length = 182

Score = 68.9 bits (167), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 51/158 (32%), Positives = 77/158 (48%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-GVVAGIAYAGP 76
AA+ +I+N I ST + P+ P+ + + +P + A E G + G A G

Sbjct: 22 AAILEILNDAIVNSTALYDYRPRPPEAMVTFATKRASGFPVVGAVDESGTLVGFASWGT 81

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
++A A+ +TVE +VYV H+ GLG L L++ +V + N SV L

Sbjct: 82 FRAFPAPFKYTVESVYVHRDHRGRGLGELLRELIRRAREADVHVLVGCVDAAANGGSVAL 141

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
H LG+ GT+ AG+K G W D F+Q + PA P

Sbjct: 142 HTRLGFVHSGTITEAGFKFGRWLDAAFYQLKLDTPAQP 179

>ref|ZP_00238331.1| acetyltransferase, GNAT family [Bacillus cereus G9241]
gb|EAL13939.1| acetyltransferase, GNAT family [Bacillus cereus G9241]
Length = 124

Score = 68.9 bits (167), Expect = 2e-10, Method: Compositional matrix adjust.
Identities = 39/123 (31%), Positives = 69/123 (56%), Gaps = 1/123 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+ + DI N I +T + +P T + ID E+ + D YP V E++ V

Sbjct: 2 IREATEKDVIYILDYINDAILNTTAVYTYKPVTLNLRIDWYEQKKADGYPIFYVELDNKV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A GP++A AY +++E +VYV +++ G+G++L L+ + + + +++A I

Sbjct: 62 VGFATFGPFRAWPAYKYSIEHSVYVDKEYRKCIGTSLIKELITIAKEREYMTLIAGIDA 121

Query: 129 PND 131
N+

Sbjct: 122 ENE 124

>ref|ZP_02890613.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria IOP40-10]
 gb|EDT03812.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria IOP40-10]
 Length = 182

Score = 68.9 bits (167), Expect = 3e-10, Method: Compositional matrix adjust.
 Identities = 53/167 (31%), Positives = 80/167 (47%), Gaps = 2/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVE-GV 67
 I + A AA+ +I+N I ST + P+ P+ + + +P + A E G
 Sbjct: 13 IDCSEAEHAAAILEILNDAIVNSTALYDYRPRPPEAMVTFATKRASGFPVVGAVDESGT 72

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A G ++A A+ +TVE +VYV H+ GLG L L++ +V +
 Sbjct: 73 LVGFASWGTFRAFPAPFKYTVESVYVHRDHRGRGLGELLLRELIRRAREADVHVLVGCVD 132

Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 N SV LH LG+ GT+ AG+K G W D F+Q + PA P
 Sbjct: 133 ATNGGSVALHTRLGTFVHSGTITEAGFKFGRWLDAAFYQLRLDTPAQP 179

>ref|ZP_08079389.1| acetyltransferase, GNAT family [Succinatimonas hippei YIT 12066]
 gb|EFY06168.1| acetyltransferase, GNAT family [Succinatimonas hippei YIT 12066]
 Length = 197

Score = 68.9 bits (167), Expect = 3e-10, Method: Compositional matrix adjust.
 Identities = 54/175 (30%), Positives = 80/175 (45%), Gaps = 2/175 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR ATA D AA+ +I YI+T + E + E I ++ + YP+LV E V
 Sbjct: 4 IRLATADDAALIEISKQYIDTP-ITLAYEVPPLAESIAKIDAISRSYPFLVVEDNKNVV 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G AYA + A W E ++ + G G + L+ + QG +V + +
 Sbjct: 63 GFAYAHRNLEQPAMSWNAELRAFIDLSQRGHGYGFVMMEVLLIDILRLQGVYINVYSSVTEG 122

Query: 130 NDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQD-FELPAPPRPVRPVTQI 183
 N S LH LG+ G + GYK+G W DV +R E+ P P P+ +I
 Sbjct: 123 NPRSESLHRKLGFDKTGVMHKTGYKNGRWLDVHLLERRILEVDGEPSPFIPLRI 177

>ref|ZP_08019786.1| phosphinothricin acetyltransferase [Lautropia mirabilis ATCC 51599]
 gb|EFV93739.1| phosphinothricin acetyltransferase [Lautropia mirabilis ATCC 51599]
 Length = 215

Score = 68.9 bits (167), Expect = 3e-10, Method: Compositional matrix adjust.
 Identities = 59/201 (29%), Positives = 78/201 (38%), Gaps = 48/201 (23%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-----QDRYPWLVA 62
 IRPA D+ A+ I N I TST + P +D ER+ + +P LVA
 Sbjct: 7 IRPARPDDLPAILAIFNDLIATSTAVYTETP-----VDLAERMAWFRARQEGGFPVLVA 60

Query: 63 EVEGV-----VAGIAYAGPWKAR-NAYDWT 87
 E G V G A GP++ Y TV
 Sbjct: 61 EETGTPDDRADDAQAQAVADQGEAASMAGGPQGANAGSRVLGYATFGPFRGSPVGYRHTV 120

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGL 147
 E +V+V + GLG+ L L +AQG +V I N S+RLH LG+ G
 Sbjct: 121 EHSVHVRQDQRGRGLGTALIQALFPLAQAGVHVMVGAIASNTGSLRLHARLGFVQTGL 180

Query: 148 LRAAGYKHGGWHDVGFQWQDF 168
 + G K G W D+ QR F

Sbjct: 181 MPQVGRKFGRWLDLALVQRTF 201

>ref|ZP_06458223.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas syringae pv. aesculi str. NCPPB3681]
 ref|ZP_06479138.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas syringae pv. aesculi str. 2250]
 Length = 180

Score = 68.9 bits (167), Expect = 3e-10, Method: Compositional matrix adjust.
 Identities = 56/177 (31%), Positives = 77/177 (43%), Gaps = 12/177 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
 IR A D+ + I N + +T + +P Q W R YP LVA +
 Sbjct: 5 IRDALPVDLPILAIYNDAVLNTTAIWNEQPVDLANRQAWY--AARQSQAYPILVAVDHA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G + G W+ + TVE +VYV + GLG L L++ +VA
 Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMASLIERARDCEKHMMVAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFE--LPAP----PRP 176
 I N S+ LHE LG+ G + G K G W D+ F Q D +PAP P+P
 Sbjct: 123 IESGNAASIALHERLGFKTTGMPQVGTGKFRWLDLTFMQLDLSPGVPAPASQAPKP 179

>ref|YP_003705558.1| GCN5-related N-acetyltransferase [Truepera radiovictrix DSM 17093]
 gb|ADI15015.1| GCN5-related N-acetyltransferase [Truepera radiovictrix DSM 17093]
 Length = 179

Score = 68.9 bits (167), Expect = 3e-10, Method: Compositional matrix adjust.
 Identities = 52/164 (31%), Positives = 73/164 (44%), Gaps = 7/164 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG- 66
 + +RPATAAD+ + I N I + F T ++P E LER Q +P LVAE G
 Sbjct: 11 LRVRPATAADLPCIRIYNEGIRSGRATFETRERSPGELSAWLERPQ--HPVLVAERGGN 68

Query: 67 ----VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 V G A P++ R Y E +VYV + G+GS L +++ E G +
 Sbjct: 69 AGGWTTVGWIAAAPYRPRACYGGVAEFSVYVGAEGRGVGSALMAAFVRACEDAGLWKL 128

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166
 VA + + N S L G+ G G W DV +R
 Sbjct: 129 VARVFVDNAASRALLYRHGFREVGVEKHAQLRGVWRDVVIVER 172

>ref|YP_772917.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria AMMD]
 gb|ABI86583.1| GCN5-related N-acetyltransferase [Burkholderia ambifaria AMMD]
 Length = 182

Score = 68.9 bits (167), Expect = 3e-10, Method: Compositional matrix adjust.
 Identities = 54/167 (32%), Positives = 80/167 (47%), Gaps = 2/167 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVE-GV 67
 I + A AA+ +I+N I ST + P+ P+ + + +P + A E G
 Sbjct: 13 IDCSEAEHAAAILEILNDAIVNSTALYDYRPRPPEAMVAWFATKRASGFPPVVGAVDESGT 72

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A G ++A A+ +TVE +VYV H+ GLG L L++ +V I
 Sbjct: 73 LVGFASWGTFRAFPAPFKYTVESVYVHCDHRGRGLGELLLRELIRRAREADVHVLVGCID 132

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPP 174
 N SV LH LG+ GT+ AG+K G W D F+Q + PA P

Sbjct: 133 ATNGGSVALHTRLGFVHSGTITDAGFKFGRWLDAAFYQLTLDTPAQP 179

>ref|ZP_05780962.1| phosphinothricin N-acetyltransferase [Citricella sp. SE45]
 gb|EEX14726.1| phosphinothricin N-acetyltransferase [Citricella sp. SE45]
 Length = 159

Score = 68.6 bits (166), Expect = 4e-10, Method: Compositional matrix adjust.
 Identities = 49/158 (31%), Positives = 74/158 (46%), Gaps = 4/158 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
 +RPA A+D AA+ + N +IET+ + F TE +T D+ R P + VAE G +
 Sbjct: 3 VRPANASDAAALEALWNPWIETTAITFSTELRTTDGIATDI---AARGPAFQVAEDAGTL 59

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 G A P++ Y T E TV +S + G G L + + QG S+ A +
 Sbjct: 60 LGFATFFPFRGGPGYARTKEHTVILSPEARGRGAGRALMDAIEEVARGQGVHSLFAGVSS 119

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N + H A+G+ L G+K G W D+ Q+
 Sbjct: 120 ENPAGIAFHAAIGFREARLPQVGWKFGRWMDLVLMQK 157

>ref|ZP_07006942.1| GCN5-related N-acetyltransferase [Pseudomonas savastanoi pv.
 savastanoi NCPPB 3335]
 gb|EFH97689.1| GCN5-related N-acetyltransferase [Pseudomonas savastanoi pv.
 savastanoi NCPPB 3335]
 Length = 180

Score = 68.2 bits (165), Expect = 4e-10, Method: Compositional matrix adjust.
 Identities = 56/177 (31%), Positives = 77/177 (43%), Gaps = 12/177 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
 IR A D+ + I N + +T + +P Q W R YP LVA +
 Sbjct: 5 IRDALPVDLPGLAIYNDVAVLNTTAIWNEQPVDLANRQVWY--AARQSQAYPILVAVDHA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125
 G V G + G W+ + TVE +VYV + GLG L L++ +VA
 Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMASLIERARDCEKHMMAV 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDQFE--LPAP----PRP 176
 I N S+ LHE LG+ G + G K G W D+ F Q D +PAP P+P
 Sbjct: 123 IESGNAASIALHERLGFKTTGMPQVGTGKFRWLDLTFMQLDLSPGVPAPASQAPKP 179

>ref|ZP_02161988.1| Phosphinothricin N-acetyltransferase [Kordia algicida OT-1]
 gb|EDP96262.1| Phosphinothricin N-acetyltransferase [Kordia algicida OT-1]
 Length = 166

Score = 67.8 bits (164), Expect = 5e-10, Method: Compositional matrix adjust.
 Identities = 42/160 (26%), Positives = 67/160 (41%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
 + EIR T D V DI N YI+ T + +T + +E+ +R V
 Sbjct: 3 KNTREIREITTTDYQTVADIYNEYIKLGTASMEETMKTSADVAGWIEKFHEREKLFVFTEH 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125
 +V G + R Y + E+ VY + G G+ + L+ + +K +VA
 Sbjct: 63 DIVIGWGIKRYSDREGYRFACETAVYFTESKLGKGYGTAMKKFLIVQCKQLQYKHLVAK 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 + N S+ +E LGYT G G+K+ W D+ Q
 Sbjct: 123 VFATNTGSIAYNEKLGYTIVGRQNQIGFKNNQWVDMIIMQ 162

>ref|YP_001186194.1| GCN5-related N-acetyltransferase [Pseudomonas mendocina ymp]
gb|ABP83462.1| GCN5-related N-acetyltransferase [Pseudomonas mendocina ymp]
Length = 166

Score = 67.8 bits (164), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 51/165 (30%), Positives = 74/165 (44%), Gaps = 6/165 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVA-EV 64
I A AD+ + I N ++ +T + + W+ ER +P LVA +
Sbjct: 4 SIVNAGEADLPGILAIYNDAVQHHTTAIWNETLVDLANRRRAWLA--ERTAAGFPVLVARDT 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
G V G A G W+ + TVE +VYV + GLG L L++ A +VA
Sbjct: 62 CGEVIGYASYGTWRTIQGFRHTVEHSVYVRADQRGQGLPALMQALIERARAANLHVMVA 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
I N S+RLH+ LG+ G + G K G W D+ F Q E
Sbjct: 122 AIESENAASIRLHQRLGFVTTGQMPQVGRKFGRWLDLTFMQLILE 166

>ref|YP_001279533.1| GCN5-related N-acetyltransferase [Psychrobacter sp. PRwf-1]
gb|ABQ93583.1| GCN5-related N-acetyltransferase [Psychrobacter sp. PRwf-1]
Length = 202

Score = 67.8 bits (164), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 46/164 (28%), Positives = 81/164 (49%), Gaps = 3/164 (1%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIET--STVNFRTEPQTP-QEWIDDLERLQDRY 57
+ + +P I+ ATAAD+ A+ +I N I T ST + + Q W D+ + R
Sbjct: 32 LDGQNQPFVIKLATAADLPAIVEIYNQSIITTKASTADLHSVTVADRQPFDEHYQHPTRP 91

Query: 58 PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
+++ +E V K+R+AYD + E ++YV + R LGS L T +++ +
Sbjct: 92 IYVLKNLEDDVMAWGSFSDVKRSAYDISSEISIYVGQQFHRRRLGSLLLTWMMQQAPSL 151

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
G ++++A+I N PS+ L G+ G L + G + D+
Sbjct: 152 GIQNILALIFGHNQPSIALFNKFGFEPWGRLPSVCDMQGFYADI 195

>ref|YP_002467454.1| GCN5-related N-acetyltransferase [Methanosphaerula palustris E1-9c]
gb|ACL17731.1| GCN5-related N-acetyltransferase [Methanosphaerula palustris E1-9c]
Length = 167

Score = 67.8 bits (164), Expect = 5e-10, Method: Compositional matrix adjust.
Identities = 45/155 (29%), Positives = 71/155 (45%), Gaps = 2/155 (1%)

Query: 14 TAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVA-EVEGVVAGIA 72
TA D A+ I NHYIE S F +P + + L YP + A + + + G
Sbjct: 13 TATDGPALIGIFNHYIEQSDAAFLDP-VSSAFFERLLPYLKIYPSVAARDDQRTLVGFG 71

Query: 73 YAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDP 132
P A+ T E T ++S G+GS + HL + G ++++A I N+
Sbjct: 72 MLRPHNQMPAFRHTAEVTCFISPDRTGQIGSRMLEHLETEGKKAGIRNLLACISSKNEG 131

Query: 133 SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 167
S+R H G+T G + AG K G + D + Q++
Sbjct: 132 SIRFHIRAGFTEVGRFKDAGKKWGAFFDTVWMQKE 166

>ref|ZP_01858609.1| hypothetical protein BSG1_03775 [Bacillus sp. SG-1]
 gb|EDL66441.1| hypothetical protein BSG1_03775 [Bacillus sp. SG-1]
 Length = 176

Score = 67.8 bits (164), Expect = 6e-10, Method: Compositional matrix adjust.
 Identities = 46/152 (30%), Positives = 66/152 (43%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR A D+ + I N IE TEP+ + L+ Q RY +VAE+EG V
 Sbjct: 17 IRKAEIRDIDRILTIYNQGIEDRVATLETEPKDRTYMAEWLKAHQGRYTGIVAELEGEVI 76

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A P+ R AY + +VY+ + G+G L + L GF +V
 Sbjct: 77 GWASLNYPSPRKAYAGVADISVYIERNSRGKGIGRKLSSLEVKAENGFKLVLFTHFPF 136

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 N +L++ GY GT + G G + DV
 Sbjct: 137 NKLGGQLYQKCGYREVGTGFKNQGILDGIYVDV 168

>gb|EFW78864.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas
 syringae pv. glycinea str. B076]
 gb|EFW86422.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas
 syringae pv. glycinea str. race 4]
 Length = 180

Score = 67.8 bits (164), Expect = 6e-10, Method: Compositional matrix adjust.
 Identities = 55/177 (31%), Positives = 77/177 (43%), Gaps = 12/177 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
 IR A D+ + +I N + +T + P Q W R YP L+A +
 Sbjct: 5 IRDALPDDLPGILEIYNDAVLNTTAIWNERPVDLANRQAWY--AARQSQAYPILLAVDHA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G + G W+ + TVE +VYV + GLG L L++ +VA
 Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMASLIERARDCEKHMMAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDQFE--LPAP----PRP 176
 I N S+ LHE LG+ G + G K G W D+ F Q D +PAP P+P
 Sbjct: 123 IESGNAASIALHERLGFKTTGQMPQVGTKFGRWLDLTFMQLDLSPGVPAPASQAPKP 179

>ref|ZP_01386326.1| GCN5-related N-acetyltransferase [Chlorobium ferrooxidans DSM
 13031]
 gb|EAT58800.1| GCN5-related N-acetyltransferase [Chlorobium ferrooxidans DSM
 13031]
 Length = 197

Score = 67.8 bits (164), Expect = 6e-10, Method: Compositional matrix adjust.
 Identities = 43/160 (26%), Positives = 68/160 (42%), Gaps = 2/160 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG- 66
 + + P T D A+ DI N Y E+ + TE E + + YP + A E
 Sbjct: 37 ISLEPVTLHDREAIIDIFNFYTESGFAAY-TESPLSYEMFESFVQFSSGYPAVTARDES 95

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 +V G P+ + A+ T E T ++ H + G+G + L + + G S++ I
 Sbjct: 96 IVVGFGLRPYSSIPAFSSAELTCFLKHGYTGRGIGKHILHCLEQKAQGMGITSILVSI 155

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ H G+T G L G K G DV + Q+
 Sbjct: 156 SSRNPGSIDFHRNNGFTECGRLTGVGKEKRGVRFDVVCYQK 195

```
>ref|YP_003840370.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor
obsidiansis
      OB47]
gb|ADL42384.1| GCN5-related N-acetyltransferase [Caldicellulosiruptor obsidiansis
      OB47]
      Length = 122
```

Score = 67.8 bits (164), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 35/110 (31%), Positives = 55/110 (50%)

```
Query: 56 RYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
      RYP VAE + G Y P+ + AY TVE T+Y+ ++ G+G + L+K +
Sbjct: 10 RYPIYVAEENSTILGYGYLSPFSEKEAYSITVEDTIYIHPLYRGRGIGKQILKFLIKRAK 69
```

```
Query: 116 AQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
      G +++A + N S+ LH++ G+ G L G K G + DV Q
Sbjct: 70 DTGAANIIAKVCAENCM SLHLHKSFGFVEVGKLT KVGSKFGRFLDVIIQ 119
```

```
>ref|YP_003696266.1| GCN5-related N-acetyltransferase [Starkeya novella DSM 506]
gb|ADH91647.1| GCN5-related N-acetyltransferase [Starkeya novella DSM 506]
      Length = 162
```

Score = 67.8 bits (164), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 50/163 (30%), Positives = 75/163 (46%), Gaps = 7/163 (4%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR----YPWLVAEVE 65
      +R A AD+ + I N+ + ST + TP + L L+DR YP +VAE
Sbjct: 3 LRDAVDADLP GILAIYNYAVLNSTAIWN---DTPTDLSGRLGWLDRDQAKSYPVIVAEAA 59
```

```
Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
      G V G A G ++ + +VE +VYV+ Q GLG L L + A G K ++
Sbjct: 60 GEVLGYASF GDFRPFEGFRISVEHSVYVAEHAQGRGLGRRLVEALFEPARAIGKKVMIGG 119
```

```
Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ RDF 168
      I N+ S+ LH LG+ + G K G D+ Q++
Sbjct: 120 ITAGNEASLALHTKLGFVQSAYMPGIGIKFGNRLDLVLMQKEL 162
```

```
>ref|ZP_05843895.1| GCN5-related N-acetyltransferase [Rhodobacter sp. SW2]
gb|EEW25127.1| GCN5-related N-acetyltransferase [Rhodobacter sp. SW2]
      Length = 162
```

Score = 67.8 bits (164), Expect = 6e-10, Method: Compositional matrix adjust.
Identities = 49/160 (30%), Positives = 75/160 (46%), Gaps = 5/160 (3%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQT---PQEWIDDLERLQDRYPWLVAEVEG 66
      IR A AAD+ A+ N I + V F + ++ Q+ +DD + + +LVAE G
Sbjct: 2 IRAAVAADLPAILGFWNPLIRDTLVTFSSAQKSLADMQKMLDD--KAAEGRAFLVAEAAAG 59
```

```
Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
      V G G ++A N Y T+E T+ + GLG L T + +G S++A +
Sbjct: 60 AVVGFCSYGQFRAGNGYAHTMEHTIILDPAVHGRGLGRALLTGIEADARTKGAHSILAGV 119
```

```
Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ R 166
      N S H A+GY + AG+K G W D+ Q+
Sbjct: 120 SGGNPESRAFHAAMGYGDPIIVPQAGWKFGRWWDLWLMQK 159
```

```
>ref|ZP_06064160.1| acetyltransferase [Acinetobacter johnsonii SH046]
gb|EEY95241.1| acetyltransferase [Acinetobacter johnsonii SH046]
      Length = 168
```

Score = 67.8 bits (164), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 44/159 (27%), Positives = 74/159 (46%), Gaps = 3/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGV- 67
IR AT D+ + +I N + + + L Q +++P+ V E + +
Sbjct: 5 IRLATEHDLPEIQNIYNAEVLHGMATWNEHAYDLAHFQKQLLHFQQNQFPFCVVEDQEMQ 64

Query: 68 -VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
+AG A ++ + Y +TVE ++Y+S + R GLG L +L++ + Q +VA I
Sbjct: 65 AIAGFADYATFRNFSGYRYTVEHSIYISPNYARQGLGQQLLAYLIEQAKLQQMHVMVAGI 124

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
N S+ LHE G+ G + G K G W D+ Q
Sbjct: 125 DHANLASIALHEKFGFVQTGYMPQVGQKFGQWRDLVLMQ 163

>ref|ZP_04635815.1| hypothetical protein yinte0001_16760 [Yersinia intermedia ATCC 29909]
gb|EEQ19936.1| hypothetical protein yinte0001_16760 [Yersinia intermedia ATCC 29909]
Length = 162

Score = 67.8 bits (164), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 48/159 (30%), Positives = 74/159 (46%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ +R D AV I I T F+TE + +W +D Q RY VA ++G
Sbjct: 1 MHVREMAENDWFAVSTIYQDGIHTGHATFQTESPSWHDW-NDSHMDQCRY---VALIDGK 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G + R+AY E ++YV+ + G+G L +H++ + EA G +++A I
Sbjct: 57 IEGWIALSAFSAKRHAYRGVAEVSIVVNPQISGQIGYRLMSHVINASEAVGIWTLIAGIF 116

Query: 128 LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+RLHE G+ G G G W DV +R
Sbjct: 117 PENTGSIRLHEKSGFRVIGIREKVGEMRGVWRDVMLMER 155

>ref|ZP_06496516.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae FF5]
Length = 180

Score = 67.4 bits (163), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 55/177 (31%), Positives = 76/177 (42%), Gaps = 10/177 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
IR A D+ + DI N + +T + +P Q W R YP LVA +
Sbjct: 5 IRDALPDDLPGILDIYNDVAVLNTTAIWNEQPVDLANRQAWY--AARQSQAYPILVAVDNA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125
G V G + G W+ + TVE +VYV + LG L L++ +VA
Sbjct: 63 GDVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKRLGPRLMAALIERARDCDKHMMVAA 122

Query: 126 IGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFELPAPPRPVPRVPTQ 182
I N S+ LH+ LG+ G + G K G W D+ F Q D A P PV+Q
Sbjct: 123 IESGNAASIALHDLRGFKTTGQMPQVGTKFGRWLDLTFMQLDLSPGAQP----PVSQ 175

>ref|YP_003997004.1| gcn5-related N-acetyltransferase [Leadbetterella byssophila DSM 17132]
gb|ADQ16651.1| GCN5-related N-acetyltransferase [Leadbetterella byssophila DSM

17132]
Length = 163

Score = 67.4 bits (163), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 43/146 (29%), Positives = 67/146 (45%), Gaps = 4/146 (2%)

Query: 21 VCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKAR 80
+ +I I T F+ E + +EW D L LVA +EG + G A P +R
Sbjct: 14 IVEIYLQGISTQIATFQNEAPSWEW--DKSHLSSCR--LVALLEGKICGWAALSPVSSR 69

Query: 81 NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPSVRLHEAL 140
Y E ++Y+ H+ G+G L L+ E +G ++ + I N PS++LHE+
Sbjct: 70 CVYSGVAEVSIIYQEHKGKIGKALLHELIHQSEKEGIWTLQSSIFSENLPISIKLHESC 129

Query: 141 GYTARGTLRAAGYKHGGWHDVGFWR 166
G+ G G K+G W D +R
Sbjct: 130 GFRMVGyreKIGLKNVWKNVLMER 155

>ref|YP_502905.1| GCN5-related N-acetyltransferase [Methanospirillum hungatei JF-1]
gb|ABD41186.1| GCN5-related N-acetyltransferase [Methanospirillum hungatei JF-1]
Length = 166

Score = 67.4 bits (163), Expect = 7e-10, Method: Compositional matrix adjust.
Identities = 41/155 (26%), Positives = 69/155 (44%), Gaps = 1/155 (0%)

Query: 14 TAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAY 73
T +D V + N+YIE + F P P + D L + ++YP + + G + G
Sbjct: 13 TESDKPEVIALFNYYIEHTNAAFLESP-LPSSYFDVLLPVIEQYPSVSVKENGALIGFGL 71

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPNDPS 133
P A+ T + ++ + G+GS + L++ +G +S++A I N S
Sbjct: 72 LRPHNPMPAFRNTAVISYFLDPAYTGKIGSKMLNFLIEKAREKGIRSILAEISSLNPGS 131

Query: 134 VRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168
VR HE G+ RG G K+G D + Q+
Sbjct: 132 VRFHEKNGFIHRGRFERVGVKNGKEFDTIWMQKSL 166

>ref|ZP_07048308.1| phosphinothricin N-acetyltransferase [Lysinibacillus fusiformis
ZC1]
gb|EFI70169.1| phosphinothricin N-acetyltransferase [Lysinibacillus fusiformis
ZC1]
Length = 163

Score = 67.4 bits (163), Expect = 8e-10, Method: Compositional matrix adjust.
Identities = 46/151 (30%), Positives = 67/151 (44%), Gaps = 4/151 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR D+ V I IET F T + Q W D+ R+ VAE V
Sbjct: 6 IRKMENKDLQKVLKIYKEGIETGMATFETIVPSEQVW-DERHHATLRF---VAEEHNRVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G P R+ Y E +VY+S ++ G+ S L+ L++ E GF ++ + I
Sbjct: 62 GWIAISPVSTRSVYSGVGEVSVYISSDYKNGIASKLKFVLIIESEKAGFWTLQSSIFAI 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
N S++LH+ +G+ GT HG WHD
Sbjct: 122 NASSIQLHKKMGFRVVGTRKIAQLHGQWHD 152

>ref|ZP_08206859.1| sortase [Gordonia neofelifaecis NRRL B-59395]
gb|EGD53303.1| sortase [Gordonia neofelifaecis NRRL B-59395]

Length = 168

Score = 67.4 bits (163), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 51/160 (31%), Positives = 75/160 (46%), Gaps = 4/160 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVAEVEGV- 67
IRPAT D A+ DI HY+E S F + T EW L + + P+LV E +
Sbjct: 4 IRPATDDDCDAIADIYRHVENS VATFDLDSMTVDEWRVKLASIIESGRPFLLVVESDDGS 63

Query: 68 --VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VAV 125
V G AY G ++ + ++WT E ++Y+ G+GS L LL + + ++V+AV
Sbjct: 64 HDVLGYAYLGVYRGKAGWNWTAEDSIYLRPEAAGRIGSRLLRELLDAADPAVTRTVMVAV 123

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
I SV LH +G+ G G K W + Q
Sbjct: 124 ISDEVPEVALHRKVGFEVGRSPGVGRKFDRWIGCVYLQ 163

>ref|YP_785269.1| N-acetyltransferase [Bordetella avium 197N]
emb|CAJ48349.1| probable N-acetyltransferase [Bordetella avium 197N]
Length = 180

Score = 67.0 bits (162), Expect = 9e-10, Method: Compositional matrix adjust.
Identities = 61/182 (33%), Positives = 87/182 (47%), Gaps = 11/182 (6%)

Query: 1 MSPERRPVEIRPATAAD-MAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDR 56
MS V + T A+ AA+ DI+N I ST + P+ P W +
Sbjct: 1 MSASHAEVRLIDCTEAHSAAML DILNDAIVNSTALYDYHPRPPSAMA AWF--AAKRAGG 58

Query: 57 YPWLVAEVEGVVAGIAYA--GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-S 113
YP +V V+G +A+A G ++A A+ +TVE ++YV + GLG L L++ +
Sbjct: 59 YP-VVGAVDGEGRLLAFASWGVFRAPAFKYTV EHSIYVHGDQGRGLGGLLLRELIRRA 117

Query: 114 MEAQGFKS VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ R D F E L P A P 173
EAQ +V I N S+ LHE LG+ GTL G+K G W D F+Q P
Sbjct: 118 CEAQ-VHVLVGCIDASN RGSIALHEKLGFKHSGT L S Q V G F K F G R W L D A S F Y Q L T L T T P E E 176

Query: 174 PR 175
PR
Sbjct: 177 PR 178

>gb|ADZ76815.1| GCN5-related N-acetyltransferase [Sphingobacterium sp. 21]
Length = 163

Score = 67.0 bits (162), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 50/160 (31%), Positives = 77/160 (48%), Gaps = 6/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E+R D AV I I T F+TE + ++W D + R+ +A ++G
Sbjct: 1 MELRTMNDTDWPAVRTIYLQGIATGQATFQTEAPSWEDW-DGSHLKRSRF---IASIDGH 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIG 127
+AG A P +R Y E +VY+ ++ G+GS L L++S E QG ++ + I
Sbjct: 57 IAGWAALSPVSSRCVYAGVAEVS VYIHEDYRGKGVGSFLMNALVESSEKQGLWTLQSGIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGG-WHDVGFQWQR 166
N+ S+RLHE G+ G G KHG W D +R
Sbjct: 117 PENEASIRLHEKHGFRQLGYREKVG-KHGNTWRD T T L M E R 155

>ref|YP_001532082.1| GCN5-like N-acetyltransferase [Dinoroseobacter shibae DFL 12]
gb|ABV92481.1| GCN5-related N-acetyltransferase [Dinoroseobacter shibae DFL 12]

Length = 161

Score = 67.0 bits (162), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 48/153 (31%), Positives = 70/153 (45%), Gaps = 1/153 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
IRPAT D A + + + I +TV F + +T + L P+LVA G V
Sbjct: 2 IRPATQDDAAQIAALWSALIRDTTVTFNSHEKTAADITALLADKAAADQPFLVALHAGRV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
AG A GP++ Y T+E ++ + + GLG L + L +G ++ A +
Sbjct: 62 AGFATYGPFRNGPGYARTIEHSILLDTAARGQGLGRGLMSALEDHARTRGMHTLWAGVSG 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N V H LG+ TLR GYK G W D+
Sbjct: 122 ENPAGVTFHRHLGFAEVATLREVGKFGRWIDL 154

>ref|ZP_05366549.1| phosphinothricin N-acetyltransferase [Corynebacterium
tuberculoostearicum SK141]
gb|EET76844.1| phosphinothricin N-acetyltransferase [Corynebacterium
tuberculoostearicum SK141]
Length = 196

Score = 66.6 bits (161), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 49/152 (32%), Positives = 77/152 (50%), Gaps = 3/152 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL-QDRYPWLVAEVE-GV 67
IRPA AD+ A+ + +N IE + V FRT P + E L + ++ P +AE + G
Sbjct: 35 IRPAGLADVPAMTETLNWAIETDVFIRTPASIAEREAYLRHIWEEGCPFCFIAESDSGA 94

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVAVI 126
G A P++ + E+T+Y+S Q G+G+ L L+ + A S++A+I
Sbjct: 95 YLGWALYHPYRDPQVWTGCVETIYLSPTAQGGVGTALLGALVDAARADTKVHSLALLI 154

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
N S++LHE G+ GTL+ YK W
Sbjct: 155 VSTNAASLKLHEKFGFENVGTLEKVCYKFDHW 186

>ref|ZP_07377158.1| GCN5-related N-acetyltransferase [Pantoea sp. aB]
gb|EFM21890.1| GCN5-related N-acetyltransferase [Pantoea sp. aB]
Length = 169

Score = 66.6 bits (161), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 50/160 (31%), Positives = 75/160 (46%), Gaps = 6/160 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVA-EVE 65
IR A +D + +I N + +T R + WI R Q +P +VA + +
Sbjct: 3 IRAAIESDADVIAEINYNDVAVLNTTAIWNESRVDVANRIAWIH--SRQQAGFPVIVATDND 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
V G A G W+ + Y TVE +VYV + + G+G L L++ +VA
Sbjct: 61 ESVLGYASFQDWRPQWGYRHTVEHSVYVHNHARGQGIGDALMRTLILQLACKSKKHVMVAG 120

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
I N S+ LH+ LG+T GT++ G K G W D+ F Q
Sbjct: 121 IESENVASITLHKKLGFTEAGTMKEVGNGKFGRWLDLTFMQ 160

>ref|ZP_00958271.1| putative acetyltransferase, GNAT family protein [Roseovarius
nubinihibens ISM]
gb|EAP76733.1| putative acetyltransferase, GNAT family protein [Roseovarius

nubinhbens ISM]
Length = 161

Score = 66.6 bits (161), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 48/157 (30%), Positives = 78/157 (49%), Gaps = 1/157 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IRPATAAD A+ N I + V F + +TP++ D+ Q + + +LV E++G
Sbjct: 2 IRPATAADAEIAAFWNPQIRDTLVTFNSIEKTPEDIARDIAAKQGGHGLVTEIDGAT 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A G ++ Y ++E T+ + R Q G+G L LL G ++A +
Sbjct: 62 LGFASYGQFRGGIGYAQSMEHTIILDPRAGRGVGRGLMAALLDHARDAGVHVMMAGVCA 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
ND +R HEA+G+ + G+K+G + D+ Q
Sbjct: 122 ENDGGLRFHEAMGFAEVAQVPEVGFKYGRYLDLVLQM 158

>ref|YP_003962714.1| N-acetyltransferase yncA [Ketogulonicigenium vulgare Y25]
gb|ADO41414.1| N-acetyltransferase yncA [Ketogulonicigenium vulgare Y25]
Length = 176

Score = 66.6 bits (161), Expect = 1e-09, Method: Compositional matrix adjust.
Identities = 49/171 (28%), Positives = 76/171 (44%), Gaps = 7/171 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTV---NFRTEPQTPQEWIDDLERLQDRYPWLVAEV 64
+ I T +D+ A+ I N + +T + + + W++ +R +P VA+
Sbjct: 5 MRILDGTESDLPAIVAIFNDAVVNTTAIWSVDLATVEARKTWME--QRRAGGFPPVFAKN 62

Query: 65 EG-VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMV 123
E V G A GP++ + + TVE +VYV + G+G L L+ G +V
Sbjct: 63 EADEVVGAFASYGPYPFDFGRLTVEHSVYVRPDQRGKGVGGKLLDALITHARGAGLHVMV 122

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF-ELPAP 173
I N S+ LHE G+ G L G K G W D+ F Q +LP P
Sbjct: 123 GGITADNAASITLHERRGFQQVGLLPQVGKFGRWLDLAFQLKLDDLPH 173

>ref|ZP_07714681.1| phosphinothricin acetyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
gb|EFQ80450.1| phosphinothricin acetyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
Length = 164

Score = 66.2 bits (160), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 49/152 (32%), Positives = 77/152 (50%), Gaps = 3/152 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL-QDRYPWLVAEVE-GV 67
IRPA AD+ A+ + +N IE + V FRT P + E L + ++ P +AE + G
Sbjct: 3 IRPAGLADVPAETETLNWAIEHTDVIFRTTPASIAEREAYLRHIWEEGCPCFIAESDSGA 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVMVAVI 126
G A P++ + E+T+Y+S Q G+G+ L L+ + A S++A+I
Sbjct: 63 YLGWALYHPYRDPQVWTGCTYETIYLSPPAAQGGVGTALLGALVDAARADTKVHSLALI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
N S++LHE G+ GTL+ YK W
Sbjct: 123 VSTNAASLKLHEKFGFENVGTLKEVCYKFDHW 154

>ref|YP_080971.1| putative phosphinothricin acetyltransferase [Bacillus licheniformis
ATCC 14580]

ref|YP_093400.1| YwnH [Bacillus licheniformis ATCC 14580]
 gb|AAU25333.1| putative phosphinothricin acetyltransferase [Bacillus licheniformis
 ATCC 14580]
 gb|AAU42707.1| YwnH [Bacillus licheniformis ATCC 14580]
 Length = 165

Score = 66.2 bits (160), Expect = 2e-09, Method: Compositional matrix adjust.
 Identities = 44/141 (31%), Positives = 73/141 (51%), Gaps = 3/141 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-- 65
 +++R A D+ AV DI N I + V TEP TP+E ++ + P +AE E
 Sbjct: 1 MKLRIANREDLPAVVDIYNSTIASRMVTADTEPVTPEERLNNWFLSHTEERPLYIAENEKR 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 +V I++ + R AY T E ++Y+ H+ G GS + L++ G +S++A
 Sbjct: 61 DIVGWISFES-FYGRPAYAKTAEVSIYLHEDHRGKGAGSAVLEKALEAAPKLGIRSLMAF 119

Query: 126 IGLPNDPSVRLHEALGYTARG 146
 I N+PS++L + G+T G
 Sbjct: 120 IFAHNEPSMKLFKKYGFTEWG 140

>ref|NP_786466.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum
 WCFS1]
 ref|ZP_07079398.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum
 subsp. plantarum ATCC 14917]
 ref|YP_003925929.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum
 subsp. plantarum ST-III]
 emb|CAD65337.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum
 WCFS1]
 gb|EFK28109.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum
 subsp. plantarum ATCC 14917]
 gb|ADN99835.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum
 subsp. plantarum ST-III]
 Length = 165

Score = 66.2 bits (160), Expect = 2e-09, Method: Compositional matrix adjust.
 Identities = 45/145 (31%), Positives = 73/145 (50%), Gaps = 7/145 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYP-WLVAE 63
 V +R AT +D+ + DI N I + V +P T ++ W L + YP W+V +
 Sbjct: 3 VSLRTATMSDLPIIVDIYNQTIPSHQVTADLKPVTVEQRRNWF--LSHTPEHYPLWVVVK 60

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + VV ++ + P+ R AY T E +VY+ Q G+GS + T + K + G +++
 Sbjct: 61 DDSVVGWVSL- PFYGRAAYAKTTEISVYLD RSVQGGIGSQVLTLPVKQLPVLGLTTII 119

Query: 124 AVIGLPNDPSVRLHEALGYTARGTL 148
 A I N PS++L + GY G L
 Sbjct: 120 AYIFSSNIPSIKLFKKFGYEQWGFL 144

>ref|ZP_07265426.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv.
 syringae
 642]
 Length = 180

Score = 66.2 bits (160), Expect = 2e-09, Method: Compositional matrix adjust.
 Identities = 52/169 (30%), Positives = 72/169 (42%), Gaps = 6/169 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVA-EVE 65
 IR A D+ + DI N + +T + +P Q W R YP LVA +
 Sbjct: 5 IRDAGPDDLPGILDIYNDVLTNTAIWNEQPVDLANRQAWY--AARQSQGYPI LVAVDSA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G + G W+ + TVE +VYV + LG L L++ +VA
 Sbjct: 63 GEVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKRLGPRMLAALIERARDCEKHMMAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
 I N S+ LH+ LG+ G + G K G W D+ F Q D A P
 Sbjct: 123 IESGNAASIALHDRLGFKTTGQMPQVGTKFGRWLDLTFMQLDLSPGAQP 171

>gb|EFW79832.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 glycinea str. B076]
 Length = 179

Score = 66.2 bits (160), Expect = 2e-09, Method: Compositional matrix adjust.
 Identities = 41/120 (34%), Positives = 64/120 (53%), Gaps = 1/120 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVV 68
 +R A D+ AV I ++ +F +P + E + + L + P+LVAE+ G V
 Sbjct: 7 LRDACDQDIPAVQAIYADHVLHGSISSFELDPPSVAELLQRRQVVLNGLPYLVAELAGEV 66

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G YA P++ R AY +TVE +VYV G+G L L++ E G++ +VAVIG+
 Sbjct: 67 VGYGYATPYRPRPAYRFTVEDSVYVRDGMGGRGIGLALLGELVQRCEQGWRQMVAVIGI 126

>ref|ZP_06884360.1| GCN5-related N-acetyltransferase [Clostridium lentocellum DSM
 5427]
 gb|EFG98260.1| GCN5-related N-acetyltransferase [Clostridium lentocellum DSM 5427]
 gb|ADZ82808.1| GCN5-related N-acetyltransferase [Clostridium lentocellum DSM 5427]
 Length = 165

Score = 65.9 bits (159), Expect = 2e-09, Method: Compositional matrix adjust.
 Identities = 41/158 (25%), Positives = 72/158 (45%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
 + T + AV +I +YI ST F + T QE + + +Y + + E +
 Sbjct: 5 KFEKITEEHVEAVREIYLYINNSTATFHKKEITTQEMSELVLFKNPKYESYIIKAEDI 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G +K R A+D T E T+Y+ + ++ G+G T + + + F ++VA+I
 Sbjct: 65 CGYVILTQYKTREAFDKTAEVTIYLKNGYEGKGIGKAITFIEERAKEKEFHTLVALICG 124

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ L E GY + G K W D+ +Q+
 Sbjct: 125 ENTGSIALFEKCGYIKCAHYKEVGKFNRLDLDSYQK 162

>ref|YP_003064133.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum
 JDM1]
 gb|ACT63436.1| phosphinothricin N-acetyltransferase [Lactobacillus plantarum JDM1]
 Length = 165

Score = 65.9 bits (159), Expect = 2e-09, Method: Compositional matrix adjust.
 Identities = 45/145 (31%), Positives = 73/145 (50%), Gaps = 7/145 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYP-WLVAE 63
 V +R AT +D+ + DI N I + V +P T++ W L + YP W+V +
 Sbjct: 3 VSLRTATMSDLPIIVDIYNQTIPSHQVTADLKPVTVEQRRNWF--LSHTPEHYPLWVVLK 60

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + VV ++ + P+ R AY T E +VY+ Q G+GS + T + K + G +++
 Sbjct: 61 DDSVVGWVSL-PPYGRAAYAKTTEISVYLDRSVQGGIGSQVLTLPKQLPVLGLTTII 119

Query: 124 AVIGLPNDPSVRLHEALGYTARGTL 148

A I N PS++L + GY G L

Sbjct: 120 AYIFSSNIPSIKLFKKFGYEQWGFL 144

>ref|XP_756087.1| GNAT family N-acetyltransferase [Aspergillus fumigatus Af293]
gb|EAL94049.1| GNAT family N-acetyltransferase, putative [Aspergillus fumigatus Af293]
Length = 220

Score = 65.9 bits (159), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 60/209 (28%), Positives = 89/209 (42%), Gaps = 39/209 (18%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA-EVE 65

+ IR AT D++ + I + Y+ S F +P + I +Q R P+ VA +

Sbjct: 3 IHIREATQDDISQIHTIYSFYVRESVATFLRQPPPLESLISSFREIQSRGLPYRVAIDTT 62

Query: 66 GVVAGIAYAGPWKA-RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG----- 118

G V G Y P+ R AY TVE ++YV + G+GS L + +L+S+E++

Sbjct: 63 GKVLGYGYLAPFNGTRMAYAPTVEVSLYVHPEYTSKGVGSRLSSILESVESEAGVWHRA 122

Query: 119 -----FKSVVAVI-----GLPNDPSVRL-HEALGYTARGTLRAAGY 153

++S V VI G N +R +E G+ RG L+ GY

Sbjct: 123 CEHKEYESHVQVIPEDGRVCSIIACMAVDTTGKENGEGLRKWYEQRGFVERGRLKNVGY 182

Query: 154 KHGGWHDVG--FWQPDFELPAPPRPVRPV 180

K G W D W F LP R + V

Sbjct: 183 KQGRWCDSLSILW--FSLPTDMRRIDTV 208

>gb|EDP55256.1| GNAT family N-acetyltransferase, putative [Aspergillus fumigatus A1163]
Length = 220

Score = 65.9 bits (159), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 60/209 (28%), Positives = 89/209 (42%), Gaps = 39/209 (18%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA-EVE 65

+ IR AT D++ + I + Y+ S F +P + I +Q R P+ VA +

Sbjct: 3 IHIREATQDDISQIHTIYSFYVRESVATFLRQPPPLESLISSFREIQSRGLPYRVAIDTT 62

Query: 66 GVVAGIAYAGPWKA-RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG----- 118

G V G Y P+ R AY TVE ++YV + G+GS L + +L+S+E++

Sbjct: 63 GKVLGYGYLAPFNGTRMAYAPTVEVSLYVHPEYTSKGVGSRLSSILESVESEAGVWHRA 122

Query: 119 -----FKSVVAVI-----GLPNDPSVRL-HEALGYTARGTLRAAGY 153

++S V VI G N +R +E G+ RG L+ GY

Sbjct: 123 CEHKEYESHVQVIPEDGRVCSIIACMAVDTTGKENGEGLRKWYEQRGFVERGRLKNVGY 182

Query: 154 KHGGWHDVG--FWQPDFELPAPPRPVRPV 180

K G W D W F LP R + V

Sbjct: 183 KQGRWCDSLSILW--FSLPTDMRRIDTV 208

>ref|NP_615734.1| phosphinothricin acetyltransferase [Methanosarcina acetivorans C2A]
gb|AAM04214.1| phosphinothricin acetyltransferase [Methanosarcina acetivorans C2A]
Length = 179

Score = 65.9 bits (159), Expect = 2e-09, Method: Compositional matrix adjust.
Identities = 43/164 (26%), Positives = 75/164 (45%), Gaps = 4/164 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNF---RTEPQTPQEWIDDLERLQDRY-PWLVAEVE 65

IR ATA D++ + ++ N+Y+E S + P+ Q + E ++ Y P+ V E
 Sbjct: 12 IREATAEDISGMLEVFNYVENSFAAYLETSVGPEFFQAVQSEKEEDENEYFPFYVIEER 71

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + GI P+ + T + ++ H R GLGS + L + +S++A
 Sbjct: 72 GKIIGIGTLRPYFPFPNFRHTGVVSYFILPGHTRKGLGSRMLDKLCTEAREKKMRSLLAN 131

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 + N+ S+ H G+ G R G K G + D+ + Q+ E
 Sbjct: 132 VSSKNEASLNFHLKHGFIIECGKFREVGTGFGYYFDIVWLQKFLE 175

>ref|YP_003194019.1| phosphinothricin N-acetyltransferase [Robiginitalea biformata
 HTCC2501]
 gb|EAR16240.1| phosphinothricin N-acetyltransferase [Robiginitalea biformata
 HTCC2501]
 Length = 163

Score = 65.9 bits (159), Expect = 3e-09, Method: Compositional matrix adjust.
 Identities = 49/159 (30%), Positives = 68/159 (42%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR D V I I T F T ++W +R + LVAE+ G
 Sbjct: 1 MQIRDMQPEDWHEVARIYEEGIATGYATFETRVPAYEDW---DRAHLPFGRLVAEISGQ 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 VAG A P R Y E +VYVS + G G L L+ E QG ++ + I
 Sbjct: 57 VAGWAALSPVSGRCVYGGVAEVSIVYSSAQRGKGTGKALLRKLIAESEQQGIWTLQSGIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+RLHEA+G+ G + G W D ++R
 Sbjct: 117 PQNAGSIRLHEAVGFRRLLGYREKIAKRDGIWQDNILFER 155

>ref|YP_276592.1| phosphinothricin N-acetyltransferase [Pseudomonas syringae pv.
 phaseolicola 1448A]
 gb|AAZ33393.1| phosphinothricin N-acetyltransferase, putative [Pseudomonas
 syringae pv. phaseolicola 1448A]
 Length = 180

Score = 65.5 bits (158), Expect = 3e-09, Method: Compositional matrix adjust.
 Identities = 54/177 (30%), Positives = 76/177 (42%), Gaps = 12/177 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVA-EVE 65
 IR A D+ + +I N + +T + P Q W R YP L+A +
 Sbjct: 5 IRDALPDDLPGILEIYNDVAVLNTTAIWNERPVDLANRQAWY--AARQSQAYPILLAVDHA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G + W+ + TVE +VYV + GLG L L++ +VA
 Sbjct: 63 GEVLGYSSFSWDRPFEGFRHTVEHSVYVRADQRGKGLPRLMASLIERARDCEKHMMAA 122

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE--LPAP----PRP 176
 I N S+ LHE LG+ G + G K G W D+ F Q D +PAP P+P
 Sbjct: 123 IESGNAASIALHERLGFKTTGQMPQVGTGFRWLDLTFMQLDLSPGVPAPASQSPKP 179

>ref|ZP_07388746.1| Phosphinothricin acetyltransferase [Paenibacillus curdolanolyticus
 YK9]
 gb|EFM09919.1| Phosphinothricin acetyltransferase [Paenibacillus curdolanolyticus
 YK9]
 Length = 166

Score = 65.5 bits (158), Expect = 3e-09, Method: Compositional matrix adjust.

Identities = 46/157 (29%), Positives = 72/157 (45%), Gaps = 5/157 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAEV 64
 +E+ AT D+ + DI N + + V EP T + +W ER P VA
 Sbjct: 5 LEVMNATEQDLPTIVDIYNSTVASRMVTADLEPVTVESRMKWFH--ERDWATRPIWVARQ 62

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 G + G P+ AR AY T E ++Y+ ++ G+G L H L+ + G K+++
 Sbjct: 63 GGQIVGWVSFQPPYYAREAYRATAELSIYIGSDYRGSGIGGALLEHALRGCDKLGKTLIG 122

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 ++ N+PS+RL G+ G L A G DV
 Sbjct: 123 LVFGHNEPSLRLLAKFGFQQWGLLPGACELDGIERDV 159

>ref|YP_003650967.1| GCN5-related N-acetyltransferase [Thermobispora bispora DSM 43833]
 gb|ADG87074.1| GCN5-related N-acetyltransferase [Thermobispora bispora DSM 43833]
 Length = 177

Score = 65.5 bits (158), Expect = 3e-09, Method: Compositional matrix adjust.
 Identities = 51/160 (31%), Positives = 72/160 (45%), Gaps = 4/160 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV-EG 66
 + IRP D A V I ++ F T T + + D +L R+ ++ A+ G
 Sbjct: 14 ILIRPMRETDAAQVLAIYQAGLDGGNAGFETTAPTWEAF--DAAKLP-RHRYVAADTASG 70

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 126
 V G A R Y VE +VYV H G+G L L++S EA+G ++ A +
 Sbjct: 71 QVVGWVAASAVSDRCVYAGVVEDSVYVHPDHGGRGIGLALLNALIRSTEAEGIWTIQAGV 130

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+RLHE G+ GT G HG W DV +R
 Sbjct: 131 FPENTASLRLEKAGFRVVGTRHRIGRHHGRWRDVILLER 170

>ref|YP_002778658.1| acetyltransferase [Rhodococcus opacus B4]
 dbj|BAH49713.1| putative acetyltransferase [Rhodococcus opacus B4]
 Length = 162

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 73/160 (45%), Gaps = 4/160 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 V +R A D AV I + I T F T+ T E +D R D + W VAEV+G
 Sbjct: 3 TVAVRRLDATDWDVAVLRIYSEGIATRRATFDTQTPTRSE-LD--ARWLDGHRW-VAEVDG 58

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 126
 VAG A P +R + E++VY + + +G+G+ L L+ + G ++ A +
 Sbjct: 59 TVAGWATLSPVSSRRCFRGVAENS VYTAGFEFRGVGVTALMRRLIDEADFSGIWTLQASV 118

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ LH A+GY G G WHD +R
 Sbjct: 119 LAVNAGSIALHHAVGYRTVGMRRERLAQIDGVVHDSVLLER 158

>ref|YP_001118910.1| GCN5-related N-acetyltransferase [Burkholderia vietnamiensis G4]
 gb|ABO54075.1| GCN5-related N-acetyltransferase [Burkholderia vietnamiensis G4]
 Length = 182

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 50/158 (31%), Positives = 76/158 (48%), Gaps = 2/158 (1%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVA-EVEGVVAGIAYAGP 76
 AA+ +I+N I ST + P+ P+ + + +P + A + G + G A G
 Sbjct: 22 AAILEILNDAIVNSTALYDYRPRPPEAMVTFATKRAGGFPVVGAVDGSGLTLLGFASWGT 81

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
 ++A A+ +TVE +VYV H+ GLG L L+K +V I N SV L
 Sbjct: 82 FRAFPAPKYTVEHSVYVHRDHRGRGLGELLLLRELKRRARDAEVHVLVGCIDATNAGSVAL 141

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAPP 174
 H +G+ GT+ AG+K G W D F+Q + P P
 Sbjct: 142 HTRVGFVHSGTIAEAGFKFGRWLDAAFYQLKLDTPMQP 179

>ref|ZP_01447778.1| phosphinothricin N-acetyltransferase [alpha proteobacterium
 HTCC2255]
 gb|EAU51960.1| phosphinothricin N-acetyltransferase [alpha proteobacterium
 HTCC2255]
 Length = 162

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 40/159 (25%), Positives = 73/159 (45%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR +D +V I I+T F+ + + EW + R +VAE+
 Sbjct: 1 MKIRNFKKSDFTSVKSIYQQGIDTGNATFQKKAKGWNEWNSSF-LITCR---IVAELNNE 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G A R Y+ E ++Y++ + G+G++L + L+ + E +G ++ A I
 Sbjct: 57 VVGWAALSAASNRTVYNGVAEVSIIYAKNYANYGIGNSLSELISTSENEGIWTLQAGIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 N+ S+ +H G+ G G +G W D+ F +R
 Sbjct: 117 PENESSIAHKSNGFKIIGVREKLGMNGAWRDILFMER 155

>ref|YP_001196742.1| GCN5-related N-acetyltransferase [Flavobacterium johnsoniae
 UW101]
 gb|ABQ07423.1| GCN5-related N-acetyltransferase [Flavobacterium johnsoniae UW101]
 Length = 168

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 47/161 (29%), Positives = 74/161 (45%), Gaps = 4/161 (2%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
 + +EIR + V I I+T F+T + ++W D L+ +V + +
 Sbjct: 6 KNMEIRKLSDKHWDQVKIYQKGIDTGNATFQTSAPSWEDW--DQSHLKSCR--VVMQED 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G A P +R Y E +VY+ H G+G TL L++ EA+G ++ A
 Sbjct: 62 GKVIGWAALTPVSSRCVYAGVAEVSVMYDPSSHSGKIGLTLNELLVLRQSEAEGIWTLQAG 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 I N S+R+HE G+ GT G ++G W D +R
 Sbjct: 122 IFPENTASLRIHEKAGFRILGTREKIGKQNGIWRDTALLER 162

>ref|YP_100962.1| putative acetyltransferase [Bacteroides fragilis YCH46]
 dbj|BAD50428.1| putative acetyltransferase [Bacteroides fragilis YCH46]
 Length = 177

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 41/160 (25%), Positives = 71/160 (44%), Gaps = 1/160 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV-EG 66
 + +R T D+ V DI ++Y +TV + + E + + Y + E EG
 Sbjct: 8 ITLRTLTLTENDLPFVKDIYDYTLHTTVVYFVHCASIDELKNYIPVGDPVYRSFIETPEG 67

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 G Y +K R A+ +VE T+Y+ G G L + + +GF +++A+I
 Sbjct: 68 APCGFCYFARFKPREAFRISVELTLYLKPEFTGRGYGKQAILRLEEIIIRQEGFSNIMALI 127

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N+ S+RL E G+ +R K G D+ +Q+
 Sbjct: 128 SGENEASIRLFEKCGFECCANIRQVAEKFGKKLDLKMYYK 167

>ref|YP_003085267.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM 18053]
 gb|ACT92102.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM 18053]
 Length = 165

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 49/157 (31%), Positives = 71/157 (45%), Gaps = 4/157 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP T AD + V I I+T + TE P+ +D L+ P LV E G V
 Sbjct: 5 IRPLTEADWSQVKQIYQLGIDTGDATYETE--APE--VDVLKAKFLAEPQLVVEENGQVI 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A+ +R Y E+++Y+ G+G L + L+ E GF ++ A I
 Sbjct: 61 GWAFLSAVSSRCVYGGVAETSIYIHPEFHGRGVGRALLSDLVPLSEKLGFWTLQAQIFPE 120

Query: 130 NDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N S+ LHE G+ G G ++G W DV +R
 Sbjct: 121 NKASIALHERYGFVKVGYREKLGKRNGIWRDVILLER 157

>ref|YP_003191605.1| GCN5-related N-acetyltransferase [Desulfotomaculum acetoxidans DSM 771]
 gb|ACV62982.1| GCN5-related N-acetyltransferase [Desulfotomaculum acetoxidans DSM 771]
 Length = 163

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
 Identities = 40/154 (25%), Positives = 68/154 (44%), Gaps = 2/154 (1%)

Query: 14 TAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL-VAEVEGVVAGIA 72
 + D V DI NHYIE S + E + ++ + R+ + YP + V G + G A
 Sbjct: 9 SNEDRKPVIDIFNHYIENSFAAY-FENKVSYDFNFGFMRISEGYPRIAVKSNNGELIGFA 67

Query: 73 YAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDP 132
 P+ + T + ++ H R G+G ++ +L+ + G S++A I N+
 Sbjct: 68 LLRPYNPIPTFRRTAVISYFIKPTHIRKGIGKSILENLIGKAKEMGIDSILASISSLNEI 127

Query: 133 SVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 S+ H G+ G L G+K G D Q+
 Sbjct: 128 SINFHLKNGFMKCGVLSKVGHKFGKDFDEILMQK 161

>ref|ZP_01059494.1| phosphinothricin N-acetyltransferase [Leeuwenhoekiella blandensis MED217]
 gb|EAQ51326.1| phosphinothricin N-acetyltransferase [Leeuwenhoekiella blandensis MED217]
 Length = 163

Score = 65.1 bits (157), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 45/157 (28%), Positives = 69/157 (43%), Gaps = 4/157 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IRP D V I + I+T F TE + W ++ LVA+ + +A
Sbjct: 5 IRPFKPEDYPEVAKIYHAGIDTQIATFETEAPDFEAWNLRFCVKVCR----LVAQFDNEIA 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G A R Y E TVYV+ +HQ +G L L+++ E +GF ++ A I
Sbjct: 61 GWAALSLVSKRQVYHGAEVTVYVAPQHKGKIGFQLLEALIQASEQEGFWTLTAHIFPQ 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
N S+ +H+ LG+ G ++G W D +R
Sbjct: 121 NKASIHVHQKLGFRLLGIHEKIAKRNGKWQDNALLER 157

>ref|ZP_05122029.1| phosphinothricin acetyltransferase [Rhodobacteraceae bacterium
KLH11]
gb|EEE36661.1| phosphinothricin acetyltransferase [Rhodobacteraceae bacterium
KLH11]
Length = 162

Score = 64.7 bits (156), Expect = 4e-09, Method: Compositional matrix adjust.
Identities = 47/160 (29%), Positives = 75/160 (46%), Gaps = 4/160 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEG 66
+ IR AT D A+ I N I ++ F T+ ++ + D+ R P +LVAE+
Sbjct: 1 MSIRQATIKDAPAIAAISNSVIGDTLITFTTDLRSTENVAADI---HTRGPAFLVAEIGD 57

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+AG A GP+++ Y E ++ ++ + + G+G TL L A +VA I
Sbjct: 58 TIAGYATYGPFRSGPGYAQCKEHSIALTPQARGQGVGRTLMAALEGRARADNVHVLVACI 117

Query: 127 GLPNDSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
N +V H ALG+T G + G K G D+ Q+
Sbjct: 118 SSANPQAVAFHLALGFTQVGQMPEVGLKWGQRLDLVLMQK 157

>ref|ZP_04586796.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. oryzae
str. 1_6]
Length = 180

Score = 64.7 bits (156), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 49/164 (29%), Positives = 70/164 (42%), Gaps = 6/164 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVE 65
IR A D+ + I N + +T + +P Q W R YP L+A +
Sbjct: 5 IRDALPGDLPILAIYNDAVLNTTAIWNEQPVDLANRQAWY--ASRQAQGYPIIIAIDSA 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G + G W+ + TVE +VYV + GLG L L++ +VA
Sbjct: 63 GDVLGYSSFGDWRPFEGFRHTVEHSVYVRADQRGKGLGPRLMAALIERARTCDKHHMVAA 122

Query: 126 IGLPNDSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFE 169
I N S+ LH+ LG+ G + G K G W D+ F Q D
Sbjct: 123 IESGNAASIALHDLRGFKITGMPQVGTKFGRWLDLTFMQLDLS 166

>ref|ZP_03489074.1| hypothetical protein EUBIFOR_01660 [Eubacterium biforme DSM 3989]
gb|EEC89704.1| hypothetical protein EUBIFOR_01660 [Eubacterium biforme DSM 3989]
Length = 318

Score = 64.7 bits (156), Expect = 5e-09, Method: Compositional matrix adjust.

Identities = 40/153 (26%), Positives = 68/153 (44%), Gaps = 1/153 (0%)

```
Query: 9   EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
          E+R   D+ ++ I  HY++TS  F    +   + + + +   P+ VA  E V+
Sbjct: 3   ELRLQLQEKDLESIYPIYVHYVKTSAIFDVVSDSFDFVKEHMMIEISKTNPFYVALNEDVL 62

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
          G  Y  P  ++ AY + VE T+Y    +  GL S +   L    + +++ I
Sbjct: 63  IGYGYVHPAFSKEAYKYCVELTIYFK-EGKHYGLPSKMLDQLEADCRKLNMRWIISCITD 121

Query: 129  PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
          N+ S+  H+  G+T  G L + G K    WH V
Sbjct: 122  SNEESIAFHKKHGFTMYGALPSCGIKFDVWHGV 154
```

```
>ref|YP_213080.1| putative acetyltransferase [Bacteroides fragilis NCTC 9343]
ref|ZP_04843522.1| conserved hypothetical protein [Bacteroides sp. 3_2_5]
ref|ZP_06094646.1| conserved hypothetical protein [Bacteroides sp. 2_1_16]
emb|CAH09166.1| putative acetyltransferase [Bacteroides fragilis NCTC 9343]
gb|EES85610.1| conserved hypothetical protein [Bacteroides sp. 3_2_5]
gb|EEZ24670.1| conserved hypothetical protein [Bacteroides sp. 2_1_16]
Length = 172
```

Score = 64.7 bits (156), Expect = 5e-09, Method: Compositional matrix adjust.
Identities = 41/160 (25%), Positives = 71/160 (44%), Gaps = 1/160 (0%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV-EG 66
          + +R  T  D+  V DI ++Y  +TV +    +  E  + +    Y  + E  EG
Sbjct: 3   ITLRTLTLTENDLPFVKDIYDYTLHTTVVYFVHCASIDELKNYIPVGDPVYRSFIETPEG 62

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          G  Y  +K R A+  +VE T+Y+    G G    L + +  +GF +++A+I
Sbjct: 63  APCGFCYFARFKPREAFRISVELTLYLKPEFTGRGYGKQAILRLEEIIRQEGFSNIMALI 122

Query: 127  GLPNDSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
          N+ S+RL E  G+    +R   K G  D+  +Q+
Sbjct: 123  SGENEASIRLFEKCGFECCANIRQVAEKF GK KLDLRMYQK 162
```

```
>ref|ZP_07087704.1| phosphinothricin acetyltransferase [Chryseobacterium gleum ATCC
35910]
gb|EFK34496.1| phosphinothricin acetyltransferase [Chryseobacterium gleum ATCC
35910]
Length = 163
```

Score = 64.7 bits (156), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 43/162 (26%), Positives = 67/162 (41%), Gaps = 3/162 (1%)

```
Query: 9   EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
          E+R   D A V +I  I+    F TE  T + W  +   D  W++    V
Sbjct: 4   ELREMLPTDEARVLEIFRQIDGGISTFETEVPTAEAW--SMGYFND-CRWVLENENNEV 60

Query: 69  AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
          G    P  R  Y    E ++Y  + +Q  GLGS L  L+  E  GF ++  I
Sbjct: 61  VGWCALKPVSKRECYKGVAEVSIFYDNEYQKGGLGSVLLKKLILDSHGFWTQLQTNIFS 120

Query: 129  PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQDFEL 170
          N+ S++ H+  G+  G  +  G  +G W DV  ++  E+
Sbjct: 121  ENETSIKFHQKNGFRMVGIRKKIGKLNGEWKDVILMEKRSEI 162
```

```
>ref|ZP_03934219.1| possible Phosphinothricin acetyltransferase [Corynebacterium
striatum ATCC 6940]
```

gb|EEI79262.1| possible Phosphinothricin acetyltransferase [Corynebacterium striatum ATCC 6940]
Length = 170

Score = 64.3 bits (155), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 48/167 (28%), Positives = 79/167 (47%), Gaps = 9/167 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDRYPWLVAEVEG 66
++IR AT AD+ A+ + +N I + FR T E + L + + D PWLVAE E
Sbjct: 1 MQIRSATLADVPAMTECLNWAIRETDFIFRDTEATIAEREYYLRQNIADGCPWLVAETEP 60

Query: 67 VV-----AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QG 118
G A P++ + + E+T+Y+ Q G+G+ L L+ A +
Sbjct: 61 ETPGEKPGHGLGWAMYHPYRDPSVWKGCCYETTYLDPAQQGRGVGTALLGELVSLARADEK 120

Query: 119 FKSVMVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
+++ +I N S++LHE G+ GT + YK G W ++ Q
Sbjct: 121 VHTLLGLIVDTNVAIKLHEKFGFANVGTFFKEVSYKMGHWLNLTHLQ 167

>ref|ZP_08002273.1| YwnH protein [Bacillus sp. BT1B_CT2]
gb|EFV70501.1| YwnH protein [Bacillus sp. BT1B_CT2]
Length = 184

Score = 64.3 bits (155), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 42/140 (30%), Positives = 72/140 (51%), Gaps = 1/140 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVEG 66
+++R A D+ AV DI N I + V TEP TP+E ++ L ++R ++V +
Sbjct: 20 MKLRIANREDLPAVVDIYNSTIASRMVTADTEPVTPEERLNNWFLSHTTEERPLYIVENEKR 79

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+ G + R AY T E ++Y+ H+ G GS + L++ G +S++A I
Sbjct: 80 DIVGWISFESFYGRPAYAKTAEVSIYLLHEDHRGKGAGSAVLEKALEAAPKLGIRSLMAFI 139

Query: 127 GLPNDPSVRLHEALGYTARG 146
N+PS++L + G+T G
Sbjct: 140 FAHNEPSMKLFFKKYGFTEWG 159

>emb|CBW23960.1| putative acetyltransferase [Bacteroides fragilis 638R]
Length = 177

Score = 64.3 bits (155), Expect = 6e-09, Method: Compositional matrix adjust.
Identities = 41/160 (25%), Positives = 71/160 (44%), Gaps = 1/160 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV-EG 66
+ +R T D+ V DI ++Y +TV + + E + + Y + E EG
Sbjct: 8 ITLRTLTLTENDLPFVKDIYDYTLHTTVVYFVHCASIDELKNYIPVGDPVYRSFIETPEG 67

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
G Y +K R A+ +VE T+Y+ G G L + + +GF +++A+I
Sbjct: 68 APCGFCYFARFKPREAFRISVELTLYLKPEFTGRGYGKQAILRLEEIIIRQEGFSNIMALI 127

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N+ S+RL E G+ +R K G D+ +Q+
Sbjct: 128 SGENEASIRLFEKCGFECCANIRQVAEKF GKLDLRMYQK 167

>ref|ZP_04244771.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock1-3]
gb|EEL23517.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock1-3]
Length = 171

Score = 64.3 bits (155), Expect = 7e-09, Method: Compositional matrix adjust.
 Identities = 45/166 (27%), Positives = 70/166 (42%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 M+ R +EIR AT D+ + I N IE TE +T + ++ L + + RY +
 Sbjct: 1 MNKGERSMERKATKQDVQEIMTIYNEGIEDRIATLETEIKTDKYVMEWLFQRETRYSVI 60

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
 V E + G A P+ R AY E ++Y+ ++ GLG L L K+ + F
 Sbjct: 61 VMEENSHIVGWASINPYSHRCAYRGVGEISYIKREYRGKGLGQKLLALEKTGQQNEFY 120

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 V N+ L+ +GY G G G DV ++
 Sbjct: 121 KFVLFTFSFNNLGQGLYRKMGYREVGVFEKQGVMDGEHVDVMIMEK 166

>ref|YP_437978.1| sortase and related acyltransferase [Hahella chejuensis KCTC 2396]
 gb|ABC33553.1| Sortase and related acyltransferase [Hahella chejuensis KCTC 2396]
 Length = 171

Score = 64.3 bits (155), Expect = 7e-09, Method: Compositional matrix adjust.
 Identities = 45/140 (32%), Positives = 65/140 (46%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
 ++RPA AD+ AV DI N + + V TE + D R D P LVAE +
 Sbjct: 10 QLRPAQEADLQAVVDIYNSTVASRQVTADTEKVSASRRDWFRLRHTDERPLLVAEQADHI 69

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 G P+ +R AY T E ++Y++ + GLG+ L H + G ++V VI
 Sbjct: 70 LGWISFEPYHSRPAYRHTAELSIYLAPEQRGKGLGARLLGHAIALAPRLGVTALVGVIFS 129

Query: 129 PNDPSVRLHEALGYTARGTL 148
 N PS+ L G+ G L
 Sbjct: 130 HNAPSLALFRKHGFQCWGE 149

>ref|ZP_05283241.1| putative acetyltransferase [Bacteroides fragilis 3_1_12]
 ref|ZP_07811118.1| GNAT family acetyltransferase [Bacteroides fragilis 3_1_12]
 gb|EFR55052.1| GNAT family acetyltransferase [Bacteroides fragilis 3_1_12]
 Length = 164

Score = 63.9 bits (154), Expect = 8e-09, Method: Compositional matrix adjust.
 Identities = 41/160 (25%), Positives = 71/160 (44%), Gaps = 1/160 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV-EG 66
 + +R T D+ V DI ++Y +TV + + E + + Y + E EG
 Sbjct: 3 ITLRTLTLTENDLPFVKDIYDYTLHTTVVYFVHCASIDELKNYIPVGDPVYRSFIETPEG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 G Y +K R A+ +VE T+Y+ G G L + + +GF +++A+I
 Sbjct: 63 TPCGFCYFARFKPREAFRISVELTLYLKPEFTGQGYGKQTIFRLEEIIIRQEGFSNIMALI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 N+ S+RL E G+ +R K G D+ +Q+
 Sbjct: 123 SGENEASIRLFEFCGFECCANIRQVAEKF GKLDLRMYQK 162

>ref|ZP_07991612.1| acetyltransferase [Corynebacterium variabile DSM 44702]
 Length = 172

Score = 63.9 bits (154), Expect = 9e-09, Method: Compositional matrix adjust.
 Identities = 48/161 (29%), Positives = 73/161 (45%), Gaps = 22/161 (13%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE---- 63
+ +R + AD A+ +I N + T T W +D + +R WL A
Sbjct: 9 ISVRSSCDADFPAITEIYNDAVVT-----TVAVWNNDTVDVDNRRDWLHAHQVPG 58

Query: 64 -----VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
+G V G A G +++ + + TVE++VYVS + G+G+ L T LL
Sbjct: 59 TVALTAVGADGRVLGYATYGDFRSYDGFRTVENSIVYVSTDARTGGVGTALMTELLVRAR 118

Query: 116 AQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHG 156
+G +VA I N S+ LHE LG++ G L G K G
Sbjct: 119 DEKGHVMVAAIESGNTASLALHEKLGFTVGVLPVGVTKFG 159

>ref|YP_001195416.1| GCN5-related N-acetyltransferase [Flavobacterium johnsoniae UW101]
gb|ABQ06097.1| GCN5-related N-acetyltransferase [Flavobacterium johnsoniae UW101]
Length = 168

Score = 63.9 bits (154), Expect = 9e-09, Method: Compositional matrix adjust.
Identities = 47/161 (29%), Positives = 73/161 (45%), Gaps = 4/161 (2%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
+ +EIR + V I I+T F+T + ++W D L+ +V + +
Sbjct: 6 KNMEIRKLSDKHWDEVKIIYQKGIDTGNATFQTSAPSWEDW--DQSHLKSCR--VVMQED 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G A P +R Y E +VYV H G+G TL L++ E +G ++ A
Sbjct: 62 GKVIGWAALTPVSSRCVYAGVAEVSIVYVDPAHSGKGIGLTLKELVRQSETEGIWTLQAG 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
I N S+R+HE G+ GT G ++G W D +R
Sbjct: 122 IFPENTASLRIHEKAGFRILGTREKIGKQNGIWRDTALLER 162

>ref|ZP_01902912.1| phosphinothricin N-acetyltransferase, putative [Roseobacter sp. AzwK-3b]
gb|EDM71733.1| phosphinothricin N-acetyltransferase, putative [Roseobacter sp. AzwK-3b]
Length = 162

Score = 63.9 bits (154), Expect = 9e-09, Method: Compositional matrix adjust.
Identities = 49/160 (30%), Positives = 74/160 (46%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
+R A AAD+ A+ +VN I +T+ F T +T Q+ DD+ +D + LV E G +
Sbjct: 3 LRDAEAADVQAIAGLVNPVIRDTTITFTTREKTAQDVADDIAAKRDLGHGLLVVEEAGAL 62

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G+A G ++ Y T E ++ + + GLG L L G S++A +
Sbjct: 63 LGVASYGQFRPGPGYARTAEHSITLDPSARGRGLGRLLLLHRLLEDHARGAGMHSMIAAVSG 122

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168
N V HE LGY L G+K G W D+ Q+
Sbjct: 123 ENPGGVAFHERLGYARVAVLPQIGWKFGRWLDLILLQKQL 162

>ref|YP_003059578.1| GCN5-related N-acetyltransferase [Hirschia baltica ATCC 49814]
gb|ACT58881.1| GCN5-related N-acetyltransferase [Hirschia baltica ATCC 49814]
Length = 165

Score = 63.9 bits (154), Expect = 1e-08, Method: Compositional matrix adjust.
Identities = 45/156 (28%), Positives = 75/156 (48%), Gaps = 7/156 (4%)

Query: 18 MAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVA-EVEGVVAGIAY 73
 + + +I NH + S + T + WI+ L+ + Y +VA + + V G A
 Sbjct: 11 LNGILEIYNHAVRESFAVWTEREDTLNDRRAWINKLQ--ANGYACIVAVDSKNDVLGYAG 68

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL-KSMEAQGFKS VVAVIGLPNDP 132
 G ++ + YD TVE +VYV+ Q G+G+ L T L+ + + + +V I N
 Sbjct: 69 YGVFRGKPGYDITVEHSVYVADSAQKG VGNALMTELINRGIADTRLEKMVG AIDAGNPI 128

Query: 133 SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 S++LHE G+ +G LR K G D+ F +D
 Sbjct: 129 SIKLHEKFGFQTQGILRGVATKWGEHRDLQFMVKDI 164

>ref|YP_001678727.1| phosphinothricin n-acetyltransferase, putative [Heliobacterium
 modesticaldum Icel]
 gb|ABZ82716.1| phosphinothricin n-acetyltransferase, putative [Heliobacterium
 modesticaldum Icel]
 Length = 164

Score = 63.5 bits (153), Expect = 1e-08, Method: Compositional matrix adjust.
 Identities = 44/142 (30%), Positives = 69/142 (48%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 +R A +D+ A+ I N I + V T P + + W D D P V E++G
 Sbjct: 3 LRNAVESDLP AIVAIYNSTIASRMVTADTTPISVESRLPWFHDHN--PDGRPLWVLEMDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVI 126
 V+AG + R AYD TVE ++Y++ + G+G L +++ A G +++ I
 Sbjct: 61 VIAGWLSFQSFYGRPAYDGTVEVSIYIAESFRGQGIGRFLQRAIEAAPAMGVHTLLGFI 120

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
 N PS+ L EALG+ G L
 Sbjct: 121 FAHNLP SLGLFEALGFARWGHL 142

>ref|ZP_06898661.1| acetyltransferase [Roseomonas cervicalis ATCC 49957]
 gb|EFH09634.1| acetyltransferase [Roseomonas cervicalis ATCC 49957]
 Length = 194

Score = 63.5 bits (153), Expect = 1e-08, Method: Compositional matrix adjust.
 Identities = 47/176 (26%), Positives = 79/176 (44%), Gaps = 10/176 (5%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA--- 62
 PV + PA + + I N + +ST + +P+T ++ + Q R +P LVA
 Sbjct: 22 PVLVLPA GPLHLPGMLAIFNEVVASSTAVYTDQPETLEQRAAWCAQRQSRGFPVLVALGA 81

Query: 63 ---EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 +V G + + G W + TVE +V++ + GLG+ L L++ G
 Sbjct: 82 DERDVLGFASF AEFRRGGWPG---FRHTVEHSVHIRADCRGRGLGTRLVAALVEQAVLLGK 138

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELPAPPR 175
 +VA I N PS+R+H+ +G+ + G K G W D+ Q+ P R
 Sbjct: 139 HVMVASIDAENAPSIRMHQRMGFRQVAHMPQVGCKFGRWLDLVLQMQLSEKQPER 194

>ref|ZP_07329309.1| GCN5-related N-acetyltransferase [Acetivibrio cellulolyticus CD2]
 gb|EFL59403.1| GCN5-related N-acetyltransferase [Acetivibrio cellulolyticus CD2]
 Length = 164

Score = 63.2 bits (152), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 40/144 (27%), Positives = 66/144 (45%)

Query: 23 DIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNA 82

DI +Y+ +T F +P + E + + +Y V + + G K R A
 Sbjct: 19 DIYTYYYVLNLTATTFHEKPLSISEMRELVIKDSKYETYVIKDGTLQCGYVILTQHKKREA 78

Query: 83 YDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGY 142
 YD T E T+Y+ + G+GS T + +++GF ++A I N+ S+RL E GY
 Sbjct: 79 YDNTGEITIYKSDYIGKGIGSRAITFIECIAKSKGFHVLIATICGENEKSIRLFFERNGY 138

Query: 143 TARGTLRAAGYKHGGWHDVGFWR 166
 + G K G W D+ +Q+
 Sbjct: 139 VKCAHYKEVGRKFGNWLDLVAYQK 162

>ref|YP_028878.1| hypothetical protein BAS2619 [Bacillus anthracis str. Sterne]
 ref|ZP_00393061.1| COG1247: Sortase and related acyltransferases [Bacillus anthracis str. A2012]
 gb|AAT54929.1| hypothetical protein BAS2619 [Bacillus anthracis str. Sterne]
 Length = 87

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 28/87 (32%), Positives = 50/87 (57%), Gaps = 2/87 (2%)

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRA 150
 +YV +++ G+G++L L+ + + + +++A I N+ S+ LHE G+ GT++
 Sbjct: 1 MYVDKEYRKCIGTSLMRALITIAKEREYMTLIAGIDAENEKSIALHENYGFVHAGTIKK 60

Query: 151 AGYKHGGWHDVGFWRDFELPAPPRPV 177
 AGYK W D+ F+Q EL P P+
 Sbjct: 61 AGYKFNKWLDAFYQ--LELCGPKNPL 85

>ref|ZP_08109933.1| Phosphinothricin acetyltransferase [Desulfovibrio sp. ND132]
 gb|EGB13818.1| Phosphinothricin acetyltransferase [Desulfovibrio sp. ND132]
 Length = 162

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 40/136 (29%), Positives = 65/136 (47%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEG 66
 ++PAT D+ + +I N + T TEP + + W + + R P +V ++G
 Sbjct: 1 MQPATEQDLPRIVEIYNSTVATRISTADTEPVSVEARRPWFE--HHVPGRRPIMVERIDG 58

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VA + R AYD T E ++Y++ H+R GLG L L A G +V+ I
 Sbjct: 59 EVAAWVSFESFYGRPAYDHTAEISIIYIAPEHRRQGLGRKLLREALDMTPALGINTVLGYI 118

Query: 127 GLPNDPSVRLHEALGY 142
 N+ S+RL + G+
 Sbjct: 119 FSHNEGSMRLFASFGF 134

>ref|ZP_03338523.1| putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. 404ty]
 Length = 129

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 47/129 (36%), Positives = 66/129 (51%), Gaps = 5/129 (3%)

Query: 10 IRPATAADMAAVCDIVNHYI-ETSTV-NFRT-EPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR A AD AA+ +I N + T+ + N RT + W + + L YP LV+E G
 Sbjct: 3 IRFADKADCAAITEIYNRAVLHTAAIWNDRVTDTNRLAWYEARQLLG--YPVLVSEENG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV G A G W++ + + +TVE +VYV HQ GLG L + L+ G +VA I

Sbjct: 61 VVTGYASFGDWRSFDGFRYTVEHSSVYVHPAHQKGKLGKLLSRLIDEARRCGKHMVAGI 120

Query: 127 GLPNDPSPVR 135

N S+R

Sbjct: 121 ESQNAASIR 129

>ref|XP_003034026.1| hypothetical protein SCHCODRAFT_107275 [Schizophyllum commune H4-8]

gb|EFI99123.1| hypothetical protein SCHCODRAFT_107275 [Schizophyllum commune H4-8]

Length = 194

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.

Identities = 55/183 (30%), Positives = 79/183 (43%), Gaps = 27/183 (14%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDRYPWLVAEV---- 64

+RPA D + + I NHYIE+S FRTE +D ++ R P++VA

Sbjct: 6 LRPARPEDFSQIAVIFNHYIESSLATFRTERVDRAALLDTFYSVVEQRLPYIVAIAFDDP 65

Query: 65 -EGVVAGIAYAGPWK-ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122

E V G AYA ++ R+AY T E ++YV H G+G+ + ++L + S+

Sbjct: 66 DEPFVLGYAYASRYRPERDAYRHTAELSIYVHPDHLGAGIGTLMLDNVLGLLRQTTKPSL 125

Query: 123 V--AVIGLPNDPSVRLHEAL-----GYTARGTLRAAGYKHGGWHDVG 162

+ AV L V + AL G+ G LR GYK G W D

Sbjct: 126 LLGAVAELAPVRQVLVVMALDTEGHKGGFGQRDWWYVKGFGVQVGHLEVGKFGRWVDTI 185

Query: 163 FWQ 165

Q

Sbjct: 186 ILQ 188

>ref|ZP_01852414.1| Putative phosphinothricin N-acetyltransferase [Planctomyces maris DSM 8797]

gb|EDL61649.1| Putative phosphinothricin N-acetyltransferase [Planctomyces maris DSM 8797]

Length = 192

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.

Identities = 43/144 (29%), Positives = 70/144 (48%), Gaps = 3/144 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEG 66

+ R AT D+ A+ DI N I T T+P T + + ++ P VAE E

Sbjct: 25 ITTRDATLDDLPAIVDIYNESIPAGTATADTKPITVESRLQWFAQFSPEKRPIWVAEDEA 84

Query: 67 --VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124

+V I + R AYD T E ++Y+S+ HQ+ GLG+ L ++ + A G ++V

Sbjct: 85 RQIVGCIYVTSFYAGRPAYDKTAEVSLYLSNSHQKQGLGTFLQKIDACPALGITTLLVG 144

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148

+ N+ + L+E G+ G L

Sbjct: 145 MHFDHNEGTRHLNEKFGFEVCGHL 168

>ref|YP_002794590.1| Phosphinothricin acetyltransferase [Laribacter hongkongensis HLHK9]

gb|ACO73581.1| Phosphinothricin acetyltransferase [Laribacter hongkongensis HLHK9]

Length = 179

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.

Identities = 44/143 (30%), Positives = 69/143 (48%), Gaps = 6/143 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYP-WLVAEVE 65

IRPA AAD+ + I N + TV TEP + Q W D D +P W++ + E
 Sbjct: 12 IRPARAADLPGIVAIYNSTVPLRTVTADTEPVSVASRQAWFD--AHHPDHHPLWVIEDAE 69

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + G A P+ R AY T E ++Y++ + GLG L +++ A G ++++

Sbjct: 70 GQLLGWASLSPFYGRPAYAATAEVSIIYLAGPARGHGLGRWLLDYVMARSPALGIRTLLGF 129

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148

I N S+ L G+ + G L

Sbjct: 130 IFSHNPASLALFARAGFASWGEL 152

>ref|YP_001865339.1| GCN5-related N-acetyltransferase [Nostoc punctiforme PCC 73102]
 gb|ACC80396.1| GCN5-related N-acetyltransferase [Nostoc punctiforme PCC 73102]
 Length = 168

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 42/144 (29%), Positives = 65/144 (45%), Gaps = 5/144 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEV 64

+ IR AT D+ A+ I N I + EP + + W R + P V EV

Sbjct: 1 MTIRHATETDLPAIVAIYNAAIPSCMATADLEPVSVESRLPWFR--ARSPSQRPLWVIEV 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124

EG +AG + R AY+ T E ++Y++ + R GLG L + + G +++

Sbjct: 59 EGAIAGWLSFSQSFYGRPAYNTTAEISIIYIAPQFHRCGLGRQLLAQAISESRSLGLNTLLG 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148

I N PS++L E G+ G L

Sbjct: 119 FIFAHNQPSLKLFFETFGFQHWGYL 142

>gb|EFU15691.1| acetyltransferase, GNAT family [Enterococcus faecalis TX1342]
 Length = 163

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 48/160 (30%), Positives = 72/160 (45%), Gaps = 5/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

++I P T +D V I +T FR+E T EW D + R L+A+ E

Sbjct: 1 MKIAPMTSDWEDVSRIFLTGTQTENATFRSELPTFDEW-DSGHFKECR---LIAKQENQ 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G A P R Y E ++YV ++ G+G++L + E F + A I

Sbjct: 57 IIGWAALSPISTRKEYQGVAEVSIYVDQPNEGKGIGTSLKKEFVHLSEVSNFWMLQASIF 116

Query: 128 LPNDPSVRLHEALGYTARG-TLRAAGYKHGGWHDVGFVQR 166

N S++LH+ LG+ G + A K G WHDV +R

Sbjct: 117 RENMASIQLHKKLGFREVGYREKIAQTKSGIWHDVVLMER 156

>ref|YP_686313.1| GNAT family acetyltransferase [uncultured methanogenic archaeon RC-I]
 emb|CAJ36987.1| putative acetyltransferase (GNAT family) [uncultured methanogenic archaeon RC-I]
 Length = 162

Score = 62.8 bits (151), Expect = 2e-08, Method: Compositional matrix adjust.
 Identities = 43/136 (31%), Positives = 65/136 (47%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQ---EWIDDLERLQDRYPWLVAEVEG 66

IR AT +D+ + +I N + V TEP T +W E P VAE++G

Sbjct: 3 IRDATGSDLPRIVEIYNSTVPGRMVTADTEPVTVASRLQWFG--EHNPATRPLWVAEIDG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G + R AY+ TVE +VYV+ H+ G+G TL + A G K+++ I
 Sbjct: 61 EICGWLSSFSSFYGRPAYNATVEISVYVAPEHRGKGIGGTLLGKAIDHSPAIGVKTLLGFI 120

Query: 127 GLPNDPSVRLHEALGY 142
 N PS+ L + G+
 Sbjct: 121 FAHNAPSLSLFKKFGF 136

>ref|ZP_04322990.1| GCN5-related N-acetyltransferase [Bacillus cereus m1293]
 gb|EEK45166.1| GCN5-related N-acetyltransferase [Bacillus cereus m1293]
 Length = 164

Score = 62.4 bits (150), Expect = 3e-08, Method: Compositional matrix adjust.
 Identities = 44/159 (27%), Positives = 67/159 (42%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +EIR A D+ + I N IE TE +T + ++ L R Q+RY +V E
 Sbjct: 1 MEIRRAAEQDVKEIMTIYNEGIEDRIATLETEIKTDKYVMEWLFRRQNRYSVIVIEENSK 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A P+ R AY E ++Y+ ++ GLG L L K+ + F V
 Sbjct: 61 IVGWASINPYSHRCAYRGVGEISYIKREYRGKGLGQKLLLALEKTGQQNEFYKFVLFVTF 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
 N+ L+ +GY G G G DV ++
 Sbjct: 121 SFNNLGQGLYRKMGYREVGVFQKQIMDGVHVDVMIMEK 159

>ref|YP_146446.1| phosphinothricin N-acetyltransferase [Geobacillus kaustophilus HTA426]
 dbj|BAD74878.1| phosphinothricin N-acetyltransferase [Geobacillus kaustophilus HTA426]
 Length = 163

Score = 62.4 bits (150), Expect = 3e-08, Method: Compositional matrix adjust.
 Identities = 47/159 (29%), Positives = 70/159 (44%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR D V +I I T F T + ++W E LVAE E
 Sbjct: 1 MNIRSFRRKEDWMQVKEIYEQGIATGQATFETTAPSFEKW----ESTIAANLCLVAENEEG 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G R Y+ E +VYV + G+G L ++K EA+GF ++ A I
 Sbjct: 57 IQGWCKISKVSDRCVYEGVGEVSVYVRDVSRGKGVGKLLQAMIKSEAKGFWTTLTAGIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
 N PS+RLH+++G+ G + G +G W DV +R
 Sbjct: 117 PENIPSLRLHQSVGFREVGIRQIRIGKLNQVWRDVLVLLER 155

>ref|ZP_02140906.1| acetyltransferase, putative [Roseobacter litoralis Och 149]
 gb|EDQ17577.1| acetyltransferase, putative [Roseobacter litoralis Och 149]
 Length = 158

Score = 62.4 bits (150), Expect = 3e-08, Method: Compositional matrix adjust.
 Identities = 46/159 (28%), Positives = 73/159 (45%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRPA+ D +A+ + N I+ + F T +T E + ++ VAE +GV A
 Sbjct: 2 IRPASPEDSSAIVALWNWMIQDTLATFTTTTKTRAELETRITAQPSQF--YVAENKGVFA 59

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G GP++ Y TVE T+ + + G+G L + A G K ++ I
 Sbjct: 60 GFVTFGPFRPGPGYAATVEHTIIIDPKAHGFGIGRALMAQAETAHAAGKKVMIGAISSH 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 N +++ HE L Y G L G+K G W D+ Q++
 Sbjct: 120 NPAAIKFHERLEYMKVGHLPVGVGHKQGHWLDLILMQKNL 158

>ref|ZP_01446058.1| GCN5-related N-acetyltransferase [Pelagibaca bermudensis HTCC2601]
 gb|EAU43721.1| GCN5-related N-acetyltransferase [Roseovarius sp. HTCC2601]
 Length = 181

Score = 62.0 bits (149), Expect = 3e-08, Method: Compositional matrix adjust.
 Identities = 48/162 (29%), Positives = 75/162 (46%), Gaps = 8/162 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR---YPWLVA-E 63
 +I A+ AD+ + +I N + + + +TP + + L+ Q R YP LVA +
 Sbjct: 13 QIDDASEADLPGILEIYNDAVHHTLAIWN---ETPVDLANRLDWWQARRAQGYPVLVARD 69

Query: 64 VEGVVGIAIYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSJV 123
 +G V G A G W+ + TVE +VY+ + G+ L T L++ +V
 Sbjct: 70 ADGAVLGYASFCDWRPFEGFRHTVEHSVYIHPSARGRGVARGLMTALIERAREASKHVMV 129

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 A I N S+ LH LG+T + G K G W D+ F Q
 Sbjct: 130 AGIESGNAASLALHRRLGFTVTAEMPQVGCKFGRWLDLTFMQ 171

>ref|ZP_05475424.1| phosphinothricin N-acetyltransferase [Enterococcus faecalis ATCC
 4200]
 gb|EEU17281.1| phosphinothricin N-acetyltransferase [Enterococcus faecalis ATCC
 4200]
 Length = 163

Score = 62.0 bits (149), Expect = 3e-08, Method: Compositional matrix adjust.
 Identities = 48/160 (30%), Positives = 72/160 (45%), Gaps = 5/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++I P T +D V I +T FR+E T EW D + R L+A+ E
 Sbjct: 1 MKIAPMTSDSDWEDVSRIFLTGTQTENATFRSELPTFDEW-DSGYFKECR---LIAKQENQ 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A P R Y E ++YV ++ G+G++L + E F + A I
 Sbjct: 57 IIGWAALSPISTRKEYQGVAEVSIYVDQPNEGKGIGTSLKKEFVHLSVSNFWMLQASIF 116

Query: 128 LPNDPSVRLHEALGYTARG-TLRAAGYKHGGWHDVGFQWQ 166
 N S++LH+ LG+ G + A K G WHDV +R
 Sbjct: 117 RENMASIQLHKKLGFREVGyreKIAQTKSGIWHDVVLMER 156

>ref|ZP_00048643.1| COG1247: Sortase and related acyltransferases [Magnetospirillum
 magnetotacticum MS-1]
 Length = 133

Score = 62.0 bits (149), Expect = 3e-08, Method: Compositional matrix adjust.
 Identities = 30/79 (37%), Positives = 46/79 (58%)

Query: 82 AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALG 141
 Y +T++ ++YV H G+G L L+++ A G++ ++ I N+ S+RLHEA G
 Sbjct: 21 GYRFTLKHSIYVHPDHLHAGIGRRLPALVEACAAGGYRQMIGYIDAKNEASRLHEACG 80

Query: 142 YTARGTLRAAGYKHGGWHD 160

+T G L A GYK G W D
Sbjct: 81 FTRVGYLPAIGYKFGWRSD 99

>gb|EGC98046.1| GCN5-related N-acetyltransferase [Burkholderia sp. TJI49]
Length = 104

Score = 62.0 bits (149), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 34/99 (34%), Positives = 49/99 (49%), Gaps = 1/99 (1%)

Query: 83 YDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG-LPNDPSVRLHEALG 141
Y T+E ++Y+ + G+GS L L+ EA ++ ++AVI S LH A G
Sbjct: 1 YRHTIEDSIYIDDTQRGRGIGSALLAALIARCEAGPWRQMIADGGTGGSTSLHRAFG 60

Query: 142 YTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRPV 180
+ GTL+A G+KHG W D QR A +P P
Sbjct: 61 FEPAGTLKAVGFKHGRWIDTALLQRTLGDGARTQPASPA 99

>ref|ZP_06971607.1| transcriptional regulator, ArsR family [Ktedonobacter racemifer
DSM

44963]
gb|EFH84327.1| transcriptional regulator, ArsR family [Ktedonobacter racemifer DSM
44963]
Length = 279

Score = 62.0 bits (149), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 48/166 (28%), Positives = 71/166 (42%), Gaps = 1/166 (0%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 61
S E + +EIR AT D A+ I N IE + T+ +TP+E + L R+P LV
Sbjct: 111 SLEEQHMEIREATREDATAIASIYNQGIEDRSATLETQLRTPPEERAEWLNSRTHRPVLV 170

Query: 62 AEVEGVVAGI-AYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
A + R AYD V+ +VYV+ + G+G L + L G+
Sbjct: 171 AVDAAGAVVGWGSLSNAPNRPAYDHVVDVSVYVAREQGRGIGDALLSALEVRARTLGYH 230

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
+V N P +RL+E + G G G W DV ++
Sbjct: 231 KMVLAAPPSNAPGMRLYERHEFRKVGVEHQGLLDGQWVDVVLMEK 276

>ref|ZP_04946138.1| hypothetical protein BDAG_02064 [Burkholderia dolosa AU0158]
gb|EAY69309.1| hypothetical protein BDAG_02064 [Burkholderia dolosa AU0158]
Length = 182

Score = 62.0 bits (149), Expect = 4e-08, Method: Compositional matrix adjust.
Identities = 50/169 (29%), Positives = 78/169 (46%), Gaps = 6/169 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVA-EVE 65
I + A +A+ +I+N I ST + P+ P+ W + +P + A +
Sbjct: 13 IDCSEAEHASAILEILNDAIVNSTALYDYRPRPPEAMAAWF--ATKRAGGFPVIGAVDAA 70

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125
+ G A G ++A A+ +TVE +VYV H+ GLG L L++ +V
Sbjct: 71 DTLGFAWGTFRAFPAPKYTVEHSVYVHRDHRGRGLGELLRLRIRARDADVHVLVGC 130

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
I N S+ LH LG+ GT+ AG+K G W D F+Q + P P
Sbjct: 131 IDATNAGSIALHTRLGFVHSGTVAEAGFKFGRWLDAAFYQLRLDTPMQP 179

>ref|YP_003996590.1| phosphinothricin acetyltransferase [Leadbetterella byssophila DSM

17132]

gb|ADQ16237.1| Phosphinothricin acetyltransferase [Leadbetterella byssophila DSM

17132]

Length = 166

Score = 61.6 bits (148), Expect = 4e-08, Method: Compositional matrix adjust.

Identities = 41/143 (28%), Positives = 67/143 (46%), Gaps = 1/143 (0%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDRYPWLVAEVE 65

P+ R A D+A + +I N I + V EP + + +D ++YP V E E

Sbjct: 3 PINYRTADIKDLAGIVEIYNSTIPSRLVTAHLEPVSVESRVDWFRSHTPEKYPLWVIESE 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125

G + G P+ R AY T E ++Y++ + GLG L+ G ++++ +

Sbjct: 63 GKMLGWLGFQPFHPRPAYAPTAEISLYLAPSARGKGLGYQSLQFALEKAPEFGIQTTLIGL 122

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148

I N+PS+RL E G+ G L

Sbjct: 123 IFAHNEPSIRLFEKAGFEEWGYL 145

>ref|ZP_05571308.1| hypothetical protein Faci_07786 [Ferroplasma acidarmanus fer1]

Length = 165

Score = 61.2 bits (147), Expect = 5e-08, Method: Compositional matrix adjust.

Identities = 38/150 (25%), Positives = 69/150 (46%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAG 70

R A+ D+ + DI N I++ F + + P D L + RY LVA + G

Sbjct: 8 RKASLDDVPYIADIWNQGIDSGNATFEIKRDPVWTSDWLVKRDPRYVVLVAGNRNNILG 67

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLPN 130

P+ +R AY + + ++YV + + G+GS L H + + GF +V + N

Sbjct: 68 WLSLNPFSREAYRFVADISIYVENSYHGRGIGSGLLDHGII EAKINGFHKLVLTMLRDN 127

Query: 131 DPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

+ + +L+ + G++ G + G + W D

Sbjct: 128 EIARKLYISRGFSTVGIMHEQGILNNKWID 157

>ref|ZP_06968560.1| GCN5-related N-acetyltransferase [Ktedonobacter racemifer DSM

44963]

gb|EFH86100.1| GCN5-related N-acetyltransferase [Ktedonobacter racemifer DSM

44963]

Length = 175

Score = 61.2 bits (147), Expect = 6e-08, Method: Compositional matrix adjust.

Identities = 45/157 (28%), Positives = 70/157 (44%), Gaps = 9/157 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAEV 64

+ +R AT AD +A+ I N IE F T+ +T W D + +P +V E

Sbjct: 1 MRVRVATVADASAIATIYNQGIEDRVGTFTETQLRTEAMVASWFDGM-----HPIVVVEQ 54

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 124

E + A +++R Y E +VYV + G G T+LL+ A GF +++

Sbjct: 55 EQDIIAYASTSSYRSRPCYAGIAEFSVYVRRDWRGKGAGRLAITYLLQESAAAGFWKLLS 114

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

+ + N+ S L +LG+ G G G W DV

Sbjct: 115 RVFVENEASRGLLRSLGFREVGIIYKKGQLDGIWRDV 151

>ref|YP_004205490.1| putative phosphinothricin acetyltransferase [Bacillus subtilis
BSn5]
gb|ADV94463.1| putative phosphinothricin acetyltransferase [Bacillus subtilis
BSn5]
Length = 165

Score = 61.2 bits (147), Expect = 6e-08, Method: Compositional matrix adjust.
Identities = 47/160 (29%), Positives = 72/160 (45%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68
+R A D+ AV I N I + V TEP TP++ ++ + P VAE E G V
Sbjct: 5 LRLAENKDLEAVVAIYNSTIASRMVTADTEPVTPEDRMEWFSGHTEARPLYVAEDENGNV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
A + R AY+ T E ++Y+ + G+GS L L+ G +S++A I
Sbjct: 65 AAWISFETFYGRPAYNKTAEVSIYIDEACRGKGVGSYLLQEALRIAPNLGIRSLMAFIFG 124

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF 168
N PS++L E G+ G G +D+ R+
Sbjct: 125 HNKPSLKLFEKHGFAEWGLFPGIAEMDGKRYDLKILGREL 164

>ref|ZP_08000132.1| hypothetical protein HMPREF1012_01166 [Bacillus sp. BT1B_CT2]
gb|EFV72449.1| hypothetical protein HMPREF1012_01166 [Bacillus sp. BT1B_CT2]
Length = 164

Score = 61.2 bits (147), Expect = 6e-08, Method: Compositional matrix adjust.
Identities = 42/154 (27%), Positives = 65/154 (42%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR A +AD+ + I N IE + + + + Q RY LVAE +G
Sbjct: 4 INIRKAISADLPFILTIYNQGIEDRIATLEQDLKEMSDIEIWFQEHQGRYSVLVAESKGE 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G A P+ R AY + +VYV + G+G L L K+ + F +V
Sbjct: 64 IVGWASLNYPYSHRCAYQGVADLSVYVDRACRGKGIGGLLLQALEKTAKENNFYKIVLFTF 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N+ L+ +GY G + G G + DV
Sbjct: 124 PFNELGQNLYNKMGYRQVGIFKNQGILDGRFIDV 157

>ref|YP_079109.1| GCN5-related N-acetyltransferase [Bacillus licheniformis ATCC
14580]
ref|YP_091522.1| hypothetical protein BLi01935 [Bacillus licheniformis ATCC 14580]
gb|AAU23471.1| GCN5-related N-acetyltransferase [Bacillus licheniformis ATCC
14580]
gb|AAU40829.1| putative protein [Bacillus licheniformis ATCC 14580]
Length = 164

Score = 61.2 bits (147), Expect = 6e-08, Method: Compositional matrix adjust.
Identities = 42/154 (27%), Positives = 65/154 (42%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR A +AD+ + I N IE + + + + Q RY LVAE +G
Sbjct: 4 INIRKAISADLPFILTIYNQGIEDRIATLEQDLKEMSDIEIWFQEHQGRYSVLVAESKGE 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G A P+ R AY + +VYV + G+G L L K+ + F +V
Sbjct: 64 IVGWASLNYPYSHRCAYQGVADLSVYVDRACRGKGIGGLLLQALEKTAKENSFYKIVLFTF 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

N+ L+ +GY G + G G + DV
 Sbjct: 124 PFNELGQNLYNKMGYRQVGIFKNQGILDGRFIDV 157

>ref|YP_001636579.1| GCN5-related N-acetyltransferase [Chloroflexus aurantiacus J-10-fl]
 ref|YP_002570940.1| GCN5-related N-acetyltransferase [Chloroflexus sp. Y-400-fl]
 gb|ABY36190.1| GCN5-related N-acetyltransferase [Chloroflexus aurantiacus J-10-fl]
 gb|ACM54614.1| GCN5-related N-acetyltransferase [Chloroflexus sp. Y-400-fl]
 Length = 168

Score = 60.8 bits (146), Expect = 6e-08, Method: Compositional matrix adjust.
 Identities = 45/163 (27%), Positives = 68/163 (41%), Gaps = 3/163 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 V R A D AA+ +I N I F T +T Q D DR+P +V V
 Sbjct: 3 SVFTRMANPHDAAIAEINYQGIADRIATFETNARTAQ---DVAWFNDRFPPIVVTIVND 59
 Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V A P++AR Y E +VYV+ + G+G LL++ GF +++ +
 Sbjct: 60 QVVAFAATFPYRARECYAGVAEFSVYVAREWRGRGIGRLTMLALLEAASRAGFWKLLSRV 119
 Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 + N S + ++G+ G G W DV +R E
 Sbjct: 120 FVENTASRAMLASVGFREVGIIYK HARLDGRWRDVVIVERLIE 162

>ref|YP_001126960.1| phosphinothricin N-acetyltransferase [Geobacillus
 thermodenitrificans NG80-2]
 gb|ABO68215.1| Probable phosphinothricin N-acetyltransferase [Geobacillus
 thermodenitrificans NG80-2]
 Length = 173

Score = 60.8 bits (146), Expect = 7e-08, Method: Compositional matrix adjust.
 Identities = 40/136 (29%), Positives = 64/136 (47%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR ATAAD+ + I N I + V EP ++ + W + + P V E +G
 Sbjct: 13 IRDATAADLPQIVRIYNETIPSRMVTADLEPVSVESRRRAWFEAHD--PHHRPLWVVEDDG 70
 Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V+ + R AY T E ++Y++ H+ GLG+ L + A G K+++ I
 Sbjct: 71 VICAWLSFQSFYGRPAYRHTAEVSIYIAESHRGQGLGTLLKRAIDKAPALGMKTLLGFI 130
 Query: 127 GLPNDPSVRLHEALGY 142
 N+PS+RL G+
 Sbjct: 131 FAHNEPSLRLFSRFGF 146

>ref|YP_353862.1| GNAT family acetyltransferase [Rhodobacter sphaeroides 2.4.1]
 gb|ABA79961.1| putative acetyltransferase, GNAT family [Rhodobacter sphaeroides
 2.4.1]
 Length = 158

Score = 60.8 bits (146), Expect = 7e-08, Method: Compositional matrix adjust.
 Identities = 51/159 (32%), Positives = 73/159 (45%), Gaps = 7/159 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAE-VEGV 67
 IRPA AAD+ A+ I N I + V F E ++ D+L L P +LVA+ EG
 Sbjct: 2 IRPAVAADVPALLAIWNPIIRDTLVTFNAAEEKSA----DELRTLIAARPAFLVADPGE GP 57
 Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V +YA ++ Y T+E T+ + + GLG L T + A G S+ A +

Sbjct: 58 VGFASYA-QFRGGVGYRHTMEHTIILGPAARGRGLGRALMTAIEDHARAGGTHSLFAGVS 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166

N H A+G+ L GYK G W D+ Q+

Sbjct: 117 AGNPEGRAFHAAAMGFAETAFLPQVGYKFGRWLDLVLMOQK 155

>ref|ZP_03149547.1| GCN5-related N-acetyltransferase [Geobacillus sp. G11MC16]

gb|EDY04365.1| GCN5-related N-acetyltransferase [Geobacillus sp. G11MC16]

Length = 166

Score = 60.8 bits (146), Expect = 8e-08, Method: Compositional matrix adjust.

Identities = 40/136 (29%), Positives = 64/136 (47%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP--QTPQEWIDDLERLQDRYPWLVAEVEG 66

IR ATAAD+ + I N I + V EP ++ + W + + P V E +G

Sbjct: 6 IRDATAADLPQIVRIYNETIPSRMVTADLEPVSVESRRRAWFEAHD--PHHRPLWVVEDDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126

V+ + R AY T E ++Y++ H+ GLG+ L + A G K+++ I

Sbjct: 64 VICAWLSFQSFYGRPAYRHTAEVSIYIAESHRGQGLGKLLKRAIDKAPALGMKTLLGFI 123

Query: 127 GLPNDPSVRLHEALGY 142

N+PS+RL G+

Sbjct: 124 FAHNEPSLRLFSRFGF 139

>ref|ZP_05076285.1| phosphinothricin N-acetyltransferase [Rhodobacterales bacterium HTCC2083]

gb|EDZ43945.1| phosphinothricin N-acetyltransferase [Rhodobacteraceae bacterium HTCC2083]

Length = 161

Score = 60.8 bits (146), Expect = 8e-08, Method: Compositional matrix adjust.

Identities = 42/157 (26%), Positives = 68/157 (43%), Gaps = 2/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

+R A D +C + N I+ + F ++ +T D+E + Y VAE +

Sbjct: 3 VRAALIGDAKGICAVWNPLIQDTATTFTSDMKTVAGIQQDIEARKGAY--FVAENNDDEII 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129

G A P++ Y +T E ++ ++ + + G G L L + QG S+ A I

Sbjct: 61 GFASYFPPFRGGPGYAYTKEHSINLAPQARGQGAGRALMQALEQHAADQGVHSLWAGISAE 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166

N V HE LG+T L G+K W D+ Q+

Sbjct: 121 NPSGVSFHEKLGFTHIARLPEVGFKFDRWMDLILMOQK 157

>ref|ZP_03593460.1| hypothetical protein Bsubs1_19761 [Bacillus subtilis subsp. subtilis str. 168]

ref|ZP_03597745.1| hypothetical protein BsubsN3_19677 [Bacillus subtilis subsp. subtilis str. NCIB 3610]

ref|ZP_03602146.1| hypothetical protein BsubsJ_19625 [Bacillus subtilis subsp. subtilis str. JH642]

ref|ZP_03606431.1| hypothetical protein BsubsS_19791 [Bacillus subtilis subsp. subtilis str. SMY]

Length = 165

Score = 60.8 bits (146), Expect = 8e-08, Method: Compositional matrix adjust.

Identities = 47/160 (29%), Positives = 72/160 (45%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68

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+R A   D+ AV   I N   I +   V   TEP TP++ ++           +   P   VAE E G V
Sbjct: 5   LRLAEHRDLEAVVAIYNSTIASRMVTADTEPVTPEDRMEWFSGHTESRPLYVAEDENGNV 64

Query: 69   AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
A           +   R AY+ T E ++Y+           +   G+GS L   L+           G +S++A I
Sbjct: 65   AAWISFETFYGRPAYNKTAEVSIYIDEACRGKGVGSYLLQEALRIAPNLGIRSLMAFIFG 124

Query: 129   PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRDF 168
N PS++L E   G+   G           G +D+   R+
Sbjct: 125   HNKPSLKLFEKHGFAEWGLFPGIAEMDGKRYDLKILGREL 164

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>ref|YP_004091673.1| GCN5-related N-acetyltransferase [Ethanoligenens harbinense
YUAN-3]
gb|ADU26942.1| GCN5-related N-acetyltransferase [Ethanoligenens harbinense YUAN-3]
Length = 168

```

Score = 60.8 bits (146), Expect = 8e-08, Method: Compositional matrix adjust.
Identities = 43/172 (25%), Positives = 76/172 (44%), Gaps = 12/172 (6%)

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Query: 1   MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQD----- 55
M           +   RP   D++ + +I   +YI   ST   F   Q   +   ID++   L
Sbjct: 1   MHVHEEQITFRPVQERDISGLLEIYLYYIRNSTGTGTF----QIAEIGIDEMRALVTPENAG 56

Query: 56   -RYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
R   +   A   E   +   G   A   ++ R A+   T E ++Y+ + +   G+GS   L
Sbjct: 57   YRSFSIFAGCE--LCGYASYHKYREREAFSKTAEISIYLKNEYAGCGIGSKALQMLEPLA 114

Query: 115   EAQGFKSVMVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
+   G   +++A++   N   S+RL +   GY   +   L+   GYK G + D+   Q+
Sbjct: 115   KNAGVHTLLALVCHENTESIRLFRSGYMMQSLKEVGKFGRYLDLVILQK 166

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>ref|NP_391537.1| phosphinothricin acetyltransferase [Bacillus subtilis subsp.
subtilis str. 168]
sp|P71043.1|YWNH_BACSU RecName: Full=Putative phosphinothricin acetyltransferase
YwnH;
Short=PPT N-acetyltransferase
emb|CAA69854.1| Unknown, similar to Streptomyces coelicolor phosphinothricin
N-acetyltransferase [Bacillus subtilis subsp. subtilis
str. 168]
emb|CAB15673.1| putative phosphinothricin acetyltransferase [Bacillus subtilis
subsp. subtilis str. 168]
Length = 163

```

Score = 60.8 bits (146), Expect = 8e-08, Method: Compositional matrix adjust.
Identities = 47/160 (29%), Positives = 72/160 (45%), Gaps = 1/160 (0%)

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Query: 10   IRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68
+R A   D+ AV   I N   I +   V   TEP TP++ ++           +   P   VAE E G V
Sbjct: 3   LRLAEHRDLEAVVAIYNSTIASRMVTADTEPVTPEDRMEWFSGHTESRPLYVAEDENGNV 62

Query: 69   AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
A           +   R AY+ T E ++Y+           +   G+GS L   L+           G +S++A I
Sbjct: 63   AAWISFETFYGRPAYNKTAEVSIYIDEACRGKGVGSYLLQEALRIAPNLGIRSLMAFIFG 122

Query: 129   PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRDF 168
N PS++L E   G+   G           G +D+   R+
Sbjct: 123   HNKPSLKLFEKHGFAEWGLFPGIAEMDGKRYDLKILGREL 162

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>ref|ZP_01129948.1| phosphinothricin acetyltransferase protein [marine
actinobacterium

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PHSC20C1]
gb|EAR25049.1| phosphinothricin acetyltransferase protein [marine actinobacterium
PHSC20C1]
Length = 168

Score = 60.5 bits (145), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 41/150 (27%), Positives = 71/150 (47%), Gaps = 3/150 (2%)

Query: 23 DIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGV-VAGIAYAGPWKAR 80
+I +Y+ T+ V F TP+ +++ P++VA + V G A PW+ +
Sbjct: 18 EIYGYVSTTVVTFDIVEVTPPEIMTAKRTAVEESGLPFIVAVDDSERVLGYAAMFPWRPK 77

Query: 81 NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP-NDPSVRLHEA 139
AY T E ++Y+S G+G L L++ G + ++AVI + SV LH+
Sbjct: 78 AAYKRTAEGSIYLSAATGQGVGGALLNELIERGRQVGIREIIAVISDEGTEASVHLHKK 137

Query: 140 LGYTARGTLRAAGYKHGGWHDVGFWRDQFE 169
LG+ + G L+ G+K W Q+ +
Sbjct: 138 LGFESIGHLKRVGFKFDRWVGTFMLMQKSID 167

>ref|XP_003034027.1| hypothetical protein SCHCODRAFT_52412 [Schizophyllum commune H4-8]
gb|EFI99124.1| hypothetical protein SCHCODRAFT_52412 [Schizophyllum commune H4-8]
Length = 196

Score = 60.5 bits (145), Expect = 9e-08, Method: Compositional matrix adjust.
Identities = 55/189 (29%), Positives = 83/189 (43%), Gaps = 33/189 (17%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVA-EVEGV 67
+RPA D+ A+ I +HYI S FRT+ P +D Q+ ++P+LVA EG
Sbjct: 5 VRPALTEDLPAITSIYDHYINHSVATFRTKRVEPSVLLDTYRSAQNSQHPFLVAVSHEGT 64

Query: 68 -VAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME----- 115
+ G AY ++A + AY TVE ++YV H G+GS L+T L ++
Sbjct: 65 EIVGYAYVSGYRASHPAYWHTVELSIYVHPNHLFGVGSRSLWTALEDALRQRNCALVDDK 124

Query: 116 -----AQGFKSVVAVIGLPNDPSV-----RLHEALGYTARGTLRAAGYKHG 156
A + V++V+ L + S + G+ +G L GYK G
Sbjct: 125 GHSPSLDERTSPGATPIRHVLSVMALDTEGSEGGYGLRDWYVKRGFVQKGHLEEVGYKFG 184

Query: 157 GWHDVGFQW 165
W D Q
Sbjct: 185 RWIDTIILQ 193

>ref|YP_003729814.1| acyltransferase [Pantoea vagans C9-1]
gb|ADI78142.1| putative acyltransferase [Pantoea vagans C9-1]
Length = 127

Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 39/107 (36%), Positives = 51/107 (47%)

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G A G W+ + Y TVE +VYV + G G L L++ QG +VA I
Sbjct: 21 VLGYSYSGDWRPWDGYCHTVEHSVYVHKSARGQGAGKALMEKLIRLATDQKGHVMVAGIE 80

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQFELPAPP 174
N S+ LH+ LG+T G L G K G W D+ F Q + A P
Sbjct: 81 SENVASISLHKKLGFTEAGRLSEVGNKFGHWLDLTLQLRLDTRAHP 127

>ref|ZP_04292465.1| GCN5-related N-acetyltransferase [Bacillus cereus R309803]

gb|EEK75819.1| GCN5-related N-acetyltransferase [Bacillus cereus R309803]
Length = 162

Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 43/159 (27%), Positives = 67/159 (42%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGV 67
+EIR AT D+ + I N IE TE +T + ++ L + + RY +V E
Sbjct: 1 MEIRKATEQDVQEITTIYNIEGIEDRIATLETEIRTDKYVMEWLFQREKRYSVIVMEENSH 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G A P+ R AY E ++Y+ ++ GLG L L K+ + F V
Sbjct: 61 IVGWASINPYSHRCAYRGVGEISYIKREYRGKGLGQNLLLALEKNGQQNEFYKFVLF 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N+ L+ +GY G G G DV ++
Sbjct: 121 SFNNLGQGLYRKMGYREVGVFEKQGIMDGEHVDVMIMEK 159

>ref|YP_333836.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei
1710b]
ref|ZP_04814366.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 1106b]
ref|ZP_04886066.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 1655]
gb|ABA47451.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei
1710b]
gb|EDU07050.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 1655]
gb|EES24991.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 1106b]
Length = 179

Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 47/141 (33%), Positives = 68/141 (48%), Gaps = 5/141 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAEEGV 67
R AT AD+ A+ I N + + V TEP T + W D R W+V E V
Sbjct: 18 RDATEPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 76

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+A ++++ + R AY T E ++Y+ + GLGS L L A G + + I
Sbjct: 77 IAWLSFSD-FYGRPAYGHTAEISIYLDEAARGSGLSRLLEAALAKAPALGVHTALGFIF 135

Query: 128 LPNDPSVRLHEALGYTARGTL 148
N+PS+RL G+TA GTL
Sbjct: 136 GHNEPSLRLFARYGFTAWGTL 156

>gb|EFS50244.1| acetyltransferase, GNAT family [Propionibacterium acnes HL025PA1]
Length = 166

Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 46/162 (28%), Positives = 75/162 (46%), Gaps = 6/162 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNF---RTEPQTPQEWIDDLERLQDRYPWLVAEV 64
V IR D+ A I N +T ++ T + W +L + D P LVAEV
Sbjct: 3 VNIRTMEERDLPAASRIYNQSAVATTYSYTVVNTNIEDRLSWWREL--IADSRPLLVAEV 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL-KSMEAQGFKSVV 123
+G +AG A ++ YD T E T+++ + + G+G L T L+ ++ +++
Sbjct: 61 DGTMAGYANYHRFREGGYDVTAEVTIWLDPQARGQGVGRKLMTELIRRARADDRLRNLL 120

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
+VI N+ S+ H A+G+ G L YK G W Q
Sbjct: 121 SVIDSDNERSISFHSAMGFVEVGRLPHIAYKLGWRTAVLMQ 162

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>ref|ZP_06427550.1| acetyltransferase, GNAT family [Propionibacterium acnes SK187]
ref|ZP_06428459.1| acetyltransferase, GNAT family [Propionibacterium acnes J165]
ref|YP_003580861.1| acetyltransferase, GNAT family [Propionibacterium acnes SK137]
gb|EFD02446.1| acetyltransferase, GNAT family [Propionibacterium acnes SK187]
gb|EFD08233.1| acetyltransferase, GNAT family [Propionibacterium acnes J165]
gb|ADE01244.1| acetyltransferase, GNAT family [Propionibacterium acnes SK137]
gb|EFS35306.1| acetyltransferase, GNAT family [Propionibacterium acnes HL013PA1]
gb|EFS37493.1| acetyltransferase, GNAT family [Propionibacterium acnes HL074PA1]
gb|EFS39715.1| acetyltransferase, GNAT family [Propionibacterium acnes HL110PA1]
gb|EFS43543.1| acetyltransferase, GNAT family [Propionibacterium acnes HL110PA2]
gb|EFS46661.1| acetyltransferase, GNAT family [Propionibacterium acnes HL087PA2]
gb|EFS52645.1| acetyltransferase, GNAT family [Propionibacterium acnes HL059PA1]
gb|EFS56667.1| acetyltransferase, GNAT family [Propionibacterium acnes HL046PA2]
gb|EFS58497.1| acetyltransferase, GNAT family [Propionibacterium acnes HL036PA1]
gb|EFS60167.1| acetyltransferase, GNAT family [Propionibacterium acnes HL036PA2]
gb|EFS63466.1| acetyltransferase, GNAT family [Propionibacterium acnes HL063PA1]
gb|EFS65808.1| acetyltransferase, GNAT family [Propionibacterium acnes HL063PA2]
gb|EFS68613.1| acetyltransferase, GNAT family [Propionibacterium acnes HL007PA1]
gb|EFS71040.1| acetyltransferase, GNAT family [Propionibacterium acnes HL056PA1]
gb|EFS76798.1| acetyltransferase, GNAT family [Propionibacterium acnes HL086PA1]
gb|EFS78811.1| acetyltransferase, GNAT family [Propionibacterium acnes HL005PA4]
gb|EFS82530.1| acetyltransferase, GNAT family [Propionibacterium acnes HL050PA1]
gb|EFS84334.1| acetyltransferase, GNAT family [Propionibacterium acnes HL050PA3]
gb|EFS89529.1| acetyltransferase, GNAT family [Propionibacterium acnes HL036PA3]
gb|EFS96008.1| acetyltransferase, GNAT family [Propionibacterium acnes HL067PA1]
gb|EFS98963.1| acetyltransferase, GNAT family [Propionibacterium acnes HL027PA1]
gb|EFT02748.1| acetyltransferase, GNAT family [Propionibacterium acnes HL002PA1]
gb|EFT03851.1| acetyltransferase, GNAT family [Propionibacterium acnes HL002PA2]
gb|EFT06424.1| acetyltransferase, GNAT family [Propionibacterium acnes HL082PA1]
gb|EFT12344.1| acetyltransferase, GNAT family [Propionibacterium acnes HL037PA1]
gb|EFT17882.1| acetyltransferase, GNAT family [Propionibacterium acnes HL053PA1]
gb|EFT20531.1| acetyltransferase, GNAT family [Propionibacterium acnes HL045PA1]
gb|EFT23226.1| acetyltransferase, GNAT family [Propionibacterium acnes HL072PA2]
gb|EFT27376.1| acetyltransferase, GNAT family [Propionibacterium acnes HL005PA1]
gb|EFT30780.1| acetyltransferase, GNAT family [Propionibacterium acnes HL005PA2]
gb|EFT33521.1| acetyltransferase, GNAT family [Propionibacterium acnes HL005PA3]
gb|EFT49470.1| acetyltransferase, GNAT family [Propionibacterium acnes HL053PA2]
gb|EFT52131.1| acetyltransferase, GNAT family [Propionibacterium acnes HL078PA1]
gb|EFT56012.1| acetyltransferase, GNAT family [Propionibacterium acnes HL027PA2]
gb|EFT61122.1| acetyltransferase, GNAT family [Propionibacterium acnes HL072PA1]
gb|EFT68538.1| acetyltransferase, GNAT family [Propionibacterium acnes HL038PA1]
gb|EFT70945.1| acetyltransferase, GNAT family [Propionibacterium acnes HL059PA2]
gb|EFT72766.1| acetyltransferase, GNAT family [Propionibacterium acnes HL046PA1]
gb|EFT79984.1| acetyltransferase, GNAT family [Propionibacterium acnes HL030PA2]
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Length = 166

Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.

Identities = 46/162 (28%), Positives = 75/162 (46%), Gaps = 6/162 (3%)

```
Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNF---RTEPQTPQEWIDDLERLQDRYPWLVAEV 64
V IR D+ A I N +T ++ T + W +L + D P LVAEV
Sbjct: 3 VNIRTMEERDLPAASRIYNQSAVATTYSYTVVNTNVEDRLSWWREL--IADSRPLLVAEV 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL-KSMEAQGFKSVV 123
+G +AG A ++ YD T E T+++ + + G+G L T L+ ++ +++++
Sbjct: 61 DGTMAGYANYHRFREGGGYDVTAEVTIWLDPQARGQGVGRKLMTELIRRARADDRLRNLL 120

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQ 165
+VI N+ S+ H A+G+ G L YK G W Q
Sbjct: 121 SVIDSDNERSISFHSAMGFVEVGRPLPHIAYKLGWRTAVLMQ 162
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>ref|YP_108060.1| putative acetyltransferase [Burkholderia pseudomallei K96243]
ref|YP_001066582.1| acetyltransferase [Burkholderia pseudomallei 1106a]
ref|ZP_02410942.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei 14]
ref|ZP_02447034.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei 91]
ref|ZP_02455234.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei 9]
ref|ZP_02470815.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei
B7210]
ref|ZP_02481253.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei
7894]
ref|ZP_02497632.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei 112]
ref|ZP_02505658.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei
BCC215]
ref|ZP_03792858.1| acetyltransferase, GNAT family [Burkholderia pseudomallei
Pakistan
9]
ref|ZP_04895657.1| acetyltransferase, GNAT family [Burkholderia pseudomallei Pasteur
52237]
ref|ZP_04950757.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 1710a]
ref|ZP_04964801.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 406e]
emb|CAH35440.1| putative acetyltransferase [Burkholderia pseudomallei K96243]
gb|ABN88846.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 1106a]
gb|EDO83908.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 406e]
gb|EDO92495.1| acetyltransferase, GNAT family [Burkholderia pseudomallei Pasteur
52237]
gb|EEH26670.1| acetyltransferase, GNAT family [Burkholderia pseudomallei Pakistan
9]
gb|EET07776.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 1710a]
Length = 168

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Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 47/141 (33%), Positives = 68/141 (48%), Gaps = 5/141 (3%)

```

Query: 11  RPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEEVEG 67
          R AT AD+ A+ I N + + V TEP T + W D R W+V E V
Sbjct: 7   RDATPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 65

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
          +A +++ + R AY T E ++Y+ + GLGS L L A G + + I
Sbjct: 66  IAWLSFS-DFYGRPAYGHTAEISIYLDEAARGSGLSRLLEAALAKAPALGVHTALGFIF 124

Query: 128  LPNDPSVRLHEALGYTARGTL 148
          N+PS+RL G+TA GTL
Sbjct: 125  GHNEPSLRLFARYGFTAWGTL 145

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>ref|ZP_06308276.1| GCN5-related N-acetyltransferase [Cylindrospermopsis raciborskii
CS-505]
gb|EFA69776.1| GCN5-related N-acetyltransferase [Cylindrospermopsis raciborskii
CS-505]
Length = 164

```

Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.
Identities = 43/142 (30%), Positives = 64/142 (45%), Gaps = 5/142 (3%)

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Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEEVEG 66
          IR AT D+ A+ I N + T EP T + W ER+ + P V E+
Sbjct: 3   IRNATELDLPAIVAIYNAVPTRMATADLEPVTLESRMTWFQ--ERVPSQRPLWVVEINY 60

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
          +AG + R AY T E ++Y+S R GLG TL + + G K++++ I
Sbjct: 61  NIAGWLSFQSFYGRPAYHATAEISIIYISPSFHRRGLGKTLTLLKAIDESPSLGIKTLLSFI 120

Query: 127  GLPNDPSVRLHEALGYTARGTL 148

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N PS++L G+ G L
 Sbjct: 121 FAHNQPSLQLFAQFGFQHWGLL 142

>ref|ZP_04386509.1| transcriptional regulator, ArsR family [Rhodococcus erythropolis SK121]
 gb|EEN86187.1| transcriptional regulator, ArsR family [Rhodococcus erythropolis SK121]
 Length = 273

Score = 60.5 bits (145), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 48/162 (29%), Positives = 76/162 (46%), Gaps = 4/162 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V +R + D AV I I+T T F T + ++ D + L D + W VAE++G
 Sbjct: 112 VVVRMESGDWDAVRSIYREGIDTGTATFTTSVPSAEKL--DAQWLPD-HRW-VAEIDGR 167

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 V G A P +R+ Y E+++Y+ + G+G L +++ +A +V + I
 Sbjct: 168 VEGWASLSPVSSRDCYRGVAENSIYIGSGARGRGVGLLLRRQVQAADASEIWTVQSSIF 227

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N SV LH+A+G+ GT G W D F +R E
 Sbjct: 228 PENRASVALHQAVGFRVVGTRSRIAQLGGRWRDTLFLERRSE 269

>ref|ZP_01078874.1| Phosphinothricin N-acetyltransferase, putative [Marinomonas sp. MED121]
 gb|EAQ63015.1| Phosphinothricin N-acetyltransferase, putative [Marinomonas sp. MED121]
 Length = 71

Score = 60.1 bits (144), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 28/69 (40%), Positives = 39/69 (56%), Gaps = 2/69 (2%)

Query: 106 LYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 +Y LL ++ + K+++A+I LPND S+ LHE +G GYK G W DVG+WQ
 Sbjct: 1 MYQALLDAISKRPKLNLLAIIALPNDASIALHEKIGMKKVAHFEKVGYKFGQWVDVGYWQ 60

Query: 166 RDFELPAPP 174
 LP P
 Sbjct: 61 --MSLPDNP 67

>ref|YP_001059314.1| acetyltransferase [Burkholderia pseudomallei 668]
 ref|ZP_01764555.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 305]
 ref|ZP_02402401.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei DM98]
 gb|ABN81999.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 668]
 gb|EBA51569.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 305]
 Length = 168

Score = 60.1 bits (144), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 47/141 (33%), Positives = 68/141 (48%), Gaps = 5/141 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEVEGV 67
 R AT AD+ A+ I N + + V TEP T + W D R W+V E V
 Sbjct: 7 RDATPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 +A ++++ + R AY T E ++Y+ + GLGS L L A G + + I
 Sbjct: 66 IAWLSFS-DFYGRPAYGHTAEISIYLDEAARGSGLSRLLEAALAKAPALGVHTALGFIF 124

Query: 128 LPNDPSVRLHEALGYTARGTL 148

N+PS+RL G+TA GTL

Sbjct: 125 GHNEPSLRLFARYGFTAWGTL 145

>ref|ZP_03918120.1| Phosphinothricin acetyltransferase [Corynebacterium
glucuronolyticum ATCC 51867]

gb|EEI27618.1| Phosphinothricin acetyltransferase [Corynebacterium
glucuronolyticum ATCC 51867]

Length = 163

Score = 60.1 bits (144), Expect = 1e-07, Method: Compositional matrix adjust.

Identities = 54/167 (32%), Positives = 73/167 (43%), Gaps = 20/167 (11%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR A A+D A+ I N E ST F P T + +R WL E VA

Sbjct: 5 IRLALASDAPALARIRNWAAEESTALFDNTPVT-----VANRTRWLAEEPVVVFA 54

Query: 70 GI-----AYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GF 119

+ A GP++ Y TVE++VYV + G+G L L+ EA

Sbjct: 55 DVDGDGDGIGYASYGPFRLVTGYRHTVENSIVYVLPNGHGAGIGTGLLQTLIAHAEANPDV 114

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

+VA I N+ S+ LH G+ +G L GYK G W DV +R

Sbjct: 115 HRMVAVIESTNEASLALHRRHGFEKGRLTEVGYKCGRWLDVTILER 161

>ref|ZP_06263749.1| acetyltransferase, GNAT family [Propionibacterium acnes J139]

gb|EFB89245.1| acetyltransferase, GNAT family [Propionibacterium acnes J139]

gb|EFS86648.1| acetyltransferase, GNAT family [Propionibacterium acnes HL001PA1]

gb|EFT10347.1| acetyltransferase, GNAT family [Propionibacterium acnes HL082PA2]

gb|EFT24868.1| acetyltransferase, GNAT family [Propionibacterium acnes HL110PA3]

gb|EFT62230.1| acetyltransferase, GNAT family [Propionibacterium acnes HL110PA4]

gb|EFT65388.1| acetyltransferase, GNAT family [Propionibacterium acnes HL060PA1]

Length = 166

Score = 60.1 bits (144), Expect = 1e-07, Method: Compositional matrix adjust.

Identities = 46/162 (28%), Positives = 75/162 (46%), Gaps = 6/162 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNF--RTEPQTPQEWIDDLERLQDRYPWLVAEV 64

V IR D+ A I N +T ++ T + W +L + D P LVAEV

Sbjct: 3 VNIRTMEERDLPAASRIYNQSAVATTYSYTVNTNVEDRLSWWREL--IADSRPLLVAEV 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL-KSMEAQGFKSVV 123

+G +AG A ++ YD T E T+++ + + G+G L T L+ ++ +++++

Sbjct: 61 DGTMAGYANYHRFREGGGYDVTAEVTIWLDPQARGQGVGRKLMTELIRRARADDRLRNLL 120

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165

+VI N+ S+ H A+G+ G L YK G W Q

Sbjct: 121 SVIDSDNERSISFHSAMGFVEVGRLPHIAYKLGDWRTAVLMQ 162

>gb|AAV70501.1| unknown [Bacillus sp. MB24]

Length = 164

Score = 60.1 bits (144), Expect = 1e-07, Method: Compositional matrix adjust.

Identities = 43/159 (27%), Positives = 66/159 (41%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+EIR AT D + I N IE TE +T + ++ L + + RY +V E

Sbjct: 1 MEIRKATEQDAQEIMTIYNEGIEDRIATLETEIKTDKYVMEWLFQREKRYSVIVMEENSH 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G A P+ R AY E ++Y+ ++ GLG L L K+ + F V
 Sbjct: 61 IVGWASINPYSHRCAYRGVGELSIYIKREYRGKGLGQKLLLALEKTGQKNEFYKFVLFTF 120

Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGVFWQR 166

N+ L+ +GY G G G DV ++
 Sbjct: 121 SFNNLGQGLYRKMGYREVGVFEKQGIMDGEHVDVMIMEK 159

>ref|YP_001812670.1| GCN5-related N-acetyltransferase [Exiguobacterium sibiricum 255-15]

gb|ACB59653.1| GCN5-related N-acetyltransferase [Exiguobacterium sibiricum 255-15]
 Length = 159

Score = 60.1 bits (144), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 43/159 (27%), Positives = 71/159 (44%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ +R TA D V I IET FRTE W + ++ LVAE +G
 Sbjct: 1 MNVRAMTATDYPEVGRIYQQGIETQNATFRTEVPFPDYW----DAHHHKHSRLVAEEDGK 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

+ G P+ + AY E ++Y+ + + G+G+ L ++++ EA G ++ + I
 Sbjct: 57 LLGWVAISPFFSSIPAYRGVAEVSLEYIDEKLRGKGVGTALMQAVIEASEAAGIWTLSQIF 116

Query: 128 LPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGVFWQR 166

N S++LH+ G+ G G G W D +R
 Sbjct: 117 PENTASLKLHQRFGRFREVGRERIGQLAGVWRDTILLER 155

>ref|YP_574837.1| GCN5-related N-acetyltransferase [Chromohalobacter salexigens DSM 3043]

gb|ABE60138.1| GCN5-related N-acetyltransferase [Chromohalobacter salexigens DSM 3043]
 Length = 172

Score = 60.1 bits (144), Expect = 1e-07, Method: Compositional matrix adjust.
 Identities = 43/142 (30%), Positives = 64/142 (45%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEG 66

IR A D+A V +I N + + TEP + EW + +R P LV E+
 Sbjct: 3 IRNAEEQDLARVVEIYNAAVPSKRSTADTEPVSIASKSEWFR--KHNPERRPLLVYEIND 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 126

VA + R AY +T E ++Y+S HQ LG TL L+ K+++ +
 Sbjct: 61 EVAAWVSFEDFYGRPAYHYTAEISYISPEHQGQRLGQTLREALELAPKLELKTIGYV 120

Query: 127 GLPNDPSVRLHEALGYTARGL 148

N+PS+RL G+ G L
 Sbjct: 121 FAHNEPSIRLLRGFGFQEWGRL 142

>ref|YP_002776597.1| putative ArsR family transcriptional regulator [Rhodococcus opacus

B4]
 dbj|BAH55745.1| putative ArsR family transcriptional regulator [Rhodococcus opacus B4]
 Length = 289

Score = 59.7 bits (143), Expect = 2e-07, Method: Compositional matrix adjust.
 Identities = 50/164 (30%), Positives = 70/164 (42%), Gaps = 14/164 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL-----VA 62

V +RP T D V I I T T F T E T +E +D WL VA

Sbjct: 129 VTVRPMTEQDWDVRRRIYEGEATRTATFTTEVPT-RETLD-----AQWLPGHRWVA 179

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122

E++GVV G A P R+ Y E++VYV+ + G+G TL + + + G ++

Sbjct: 180 EIDGVVVGWAALSPTSGRDCYRGVAENSVYVADGMRGRGVGKTLRLTQVIAADEAGIWT 239

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166

I N S+ LH + G+ G G W D F +R

Sbjct: 240 QTSIFPENRASIALHHSAGFRTIGVRERIRLDGIWRDVFLE 283

>ref|ZP_07468658.1| phosphinothricin acetyltransferase [Corynebacterium accolens ATCC 49726]

gb|EFM44049.1| phosphinothricin acetyltransferase [Corynebacterium accolens ATCC 49726]

Length = 151

Score = 59.7 bits (143), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 44/141 (31%), Positives = 71/141 (50%), Gaps = 3/141 (2%)

Query: 21 VCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDR-YPWLVAEVE-GVVAGIAYAGPWK 78

+ D +N IE + V F + P T E + L +Q+ P+LVAE + G G A P++

Sbjct: 1 MTDTLNWAEHTDVFIDSTPVTVAEREHLRHIQELGCPFLVAETDAGEYLGWALYHPYR 60

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQF-KKSVVAVIGLPNDPSVRLH 137

+ E+T+Y+S Q G+G+ L + L+ A +++A+I N S++LH

Sbjct: 61 DPRIWQGCYETTYLSPNAQGGVGTALMSELVDRAADKVVHALLALIVSTNTASLKLH 120

Query: 138 EALGYTARGTLRAAGYKHGGW 158

E G+ GTL+ YK W

Sbjct: 121 EKFGFENVGTLKEVYKFDHW 141

>ref|YP_002766834.1| ArsR family transcriptional regulator [Rhodococcus erythropolis PR4]

dbj|BAH34095.1| putative ArsR family transcriptional regulator [Rhodococcus erythropolis PR4]

Length = 278

Score = 59.7 bits (143), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 48/162 (29%), Positives = 76/162 (46%), Gaps = 4/162 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

V +R + D AV I I+T T F T + ++ D + L D + W VAE++G

Sbjct: 112 VVLRRMESGDWDVAVRSIYREGIDTGTATFTTSVPSAEKL--DAQWLPD-HRW-VAEIDGR 167

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

V G A P +R+ Y E+++Y+ + G+G L +++ +A +V + I

Sbjct: 168 VEGWASLSPSSRDCYRGVAENSIYIGSGARGRGVKGKLLRRQVQAADASEIWTQSSIF 227

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169

N SV LH+A+G+ GT G W D F +R E

Sbjct: 228 PENRASVALHQAVGFRIVGTRSRQAQLGGRWRDTLFLERRSE 269

>ref|YP_001137970.1| hypothetical protein cgR_1092 [Corynebacterium glutamicum R]

dbj|BAF54068.1| hypothetical protein [Corynebacterium glutamicum R]

Length = 176

Score = 59.7 bits (143), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 45/173 (26%), Positives = 71/173 (41%), Gaps = 8/173 (4%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAE 64

```

      R   IRP   D   V DI   +ET   ++ T   T   ++   ++ D   V
Sbjct: 3   ERDFTIRPIREGDFPQVRDIYELGLETGHASYETSGPTWDQF--SQSKIMDTVMVAVENN 60

Query: 65   E-GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
      +   + G   A P   +R   +   VE ++Y+   + Q   G+G   L   L+   E+ G   S+
Sbjct: 61   DPDFILGWVSAAPISSRQVFHGVVEDSIYIHPQGQGRGIGGALLDALITYCESNGIWSIH 120

Query: 124  AVIGLPNDPSVRLHEALGYTARGTLRAA-----GYKHGGWHDVGVFWQRDFELP 171
      + I   N   S +LHE+ G+   GT+   G   G W D   W+R   +P
Sbjct: 121  SWIFPENLGS AKLHESKGFVKVGTMHQMARMYPY GEMEGQWRDCDLWERLLSVP 173

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>ref|YP_003086321.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM
18053]
gb|ACT93156.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM 18053]
      Length = 164

```

Score = 59.3 bits (142), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 47/157 (29%), Positives = 63/157 (40%), Gaps = 3/157 (1%)

```

Query: 10   IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
      IR   +D   AV DI   I T   T P   W D   RY   +   G VA
Sbjct: 3   IRELLPSDWP AVRDIYAQGIATGQATLETSPPEWAVW-DQSHVANLRY--VAVSDHGEVA 59

Query: 70   GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
      G A   P   R Y   E ++Y++   +   +G   L   HL+   E +G+ ++ A I
Sbjct: 60   GWAALTPVSGRCVYTGVAEVSIIYIAKAFRGQKIGDLLLLKHLIIIESEGKGYWTLQAGIFPE 119

Query: 130  NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
      N S+RLHE G+   G   G   G W DV   +R
Sbjct: 120  NPASIRLHENNGFRIIGYREKIGKMKGAWRD VNLLER 156

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>ref|ZP_06735037.1| putative phosphinothricin N-acetyltransferase [Neisseria elongata
      subsp. glycolytica ATCC 29315]
gb|EFE49373.1| putative phosphinothricin N-acetyltransferase [Neisseria elongata
      subsp. glycolytica ATCC 29315]
      Length = 167

```

Score = 59.3 bits (142), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 41/142 (28%), Positives = 66/142 (46%), Gaps = 5/142 (3%)

```

Query: 10   IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP--QE WIDDLERLQDRYPWLVAEVEG 66
      I A   D+AA+ DI N I++   P T   Q W+D   +R   +++   EG
Sbjct: 6   ITEARQDDLAAIVDIYNSTIDSR LATADLSPATVESRQSWLD--AHGGNRPLYVLKNQEG 63

Query: 67   VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
      +   +   R AY   T E ++YV H   + +G+G   L   ++L+   + G K+++AVI
Sbjct: 64   ELLAWGGFSDYYPREAYSITAEISIIYVRHDMRGVGVGKILVRYMLEKAPSLGIKNIIAVI 123

Query: 127  GLPNDPSVRLHEALGYTARGTL 148
      N S+RL   G+   G L
Sbjct: 124  FGHNHASIRLFHTFGFQEWGRL 145

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>ref|YP_002526507.1| GCN5-related N-acetyltransferase [Rhodobacter sphaeroides KD131]
gb|ACM02006.1| GCN5-related N-acetyltransferase [Rhodobacter sphaeroides KD131]
      Length = 158

```

Score = 59.3 bits (142), Expect = 2e-07, Method: Compositional matrix adjust.
Identities = 50/159 (31%), Positives = 72/159 (45%), Gaps = 7/159 (4%)

```

Query: 10   IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAE-VEGV 67

```

IRPA AAD+ A+ I N I + V F E ++ D+L L P +LVA+ EG
 Sbjct: 2 IRPAVAADVPALLAIWNPIIRDTLVTFNAEEKSA----DELRALIAARPAFLVADPGEGP 57

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 V +YA ++ Y T+E T+ + + GLG L T + G S+ A +
 Sbjct: 58 VGFASYA-QFRGGVGYRHTMEHTIILGPAARGRGLGRALMTAIEDHARRGGVHSLFAGVS 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N H A+G+ L GYK G W D+ Q+
 Sbjct: 117 AGNPEGRAFHAAAMGFAETAVLPQVGKFGRWLDLVLQM 155

>ref|YP_001271389.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri DSM 20016]
 ref|YP_001841755.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri JCM 1112]
 ref|ZP_03848980.1| acetyltransferase [Lactobacillus reuteri MM2-3]
 ref|ZP_08161957.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri MM4-1A]
 gb|ABQ83052.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri DSM 20016]
 dbj|BAG25275.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri JCM 1112]
 gb|EEI08402.1| acetyltransferase [Lactobacillus reuteri MM2-3]
 gb|EGC15229.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri MM4-1A]
 Length = 164

Score = 59.3 bits (142), Expect = 2e-07, Method: Compositional matrix adjust.
 Identities = 41/159 (25%), Positives = 69/159 (43%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAG 70
 R AT D+ + +I N I + P T ++ + E + YP V E + V G
 Sbjct: 6 RKATLEDLPKIVEIYNQIIPSRLATADLTPTVEKRKEWFEAFDENYPIWVIEYQKEVLG 65

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPN 130
 + R AYD T E +Y+ R ++ G+G+ ++ + ++VA I N
 Sbjct: 66 WVALEHFYGRPAYDHTSEIAIYLDQRLRKQGVGKTMEFIIGQLPKLTVDTIVAYIFGHN 125

Query: 131 DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRD 169
 PS++L ++ G+T G L G D+ R F+
 Sbjct: 126 IPSLKLKFSFGFTQWGLLPQVAELDGIKRDVLILGRHFK 164

>dbj|BAI87305.1| hypothetical protein BSNT_05581 [Bacillus subtilis subsp. natto BEST195]
 Length = 165

Score = 58.9 bits (141), Expect = 2e-07, Method: Compositional matrix adjust.
 Identities = 47/160 (29%), Positives = 72/160 (45%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68
 +R A D+ AV I N I + V TEP TP++ ++ + P VAE E G V
 Sbjct: 5 LRLAEHRDLEAVVAIYNSTIASRMVTADTEPVTPEDRMEWFLGHTEARPLYVAEDENG 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGL 128
 A + R AY+ T E ++Y+ + G+GS L L+ G +S++A I
 Sbjct: 65 AAWISFETFYGRPAYNKTAEVSIYIDEACRGKGVSYLLQEALRIAPDLGIRSLMAFIFG 124

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRD 168
 N PS++L E G+ G G +D+ R+
 Sbjct: 125 HNKPSLKLFEKHGFAEWGLFPGIAEMDGKRYDLKILGREL 164

>ref|YP_003832435.1| GNAT family acetyltransferase [Butyrivibrio proteoclasticus B316]

gb|ADL35853.1| acetyltransferase GNAT family [Butyrivibrio proteoclasticus B316]
Length = 154

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 42/146 (28%), Positives = 64/146 (43%), Gaps = 5/146 (3%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGP 76
D V +I +E T F TE + EW + + V E EG V G P
Sbjct: 5 DWGTVAEIIYKQGLEEGTSTFNTECPSTFEWNEG----HVKNCRFVFEEEGKVVGWIALSP 60

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
+R AY VE +VYV ++ G+G+ L +++ E G+ S+ + I N S+ L
Sbjct: 61 SSSRCAYKGCVEMSVYVDRNYRGHGIGITALVNTIIREAEKDGYSIYSAIFSINKASIAL 120

Query: 137 HEALGYTARGTL-RAAGYKHGGWHDV 161
H+ G+ G R A + G W +
Sbjct: 121 HKKCGFREIGYRERIAKDRFGKWQNT 146

>gb|EFS74684.1| acetyltransferase, GNAT family [Propionibacterium acnes HL037PA2]
gb|EFS93270.1| acetyltransferase, GNAT family [Propionibacterium acnes HL044PA1]
gb|EFT15574.1| acetyltransferase, GNAT family [Propionibacterium acnes HL037PA3]
Length = 166

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 47/162 (29%), Positives = 73/162 (45%), Gaps = 6/162 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPWLVAEV 64
V IR D+ I N +T ++ T+ + W +L + D P LVAEV
Sbjct: 3 VNIRAMEERDLPTASRIYNQSAVATTYSYTLVDTKVEDRLSWWHEL--VADGRPVLVAEV 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QGFKSVV 123
+ +AG A ++ YD T E T+++ + G+G L L++ A +++
Sbjct: 61 DETMAGYATYHRFRGGGYDVTAEVTIWLDAPARGRGVGRKLMAELIRHARADHHLNLL 120

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
AVI N+ S+ H A+G+T G L YK G W F Q
Sbjct: 121 AVIDSQNERSIGFHSAMGFTEVGRLPHIAYKLGDWRTAVFMQ 162

>ref|YP_001044314.1| GCN5-related N-acetyltransferase [Rhodobacter sphaeroides ATCC
17029]
gb|ABN77542.1| GCN5-related N-acetyltransferase [Rhodobacter sphaeroides ATCC
17029]
Length = 158

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 47/158 (29%), Positives = 68/158 (43%), Gaps = 5/158 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
IRPA AAD+ A+ I N I + V F E ++ D+L L P +LVA+
Sbjct: 2 IRPAVAADVPALLAIWNPIIRDTLVTFNAEEKSA----DELHALIAARPAFLVADPGDGP 57

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A ++ Y T+E T+ + + GLG L T + G S+ A +
Sbjct: 58 VGFASYAQFRGGVGYRHTMEHTIILGPAARGRGLGRALMTAIEDHARRGGVHSLFAGVSA 117

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 166
N H A+G+ L GYK G W D+ Q+
Sbjct: 118 GNPEGRAFHAAMGFAETAVLPQVGKFGRWLDLVLQM 155

>ref|YP_001029322.1| phosphinothricin acetyltransferase [Burkholderia mallei NCTC 10229]
 ref|ZP_04904092.1| acetyltransferase, GNAT family [Burkholderia pseudomallei S13]
 gb|ABN02247.1| phosphinothricin acetyltransferase [Burkholderia mallei NCTC 10229]
 gb|EDS87104.1| acetyltransferase, GNAT family [Burkholderia pseudomallei S13]
 Length = 179

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
 Identities = 46/141 (32%), Positives = 67/141 (47%), Gaps = 5/141 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEVEGV 67
 R AT AD+ A+ I N + + V TEP T + W D R W+V E V
 Sbjct: 18 R DATPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 76

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 +A +++ + R AY T E ++Y+ + GLGS L L A G + + I
 Sbjct: 77 IAWLSFSD-FYGRPAYGHTAEISIYLDEAARGSGLSRLLEAALAKAPALGVHTALGFIF 135

Query: 128 LPNDPSVRLHEALGYTARGTL 148
 N+PS+RL G+T GTL
 Sbjct: 136 GHNEPSLRLFARYGFTTWGTL 156

>ref|ZP_03931541.1| Phosphinothricin acetyltransferase [Corynebacterium accolens ATCC 49725]
 gb|EEI15480.1| Phosphinothricin acetyltransferase [Corynebacterium accolens ATCC 49725]
 Length = 151

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
 Identities = 44/141 (31%), Positives = 70/141 (49%), Gaps = 3/141 (2%)

Query: 21 VCDIVNHYIETSTVNFRTEPQTPQE WIDDLERLQDR-YPWLVAEVE-GVVAGIAYAGPWK 78
 + D +N IE + V F + P T E + L +Q+ P+LVAE G G A P++
 Sbjct: 1 MTDTLNWAIEHTDVIFDSTPVTVAEREHLRHIQELGCPFLVAETNAGEYLGWALYHPYR 60

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG-FKSVVAVIGLPNDPSVRLH 137
 + E+T+Y+S Q G+G+ L + L+ A +++A+I N S++LH
 Sbjct: 61 DPRIWQGCYETTIYLSRNAQGGVGTALMSELVDRARADDKVHALLALIVSTNTASLKLH 120

Query: 138 EALGYTARGTLRAAGYKHGGW 158
 E G+ GTL+ YK W
 Sbjct: 121 EKFGFENVGTLKEVITYKFDHW 141

>ref|ZP_04231266.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock3-29]
 gb|EEL37022.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock3-29]
 Length = 164

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
 Identities = 43/159 (27%), Positives = 64/159 (40%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE WIDDLERLQDRYPWLVAEVEGV 67
 +EIR A D + I N IE TE +T +D L + + RY +V E
 Sbjct: 1 MEIRKAIEQDAQEIMTIYNEGIEDRIATLETEIKTDTYVMDWLFQREKRYSVIVIEENSK 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A P+ R AY E ++Y+ ++ GLG L L K+ + F V
 Sbjct: 61 IVGWASINPYSHRCAYRGVGEISYIKREYRGKGLGQKLLALEKTGQQNEFYKFVLFTF 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N+ L+ +GY G G G DV ++
 Sbjct: 121 SFNNLGQGLYRKMGYREVGVFEKQGVMDGEHVDVMIMEK 159

>ref|ZP_02186123.1| phosphinothricin N-acetyltransferase [Carnobacterium sp. AT7]
 gb|EDP67109.1| phosphinothricin N-acetyltransferase [Carnobacterium sp. AT7]
 Length = 174

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
 Identities = 43/153 (28%), Positives = 72/153 (47%), Gaps = 2/153 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
 IR A+ D+ + DI N I T + + T ++ E Q ++YP + EV+G V
 Sbjct: 13 IREASLNDLPEMVDIYNKAILTGGITCDIDVFTVEQRKSWFESHQTEKYPLFIYEVDGKV 72

Query: 69 AGIAYAGPWK-ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 AG ++ ++ R A + E + YV+ ++ G+GS L H L+ G+ +V+A+I
 Sbjct: 73 AGYSHLSGYRVGRRRAVERVAEISYYVNSDYRNRGIGSKLVEHTLQQAREIGYHNMAMIV 132

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 N S L G+ G + +G HD
 Sbjct: 133 EGN GASEYLLSKFGFQQWGRMPKVAEFNGELHD 165

>ref|YP_002897089.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei
 MSHR346]
 gb|ACQ96170.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei
 MSHR346]
 Length = 168

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
 Identities = 46/141 (32%), Positives = 67/141 (47%), Gaps = 5/141 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAEVEGV 67
 R AT AD+ A+ I N + + V TEP T + W D R W+V E V
 Sbjct: 7 R DATPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 +A +++ + R AY T E ++Y+ + GLGS L L A G + + I
 Sbjct: 66 IAWLSFS-DFYGRPAYGHTAEISIYLDEAARGSGLSRLLEAALAKAPALGVHTALGFIF 124

Query: 128 LPNDPSVRLHEALGYTARGTL 148
 N+PS+RL G+T GTL
 Sbjct: 125 GHNEPSLRLFARYGFTTWGTL 145

>ref|YP_002464793.1| GCN5-related N-acetyltransferase [Chloroflexus aggregans DSM
 9485]
 gb|ACL26357.1| GCN5-related N-acetyltransferase [Chloroflexus aggregans DSM 9485]
 Length = 170

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
 Identities = 42/162 (25%), Positives = 68/162 (41%), Gaps = 9/162 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
 V R AT AD A+ I N I F T P+T +E W DR+P +V +
 Sbjct: 4 VLTRSATVADAEIAIAIYNQGIADRIATFETRPRTAEVAGW-----FGDRFPPIVVTII 57

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 + A P++ R+ Y E +VYV + G+G L+++ GF +++
 Sbjct: 58 NDQIVAFAAATFPYRPRDCYAGIAEFSVYVEREWRGRGIGRLTMLALIEAATHAGFWKLLS 117

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
 + + N S + ++G+ G G W DV +R
 Sbjct: 118 RVFVENTASRAMLASVGFREVGIIYK HARLDGHWRDVVIVER 159

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>ref|YP_055338.1| N-acetyltransferase [Propionibacterium acnes KPA171202]
gb|AAT82380.1| N-acetyltransferase [Propionibacterium acnes KPA171202]
gb|EFT79246.1| acetyltransferase, GNAT family [Propionibacterium acnes HL030PA1]
      Length = 166
```

Score = 58.9 bits (141), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 45/162 (27%), Positives = 74/162 (45%), Gaps = 6/162 (3%)

```
Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNF---RTEPQTPQEWIDDLERLQDRYPWLVAEV 64
      V IR      D+      I N      +T ++      T +      W +L + D P LVAEV
Sbjct: 3  VNIRTMEERDLPTASRIYNQSAVATTYSYTVVNTNVEDRLSWWREL--IADSRPLLVAEV 60

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL-KSMEAQGFKSVV 123
      +G +AG A      ++      YD T E T+++ + + G+G L T L+ ++      ++++
Sbjct: 61  DGTMAGYANYHRFREGGGYDVTAEVTIWLDPQARGQGVGRKLMTELIRRARADDRLRNLL 120

Query: 124  AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
      +VI N+ S+ H A+G+ G L YK G W Q
Sbjct: 121  SVIDSDNERSISFHSAMGFVEVGRLPHIAYKLGWRTAVLMQ 162
```

```
>ref|ZP_01038277.1| phosphinothricin N-acetyltransferase, putative [Roseovarius sp.
      217]
gb|EAQ23120.1| phosphinothricin N-acetyltransferase, putative [Roseovarius sp.
      217]
      Length = 159
```

Score = 58.5 bits (140), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 43/159 (27%), Positives = 67/159 (42%), Gaps = 2/159 (1%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
      +R A D+ + N I ++V F T +T D+ + V E +GVV
Sbjct: 3  VRQAEQRDIGPILAFWNPLIRETSVTFTTVEKTADSLAGDMA--ARGLAFQVIEEQGVVL 60

Query: 70  GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
      G A G +++ Y T E TV ++ + GLG L T L A +VA +
Sbjct: 61  GFASYGGFRSGPGYARTAEHTVILAQAARGRGLGRALMTRLEDVARAADLHVLVAGVSGE 120

Query: 130  NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDF 168
      N ++ H A+GY+ + G K G W D+ Q+
Sbjct: 121  NAAAIAFHRAIGYSEVARMPFVGRKFGRWLDLVLLQKTL 159
```

```
>ref|YP_003314238.1| sortase-like acyltransferase [Sanguibacter keddieii DSM 10542]
gb|ACZ21404.1| sortase-like acyltransferase [Sanguibacter keddieii DSM 10542]
      Length = 166
```

Score = 58.5 bits (140), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 48/159 (30%), Positives = 65/159 (40%), Gaps = 3/159 (1%)

```
Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
      + +R T +D V DI I T F T T W + D + + + G+
Sbjct: 6  LTLRAMTPSDWGRVADIYTAGIATGQATFET---TVPSWEAFDQGLDTHRTVAVDASGL 62

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
      V G P AR AY VE++VYV G+G L HL+ S E G ++ A I
Sbjct: 63  VVGWCAVSPISARPAYAGVVENSVYVDPAAAGHGVGGALLAHLVASTEVTGIWTIQAGIF 122

Query: 128  LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
      N S+RLH G+ G G W DV +R
Sbjct: 123  PENTASMRLHARAGFRVVGVRERIAQLKGTWRDVALER 161
```

```
>ref|YP_103078.1| phosphinothricin acetyltransferase [Burkholderia mallei ATCC 23344]
ref|ZP_00439036.1| phosphinothricin acetyltransferase [Burkholderia mallei GB8 horse
4]
ref|YP_993233.1| phosphinothricin acetyltransferase [Burkholderia mallei SAVP1]
ref|YP_001080741.1| phosphinothricin acetyltransferase [Burkholderia mallei NCTC
10247]
ref|ZP_02264599.1| phosphinothricin acetyltransferase [Burkholderia mallei PRL-20]
ref|ZP_04885083.1| phosphinothricin acetyltransferase [Burkholderia mallei ATCC
10399]
ref|ZP_04906390.1| phosphinothricin acetyltransferase [Burkholderia mallei FMH]
ref|ZP_04912710.1| phosphinothricin acetyltransferase [Burkholderia mallei JHU]
ref|ZP_04974500.1| phosphinothricin acetyltransferase [Burkholderia mallei
2002721280]
gb|AAU47628.1| phosphinothricin acetyltransferase [Burkholderia mallei ATCC 23344]
gb|ABM50325.1| phosphinothricin acetyltransferase [Burkholderia mallei SAVP1]
gb|ABO06228.1| phosphinothricin acetyltransferase [Burkholderia mallei NCTC 10247]
gb|EDK56694.1| phosphinothricin acetyltransferase [Burkholderia mallei FMH]
gb|EDK60866.1| phosphinothricin acetyltransferase [Burkholderia mallei JHU]
gb|EDK85375.1| phosphinothricin acetyltransferase [Burkholderia mallei 2002721280]
gb|EDP89437.1| phosphinothricin acetyltransferase [Burkholderia mallei ATCC 10399]
gb|EEP84365.1| phosphinothricin acetyltransferase [Burkholderia mallei GB8 horse
4]
gb|EES47285.1| phosphinothricin acetyltransferase [Burkholderia mallei PRL-20]
Length = 168
```

Score = 58.5 bits (140), Expect = 3e-07, Method: Compositional matrix adjust.
Identities = 46/141 (32%), Positives = 67/141 (47%), Gaps = 5/141 (3%)

```
Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTP--QEWIDDLERLQDRYPWLVAEEVEGV 67
R AT AD+ A+ I N + + V TEP T + W D R W+V E V
Sbjct: 7 R DATPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+A +++ + R AY T E ++Y+ + GLGS L L A G + + I
Sbjct: 66 IAWLSFS-DFYGRPAYGHTAEISIYLDEAARGSGLGSRLLAALAKAPALGVHTALGFIF 124

Query: 128 LPNDPSVRLHEALGYTARGTL 148
N+PS+RL G+T GTL
Sbjct: 125 GHNEPSLRLFARYGFTTWGTL 145
```

```
>pdb|1VHS|A Chain A, Crystal Structure Of A Putative Phosphinothricin N-
Acetyltransferase
pdb|1VHS|B Chain B, Crystal Structure Of A Putative Phosphinothricin N-
Acetyltransferase
Length = 175
```

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 47/160 (29%), Positives = 70/160 (43%), Gaps = 1/160 (0%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEEV-GVV 68
+R A D+ AV I N I + V TEP TP++ + + P VAE E G V
Sbjct: 5 LRLAEHRDLEAVVAIYNSTIASRXVTADTEPVTPEDRXEWFSGHTESTRPLYVAEDENGNV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
A + R AY+ T E ++Y+ + G+GS L L+ G +S+ A I
Sbjct: 65 AAWISFETFYGRPAYNKTAEVSIYIDEACRGKGVGSYLLQEALRIAPNLGIRSLXAFIFG 124

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQWQDF 168
N PS++L E G+ G G +D+ R+
Sbjct: 125 HNKPSLKLFEKHGFAEWGLFPGIAEXDGKRYDLKILGREL 164
```

```
>ref|ZP_03495248.1| GCN5-related N-acetyltransferase [Alicyclobacillus acidocaldarius
LAA1]
gb|EED06032.1| GCN5-related N-acetyltransferase [Alicyclobacillus acidocaldarius
LAA1]
Length = 164
```

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 46/154 (29%), Positives = 60/154 (38%)

```
Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V++R AT DMAA+ I N IE + + + RYP VA V
Sbjct: 3 VDVRIATREDMAAILSINQGIEDRIATLEQDLKDMAYIESWFSQHNSRYPVFVATVGSN 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G A P+ R AY E +VYV + G+G L L GF +V
Sbjct: 63 VVGWADLHPYSHRCAYAGVGELSVYVERSWRGKGVGQALLRQLESHAMEHGFHKLVLATF 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N L+ +G+ G R G G W DV
Sbjct: 123 PFNQAGQGLYRKMGFREVGIFFRRHGKLDGQWVDV 156
```

```
>ref|ZP_05394037.1| GCN5-related N-acetyltransferase [Clostridium carboxidivorans P7]
ref|ZP_06856203.1| acetyltransferase, GNAT family [Clostridium carboxidivorans P7]
gb|EET85506.1| GCN5-related N-acetyltransferase [Clostridium carboxidivorans P7]
gb|EFG87206.1| acetyltransferase, GNAT family [Clostridium carboxidivorans P7]
Length = 166
```

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 43/159 (27%), Positives = 68/159 (42%), Gaps = 5/159 (3%)

```
Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+I D V I I T F+TE T+ W + + LVA E V
Sbjct: 4 KIEEMKKEDWEEVSKIYLEGINTGKATFQTEIPTWENW----DSSHTKSCLVAHFENKV 59

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G P +R Y E ++Y+ ++ G+G L T+L+ E GF ++ + I
Sbjct: 60 LGWVALSPTSSRCVYSGVAEVSIIYIGEEYRGKGIGKALLTNLIDLSEKDGFWTLQSGIIK 119

Query: 129 PNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGVFWQR 166
N S+ LH++ G+ G + + +G WHDV +R
Sbjct: 120 ENLASIALHKSCGFREIGVREKISKMSNGVWHDVVLMLER 158
```

```
>ref|ZP_04433180.1| GCN5-related N-acetyltransferase [Bacillus coagulans 36D1]
gb|EEN90936.1| GCN5-related N-acetyltransferase [Bacillus coagulans 36D1]
Length = 169
```

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.
Identities = 42/153 (27%), Positives = 68/153 (44%), Gaps = 1/153 (0%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEGVV 68
IR AT D+ + DI N I + T P T +E + + D P V E +G +
Sbjct: 7 IRNATEEDLQEILDIYNACIGNGIITADTVPVTVEEKLPWFKAHPDSRPLVWLEADGEI 66

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
A + R AY T E ++YVS + + G G L +L++ G ++++ I
Sbjct: 67 AAWISLSDFYGRPAYQPTAEVSIYVSEKWRGKGAGKHLGKMLEACPKLGVETLLGFIFS 126

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N S++L + G+ G L+ G HD+
```

Sbjct: 127 ENKASLKLFAFSGFETWGHLEKAVLDGRMHDL 159

>ref|ZP_02489505.1| phosphinothricin acetyltransferase [Burkholderia pseudomallei NCTC

13177]

ref|ZP_03453291.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 576]

gb|EEC35547.1| acetyltransferase, GNAT family [Burkholderia pseudomallei 576]

Length = 168

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.

Identities = 47/141 (33%), Positives = 67/141 (47%), Gaps = 5/141 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEVEGV 67

R AT AD+ A+ I N + + V TEP T + W D R W+V E V

Sbjct: 7 RDATPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+A +++ + R AY T E ++Y+ + GLGS L L A G + + I

Sbjct: 66 IAWLSFS-DFYGRPAYGHTAEISIYLDEAARGSGLSRLLEAALAKAPALGVHTALGFIF 124

Query: 128 LPNDPSVRLHEALGYTARGTL 148

N PS+RL G+TA GTL

Sbjct: 125 GHNVP SLRLFARYGFTAWGTL 145

>ref|YP_002005514.1| acetyltransferase; phosphinothricin acetyltransferase

[Cupriavidus

taiwanensis LMG 19424]

emb|CAQ69447.1| putative acetyltransferase; putative Phosphinothricin

acetyltransferase [Cupriavidus taiwanensis LMG 19424]

Length = 168

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.

Identities = 44/144 (30%), Positives = 64/144 (44%), Gaps = 6/144 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYP-WLVAEV 64

+R A D+ + I N + + V TEP T Q W D + R P W+

Sbjct: 4 SLRIAEPDLPGIVAIYNSTVASRMVTADTEPVTVASRQAWFDAHQ--PGRRLWVCEGA 61

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124

+G +AG + R AY T E ++Y+ RH+ GLG L + A G +++

Sbjct: 62 DGAMAGWMSFSDFYGRPAYGATAEVSIIYLDTRHRGQGLGRYLLQQAIDQAPAVGVNTLLG 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148

I N PS+ L ALG+T G L

Sbjct: 122 FIFGHNAPSLGLFAALGFTRWGDL 145

>ref|ZP_03509327.1| putative phosphinothricin N-acetyltransferase (antibiotic

resistance) protein [Rhizobium etli 8C-3]

Length = 102

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.

Identities = 28/82 (34%), Positives = 44/82 (53%)

Query: 87 VESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARG 146

+E ++Y++ + G+G L + L+ A GF+ +VAVIG + S+ LH G+ G

Sbjct: 1 MEDSIYLAPEARQGIGKALMSELIDRCTALGFRQMVAVIGGASPASIALHLKAGFVEVG 60

Query: 147 TLRAAGYKHGGWHDVGFWRQDF 168

++ GYKHG W D QR

Sbjct: 61 LMQGTGYKHGRWLDTMLMQRSL 82

>ref|ZP_01879208.1| phosphinothricin N-acetyltransferase, putative [Roseovarius sp. TM1035]
 gb|EDM32364.1| phosphinothricin N-acetyltransferase, putative [Roseovarius sp. TM1035]
 Length = 159

Score = 58.5 bits (140), Expect = 4e-07, Method: Compositional matrix adjust.
 Identities = 42/159 (26%), Positives = 67/159 (42%), Gaps = 2/159 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +R A D+A + N I ++V F T +TP+ D+ + V E G V
 Sbjct: 3 LRQAEPRDIAPILAFWNPLIRDTSVTFTTVEKTPETLAADIASRGAAFQ--VVEKAGAVL 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G A G +++ Y T E TV ++ + G+G L T L G +VA +
 Sbjct: 61 GFASYGAFRSGPGYAHTAEHTVILAPEARGHGVGRALMTRLEDVARTAGLHVLVAGVSGE 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDF 168
 N ++ H A+G+ + G K G W D+ Q+
 Sbjct: 121 NVSAIAFHRAIGFAEVARMPFVGRKFGRWMDLVLLQKTL 159

>ref|ZP_03146870.1| GCN5-related N-acetyltransferase [Geobacillus sp. G11MC16]
 gb|EDY06652.1| GCN5-related N-acetyltransferase [Geobacillus sp. G11MC16]
 Length = 163

Score = 58.2 bits (139), Expect = 4e-07, Method: Compositional matrix adjust.
 Identities = 44/159 (27%), Positives = 68/159 (42%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR D V +I I T F T + ++W+ + VAE E
 Sbjct: 1 MNIRRFREEDWLQVKEIYEQGIATGQATFETAAPSFEKWWSTIAA---NLCFVAEDEEG 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
 + G R Y E +VYV + G+G L ++K E +GF ++ A I
 Sbjct: 57 IQGWCKISKVSDRCVYQGVGEVSVYVREWSRGKGVGKRLLAEAIKESEEKGFWTLTAGIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N PS+RLH+++G+ G + G +G W DV +R
 Sbjct: 117 PENIPSLRLHQSVGFRVVGIRQRIGKLYGVWRDVMMLER 155

>ref|YP_003085328.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM 18053]
 gb|ACT92163.1| GCN5-related N-acetyltransferase [Dyadobacter fermentans DSM 18053]
 Length = 165

Score = 58.2 bits (139), Expect = 5e-07, Method: Compositional matrix adjust.
 Identities = 46/157 (29%), Positives = 70/157 (44%), Gaps = 4/157 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR +D V I ++T + T Q P+ +D L+ P LVAE G V
 Sbjct: 5 IRALIVSDWQQVKQIYQLGMDTGDATYET--QAPE--MDALKGKFLAEPQLVAEENGEVI 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
 G A+ +R Y E++VY+ + G+G L + ++ E GF ++ A I
 Sbjct: 61 GWAFLSVVSSRCVYGGVAETSVYIHPQFHGRGIGRALLSAIPLSEKFGFWTLQAQIFPE 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ LHE G+ G G ++G W DV +R
 Sbjct: 121 NKASIALHEGQGFREVGyreKLGRNGIWRDVIILLER 157

>gb|EFS03227.1| gnat family acetyltransferase [*Listeria seeligeri* FSL S4-171]
Length = 165

Score = 58.2 bits (139), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 42/158 (26%), Positives = 72/158 (45%), Gaps = 4/158 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+I P + AV I I+T F+ + T+EW D + L+ LV + V
Sbjct: 5 KILPMLPENYPVATIHQEGIDTGNATFQEKTLTLEEW--DQKYLKK--CRLVVLLNEKV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A P+ + NAY E ++Y++ + G+G L ++++ E GF ++ ++I
Sbjct: 61 VGWAALLPFSSMNAYRGVAELSIYIAKAARGKGIGKALMQEIQTSEQNGFWTLQSLIFP 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH A G+ G +G + DV +R
Sbjct: 121 ENKASIALHHAYGFQTLCIHEKLGEMNGTFRDVALER 158

>ref|YP_003975090.1| putative phosphinothricin acetyltransferase [*Bacillus atrophaeus*
1942]
gb|ADP34159.1| putative phosphinothricin acetyltransferase [*Bacillus atrophaeus*
1942]
Length = 165

Score = 58.2 bits (139), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 42/160 (26%), Positives = 71/160 (44%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68
+R A D+ AV I N + + V TEP TP++ ++ ++ P VA+ E G +
Sbjct: 5 LRRAAKKDLDAVVAIYNSTVASRMVTADTEPVTPEDRMEWFLAHTEKRPYVAQDENGTI 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
+ + R AY+ T E ++Y+ + G GS L L+ +S++A I
Sbjct: 65 SAWISFETFYGRPAYNKTAEISIIYIHEGFRGKGAGSYLLQEALRLARELDIRSLMAFIFA 124

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDF 168
N PS++L E G+ G G +D+ R+
Sbjct: 125 HNLPSIKLFEKFGFEWGLFPGIAEMDGKRYDLKILGREL 164

>ref|YP_001404157.1| GCN5-related N-acetyltransferase [*Candidatus Methanoregula*
boonei
6A8]
gb|ABS55514.1| GCN5-related N-acetyltransferase [*Methanoregula boonei* 6A8]
Length = 179

Score = 58.2 bits (139), Expect = 5e-07, Method: Compositional matrix adjust.
Identities = 41/157 (26%), Positives = 67/157 (42%), Gaps = 3/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR A D AV I NHY + +P + + L L++ Y + V + V
Sbjct: 24 IRQAHEKDCGAVLSIFNHYAVHGFAAYADKP-VRERYFTGL--LKNAYAFYVVDSPGVL 80

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G + P+ +A+ T E + ++ + G GS L L++ +G VVA +
Sbjct: 81 GFGFVKPFLPFSAFATTGELSYFIMPEYVNQGFGLLLYRLIRDSRTKGISMVVAHMASW 140

Query: 130 NPDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N+ +R H G+ G L+ G K G D+ Q+
Sbjct: 141 NEEGIRFHRKHGFYDAGRLKKVGGKFGEPFDILLMQK 177

>ref|YP_323829.1| GCN5-like N-acetyltransferase [Anabaena variabilis ATCC 29413]
 gb|ABA22934.1| GCN5-related N-acetyltransferase [Anabaena variabilis ATCC 29413]
 Length = 162

Score = 58.2 bits (139), Expect = 5e-07, Method: Compositional matrix adjust.
 Identities = 40/142 (28%), Positives = 62/142 (43%), Gaps = 1/142 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLE-RLQDRYPWLVAEVEG 66
 + IR AT D+ + I N + + EP + + + + R + P V E EG
 Sbjct: 1 MTIRHATTTDLPTIIGIYNAAVPSRMATADLEPVSVESRLAWFQGRSPNFRPLWVIEQEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V+AG + R AY T E ++Y++ R GLG L + G K+++ I
 Sbjct: 61 VIAGWLSFQSFYGRPAYSATAELSIYIAPAFHRCGLGKQLLAKAIAESPNLGLKTLGLFI 120

Query: 127 GLPNDSVRLHEALGYTARGTL 148
 N PS+ L E G+ G L
 Sbjct: 121 FAHNQPSLHLFETFGFKWGYL 142

>ref|YP_001341823.1| GCN5-like N-acetyltransferase [Marinomonas sp. MWYL1]
 gb|ABR71888.1| GCN5-related N-acetyltransferase [Marinomonas sp. MWYL1]
 Length = 167

Score = 57.8 bits (138), Expect = 6e-07, Method: Compositional matrix adjust.
 Identities = 47/160 (29%), Positives = 68/160 (42%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
 EIR A D A+ DI H ++ R + + +D LE + D +P LV E +G V
 Sbjct: 8 EIRLAVLDDAPAILDIFQHCDLFASTGHRQDHI GLIDVMDWLESVTDNHPMLVLEEQQKV 67

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 P+ A+D E +VYVS Q G+G+ L+ +L + GF +VA I
 Sbjct: 68 IAWCSVEPFYGLPAFDSACEVSVYVSPNWQKGKVGTLFQYLETNQIEFGFTHLVAYIYA 127

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDF 168
 N S + G+ G L DV R+F
 Sbjct: 128 SNLESQGFKRGQFDQWGLLPNIAQNEQIKEDVFILGREF 167

>ref|ZP_07630836.1| GCN5-related N-acetyltransferase [Clostridium cellulovorans 743B]
 Length = 197

Score = 57.8 bits (138), Expect = 6e-07, Method: Compositional matrix adjust.
 Identities = 40/158 (25%), Positives = 69/158 (43%), Gaps = 5/158 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 I D ++ +I I T F+T+ T ++W + R LVA ++ +
 Sbjct: 36 IENIVQEDWESIANIYLEGISTGKATFQTDVPTWEQW---DSSHTRTCRLVARLDDKIL 91

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G + P +R Y E ++Y+ + G+G++L L+ E GF ++ + I
 Sbjct: 92 GWSALSPTSSRCVYAGVAEVSIIYGKEFRGQGIGTSLNRLISLSEENGFWTLQSGIIRE 151

Query: 130 NDPSVRLHEALGYTARGTLRAAG-YKHGGWHDVGFWRQ 166
 N S+ LH+ G+ G G +G WHDV +R
 Sbjct: 152 NVESIELHKNCGFREIGVREKLGKMSNGKWHDVVLMER 189

>ref|YP_003842069.1| GCN5-related N-acetyltransferase [Clostridium cellulovorans 743B]
 gb|ADL50305.1| GCN5-related N-acetyltransferase [Clostridium cellulovorans 743B]

Length = 166

Score = 57.8 bits (138), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 40/158 (25%), Positives = 69/158 (43%), Gaps = 5/158 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
I D ++ +I I T F+T+ T ++W + R LVA ++ +
Sbjct: 5 IENIVQEDWESIANIYLEGISTGKATFQTDVPTWEQW----DSSHTRTCRLVARLDDKIL 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G + P +R Y E ++Y+ + G+G++L L+ E GF ++ + I
Sbjct: 61 GWSALSPTSSRCVYAGVAEVSIIYIGKEFRQGIGTSLNRLISLSEENGFWTLQSGIIRE 120

Query: 130 NDPSPVRLHEALGYTARGTLRAAG-YKHGGWHDVGVFWQR 166
N S+ LH+ G+ G G +G WHDV +R
Sbjct: 121 NVESIELHKNCGFREIGVREKLGMKMSNGKWHDVVLMER 158

>gb|EFS00154.1| gnat family acetyltransferase [Listeria seeligeri FSL N1-067]
Length = 165

Score = 57.8 bits (138), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 42/158 (26%), Positives = 72/158 (45%), Gaps = 4/158 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+I P + AV I I+T F+ + T +EW D + L+ LV + V
Sbjct: 5 KILPMLPENYPAAVAIHQEGIDTGNATFQEKTLTLEEW--DQKYLKK--CRLVLLNEKV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128
G A P+ + NAY E ++Y++ + G+G L ++++ E GF ++ ++I
Sbjct: 61 VGWAALLPFSSMNAYRGVAELSIYIAKAARGKGIGKALMQEIIQTSEQNGFWTLQSLIFP 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
N S+ LH A G+ G +G + DV +R
Sbjct: 121 ENKASIALHHAYGFQTLCIHEKLGEMNGTFRDVALLER 158

>ref|YP_591201.1| GCN5-related N-acetyltransferase [Candidatus Koribacter versatilis
Ellin345]
gb|ABF41127.1| GCN5-related N-acetyltransferase [Candidatus Koribacter versatilis
Ellin345]
Length = 165

Score = 57.8 bits (138), Expect = 6e-07, Method: Compositional matrix adjust.
Identities = 49/160 (30%), Positives = 69/160 (43%), Gaps = 6/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEW-IDDLERLQDRYPWLVAEVEG 66
+ I P +AD AAV I I T F TE T ++W +E + LVA +
Sbjct: 5 IVIAPMLSADWAARRRIYAEIATGNATFETEAPTWEKWSAGHVESCR-----LVARIGD 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVI 126
+ G A R Y E +VYV+ + G+G L L+ + E GF ++ A I
Sbjct: 60 EIVGWAALSRSVQRAVYAGVGEVSVYVAESARGKGVGLQLLHALITASETAGFWTLQAGI 119

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
N S+RLHE G+ G G +G W D +R
Sbjct: 120 FPENTASIRLHEGCGFRIVGRRERIGCLNGVWRDVLVLMER 159

>ref|YP_687122.1| GNAT family acetyltransferase [uncultured methanogenic archaeon
RC-I]
emb|CAJ37796.1| putative acetyltransferase (GNAT family) [uncultured methanogenic
archaeon RC-I]

Length = 158

Score = 57.8 bits (138), Expect = 7e-07, Method: Compositional matrix adjust.
Identities = 44/159 (27%), Positives = 71/159 (44%), Gaps = 7/159 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
I+ + +D VC I + + + + + P EWID ER ++ LVA+++ V
Sbjct: 6 IQEMSVSDQDQVCSIFRNGVASG--DHVLDADDDPAEWID-FERGEN----LVAKLDDKV 58

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G A P + V+V ++ G+G L ++ E QG S++ I
Sbjct: 59 GWAIVTPLEEAELPQGVGRIGVFVDPEYRKGKIGRLLLSAIQYSEEQGIDSLICGIVPD 118

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
N P+V LH++ G+ A G LR AG G D Q +
Sbjct: 119 NLPVAVMLHKSCGFKALGMLRDAGMCGGRKRDVALLQHTY 157

>ref|YP_644434.1| GCN5-related N-acetyltransferase [Rubrobacter xylanophilus DSM 9941]
gb|ABG04622.1| GCN5-related N-acetyltransferase [Rubrobacter xylanophilus DSM 9941]
Length = 174

Score = 57.8 bits (138), Expect = 7e-07, Method: Compositional matrix adjust.
Identities = 43/162 (26%), Positives = 66/162 (40%), Gaps = 9/162 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
V R +T D + + I N IE + F T P++P+E W D +P +V E
Sbjct: 14 VRARASTPKDASGIARIYNQGIEERSSTFETCPRSPEEVRAWYDGA-----HPIVVVEE 67

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVA 124
G + A ++ R Y E +VYV H+ G G L+ + + G +V+
Sbjct: 68 GGEIIAFAATFEYRPRECYRGVAEFSVYVDREHRGRGAGRLAMEALIPAAASAGLWLKVS 127

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 166
+ N S L + G+ GT G W DV +R
Sbjct: 128 RVFPENAASRALLRSAGFREVGYEKHARLDGRWRDVIIVER 169

>ref|ZP_05391837.1| GCN5-related N-acetyltransferase [Clostridium carboxidivorans P7]
gb|EET87749.1| GCN5-related N-acetyltransferase [Clostridium carboxidivorans P7]
Length = 151

Score = 57.4 bits (137), Expect = 7e-07, Method: Compositional matrix adjust.
Identities = 38/148 (25%), Positives = 62/148 (41%), Gaps = 3/148 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE--G 66
+ T + V DI N+YIE S + + + P E+ + +P + + E G
Sbjct: 4 KFEKMTTSHSKEVIDIFNYIENSFAAY-FDNKLPYEFTKFIEMTKNFPAYIIKSEDTG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVA 126
V G ++ + A+ T E T ++ R GLG T L + + G K ++A I
Sbjct: 63 KVVGFSLKAYSPLPAFKETAETIYFIEKDSVRSGLGKAALTLEQDAKNIGIKYLLASI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYK 154
N S++ HE G+ G G K
Sbjct: 123 SSKNTQSLKFHEKNGFNQCGRFYNIQK 150

>ref|YP_003183978.1| GCN5-like N-acetyltransferase [Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446]
gb|ACV57589.1| GCN5-related N-acetyltransferase [Alicyclobacillus acidocaldarius

subsp. acidocaldarius DSM 446]
Length = 164

Score = 57.4 bits (137), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 47/155 (30%), Positives = 64/155 (41%), Gaps = 2/155 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEG 66
V++R AT D+ A+ I N IE +P+ +ID + RYP VA V
Sbjct: 3 VDVRIATREDLPAILSIYNQGIEDRITRLEQDPKD-MAYIDTWFSQHNRRYPVVFVATVGS 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A P+ R AY E +VYV + G+G L +L GF +V
Sbjct: 62 NVVGWADLHPYSHRFAYADVGEISVYVERAWRGKGVGQALLRNLEIYAVEHGFHKLVLAT 121

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N L+ +G+ G R G G W DV
Sbjct: 122 FPFNQAGQGLYRKMGFREVGVFRRHGKLGKGVWDV 156

>ref|ZP_04217151.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock3-44]
gb|EEL51163.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock3-44]
Length = 167

Score = 57.4 bits (137), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 42/157 (26%), Positives = 65/157 (41%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
+R AT D+ + I N IE TE +T + + L + +RY +V E + V
Sbjct: 6 VRIATEQDVQEITAIYNEGIEDRIATLEITEIKTDEYVVKWLFQORDERYAVIVLEKDDQVV 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G A P+ R AY E ++Y+ ++ GLG L L K+ + F V
Sbjct: 66 GWASINPYSHRCAYRGVGEISYIKREYRGQGLGQKLLLALEKTGQQNEFYKFVLFTFSF 125

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
N+ L+ +GY G G G DV ++
Sbjct: 126 NNLGQGLYRKMGYREVGVFEKQGIMDGEHVDVMIMEK 162

>ref|YP_002130283.1| phosphinothricin N-acetyltransferase [Phenylobacterium zucineum
HLK1]
gb|ACG77854.1| phosphinothricin N-acetyltransferase [Phenylobacterium zucineum
HLK1]
Length = 169

Score = 57.4 bits (137), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 48/173 (27%), Positives = 73/173 (42%), Gaps = 17/173 (9%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE----WIDDLERLQDR 56
M+P ++ RPA +D A+ I N IE F TEP+TP++ W +L
Sbjct: 1 MTPSN--LQARPAEPSDAPAIALIYNQGIEDRIATFETEPRTPEQVEAWWAHNL----- 53

Query: 57 YPWLVAEVEGV--VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
+VA +G V G A P+ R Y E +VYV + G+G L+ +
Sbjct: 54 ---IVAVTDGAGGPVVGAAVFPYADRCCYRGIGEFVYVRRDWRGRGVGRVAMEQLIVA 110

Query: 114 MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
E+ G +++ + N S+ L LG+ G G G W D +R
Sbjct: 111 AESAGLWKLRSRVFPENRASLSLMARLGFKEVGVHEKHGKLDGVWRDCVLVER 163

>ref|ZP_07873781.1| gnat family acetyltransferase [Listeria ivanovii FSL F6-596]
gb|EFR96982.1| gnat family acetyltransferase [Listeria ivanovii FSL F6-596]

Length = 165

Score = 57.4 bits (137), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 41/158 (25%), Positives = 68/158 (43%), Gaps = 4/158 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
EI P +AV I I+T F+ + T EW + LV + G V
Sbjct: 5 EILPMLREHYSAAVAIHQEGIDTGNATFQEKTLTLGEWNQKYLTIGR----LVVILNGQV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A P+ + NAY E ++Y++ + G+G L +++ E GF ++ ++I
Sbjct: 61 VGWAALLPFSSMNAYRGVAELSIYIAKSARGKGIGKALMQAIIQTSEENGFWTLQSLIFP 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH G+ G +G + DV +R
Sbjct: 121 ENKASIALHHTFGFRTLCTIHEKLGEMNGTFRDVALER 158

>ref|ZP_03073935.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri 100-23]
gb|EDX41700.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri 100-23]
Length = 164

Score = 57.4 bits (137), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 37/138 (26%), Positives = 62/138 (44%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAG 70
R AT D+ + +I N I + P T E E + +P V E + V G
Sbjct: 6 RKATLKDLPKIVEIYNQIIPSRLATADLTPITVDERKGFWEAFDENHPIWVIEYQNEVRG 65

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130
+ R AYD T E +Y+ R ++ G+G+ +++ + ++VA I N
Sbjct: 66 WVALEHFYGRPAYDHTSEIAIYLDQRLRKQGVGKTMEFIIRQLPKLTVDTIVAYIFGHN 125

Query: 131 DPSVRLHEALGYTARGTL 148
PS++L ++ G+T G L
Sbjct: 126 IPSLKLFKSFGFTQWGLL 143

>ref|YP_684987.1| GNAT family acetyltransferase [uncultured methanogenic archaeon RC-I]
emb|CAJ35661.1| putative acetyltransferase (GNAT family) [uncultured methanogenic archaeon RC-I]
Length = 167

Score = 57.4 bits (137), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 45/149 (30%), Positives = 63/149 (42%)

Query: 18 MAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPW 77
+ AV I NHY+ +T F E+ + + RY V + G++ G
Sbjct: 16 LDAVLGIYNHYVLNNTTATFHAAHAFGRDEFRELVFVDNPRYRTYVIKEAGIICGYVLLTQH 75

Query: 78 KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLH 137
K R AYD T E TVY++ GLGS + + +G +VA I N S+ L
Sbjct: 76 KKREAYDETAEVTVYLPAGSVGKGLGSRALQFIEQVAVERGIHVLVATICGENARSIGLF 135

Query: 138 EALGYTARGTLRAAGYKHGGWHDVGFQWR 166
E GY R G K G DV +Q+
Sbjct: 136 EKNGYDKCAHYREVGRKFGQRLDVVAYQK 164

>ref|ZP_08006391.1| hypothetical protein HMPREF1013_03004 [Bacillus sp. 2_A_57_CT2]
gb|EFV76816.1| hypothetical protein HMPREF1013_03004 [Bacillus sp. 2_A_57_CT2]
Length = 165

Score = 57.4 bits (137), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 42/152 (27%), Positives = 62/152 (40%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR A D+ + +I N IE T+ + + E+ Q RY L AE V
Sbjct: 7 IREARKTDLEDILEIYNQGIEDRIATLETDAKDL SYMTNWFQHQGRYSVLAAEEGDQVI 66

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G A P+ +R AYD + +VY+S + G G L + L F +V
Sbjct: 67 GWASLNPYSSRCAYDGVADLSVYISRAFRGKGAGGKLLSALEMKARENKFHKLVLFTFPF 126

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N L++ +GY G + G G + DV
Sbjct: 127 NGLGQGLYKKMGYREVGIFQNGVLDGEFVDV 158

>ref|XP_001261229.1| GNAT family acetyltransferase, putative [Neosartorya fischeri NRRL

181]
gb|EAW19332.1| GNAT family acetyltransferase, putative [Neosartorya fischeri NRRL
181]
Length = 194

Score = 57.4 bits (137), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 48/183 (26%), Positives = 78/183 (42%), Gaps = 34/183 (18%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA-EVE 65
+ IR AT D++ + I + Y+ S F P + I +Q R P+ VA +
Sbjct: 3 IHIREATQDDISQIHTIYSFYVCESVATFLRHPPPLESLISSFRDIQSRRLPYRVAIDTT 62

Query: 66 GVVAGIAYAGPWKA-RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG----- 118
G V G Y P+ R AY TVE ++YV + G+GS L + +L+S+E++
Sbjct: 63 GKVLGYGYLAPFNGTRMAYAPTVEVSLYVHPEYTSKGVGSRLSSILESVESEAGVWHRA 122

Query: 119 -----FKSVVAVIGLPN-----DPSVRLHEALGYTARGTLRAAGY 153
+S++A + + + R +E G+ RG L+ GY
Sbjct: 123 CEHKEYETHVQIIPEDGRVRSIIACMSVDTTGKEDGEGLRRWYEQRGFVERGRLKNVG 182

Query: 154 KHG 156
K G
Sbjct: 183 KQG 185

>ref|ZP_01886255.1| phosphinothricin N-acetyltransferase [Pedobacter sp. BAL39]
gb|EDM34540.1| phosphinothricin N-acetyltransferase [Pedobacter sp. BAL39]
Length = 163

Score = 57.4 bits (137), Expect = 9e-07, Method: Compositional matrix adjust.
Identities = 45/157 (28%), Positives = 68/157 (43%), Gaps = 4/157 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR +D V I I T F+T + +EW D+ + R+ V + +G V
Sbjct: 5 IRILVPSDWEQVKLIYEKGATGNATFQTTPASFEEW-DNSHLINCRF---VDDQDGTVR 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G A P +R Y E +VYV G+GS L L++ E +G ++ A I
Sbjct: 61 GWAALTPVSSRCVYAGVAEVSIVYVDPAFSGKGIGSDLLNLLVRQSEQEGIWTLQAGIFPE 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
N S+++HE G+ G G + G W D +R
Sbjct: 121 NAASLKIHEKAGFRILGVREKIGKQLGLWRDTVLLER 157

>ref|YP_003356173.1| GCN5-related N-acetyltransferase family protein [Methanocella paludicola SANAЕ]
 dbj|BAI61190.1| GCN5-related N-acetyltransferase family protein [Methanocella paludicola SANAЕ]
 Length = 162

Score = 57.0 bits (136), Expect = 9e-07, Method: Compositional matrix adjust.
 Identities = 41/144 (28%), Positives = 64/144 (44%), Gaps = 5/144 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
 + IR AT +D+ A+ DI N I + +P T + W + P LVAE
 Sbjct: 1 MRIREATESDLPAIVDIYNGSINDGKSSTNMQPTTVRRSTGWFR--QHKATGKPILVAED 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 G + G P+ R AYD T + +YV + + G+G L + ++ G ++V
 Sbjct: 59 AGRIVGWSVRPFYGREAYDRTGKVKIYVEPQSRGKGIGKELLDKAMSCGKSSGLNLTVC 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
 + ND + RL E G+ G L
 Sbjct: 119 YMLADNDLARRLFEDSGFERWGQL 142

>ref|YP_003245194.1| GCN5-like N-acetyltransferase [Paenibacillus sp. Y412MC10]
 gb|ACX67387.1| GCN5-related N-acetyltransferase [Paenibacillus sp. Y412MC10]
 Length = 166

Score = 57.0 bits (136), Expect = 9e-07, Method: Compositional matrix adjust.
 Identities = 41/157 (26%), Positives = 74/157 (47%), Gaps = 3/157 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP--WLVAEV 64
 P I A D+ A+ DI N I + V EP T + I E + + W++
 Sbjct: 4 PYRIDYAVKEDLPAIVDIYNSTISSRKVTADLEPVTVESRIRWFEEHSNDFRPLWVMRSD 63

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +G+VA +++ + R AY+ T E ++YV+ +++ +G GS L ++ ++V
 Sbjct: 64 DGLVAWMSFQS-FYGRPAYNGTAEISIVNEKYRGVAGSLLIQKAIECPRLRVSNLVG 122

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 + N+PS++L + G+ G L A G D+
 Sbjct: 123 FVFGHNEPSLKLKKFGFDQWGLLPVAEALDGVKRD 159

>ref|ZP_05067648.1| phosphinothricin acetyltransferase [Octadecabacter antarcticus 238]
 gb|EDY92887.1| phosphinothricin acetyltransferase [Octadecabacter antarcticus 238]
 Length = 158

Score = 57.0 bits (136), Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 44/157 (28%), Positives = 66/157 (42%), Gaps = 3/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +R AT+ D A + I N I + V F + P++ E I DL + R +LV E EG
 Sbjct: 3 VRAATSEDAATIAAIWNPQILDTVVTFNSVPKSDHE-IADL--IAQRPCFLVVEAEGKT 59

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
 G A ++ Y +E T+ ++ G G L L+ A ++ A +
 Sbjct: 60 GFASYDQFRGGIGYAHAMEHTIILAPEASGRGAGRELMRALMDHARAAVHTLWAGVSAE 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N V H ALG+ L G K W D+ Q+
 Sbjct: 120 NSAGVAFHSALGFKTVAVLPEVGRKFERWMDLVLMQK 156

>gb|AAA26766.2| ORF X product (put.); putative [Streptomyces coelicolor]
Length = 99

Score = 57.0 bits (136), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 32/101 (31%), Positives = 51/101 (50%), Gaps = 24/101 (23%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG- 66
V++RP D+ + D+ NHY+ + + F TEP TP+E R PWL++ E
Sbjct: 7 VQVRPGVEEDLKPLTDLYNHVRETPTFDTEPFTPEE-----RRPWLLSHPEDG 56

Query: 67 -----VVAGIAYAGPWKARNAYDWTVESTVYVS 94
+ G A + P++A+ AY +VE+TVYV+
Sbjct: 57 PYRLRVATDAESQEILGYATSSPYRAKPAYATSVETTVYVA 97

>ref|ZP_07992477.1| acetyltransferase [Neisseria mucosa C102]
gb|EFV81521.1| acetyltransferase [Neisseria mucosa C102]
Length = 166

Score = 57.0 bits (136), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 40/140 (28%), Positives = 63/140 (45%), Gaps = 1/140 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
IRPA D+ A+ DI N + T P T E D+ P + + + +G V
Sbjct: 5 IRPALRQDLPAIVDIYNSTVATRQSTADLSPTTVAEREMWFAAHTDKRPIYALYDTDGTV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
+ R AY + E +VYV H + G+G L H+L+ + G ++V+A++
Sbjct: 65 LAWGSFSDYHPRYAYHISAEVSVYVRHDMRGAGVGKILLRHMLERALSGLIRNVIALVFG 124

Query: 129 PNDPSVRLHEALGYTARGTL 148
N PS+ L G+ G L
Sbjct: 125 HNYPSLNLFHRFGFEWGRL 144

>ref|ZP_01750878.1| putative acetyltransferase, GNAT family protein [Roseobacter sp.
CCS2]
gb|EBA12552.1| putative acetyltransferase, GNAT family protein [Roseobacter sp.
CCS2]
Length = 155

Score = 57.0 bits (136), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 48/159 (30%), Positives = 68/159 (42%), Gaps = 9/159 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL--QDRYPWLVAEVEGV 67
IR ATAAD + I NH I +T+ F P E D++ L QD W + +G
Sbjct: 2 IRAATAADAPQIAAIWNHAIRETTITFN--PVEKSE--DEVATLCAQDCLVW---DEDGQ 54

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G A P++ Y +TVE T+ + G G L L + ++ A
Sbjct: 55 VLGfARYFPFRGGEGYRFTVEHTIMLHGdGHGKGgGKQLMDALFADAKTADKHTMFAGCS 114

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
N +V H LG+ TL G+K G W D+ Q+
Sbjct: 115 AENAGAVAFHAKLGFQKVATLPEVGFKFGRWIDLVLQM 153

>ref|YP_825858.1| GCN5-related N-acetyltransferase [Candidatus Solibacter usitatus
Ellin6076]
gb|ABJ85573.1| GCN5-related N-acetyltransferase [Candidatus Solibacter usitatus
Ellin6076]
Length = 161

Score = 57.0 bits (136), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 49/157 (31%), Positives = 68/157 (43%), Gaps = 5/157 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR D AV I I T F T + W D L + LVA E ++
Sbjct: 5 IRTLLPPDWPVAVRAIYLEGIATGNATFETVAPEWERW--DAAHLP--HCRLVAAAETIL- 59

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G A P AR Y E +VYV+ + + G+G L L++ E G ++ A I
Sbjct: 60 GFAALSPVSARRVYAGVAEVSIVYVAAQSRGAGVGKALLRELIRESSETAGIWTLQAGIFPE 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N+ S+RLH++ G+ GT G G W DV +R
Sbjct: 120 NEASRLRHQSAGFRIVGTRERIGRLAGHWRDVLLE 156

>ref|YP_002777200.1| ArsR family transcriptional regulator [Rhodococcus opacus B4]
dbj|BAH48255.1| putative ArsR family transcriptional regulator [Rhodococcus opacus B4]
Length = 304

Score = 57.0 bits (136), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 47/159 (29%), Positives = 70/159 (44%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V +RP D AV I I T T F T E T +E +D + R+ W VAE++ V
Sbjct: 144 VTVRPMREQDWEAVRRIYEGGIATRTATFTTEVPT-RETLD--AQWLPRIHW-VAEIDDV 199

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIG 127
V G A P R+ Y E+++YV+ + G+G L + + + G ++ I
Sbjct: 200 VVGWAALTPTSGRDCYQGAENSIYVADGMRGRGVGKALLRTQVIAADEAGIWTLQTSIF 259

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH + G+ G G W D F +R
Sbjct: 260 PENRASIALHHSAGFRTIGVRERIAQLDGIWRDVFLE 298

>ref|YP_003095172.1| phosphinothricin N-acetyltransferase [Flavobacteriaceae bacterium
3519-10]
gb|ACU07110.1| phosphinothricin N-acetyltransferase [Flavobacteriaceae bacterium
3519-10]
Length = 165

Score = 57.0 bits (136), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 42/161 (26%), Positives = 68/161 (42%), Gaps = 3/161 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IR +D V I IE F + + + W + ++ + VA
Sbjct: 5 IREMPSDGPVNLTIIFGEGIEGGNATFDRDVPSLEAWDSKFFKC--CRFVAEDQNNVA 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGLP 129
G A P R+ + E ++Y+S+ Q GLG L L++ EA G+ ++ A I
Sbjct: 62 GWAAIQPVSKRDCFTGVAEVSIIYISNAVQGGGLDLLRKLVEESEAHGYWTLQAGIFPE 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFEL 170
N S+++HE LG+ G + G W DV +R E+
Sbjct: 122 NVASIKIHEKLGFRITVGIRQLAQMKGVWRDVLLEMERSEI 162

>gb|EFS49061.1| acetyltransferase, GNAT family [Propionibacterium acnes HL083PA1]
gb|EFT57213.1| acetyltransferase, GNAT family [Propionibacterium acnes HL002PA3]

Length = 166

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 45/162 (27%), Positives = 74/162 (45%), Gaps = 6/162 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNF---RTEPQTPQEWIDDLERLQDRYPWLVAEV 64
V IR D+ A I N +T ++ T + W +L + D P LVAEV
Sbjct: 3 VNIRTMEERDLPAASRIYNQSAVATTYSYTVVNTNVEDRLSWWREL--IADSRPLLVAEV 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL-KSMEAQGFKSVV 123
+G +AG A ++ D T E T+++ + + G+G L T L+ ++ ++++
Sbjct: 61 DGTMAGYANYHRFREGGGDDVTAEVTIWLDPQARGQGVGRKLMTELIRRARADDRLRNLL 120

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
+VI N+ S+ H A+G+ G L YK G W Q
Sbjct: 121 SVIDSDNERSISFHSAMGFVEVGRLPHIAYKLGNNWRTAVLMQ 162

>ref|YP_003841929.1| GCN5-related N-acetyltransferase [Clostridium cellulovorans 743B]
ref|ZP_07630984.1| GCN5-related N-acetyltransferase [Clostridium cellulovorans 743B]
gb|ADL50165.1| GCN5-related N-acetyltransferase [Clostridium cellulovorans 743B]
Length = 162

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 36/159 (22%), Positives = 71/159 (44%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVAEEVEG 67
V +R A D+ V I N IE T + + +E L D++ LVAE
Sbjct: 2 VIVREARIEDIPYVTAIYNQGIEERTATLESRLRNKEMEKLITRSDKHKVLVAEEFET 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G A + R ++ ++Y+ + G+G TL L+++ ++ GF+ ++
Sbjct: 62 IVGWASINEFSPRECFNANAGMSIYIEKESRGKGVGKTLIELIETAKSFGRKLILNTF 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N+ S L++++G+ G G+ G + D+ ++
Sbjct: 122 KKNNASNALYKSMGFKEVGIYEKHFGLDGEYIDIRIMEK 160

>ref|YP_001467661.1| acetyltransferase [Campylobacter concisus 13826]
gb|EAT98142.1| phosphinothricin N-acetyltransferase (PPT N-acetyltransferase)
(Phosphinothricin-resistance protein) [Campylobacter
concisus 13826]
Length = 160

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
Identities = 38/155 (24%), Positives = 64/155 (41%), Gaps = 6/155 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQE---WIDDLERLQDRYPWLVAEEVEG 66
I A +D+ A+ I N YI + P + +E W + D P + +
Sbjct: 2 IERANLSDLEAITKIYNDYILERSATADMRPVSTKEREPEWPN---AHGDSRPIFIYKEND 58

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+ G + + AYD +VE ++YV+ + + G+G L H L K+++A+I
Sbjct: 59 EILGYCSLSDFNPKIAYDISVEISYVAKKALKKGIGQLLAHSLNEARGLNLKNIIALI 118

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N S+ L G+ G L G + DV
Sbjct: 119 FSKNKASLGLFLKFGFEKWGELPGVCLMDGEYKDV 153

>ref|ZP_06873759.1| putative phosphinothricin acetyltransferase [Bacillus subtilis
subsp. spizizenii ATCC 6633]

ref|YP_003867945.1| putative phosphinothricin acetyltransferase [Bacillus subtilis
 subsp. spizizenii str. W23]
 gb|EFG92279.1| putative phosphinothricin acetyltransferase [Bacillus subtilis
 subsp. spizizenii ATCC 6633]
 gb|ADM39636.1| putative phosphinothricin acetyltransferase [Bacillus subtilis
 subsp. spizizenii str. W23]
 Length = 165

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 46/160 (28%), Positives = 70/160 (43%), Gaps = 1/160 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68
 +R A D+ AV I N I + V EP TP++ ++ + P VAE E G V
 Sbjct: 5 LRLAEYKDLEAVVAIYNSTIASRMVTADIEPVTPEDRMEWFLGHTEARPLYVAEDENG 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 A + R AY+ T E ++Y+ + G GS L L+ G +S++A I
 Sbjct: 65 AAWISFETFYGRPAYNKTAEVSIYIDEACRGKGAGSYLLQEALRIAPDLGIRSLMAFIFG 124

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168
 N PS++L E G+ G G +D+ R+
 Sbjct: 125 HNKPSLKLFEKHGFAEWGLFPGIAEMDGKRYDLKILGREL 164

>ref|YP_001031090.1| polyprenyl synthetase [Methanocorpusculum labreanum Z]
 gb|ABN07823.1| GCN5-related N-acetyltransferase [Methanocorpusculum labreanum Z]
 Length = 165

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 47/158 (29%), Positives = 67/158 (42%), Gaps = 13/158 (8%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQD-RYPWLVAEVEGVV 68
 IR D V I + F T T +EW D L+D RY L + +V
 Sbjct: 7 IREMQDYDWPRVSGIYEQALLEGISTFATVCPTFEW--DKAHLKDCRYVMLA---DDMV 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G P +R AY VE ++Y + +GLG+ L HL + EA+G+ + I
 Sbjct: 62 VGWCAVSPTSSREAYKGVVEVSIYFDKAFRGMGLGTKLDDHLCRESEAKGYWCLFVNILS 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV-GFWQ 165
 N S+ LH+ G+ R GY+ D+ G WQ
 Sbjct: 122 INTASINLHKKCGF-----REVGYRERIAKDLFGVWQ 153

>ref|YP_001488516.1| acetyltransferase [Bacillus pumilus SAFR-032]
 gb|ABV63956.1| possible acetyltransferase [Bacillus pumilus SAFR-032]
 Length = 164

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 41/154 (26%), Positives = 74/154 (48%), Gaps = 5/154 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEGV 67
 R AT D+ A+ DI N I + V TEP + ++W L + R ++ + +G
 Sbjct: 6 RIATEDDLKAIVDIYNSTIASREVTADTEPVSVEDRRQWF--LNHSEKRPLYVKTDEDGH 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G + R AY+ TVE ++Y++ ++ GLGS ++ + G ++++A I
 Sbjct: 64 IYGWLSFETFYGRPAYNGTVEMSIYLNQDYRGKGLGSLFLQEAIELAPSLGIRTLALAFIF 123

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 N+ S+RL + G+ G L G +D+
 Sbjct: 124 GHNEASIRLFFKKHGFETWGHLPRIAEMDGSRYDL 157

>ref|YP_003682387.1| ArsR family transcriptional regulator [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111]
 gb|ADH69881.1| transcriptional regulator, ArsR family [Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111]
 Length = 302

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 48/163 (29%), Positives = 67/163 (41%), Gaps = 12/163 (7%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP---WLVAE 63
 V R AD+ AV +I I + F TE + + L+DR+ W VAE
 Sbjct: 125 VTTRAMADADLDAVREIYAQGIASGHATFETE-----VPGADALKDRWTPGHRW-VAE 176

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 G V G A A P AR Y E++VYV+ + G+G L + + G ++
 Sbjct: 177 SGGRVVGWAAASPVSAREVYAGVAETSVYVAEDARGRGVKGALLYRQVTEADTAGLWTLQ 236

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 I N S+ LH +GY G HG W D +R
 Sbjct: 237 TSIFPENRASLALHHQVGYRTVGVRERVARHHGIWRDVTLLER 279

>ref|ZP_07088258.1| GNAT family acetyltransferase [Chryseobacterium gleum ATCC 35910]
 gb|EFK35050.1| GNAT family acetyltransferase [Chryseobacterium gleum ATCC 35910]
 Length = 167

Score = 56.6 bits (135), Expect = 1e-06, Method: Compositional matrix adjust.
 Identities = 38/145 (26%), Positives = 68/145 (46%), Gaps = 4/145 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVAE 63
 ++ R A +D+ + I N I + V E ++ +W ++ Q R W+V +
 Sbjct: 3 KLKFRNAELSDLNKIVAIYNSTIASRMVTADMEEVSVESKLKWFEH-HNPQTRPLWVVED 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + V G + R AY TVE ++Y+ + G G T+ + + + E G ++V
 Sbjct: 62 EQNQVIGWVSFSSFHRAAYKGTVEVSIYLDESCRGKGYGKTLQYCIDNAEKFGVLNLV 121

Query: 124 AVIGLPNDPSVRLHEALGYTARGTL 148
 A+I L N+PS++L G+ G L
 Sbjct: 122 ALIFLHNEPSLKLFRHFGFEDWGNL 146

>ref|ZP_07054844.1| GNAT family acetyltransferase [Listeria grayi DSM 20601]
 gb|EFI83725.1| GNAT family acetyltransferase [Listeria grayi DSM 20601]
 Length = 167

Score = 56.6 bits (135), Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 43/157 (27%), Positives = 71/157 (45%), Gaps = 4/157 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +R D A+ I I T F+ E +EW D + L LVA +E V
 Sbjct: 6 LRKMQPEDYPAMQAIYQEGILTKNATFQKEVMAFEW--DHKYLST--CRLVAVLEKEVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A P+ + +Y E ++Y+S + + G+GS L L+++ E +G+ ++ ++I
 Sbjct: 62 GFAALLPFSSMESYRGVAEVSIISSKARGNGIGSLLMQQLIEASEEEGYWTLQSLIFPE 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 N S+ LH G+ R G G + DV +R
 Sbjct: 122 NVASISLHHKAGFELRARHPRLGEMDGIFRDVLLER 158

>gb|EFT74943.1| acetyltransferase, GNAT family [Propionibacterium acnes HL050PA2]
Length = 166

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 45/162 (27%), Positives = 74/162 (45%), Gaps = 6/162 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNF--RTEPQTPQEWIDDLERLQDRYPWLVAEV 64
V IR D+ A I N +T ++ T + W +L + D P LVAEV
Sbjct: 3 VNIRTMEERDLPAASRIYNQSAVATTYSYTVNTNVEDRLSWWREL--IADSRPLLVAEV 60

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL-KSMEAQGFKSVV 123
+G +AG A ++ D T E T+++ + + G+G L T L+ ++ ++++
Sbjct: 61 DGTMAGYANYHRFREGGDDVTAEVTIWLDPQARGQGVGRKLMTELIRRARADDRLRNLL 120

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQ 165
+VI N+ S+ H A+G+ G L YK G W Q
Sbjct: 121 SVIDSDNERSISFHSAMGFVEVGRLPHIAYKLGDWRTAVLMQ 162

>ref|ZP_04224647.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock3-42]
gb|EEL43680.1| GCN5-related N-acetyltransferase [Bacillus cereus Rock3-42]
Length = 162

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 41/159 (25%), Positives = 66/159 (41%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++IR AT D+ + I N IE TE +T + ++ L + + RY +V E
Sbjct: 1 MKIRKATEQDVQEITTIYNEGIEDRIATLETEIKTDKYVMEWLFQREKRYSVIVMEENSH 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G A P+ R AY E ++Y+ ++ GLG L L K+ + F V
Sbjct: 61 IVGWASINPYSHRCAYRGVGEISYIKREYRGKGLQNLLLALEKNGQQNEFYKFVLFTF 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166
N+ L+ + Y G G G DV ++
Sbjct: 121 SFNNLGQGLYRKMDYREVGVFEKQGIMDGEHVDVMIMEK 159

>ref|ZP_07707784.1| GCN5-related N-acetyltransferase family protein [Bacillus sp.
m3-13]
Length = 168

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 38/141 (26%), Positives = 64/141 (45%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+++R A D+ + I N IE+ V T P T + + + P V E++
Sbjct: 6 IQLRNAVIEDLPEIVSIYNSTIESRMVTADTSPVTVESRKEWFHKHNNDRPLKVVELDNQ 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ + R AY T E ++Y+S + GLG+ L +K A +++A I
Sbjct: 66 ICAWISFQNFYGRPAYQATAEVSIIYLSVETRKGGLGALLEKAIKECPALQIENLLAFIF 125

Query: 128 LPNDPSVRLHEALGYTARGTL 148
N PS+RL E G+ G L
Sbjct: 126 AHNVP SIRLFEKYGFEGWGYL 146

>gb|ADI18697.1| sortase and related acyltransferases [uncultured Chloroflexi
bacterium HF4000_28F02]
Length = 208

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 47/166 (28%), Positives = 66/166 (39%), Gaps = 32/166 (19%)

Query: 29 IETSTVNFRTPEQTPQEWIDDLERLQDRY-----PW-----L 60
I TVN EP P++W E +++ Y PW L
Sbjct: 40 IRIKTVNCIIEPMGPEDW---EVVREIYLEGIATGHATIEATEAPPWESWNNHRPDCRL 95

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
VA V G A P +R Y E +VYV+ +R G G L L+ + E+ G
Sbjct: 96 VARDGEQVVGWAALSPVSSRAVYSGVAEVSYYVAEHFRKGTGRLLDLSLITASESAGVW 155

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+ A I + N+ S+ LH A G+ GT G +G W D +R
Sbjct: 156 TFQAGILVENEASIALHAACGFLTGTRETRIGRLNGHWRDTLLMER 201

>ref|NP_600226.1| sortase or related acyltransferase [Corynebacterium glutamicum ATCC 13032]
ref|YP_225291.1| phosphinothricin acetyltransferase protein [Corynebacterium glutamicum ATCC 13032]
dbj|BAB98394.1| Sortase and related acyltransferases [Corynebacterium glutamicum ATCC 13032]
emb|CAF19705.1| PROBABLE PHOSPHINOTHRICIN ACETYLTRANSFERASE PROTEIN [Corynebacterium glutamicum ATCC 13032]
Length = 179

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 44/173 (25%), Positives = 69/173 (39%), Gaps = 8/173 (4%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV 64
R IRP D V DI +ET + T T ++ ++ D V
Sbjct: 3 ERDFTIRPIREGDFPQVRDIYELGLETHATYETSGPTWDQF--SQSKIMDTVMVAVENN 60

Query: 65 E-GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 123
+ + G A P +R + VE ++Y+ + Q G+G L L+ E+ G S+
Sbjct: 61 DPDFILGWVSAAPISSRQVFHGVVEDSIYIHPQGQGRGIGGALLDALITYCESNGIWSIH 120

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAA-----GYKHGGWHDVGFQWRDFELP 171
+ I N S +LHE+ G+ GT+ G G W D W+ +P
Sbjct: 121 SWIFPENLGS AKLHESKGFVKVGTMHQMARMPIYEMEGQWRDCDLWECLLSVP 173

>ref|NP_488508.1| hypothetical protein alr4468 [Nostoc sp. PCC 7120]
dbj|BAB76167.1| alr4468 [Nostoc sp. PCC 7120]
Length = 163

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
Identities = 41/145 (28%), Positives = 61/145 (42%), Gaps = 7/145 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL---VAE 63
+ IR AT D+ + I N + + EP + + L Q R P V E
Sbjct: 2 MTIRHATTTDLPTIIGIYNAAVPSRMATADLEPVSV---SRLAWFQGRSPSFRPLWVIE 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 123
EGV+AG + R AY T E ++Y++ R GLG L + G K+++
Sbjct: 59 QEGVIAGWLSFQSFYGRPAYAATAELSIYIAPAFHRCGLGKQLLAKAIVESPNLGLKTLL 118

Query: 124 AVIGLPNDPSVRLHEALGYTARGTL 148
+ N PS+ L E G+ G L
Sbjct: 119 GFVFAHNQPSLHLFETFGFKWGYL 143

>ref|YP_442677.1| phosphinothricin acetyltransferase [Burkholderia thailandensis]

E264]
 ref|ZP_02374490.1| phosphinothricin acetyltransferase [Burkholderia thailandensis
 TXDOH]
 ref|ZP_02388363.1| phosphinothricin acetyltransferase [Burkholderia thailandensis
 Bt4]
 ref|ZP_05587152.1| phosphinothricin acetyltransferase [Burkholderia thailandensis
 E264]
 gb|ABC39376.1| phosphinothricin acetyltransferase [Burkholderia thailandensis
 E264]
 Length = 168

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 45/141 (31%), Positives = 66/141 (46%), Gaps = 5/141 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTP--QEWIDDLERLQDRYPWLVAEVEGV 67
 R AT AD+ A+ I N + + V TEP T + W D R W+V E V
 Sbjct: 7 RDATPADLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 +A +++ + R AY T E ++Y+ + GLGS L L G + + I
 Sbjct: 66 IAWLSFS-DFYGRPAYGHTAEISIYLDEAARGSGLSRLLEAALAKAPELGVHTALGFIF 124

Query: 128 LPNDPSVRLHEALGYTARGTL 148
 N+PS+RL G+T GTL
 Sbjct: 125 GHNEPSLRLFARHGFTTWGTL 145

>ref|YP_003464554.1| acetyltransferase, GNAT family [Listeria seeligeri serovar 1/2b
 str. SLCC3954]
 emb|CBH27468.1| acetyltransferase, GNAT family [Listeria seeligeri serovar 1/2b
 str. SLCC3954]
 Length = 165

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 41/158 (25%), Positives = 72/158 (45%), Gaps = 4/158 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
 +I P + AV I I+T F+ + T ++W D + L+ LV + V
 Sbjct: 5 KILPMLPENYPYPAVAIVHQEGIDTGNATFQEKTLTLEDW--DQKYLKK--CRLVLLNEKV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A P+ + NAY E ++Y++ + G+G L ++++ E GF ++ ++I
 Sbjct: 61 VGWAALLPFSSMAYRGVAELSIYIAKAARGKGIGKALMQEIIQTSEQNGFWTLQSLIFP 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N S+ LH A G+ G +G + DV +R
 Sbjct: 121 ENKASIALHHAYGFQTLCIHEKLGEMNGTFRDVALLER 158

>ref|YP_003357066.1| GCN5-related N-acetyltransferase family protein [Methanocella
 paludicola SANAЕ]
 dbj|BAI62083.1| GCN5-related N-acetyltransferase family protein [Methanocella
 paludicola SANAЕ]
 Length = 167

Score = 56.2 bits (134), Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 46/159 (28%), Positives = 66/159 (41%), Gaps = 9/159 (5%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLERLQDRYPWLVAEVEGV 67
 E+RP D +V I I+T F T + WI LE +VA G
 Sbjct: 9 EMRPE---DWESVARIYEGEGIDTGNSTFEQSVPTYERWISAHLEGFS-----IVARENGE 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

V G A P A R Y E ++YV +H+ G+GS L +++ E +G ++
 Sbjct: 61 VLGWAALSPVSARQVYRGVAELSLYVGEKHRGKGVSALMGAMIELSEKKGIWTLQGGTF 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166

N S+ L + G+ GT G G W DV +R
 Sbjct: 121 PENTASLALQKKFGFREVGTRELRGRMSGRWRDVLTER 159

>ref|YP_003869679.1| Sortase [Paenibacillus polymyxa E681]

gb|ADM69141.1| Sortase [Paenibacillus polymyxa E681]

Length = 170

Score = 55.8 bits (133), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 40/142 (28%), Positives = 62/142 (43%), Gaps = 1/142 (0%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY-PWLVAEV 64

+ I A D+ + DI N + V EP T + I E Q+ + P V +
 Sbjct: 5 QSFSEIFACKEDLPDIVDIYNSTVAGRMVTADLEPVTVESRIPWFEEAHQENHRPLWVLKQ 64

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124

+G +AG A + R AY+ T E ++YV + G GS L HLL G +++
 Sbjct: 65 KGAIAGWASLQSFYGRPAYNGTAEISIVYHEDSRGTGTGSRLVQHLLNECPRLGITTLG 124

Query: 125 VIGLPNDPSVRLHEALGYTARG 146

+ N+PS+ L G+ G
 Sbjct: 125 FVFGHNEPSIGLLRKFGFEQWG 146

>ref|YP_001537972.1| GCN5-related N-acetyltransferase [Salinispora arenicola CNS-205]

gb|ABV98981.1| GCN5-related N-acetyltransferase [Salinispora arenicola CNS-205]

Length = 165

Score = 55.8 bits (133), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 45/159 (28%), Positives = 69/159 (43%), Gaps = 3/159 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IRP D V +I +++ +F E P + D RL + + ++ A+ G
 Sbjct: 4 ITIRPMRRDDEKPVLEIYQAGLDSGDASF--ETVAPAWTVFDAGRLPE-HRYVAADDGGT 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 127

V G R Y VE +VYV Q G+ L T L+ + EA G ++ + +
 Sbjct: 61 VLGWIAVSSVSTRVYAGVVEHSVYVDPAAQGRGVARLLLTTLIAATEAAGIWTIQSGVF 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166

N S+ LH G+ GT G +HG W DV +R
 Sbjct: 121 PENTASLTLTRSGFRVVGTRERVGRRHGRWRDVLTER 159

>ref|ZP_04306448.1| Phosphinothricin N-acetyltransferase [Bacillus cereus 172560W]

gb|EEK61923.1| Phosphinothricin N-acetyltransferase [Bacillus cereus 172560W]

Length = 74

Score = 55.8 bits (133), Expect = 2e-06, Method: Compositional matrix adjust.

Identities = 24/74 (32%), Positives = 45/74 (60%)

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 150

+YV +++ G+GS+L L+K + + + +++A I N+ S+ LH+ G+ GT++
 Sbjct: 1 MYVDKAYRKNGIGSSLMKELIKAKEREYMTLIAGIDAENEKSIVLHQNYGFVHAGTIKK 60

Query: 151 AGYKHGGWHDVGVFW 164

AGYK W D+ F+
 Sbjct: 61 AGYKFNKWLDAFY 74

>ref|YP_001659372.1| GCN5-related N-acetyltransferase [Microcystis aeruginosa NIES-843]
 dbj|BAG04180.1| GCN5-related N-acetyltransferase [Microcystis aeruginosa NIES-843]
 Length = 163

Score = 55.8 bits (133), Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 38/142 (26%), Positives = 64/142 (45%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR A D+ + +I N + T +P ++ +EW + ++YP V +EG
 Sbjct: 3 IREAKETDLPTIIEIYNAAVPTRKATADLKPISLESRRWFK--KHNPEQYPIWVIAIEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 V G + R AY T E ++Y++ +Q G+G L + L G +++ +I
 Sbjct: 61 RVVGWLSLQMFYGRVAYQKTAEVSLYIAPDYQGRGIGKLLVEYALNRCPKLGISNLICII 120

Query: 127 GLPNDPSPVRLHEALGYTARGTL 148
 N S+RL E G+ G L
 Sbjct: 121 FAHNQASIRLFEKFGFQRWGYL 142

>ref|YP_003254040.1| GCN5-related N-acetyltransferase [Geobacillus sp. Y412MC61]
 ref|YP_004133526.1| Phosphinothricin acetyltransferase [Geobacillus sp. Y412MC52]
 gb|ACX79558.1| GCN5-related N-acetyltransferase [Geobacillus sp. Y412MC61]
 gb|ADU95383.1| Phosphinothricin acetyltransferase [Geobacillus sp. Y412MC52]
 Length = 166

Score = 55.8 bits (133), Expect = 2e-06, Method: Compositional matrix adjust.
 Identities = 38/136 (27%), Positives = 67/136 (49%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR A AAD+ + I N I + V EP ++ + W + + +R W+V +
 Sbjct: 6 IRDAAAADLPHIVRIYNETIPSRMVTADLEPVSVESRRRAWFEAHDP-HNRPLWVVEDDGA 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 V A +++ + R AY T E ++Y++ H+ GLG+ L ++ G K+++ I
 Sbjct: 65 VCAWLSFQS-FYGRPAYRHTAEVSIYIAETHRGRGLGAKLLERAVERAPELGIKTLTGFI 123

Query: 127 GLPNDPSPVRLHEALGY 142
 N+PS+RL G+
 Sbjct: 124 FAHNEPSLRLFSRFGF 139

>ref|YP_846122.1| GCN5-related N-acetyltransferase [Syntrophobacter fumaroxidans MPOB]
 gb|ABK17687.1| GCN5-related N-acetyltransferase [Syntrophobacter fumaroxidans MPOB]
 Length = 164

Score = 55.8 bits (133), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 43/156 (27%), Positives = 66/156 (42%), Gaps = 8/156 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEW--IDDLERLQDRYPWL--VAEVE 65
 P T AV DI NH++ S + P+ P E+ D L YP + +E
 Sbjct: 5 FEPITRKHREAVIDIFNHFVNSYAAY---PERPVEYDFFDYLYVEPRDYPVAVTSETA 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 125
 G+V G + P+ + ++ T E T ++ H GLG+ + +G +S++A
 Sbjct: 62 GIV-GFGFMRPYDSDESFKHTAEVTTYFILPSHTGKGLGTGMLRLFCQALHRGIRSLMAN 120

Query: 126 IGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 I ND S+ H G+ G G K G DV

Sbjct: 121 ISSLNDASISFHLKNGFQEWGRFYRVGSKFGVEFDV 156

>ref|YP_374818.1| acetyltransferase [Chlorobium luteolum DSM 273]
gb|ABB23775.1| acetyltransferase, GNAT family [Chlorobium luteolum DSM 273]
Length = 171

Score = 55.8 bits (133), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 45/166 (27%), Positives = 68/166 (40%), Gaps = 5/166 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV--E 65
+ + P D A V D I N Y T S T+ P++ + YP +A
Sbjct: 6 ILLCPLGEGDGAEVLDFNPY-TTSGFAAYTDTPLPEDAALSFIQPSAGYPACMARTLDG 64

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G G P+ A+ T E T+++ G+G+ + HL G +++A
Sbjct: 65 GYAVGFGMLRPYSPLPAFSRTAELTMFLRDGWTGRGIGTLVLLHLAGEAVPMGITTILAS 124

Query: 126 IGLPNDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELP 171
I N S+R H+ G+ G L G K G DV + Q+ ELP
Sbjct: 125 ISSLNPASIRFHQKNGFRECGRLEGVGEKFGRPFDVVCQK--ELP 168

>ref|YP_511330.1| GCN5-related N-acetyltransferase [Jannaschia sp. CCS1]
gb|ABD56305.1| GCN5-related N-acetyltransferase [Jannaschia sp. CCS1]
Length = 156

Score = 55.8 bits (133), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 41/157 (26%), Positives = 69/157 (43%), Gaps = 4/157 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
I A +D AV + N I +T+ F + P+T ++ ++RL P +A V
Sbjct: 2 IDLAGPSDADAVRRLWNEIIAETTITFTSAPKTAEQ----IDRLVADQPVFIAARDGTRVL 57

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G A ++ + Y T E +Y++ + GLG L + A G S++ I
Sbjct: 58 GFATYAQFRGGDGYRLTQEHAIIYLTGDARGRGLGRGLMRAVEDHARAAGTHSLIGGISGE 117

Query: 130 NDPVSRVLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
N + H A+G+ G L G+K G + D+ Q+
Sbjct: 118 NTDGIAFHFTAIGFIHLGRLPEVGHKFGFRFLDLVLMQK 154

>ref|ZP_03054807.1| YwnH [Bacillus pumilus ATCC 7061]
gb|EDW21234.1| YwnH [Bacillus pumilus ATCC 7061]
Length = 175

Score = 55.5 bits (132), Expect = 3e-06, Method: Compositional matrix adjust.
Identities = 41/154 (26%), Positives = 73/154 (47%), Gaps = 5/154 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEGV 67
R AT D+ A+ D I N I + V TEP + ++W L + R ++ + +G
Sbjct: 17 RIATEDDLKAIVDIYNSTIASREVTADTEPVSVEDRRQWF--LNHSEKRPLYVKTDEDGH 74

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G + R AY+ TVE ++Y++ + GLGS ++ + G +++A I
Sbjct: 75 IYGWLSFETFYGRPAYNGTVEMSIYLNQDDRKGKGLGSLFLQEAIELAPSLGIRTLLAFIF 134

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N+ S+RL + G+ G L G +D+
Sbjct: 135 GHNEASIRLFFKKHGFETWGHLPRIAEMDGSRYDL 168

>ref|YP_148773.1| phosphinothricin N-acetyltransferase [Geobacillus kaustophilus HTA426]
 dbj|BAD77205.1| phosphinothricin N-acetyltransferase [Geobacillus kaustophilus HTA426]
 Length = 220

Score = 55.5 bits (132), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 38/136 (27%), Positives = 67/136 (49%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR A AAD+ + I N I + V EP ++ + W + + +R W+V +
 Sbjct: 60 IRDAAAADLPHIVRIYNETIPSRMVTADLEPVSVESRRRAWFEAHDP-HNRPLWVVEDDGA 118

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V A +++ + R AY T E ++Y++ H+ GLG+ L ++ G K+++ I
 Sbjct: 119 VCAWLSFQS-FYGRPAYRHTAEVSIYIAETHRGRGLGTKLLERAVERAPELGIKTLLGFI 177

Query: 127 GLPNDP SVRLHEALGY 142
 N+PS+RL G+
 Sbjct: 178 FAHNEPSLRLFSRFGF 193

>ref|ZP_02463190.1| phosphinothricin acetyltransferase [Burkholderia thailandensis MSMB43]
 Length = 168

Score = 55.5 bits (132), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 45/141 (31%), Positives = 65/141 (46%), Gaps = 5/141 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEVEGV 67
 R AT D+ A+ I N + + V TEP T + W D R W+V E V
 Sbjct: 7 RDATPVDLPAIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEAGRV 65

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 VA ++++ + R AY T E ++Y+ + GLGS L L A G + + I
 Sbjct: 66 VAWLSFS-DFYGRPAYGHTAEISIYLDEAARGHGLGSRLDLAALAKAPALGVHTALGFIF 124

Query: 128 LPNDP SVRLHEALGYTARGTL 148
 N+PS+RL G+ GTL
 Sbjct: 125 GHNEPSLRLFARYGFATWGTL 145

>ref|YP_003186386.1| GCN5-related N-acetyltransferase [Alicyclobacillus acidocaldarius
 subsp. acidocaldarius DSM 446]
 gb|ACV59997.1| GCN5-related N-acetyltransferase [Alicyclobacillus acidocaldarius
 subsp. acidocaldarius DSM 446]
 Length = 168

Score = 55.5 bits (132), Expect = 3e-06, Method: Compositional matrix adjust.
 Identities = 42/164 (25%), Positives = 65/164 (39%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V +R AT D+ ++ I N IE + + + +RYP VAE +
 Sbjct: 3 VTVRVATHRDLPSILAIYNQGIEDRVATLEQDLKMDYITNWFNEHTNRYPVFVAEYQNN 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G A P+ R AY E +VYV + G+G L + L F +V
 Sbjct: 63 IIGWADLHPYSHRCAYGGVAELSVYVHRGWRAKGVGQALLSALEAFARKHDFHKLVLATF 122

Query: 128 LPNDP SVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFELP 171
 N + L+ +G+ G G G W DV + ++ EL
 Sbjct: 123 PFNSAGLALYRKMGFREVGVFMNHGRLDGKWVDVLWMEKLELKLK 166

```
>ref|ZP_04157106.1| Phosphinothricin N-acetyltransferase [Bacillus mycoides Rock3-17]
ref|ZP_04162837.1| Phosphinothricin N-acetyltransferase [Bacillus mycoides Rock1-4]
gb|EEM05411.1| Phosphinothricin N-acetyltransferase [Bacillus mycoides Rock1-4]
gb|EEM11214.1| Phosphinothricin N-acetyltransferase [Bacillus mycoides Rock3-17]
Length = 167
```

Score = 55.5 bits (132), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 33/141 (23%), Positives = 67/141 (47%), Gaps = 5/141 (3%)

```
Query: 5   RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWL 61
          + ++IR A +D++++ DI N I + V TEP ++ ++W + E P +
Sbjct: 2   KEDIKIRDAEISDLSSIVDIYNSTISSRMVTADTEPVTVKSRQWFN--EHSPSFRPLWI 59

Query: 62  AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
          E +G + G + R AY+ T E ++Y+ ++ G+G + +L + K+
Sbjct: 60  IESQGEICGWVSFQSFYGRPAYNGTAEISYIYHQMYRGRGMGKHILHKVLDTCPKLKIKT 119

Query: 122 VVAVIGLPNDPSVRLHEALGY 142
          ++A I N S++L +
Sbjct: 120 ILAFIFAHNKASLQLFSCFDF 140
```

```
>ref|ZP_06595853.1| acetyltransferase, GNAT family [Bifidobacterium breve DSM 20213]
gb|EFE89258.1| acetyltransferase, GNAT family [Bifidobacterium breve DSM 20213]
Length = 171
```

Score = 55.1 bits (131), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 43/164 (26%), Positives = 67/164 (40%), Gaps = 2/164 (1%)

```
Query: 7   PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
          P RPA +D+ A+ DI N + P+T + +E + Y VAE EG
Sbjct: 8   PYTFRPAVESDIQAITDIYNASVVVGATADLTPTRLDQRRRAWVESHKPPYGVFVAESEG 67

Query: 67  -VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAV 125
          V G + R YD + Y++ Q G G+ + +LL+ A+ + +
Sbjct: 68  GQVIGFGSLSVFYDRAGYDGVTDLAYYIAPAWQGRGAGTFMLDNLLREARARHMRKACGI 127

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGFQWRDF 168
          I N S+ L G+T G + AA G D+ +W D
Sbjct: 128 IFADNAGSIALMRRFGFTQFGLMPAAATDSTGTMRDMSYWYLDL 171
```

```
>ref|YP_004042043.1| gcn5-related N-acetyltransferase [Paludibacter propionigenes
WB4]
gb|ADQ79058.1| GCN5-related N-acetyltransferase [Paludibacter propionigenes WB4]
Length = 165
```

Score = 55.1 bits (131), Expect = 4e-06, Method: Compositional matrix adjust.
Identities = 41/160 (25%), Positives = 69/160 (43%), Gaps = 4/160 (2%)

```
Query: 7   PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
          + R TA D +V +I IET F+ E T +W D+ R +VA +E
Sbjct: 2   EITFRTMTANDWKSVAEIIYKQGIETGNATFQQEIPTWNDW-DNGHIKSCR---IVACIEN 57

Query: 67  VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVI 126
          + G A AR Y E ++YV+++++ G+G L + E + F ++ I
Sbjct: 58  EIVGWAALSSVSARKVYAGIAEVSIYVANKYRGHGIGYKLEKTIAESENENFWTLQVGI 117

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
          N S+ +H+ L + G G +G W + +R
Sbjct: 118 FPEHQASLHIHKLNFRFIEGYRERIGKMNGTWRNTVLLER 157
```

>ref|YP_003596647.1| GNAT family acetyltransferase [Bacillus megaterium DSM 319]
gb|ADF38297.1| acetyltransferase, GNAT family [Bacillus megaterium DSM 319]
Length = 180

Score = 55.1 bits (131), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 40/160 (25%), Positives = 73/160 (45%), Gaps = 2/160 (1%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWL 60
+ +RR V IRPA A+D + V IE + EP+T QE D + ++ + + ++
Sbjct: 13 AKDRREVTIRPAQASDAEHITTAVREIIEAGEFIQKDEPRTVQEEQDFIASVEKNNHMYV 72

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
VAEVEG V GIA + + + T +S + Q +G+G + L +
Sbjct: 73 VAEVEGEVLGIARVLRGEIKMKRHTGLFRTWLIS-KAQGMGIGKQFMNYTLNWCKENNLH 131

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
+ + N + L++ +G+ G ++ Y + + D
Sbjct: 132 KLSLTVFASNKVAYELYKKVGFEGVMKEQAYFNNEYVD 171

>ref|YP_756942.1| GCN5-related N-acetyltransferase [Maricaulis maris MCS10]
gb|ABI66004.1| GCN5-related N-acetyltransferase [Maricaulis maris MCS10]
Length = 170

Score = 55.1 bits (131), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 50/159 (31%), Positives = 69/159 (43%), Gaps = 10/159 (6%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-EVEGV 67
++RP T D AV I I T F E P +W+ + + P LV+ + EG
Sbjct: 3 KLRPMTPTDAPAVLAIYAEGIATGHATF--ESAAP-DWVH-FDEGKLAAPRLVSLDGEGG 58

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
V G A P +R Y E +VYV+ + GLG L L+ EA+G ++ A I
Sbjct: 59 VTGWAALSPVSSRCVYGGVGEVSVYVAEARGKGLGRILLQALVDGSEAEGLWTLTAGIF 118

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGG-----WHDV 161
N S+R+HE G+ G G G W DV
Sbjct: 119 AENTASIRMHEQCGFERLGVRCGLGKMGHGPMAGRWRDV 157

>ref|ZP_05745074.1| phosphinothricin N-acetyltransferase [Lactobacillus antri DSM
16041]
gb|EEW54285.1| phosphinothricin N-acetyltransferase [Lactobacillus antri DSM
16041]
Length = 162

Score = 55.1 bits (131), Expect = 5e-06, Method: Compositional matrix adjust.
Identities = 39/162 (24%), Positives = 68/162 (41%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++ R AT +D+ + +I N I + EP + L +P V E +
Sbjct: 1 MKFRQATHSDLPRIVEIYNQIIPSRLATADLEPVIVADREGWLASFTATHPLWVMEQDDQ 60

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G P+ R AY+ T E ++Y+ + G+G ++ + G ++VA I
Sbjct: 61 IVGWVGLEPFYGRPAYEHTAEISIIYIDQAVRHQGVGHQALQFVIAQLPQLGITAIIVAYIF 120

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
N PS++L G+T G+L G D+ R F+
Sbjct: 121 GHNQPSLKLFRHFGFTEWGS LPRVAELDGVQRDLEILGRFRD 162

>ref|YP_003945614.1| phosphinothricin n-acetyltransferase, putative [Paenibacillus polymyxa SC2]
 gb|ADO55373.1| Phosphinothricin n-acetyltransferase, putative [Paenibacillus polymyxa SC2]
 Length = 169

Score = 54.7 bits (130), Expect = 5e-06, Method: Compositional matrix adjust.
 Identities = 40/138 (28%), Positives = 60/138 (43%), Gaps = 1/138 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY-PWLVAEVEGVV 68
 I A D+ + DI N I V EP T + I E ++ + P V +G +
 Sbjct: 9 IEIACREDLPDIVDIYNSTIAGRMVTADLEPVTVESRIPWFEAHEENHRPLWVLRQKGTI 68

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 AG A + R AY+ T E ++YV + G GS L HLL G +++ +
 Sbjct: 69 AGWASLQSFYGRPAYNGTAEISIVHEDSRGTGTGSRLVQHLLNECPRLGITTLGLGFVFG 128

Query: 129 PNDPSVRLHEALGYTARG 146
 N+PS+ L G+ G
 Sbjct: 129 HNEPSIALLRKFGFEQWG 146

>ref|YP_003670212.1| Phosphinothricin acetyltransferase [Geobacillus sp. C56-T3]
 gb|ADI25635.1| Phosphinothricin acetyltransferase [Geobacillus sp. C56-T3]
 Length = 166

Score = 54.7 bits (130), Expect = 5e-06, Method: Compositional matrix adjust.
 Identities = 38/136 (27%), Positives = 62/136 (45%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP--QTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR AT D+ + I N I + V EP ++ + W + + P V E +G
 Sbjct: 6 IRDATMEDLPHIVRIYNETIPSRMVTADLEPVSVESRRRAWFEAHD--PHNRPLWVVEDDG 63

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV + R AY T E ++Y++ H+ GLG+ L ++ G K+++ I
 Sbjct: 64 VVCAWLSFQSFYGRPAYRHTAEVSIYIAETHRGRGLGAKLLERAVERAPELGIKTLLGFI 123

Query: 127 GLPNDPSVRLHEALGY 142
 N+PS+RL G+
 Sbjct: 124 FAHNEPSLRLFSRFGF 139

>ref|YP_002950799.1| GCN5-related N-acetyltransferase [Geobacillus sp. WCH70]
 gb|ACS25533.1| GCN5-related N-acetyltransferase [Geobacillus sp. WCH70]
 Length = 162

Score = 54.7 bits (130), Expect = 5e-06, Method: Compositional matrix adjust.
 Identities = 40/142 (28%), Positives = 64/142 (45%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP--QTPQEWIDDLERLQDRYPWLVAEVEG 66
 IR A D+ A+ I N I T V EP ++ + W LE P V E++G
 Sbjct: 2 IRNANREDLPAIVQIYNETIPTRMVTADLEPVTVESKKAWF--LEHDPHTRPLWVVELDG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V + R AY T E ++Y+S ++ G+G+ L ++ + K+++ I
 Sbjct: 60 RVCWLSFQSFYGRPAYRHTAEISIYISEAYRGRGIGTQLLQKAIEEAPSLEIKTLLGFI 119

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
 N+PS+RL G+ G L
 Sbjct: 120 FAHNEPSLRLFARFGFETWGHL 141

>dbj|BAJ27042.1| putative acetyltransferase [Kitasatospora setae KM-6054]
Length = 167

Score = 54.7 bits (130), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 49/164 (29%), Positives = 67/164 (40%), Gaps = 6/164 (3%)

Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA 62
P RP + P A V I IE F TE P+ D RL + ++V
Sbjct: 4 PVFRPAPMLPEHAEQ---VLAIYRAGIEEGNATFETE--APEWAAFDAARLPG-HRYVVL 57

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
+ V+G A AR AY VE +VYV H+ G+ L HL+ S E G ++
Sbjct: 58 GPDATVSGWIAASAVSARPAYAGVVEHSVYVHPDHRGRGIAGVLLAHLIDSTEEAGIWTI 117

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+ + N S+ LH A G+ GT G W D +R
Sbjct: 118 QSSVFPENTASLALHAAAGFRVVGTRERVARHRGVWRDVTVLIER 161

>ref|YP_004100431.1| GCN5-related N-acetyltransferase [Intrasporangium calvum DSM 43043]
gb|ADU49704.1| GCN5-related N-acetyltransferase [Intrasporangium calvum DSM 43043]
Length = 162

Score = 54.3 bits (129), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 50/159 (31%), Positives = 70/159 (44%), Gaps = 3/159 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++I P TAA AV DI I F + T +++ D RL V ++ V
Sbjct: 1 MQIAPMTAAHGPAVLDIYAAGIAEGDATFESTVPTWEDF--DAARLSLHRFVAVDDLTAV 58

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ IA A P +R AY E +VYV R + +G L L+ S EA G +V + I
Sbjct: 59 LGWIA-ASPSSRPAYAGVAEHSVYVDPARGRHVGRALLDALITSTEAGIWTVQSGIF 117

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH G+ G G + G W DV +R
Sbjct: 118 PENVASLALHRRAGFREVGVRERIGRQDGRWRDVVLLER 156

>emb|CA089677.1| unnamed protein product [Microcystis aeruginosa PCC 7806]
Length = 163

Score = 54.3 bits (129), Expect = 6e-06, Method: Compositional matrix adjust.
Identities = 38/142 (26%), Positives = 64/142 (45%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWIDDLERLQDRYPWLVAEVEG 66
IR A D+ + +I N + T +P ++ +EW + ++YP V +EG
Sbjct: 3 IREKETDLPTIIEIYNAAVPTRKATADLKPILESRRWFKKHD--PEQYPIWVIAIEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G + R AY T E ++Y+S +Q G+G L + L+ G +++ +I
Sbjct: 61 RVVGWLSLQMFYGRVAYQKTAEVSLYISPDYQGRGIGKLLVEYALERCPQLGISNLCII 120

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
N S+ L E G+ G L
Sbjct: 121 FAHNQASICLFKFGFQRWGYL 142

>ref|YP_003511953.1| GCN5-related N-acetyltransferase [Stackebrandtia nassauensis DSM 44728]
gb|ADD42860.1| GCN5-related N-acetyltransferase [Stackebrandtia nassauensis DSM 44728]

Length = 163

Score = 54.3 bits (129), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 47/160 (29%), Positives = 66/160 (41%), Gaps = 5/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR T D V I I+T F T T + + D L D L+A +
Sbjct: 1 MHIRAMTPTDAPDVLKIYQDGIDTGNATFETTAPTWETF--DHTHLPDHR--LIAHDDTG 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
G A P R+ Y +E ++Y++ Q G+GS L + S E G ++ A I
Sbjct: 57 PLGWIAATPTSTRHVYRGVIEHSIYIATHAQGRGVGSALLAAAFVDSCTAGIWTIQAGIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYK-HGGWHDVGFVQR 166
N PS+ LHE G+ G G G W DV +R
Sbjct: 117 PDNTPSLALHEKHGFRIIGIRHHIGQTIDGRWRDVALER 156

>ref|ZP_07729425.1| acetyltransferase, GNAT family [Lactobacillus oris PB013-T2-3]
gb|EFQ53546.1| acetyltransferase, GNAT family [Lactobacillus oris PB013-T2-3]
Length = 162

Score = 54.3 bits (129), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 38/163 (23%), Positives = 70/163 (42%), Gaps = 2/163 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEG 66
+E R A AD+ + +I N I + EP + D +P W++ + +
Sbjct: 1 MEFRKAVHADLPRIVEIYNQIIPSRLATADLEPVIVADCEDWFASFATHTPLWVMTQGDQ 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
++ +A P+ R AY+ T E ++Y+ + G+GS ++ + G ++VA I
Sbjct: 61 IIGWVALE-PFYGRPAYEHTAEISIIYIDQAVRHQGVGSRALQFVIDQLPQLGITAIWAYI 119

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQRDFE 169
N PS++L + G+L G D+ R F+
Sbjct: 120 FGHNQPSLKLFRFAFAEWGSLPRVAELDGVQRDLKILGRRFD 162

>ref|YP_003593537.1| GCN5-related N-acetyltransferase [Caulobacter segnis ATCC 21756]
gb|ADG10919.1| GCN5-related N-acetyltransferase [Caulobacter segnis ATCC 21756]
Length = 164

Score = 54.3 bits (129), Expect = 7e-06, Method: Compositional matrix adjust.
Identities = 46/163 (28%), Positives = 68/163 (41%), Gaps = 10/163 (6%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVA-EVEG 66
RPAT AD A+ I N IE F T P + + W L P +V +
Sbjct: 7 RPATLADAPAMARIYNQGIEDRIATFETSPRGVEAVEAW-----LASGLPVVVVVDAAG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A + R Y E +VYV H+ G+G L+++ +AQG +++ +
Sbjct: 61 NVVGYAATFAYSDRCCYAGIAEFSVYVDRGHRGTGVGKHALAALIEAAKAQGLHKLLSRV 120

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQRDFE 169
+ N S+ L G+ G + G G W DV +R E
Sbjct: 121 FVENSASLGLLRQGFREVGVRHQRHGLDGVWRDVAVERLIE 163

>ref|ZP_03970056.1| acetyltransferase [Sphingobacterium spiritivorum ATCC 33300]
gb|EEI90300.1| acetyltransferase [Sphingobacterium spiritivorum ATCC 33300]
Length = 163

Score = 54.3 bits (129), Expect = 7e-06, Method: Compositional matrix adjust.

Identities = 35/137 (25%), Positives = 64/137 (46%), Gaps = 2/137 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER--LQDRYPWLVAEVE 65
 ++ R A +D+ + +I N + + V TEP + I E+ + R W++ E
 Sbjct: 1 MQFRHAILSDLIRIVEIYNSTVASRVVTADTEPVSTNSRIPWFEEKHDEKRPWLWVLENEE 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G++ G + R AY TVE ++Y+ ++ GLG + ++ A G K+++
 Sbjct: 61 GLIIGWISFQSFYGRPAYQATVEISIIYLDEAYRGQGLGLAIDYAIQQAPAYGIKTLTLLGF 120

Query: 126 IGLPNDPSVRLHEALGY 142
 I N S+ L E G+
 Sbjct: 121 IFAHNTASLHLFEHFGF 137

>ref|ZP_07729782.1| acetyltransferase, GNAT family [Lactobacillus oris PB013-T2-3]
 gb|EFQ53125.1| acetyltransferase, GNAT family [Lactobacillus oris PB013-T2-3]
 Length = 172

Score = 54.3 bits (129), Expect = 7e-06, Method: Compositional matrix adjust.
 Identities = 42/165 (25%), Positives = 73/165 (44%), Gaps = 1/165 (0%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV 64
 + ++IR A A+D + +I N + ++P T + + + DR+P V +
 Sbjct: 3 KATIKIRRAEASDWETIINIFNEAVAAGIATDESKPITVADREEWFAQFDDRHLWVVD 62

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM-EAQGFKSVV 123
 +G V+G + AY T E +Y+ H R GLG L + + E FK+VV
 Sbjct: 63 DGKVS GWCALEYFSTHPAYTDTAEIAIYIHGAHRQGLGRLLAFADQQIKEELHFKTVV 122

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDF 168
 A I N S L + G+ G L A G + ++ + +++
 Sbjct: 123 AYIYERNQASQGLFKQSGFEYWGHLPAAIAKVAGEYRELKIYGKNY 167

>ref|NP_241299.1| phosphinothricin N-acetyltransferase [Bacillus halodurans C-125]
 dbj|BAB04152.1| phosphinothricin N-acetyltransferase [Bacillus halodurans C-125]
 Length = 165

Score = 54.3 bits (129), Expect = 8e-06, Method: Compositional matrix adjust.
 Identities = 45/163 (27%), Positives = 71/163 (43%), Gaps = 4/163 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 + I T D V I IET F TE + ++W D ++ R ++ E
 Sbjct: 3 SIRIEMTDNDWPEVERIYREGIETGNATFETEAPSWEKW--DAGHVK-RCRFVAKSKEK 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VV +A + P +R Y E +VYV + G+G L +++ E QG+ ++ A +
 Sbjct: 60 VVGWVALS-PVSSRCVYQGVAEVSVYVGSTGRGKG VGRKLLASVVEESEKQGYWTLQASV 118

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWQDFE 169
 N S++LH LG+ G + G W DV +R E
 Sbjct: 119 FPENVASLKLHRQLGFREVGKRERLAKREGVWRDVILLERRSE 161

>ref|ZP_06567725.1| hypothetical protein SeryN2_35005 [Saccharopolyspora erythraea
 NRRL
 2338]
 Length = 281

Score = 53.9 bits (128), Expect = 8e-06, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 68/160 (42%), Gaps = 6/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLRLQDRYPWLVAEVEG 66
 V IRP D +AV I I T F TE P + LE R + W VAEV+G
 Sbjct: 120 VTIRPLETRDWSAVRRIYAEGIATGNATFDTE--VPAR--NTLEARWLPEHRW-VAEVDG 174

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 VAG A P R+ Y +++VYV + G+G TL + + G ++ I
 Sbjct: 175 EVAGWAAITPVSNRDCYAGVGDTSVYVGDFRGRGVGKTLHLKQVTEADTHGLWTLQTSI 234

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N S+ LH + G+ G HG W D +R
 Sbjct: 235 FPNRASLALHYSAGFRTVGLRERIAAHHGTWRDVLLE 274

>ref|ZP_08206806.1| N-acetyltransferase [Gordonia neofelifaecis NRRL B-59395]
 gb|EGD53309.1| N-acetyltransferase [Gordonia neofelifaecis NRRL B-59395]
 Length = 155

Score = 53.9 bits (128), Expect = 8e-06, Method: Compositional matrix adjust.
 Identities = 43/139 (30%), Positives = 61/139 (43%), Gaps = 5/139 (3%)

Query: 29 IETSTVNFRTPEQTPQEWIDDLRLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWT 87
 I+T F T T W D D + L D + ++ + G V G A P + Y +
 Sbjct: 17 IDTGNATFATAAPT---WPDFDRDHLPD-HRFVALDPNGNVTGWIAASPASSLCVYTGV 72

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGT 147
 E +VYV H G+G+ L L+ S E G ++ I N S+ LH A G+ GT
 Sbjct: 73 EHSVYVDPNHSKGKGVGTALLQALIDSTETAGVWTIETGIFPENHASLALHHAHGFRTVGT 132

Query: 148 LRAAGYKHGGWHDVGFQWR 166
 G +G W DV +R
 Sbjct: 133 RERIGQHNGHWRDVLIER 151

>ref|ZP_00955324.1| phosphinothricin N-acetyltransferase, putative [Sulfitobacter sp.
 EE-36]
 gb|EAP83749.1| phosphinothricin N-acetyltransferase, putative [Sulfitobacter sp.
 EE-36]
 Length = 161

Score = 53.9 bits (128), Expect = 9e-06, Method: Compositional matrix adjust.
 Identities = 49/157 (31%), Positives = 74/157 (47%), Gaps = 3/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLRLQDRYPWLVAEVEGVVA 69
 IRPAT +D AV + N I + F ++P+T E ++ L + W VA+ EGV A
 Sbjct: 3 IRPATGSDAGAVTALWNVMITQTLFTFTSQPKTGAE-VEALIAGRAGQFW-VADAEV-A 59

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G G +++ Y VE ++ + Q G G L + AQG + +VA I
 Sbjct: 60 GFMTYGAFRSGVGYRDAVEHSIVLDAQAQAGAGRALMQTACDAVAQGRVMVA AISGA 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N +V H ALG+ G + G K+G D+ Q+
 Sbjct: 120 NPGAVGFHAALGFDHVGRMPRIGQKNGQQQLDLILMQK 156

>ref|ZP_01049506.2| acetyltransferase (GNAT) family protein [Dokdonia donghaensis
 MED134]
 gb|EAQ39478.2| acetyltransferase (GNAT) family protein [Dokdonia donghaensis
 MED134]
 Length = 160

Score = 53.9 bits (128), Expect = 9e-06, Method: Compositional matrix adjust.
 Identities = 46/163 (28%), Positives = 67/163 (41%), Gaps = 8/163 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERL-QDRYPWLVAEVEGV 67

IRP D I ++T F T +WI D + L Q R+ VA E V
Sbjct: 3 IRPLLKQDYTHCAQIYQDGLDTGMATFET---IVPDWISWDAKFLEQCRF---VAIKEEV 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G P+ R Y E T+Y+S + G+G L +K E GF ++ A I
Sbjct: 57 ILGWALTTPFSTREVIYKGVAEVTLYISKIARGKGIGRALLMTAIKESERAGFWTLQAKIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFEL 170

N+ S+ L + G+ G + G WHD ++ EL
Sbjct: 117 AQNEASMDLFQKCGFRIVGVREKLAMRDGIWHDNVLLLEKRSEL 159

>ref|ZP_03973496.1| acetyltransferase [Lactobacillus reuteri CF48-3A]

ref|ZP_07127575.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri SD2112]

gb|EEI66647.1| acetyltransferase [Lactobacillus reuteri CF48-3A]

gb|EFK86123.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri SD2112]

Length = 164

Score = 53.9 bits (128), Expect = 9e-06, Method: Compositional matrix adjust.

Identities = 39/162 (24%), Positives = 69/162 (42%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

++ R AT D+ + I N I + P T + E + +P V E +
Sbjct: 3 LQYRKATLEDLPKIVEIYNQIIPSRLATADLTPTITVDARKEWFEAFDENHPIWVIEHQNE 62

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

V G + R AY+ T E +Y+ R ++ G+G+ ++ + ++VA I
Sbjct: 63 VLGWVALEHFPYGRPAYNHTSEIAIYLDQRLRKQGVGKTMFEIIGQLPNLAVDTIVAYIF 122

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169

N PS++L ++ G+T G L G D+ R F+
Sbjct: 123 GHNIPSLKLFKSFGFTQWGLLPQVAELDGIKRDLVILGRHFK 164

>ref|ZP_01629051.1| GCN5-related N-acetyltransferase [Nodularia spumigena CCY9414]

gb|EAW46270.1| GCN5-related N-acetyltransferase [Nodularia spumigena CCY9414]

Length = 162

Score = 53.9 bits (128), Expect = 9e-06, Method: Compositional matrix adjust.

Identities = 43/143 (30%), Positives = 64/143 (44%), Gaps = 3/143 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 66

+ IR A D+ A+ I N I + +P + Q + + R + P V E+EG
Sbjct: 1 MTIRHANETDLPAIVAIYNAAIPSRKATADLKPVSVQSRGLGWFGGRSPSQRPVIEIEG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVS-HRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125

+V G + R AYD T E ++Y+S HQR GLGS +K G K+++
Sbjct: 61 IVVGWLSFKSFYGRPAYDSTAEISIIYLSPSVHQR-GLGSQFLALAIKESPNLGIKTLLGF 119

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148

I N S+ L G+ G L
Sbjct: 120 IFAHNQASLNLFTFRFGFEQWGYL 142

>ref|ZP_03211253.1| Sortase related acyltransferase [Lactobacillus rhamnosus HN001]

gb|EDY99343.1| Sortase related acyltransferase [Lactobacillus rhamnosus HN001]

Length = 164

Score = 53.9 bits (128), Expect = 9e-06, Method: Compositional matrix adjust.

Identities = 42/162 (25%), Positives = 69/162 (42%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +E PAT AD+ + I N I T +PQT + D D +P + +V+
 Sbjct: 2 IEFVPATTADLPKIVAIYNETIPTHQATADLQPTVDQKADWFAAHNDHFFAWMIQVDHH 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
 G + R AYD T E ++Y+ + +GS+ + + A+G +++A I
 Sbjct: 62 NVGWLTLSDRAAYDQTAEISLYLDITARGQHIGSSALAFVDQEAPARGLTIIARIF 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
 N S RL + Y G L A G D+ + + F+
 Sbjct: 122 GHNSASRRLPKKFNYDHWGHLPAIADLPEGKADLEIYGKHF 163

>ref|YP_001107169.1| hypothetical protein SACE_4980 [Saccharopolyspora erythraea NRRL
 2338]
 emb|CAM04244.1| hypothetical protein SACE_4980 [Saccharopolyspora erythraea NRRL
 2338]
 Length = 272

Score = 53.9 bits (128), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 50/160 (31%), Positives = 68/160 (42%), Gaps = 6/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG 66
 V IRP D +AV I I T F TE P + LE R + W VAEV+G
 Sbjct: 111 VTIRPLETRDWSAVRRIYAEIATGNATFDTE--VPAR--NTLEARWLPEHRW-VAEVDG 165

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
 VAG A P R+ Y +++VYV + G+G TL + + G ++ I
 Sbjct: 166 EVAGWAAITPVSNRDCYAGVGDTSVYVGDFGRGRGVGKTLHLKQVTEADTHGLWTLQTSI 225

Query: 127 GLPNDPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 N S+ LH + G+ G HG W D +R
 Sbjct: 226 FPENRASLALHYSAGFRTVGLRERIAAHHGTTWRDVTLLER 265

>ref|YP_001166607.1| GCN5-related N-acetyltransferase [Rhodobacter sphaeroides ATCC
 17025]
 gb|ABP69302.1| GCN5-related N-acetyltransferase [Rhodobacter sphaeroides ATCC
 17025]
 Length = 183

Score = 53.9 bits (128), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 45/166 (27%), Positives = 67/166 (40%), Gaps = 5/166 (3%)

Query: 3 PERRP--VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 P RP + IR A D A+ I N I + V F + ++P+E +E R +L
 Sbjct: 18 PSGRPPSLTIRQARPEDGPALLAIWNPIIRDITLVTFNADEKSPEELRAMIE---TRPAFL 74

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
 VA+ G A ++ Y T+E T+ + + G+G L + G
 Sbjct: 75 VADEGAGPMGFATYSQFRGGVGYRHTMEHTIILGPAARGRGIGRALMAAIEDHARQAGAH 134

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 S+ A + N H ALGY L G K G W D+ Q+
 Sbjct: 135 SIFAGVSAGNPEGRAFHAAALGYAETAVLPQVGCKFGRWLDLVLQM 180

>ref|ZP_02962821.1| possible N-acetyl transferase [Bifidobacterium animalis subsp.
 lactis HN019]
 ref|YP_002968443.1| N-acetyl transferase [Bifidobacterium animalis subsp. lactis Bl-
 04]
 ref|YP_002970010.1| N-acetyl transferase [Bifidobacterium animalis subsp. lactis DSM

10140]
gb|EDT89698.1| possible N-acetyl transferase [Bifidobacterium animalis subsp. lactis HN019]
gb|ACS46381.1| N-acetyl transferase [Bifidobacterium animalis subsp. lactis B1-04]
gb|ACS47948.1| N-acetyl transferase [Bifidobacterium animalis subsp. lactis DSM 10140]
gb|ADG33573.1| N-acetyl transferase [Bifidobacterium animalis subsp. lactis V9]
Length = 215

Score = 53.9 bits (128), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 46/164 (28%), Positives = 63/164 (38%), Gaps = 6/164 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV-----E 65
R AT D+A + DI N + T P T + +E D Y V E E
Sbjct: 37 RLATVDDVAVITDIYNEAVMAGGSTADTVPVTYEARRWIESHVDPYAVFVFETIAGDGE 96

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G + R YD + YV+ R QR G+G LL A+ + A+
Sbjct: 97 AEEVGFGAISVIFYDRPGYDGVCDLAYVVTARWQRRGVGRFALRTLLNECRARAMRKACAI 156

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGY-KHGGWHDVGVFWQRDF 168
I N S L E+ G+ G + A Y G HD+ +W D
Sbjct: 157 IFSDNTASNALVESFGFEPFGEMPEAAAYDSRGVLHDMSYWCLDL 200

>ref|YP_001353673.1| acetyltransferase [Janthinobacterium sp. Marseille]
gb|ABR88349.1| acetyltransferase [Janthinobacterium sp. Marseille]
Length = 165

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 43/135 (31%), Positives = 61/135 (45%), Gaps = 5/135 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWDLLERLQDRYPWLVAEEVGV 67
R AT D+ A+ I N I + V EP T Q W LE + P V E +G
Sbjct: 6 RLATLDDLPAIVAIYNSTIASRQVTADIEPVTVASRQAWF--LEHTAGQRPIWVLEEQR 63

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G + AR AY TVE ++Y+ + GLG+ L + G ++V +I
Sbjct: 64 VLGWLSYSNHFARAAYAATVELSIYLEDARGKGLGAYLLQEAIAYAPKLGHTLVGLIF 123

Query: 128 LPNDPSVRLHEALGY 142
N PS++L E G+
Sbjct: 124 GHNTPSLKLFRFGRF 138

>ref|ZP_05744891.1| phosphinothricin N-acetyltransferase [Lactobacillus antri DSM 16041]
gb|EEW54543.1| phosphinothricin N-acetyltransferase [Lactobacillus antri DSM 16041]
Length = 172

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
Identities = 42/166 (25%), Positives = 75/166 (45%), Gaps = 1/166 (0%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63
E+ + IR A A+D + +I N + + P T + + + D +P V
Sbjct: 2 EKAIMSIRRAHASDWETIINIFNEAVAAGIATDESSPITVADRAEWAQFDDWHPLWVIT 61

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSV 122
V+GVV G + AY T E +Y+ + R GLG L + + ++ + F++V
Sbjct: 62 VDGVVVRGWCALEYFYPNPAYADTAEIAIYIQQAHRQGLGRLLAFVDQQIKDRHLHFRTV 121

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRDF 168

VA I N PS L + G++ G L A G + ++ + +++
 Sbjct: 122 VAYIYERNRPSQALFKQNGFSYWGRLLPAIAKVAGEYRELKIYGKNY 167

>ref|YP_949323.1| putative phosphinothricin N-acetyltransferase [Arthrobacter
 aurescens TC1]
 gb|ABM06417.1| putative phosphinothricin N-acetyltransferase [Arthrobacter
 aurescens TC1]
 Length = 169

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 46/164 (28%), Positives = 72/164 (43%), Gaps = 8/164 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGV 67
 V +R D AV I I+T F E + P+ + RL+D + + E
 Sbjct: 3 VALRAMEPEDWPAVRGIFQEGIDTGYATF--ETKAPEWAAFNNRLKD-HRLVAVNSERE 59

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 + G P +R AY VE ++YV+ + G+G+ L L S EA+G ++ + I
 Sbjct: 60 ILGWTAVSPVSSRPAYAGVVEHSIYVARAARGQGIGARLLKALAASTEAKGIWTIQSSIF 119

Query: 128 LPNDPSVRLHEALGYTARG-----TLRAAGYKHGGWHDVGFWQR 166
 N+ S+RLH+A G+ G + G G W D +R
 Sbjct: 120 PENEASIRLHQAHGFAIVGRRDRIARLSTGPAAGQWQDTLLLER 163

>ref|ZP_05025230.1| acetyltransferase, GNAT family [Microcoleus chthonoplastes PCC
 7420]
 gb|EDX76941.1| acetyltransferase, GNAT family [Microcoleus chthonoplastes PCC
 7420]
 Length = 178

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 46/166 (27%), Positives = 70/166 (42%), Gaps = 14/166 (8%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVE--- 65
 IR AT D+ A+ +I N + + EP + + I E + +P V +
 Sbjct: 12 IRDATEVDLPAIVEIYNSAVPSRIATADLEFISVESRISWYQEHKPNSHPLWVMDCHERS 71

Query: 66 ---GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 G +AG + R AY T E +VYVS +R G+G L +K G ++
 Sbjct: 72 NSTGQIAGWLSFQAFVLRPAYHATAELSVYVSPDFRRQGIGQQLLQRAIKQTPKLGLNTL 131

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQRDF 168
 VA+I N PS+ L + G+ G L D+G +RD
 Sbjct: 132 VALIFAHNQPSLHLFQKYGFQRWGYLPQIA-----DMGHIERDL 170

>ref|YP_003838423.1| GCN5-related N-acetyltransferase [Micromonospora aurantiaca ATCC
 27029]
 gb|ADL48847.1| GCN5-related N-acetyltransferase [Micromonospora aurantiaca ATCC
 27029]
 Length = 163

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 41/147 (27%), Positives = 59/147 (40%), Gaps = 3/147 (2%)

Query: 20 AVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGVVAGIAYAGPWKA 79
 +V +I I F TEP +W + W+ + G V G
 Sbjct: 15 SVLEIYRLGIAEGNATFETEPP--DWTRFTATRLPGHRWVALDEAGDVLGWVACSAVSD 71

Query: 80 RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEA 139
 R Y VE +VYV + + G+G L L+ S EA G ++ + + N S+ LH

Sbjct: 72 RCVYAGVVEHSVYVHPKGRGRGVGRALLEALIASTEAAAGIWTIQSGVFPENTASLALHAT 131

Query: 140 LGYTARGTLRAAGYKHGGWHDVGFQWR 166

G+ GT G HG W DV +R

Sbjct: 132 CGFRVVGTRERVGRHHGTWRDVTILIER 158

>ref|YP_003961511.1| GCN5-related N-acetyltransferase [Eubacterium limosum KIST612]
 gb|ADO38548.1| GCN5-related N-acetyltransferase [Eubacterium limosum KIST612]
 Length = 174

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 41/147 (27%), Positives = 66/147 (44%), Gaps = 6/147 (4%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE--WIDDLERLQDRYPWLVA 62

+ + +R A D + DI+N I V P T + W E +P VA

Sbjct: 10 KRIAVRLAKEKDYQRILDILNAAILERRVTALLTPVTMESRRGWFK--EHSDBGVHPIYVA 67

Query: 63 EVEGVVAG-IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121

E +G+VAG +A R + E + Y++ + G+GS+L H+++ +G K+

Sbjct: 68 EKDGIWAGWMAVTAYRCGREGFKHACEISYYIAPEFRGSGIGSSLMEHVIRESRKRLKN 127

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTL 148

++AVI N S RL G+ GT

Sbjct: 128 LMAVIFADNLGSQRLAYKYGFKIWGTF 154

>ref|ZP_06500009.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv.
 syringae

FF5]

Length = 85

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 28/67 (41%), Positives = 40/67 (59%), Gaps = 1/67 (1%)

Query: 101 GLGSTLYTHLLKSMEAQGFKS VVAVIG-LPNDPSVRLHEALGYTARGTLRAAGYKHGGWH 159

G+G L + L++ EA G++ ++AVIG N S+RLHE LG+ G + G+KHG W

Sbjct: 5 GIGQALLSALVQHCEAGGWRQMIWVIGNSQNIASRLRLHERLGFRRVGVFESVGFKHGRWV 64

Query: 160 DVGFWQR 166

D QR

Sbjct: 65 DTVLMQR 71

>ref|ZP_05915841.1| putative phosphinothricin N-acetyltransferase [Brevibacterium
 linens BL2]
 Length = 168

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 36/139 (25%), Positives = 61/139 (43%), Gaps = 2/139 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ +R ++D + V D+ IET F P P W D + + +G

Sbjct: 4 LHVREMVSSDWSEVKDLYRTGIETGHATFEAAP--PAAWEDFCATRRDLRCRVAVDADGR 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIG 127

+ G AGP +R Y VE ++YV G+G+ L + + +G ++ + I

Sbjct: 62 ILGWVGAGPVSSREYRGVVEHSIYVHPDASGKGVGTQLLSEFISLTDQRGIWTIQSSIF 121

Query: 128 LPNDPSVRLHEALGYTARG 146

N S+RLHE G+ G

Sbjct: 122 PENTASLRLHEHAGFRTVG 140

>ref|YP_002469889.1| N-acetyl transferase [Bifidobacterium animalis subsp. lactis AD011]
 gb|ACL29313.1| possible N-acetyl transferase [Bifidobacterium animalis subsp. lactis AD011]
 Length = 185

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 46/164 (28%), Positives = 63/164 (38%), Gaps = 6/164 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEV-----E 65
 R AT D+A + DI N + T P T + +E D Y V E E
 Sbjct: 7 RLATVDDVAVITDIYNEAVMAGGSTADTVPVTYEARRRWIESHVDPYAVFVFETIAGDGE 66

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + R YD + YV+ R QR G+G LL A+ + A+
 Sbjct: 67 AEEVGFGAISVIFYDRPGYDGVCDLAYVYTARWQRRGVGRFALRTLLNECRARAMRKACAI 126

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGY-KHGGWHDVGVFQWRDF 168
 I N S L E+ G+ G + A Y G HD+ +W D
 Sbjct: 127 IFSDNTASNALVESFGFEPFGEMPEAAYDSRGVLHDMSYWCLDL 170

>ref|YP_340976.1| acetyltransferase [Pseudoalteromonas haloplanktis TAC125]
 emb|CAI87534.1| putative acetyltransferase [Pseudoalteromonas haloplanktis TAC125]
 Length = 161

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 40/142 (28%), Positives = 66/142 (46%), Gaps = 6/142 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQT--PQEWIDDLERLQDRYPWLVAEVEG 66
 IR A D+ + I N I + V TE + Q W D R ++ +E +
 Sbjct: 3 IRLARPDLKTIVAIYNETIASRMVTADTEEVSVTDKQAWFDS--HTSQRPIYVYSENDQ 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V+A ++Y P+ R AY+ TVE ++Y++ + Q GLG TL + K ++ I
 Sbjct: 61 VLAWLSYK-PFYGRVAYEGTVEISIIYITAKAQGKGLGKTLMEFAQTQAKQLNIKVLLGFI 119

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
 N PS++L + ++ G L
 Sbjct: 120 FSHNLPSIKLKFHFNFSVWGEL 141

>ref|ZP_04758433.1| acetyltransferase [Neisseria flavescens SK114]
 gb|EER55694.1| acetyltransferase [Neisseria flavescens SK114]
 Length = 166

Score = 53.5 bits (127), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 38/140 (27%), Positives = 61/140 (43%), Gaps = 1/140 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
 IRPA D+ A+ DI N + T P T E D+ P + + + +G V
 Sbjct: 5 IRPALRQDLPAIVDIYNSTVATRQSTADLSPTTVAEREIWFAAHTDKRPIYALYDTDGTV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 + R AY + E ++YV H + G+G L H+L+ + +V+A++
 Sbjct: 65 LAWGSFSDYHPRYAYHISAEVSIYVRHDMRGAGVGKILLRHMLEHAPSLDIHNVIALVFG 124

Query: 129 PNDPSVRLHEALGYTARGTL 148
 N PS+ L G+ G L
 Sbjct: 125 HNYPSLNLFHRFGFKEWGRL 144

```
>ref|ZP_04440177.1| acetyltransferase [Lactobacillus rhamnosus LMS2-1]
ref|YP_003175303.1| phosphinothricin N-acetyltransferase [Lactobacillus rhamnosus Lc
705]
gb|EEN81150.1| acetyltransferase [Lactobacillus rhamnosus LMS2-1]
emb|CAR91452.1| Phosphinothricin N-acetyltransferase [Lactobacillus rhamnosus Lc
705]
Length = 164
```

Score = 53.1 bits (126), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 42/162 (25%), Positives = 68/162 (41%)

```
Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E PAT AD+ + I N I T +PQT + D D +P + +V+
Sbjct: 2 IEFVPATTADLPKIVAIYNETIPTHQATADLQPTVDQKADWFAAHNDHFPAAWMIQVDHH 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
G + R AYD T E ++Y+ + +GS+ + + A+G +++A I
Sbjct: 62 NVGWLTLAYSADRAAYDQTAEISLYLDITARGHHIGSSALAFVDQEAPARGLTTIIRIF 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDFE 169
N S RL + Y G L A G D+ + + F
Sbjct: 122 GHNSASRRRLFKKFNYDHWGHLPAIADLPEGKADLEIYKHFN 163
```

```
>ref|YP_003123028.1| GCN5-related N-acetyltransferase [Chitinophaga pinensis DSM 2588]
gb|ACU60827.1| GCN5-related N-acetyltransferase [Chitinophaga pinensis DSM 2588]
Length = 163
```

Score = 53.1 bits (126), Expect = 1e-05, Method: Compositional matrix adjust.
 Identities = 40/135 (29%), Positives = 62/135 (45%), Gaps = 5/135 (3%)

```
Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEGV 67
R AT D+ + I N I V TEP ++ Q W D + + R W+V E EGV
Sbjct: 4 RNATQEDLPEIVAIYNTTIAGRMVTADTEPVTVESRQHWF--IHSPEKRPLWMV-EDEGV 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
G + R AYD T E ++Y+ + G G + + ++ A +++ I
Sbjct: 62 SVGWVSFQSFYGRPAYDGTAEISLYLHENTRGKGYGKKILEYAMEQCPAIVHTLLGFIF 121

Query: 128 LPNDPSVRLHEALGY 142
N PS++L E LG+
Sbjct: 122 AHNIPSLKLFQQLGF 136
```

```
>ref|ZP_01614149.1| putative acetyltransferase [Alteromonadales bacterium TW-7]
gb|EAW26595.1| putative acetyltransferase [Alteromonadales bacterium TW-7]
Length = 173
```

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 42/149 (28%), Positives = 66/149 (44%), Gaps = 6/149 (4%)

```
Query: 3 PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPW 59
P + + R AT D+ + I N I+ V TE T +E W + Q R +
Sbjct: 7 PLKFTMTTRLATIDDLNDIVAIYNETIKGRMVTADTEEVTVEEKKDFN--SHTQKRPIY 64

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
+ E + V+A ++Y + R AYD TVE ++Y++ Q GLG L +
Sbjct: 65 VYCENDTVLAWVSYSFY-GRPAYDGTVEMSIYITKNAQKGLGKKLMQFAQSEAKKLDI 123

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTL 148
++ I N PSV+L + G+ G L
Sbjct: 124 SVLLGFIFSHNLPSVKLFKHFQFDVWGEL 152
```


>ref|ZP_07717069.1| GNAT family acetyltransferase [Aeromicrobium marinum DSM 15272]
gb|EFQ83240.1| GNAT family acetyltransferase [Aeromicrobium marinum DSM 15272]
Length = 289

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 45/162 (27%), Positives = 67/162 (41%), Gaps = 10/162 (6%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY-PWL--VAEV 64
V +RP ADM V I + + T F T + ++L+ R+ P L VAE+
Sbjct: 130 VAVRPVADADMPRVLAIYDQGLATRNATFETT-----VPSADQLRSRWRPGLAWVAEL 182

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+G V G P R Y E++VYV+ + G+G L + +A G ++
Sbjct: 183 DGEVVGWTAVTPTSDRECYAGVGETSVYVAESARGRGVGKALLFAQVTEADAAGLWTLQT 242

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
I N S+ LH + GY G G W D +R
Sbjct: 243 SIFPENRASLALHHSAGYRTLAVRTRIGQLDGVWRDVTLLER 284

>ref|ZP_05984327.1| phosphinothricin N-acetyltransferase [Neisseria subflava NJ9703]
gb|EFC52779.1| phosphinothricin N-acetyltransferase [Neisseria subflava NJ9703]
Length = 166

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 38/140 (27%), Positives = 61/140 (43%), Gaps = 1/140 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
IRPA D+ A+ DI N + T P T E D+ P + + + +G V
Sbjct: 5 IRPALRQDLPAIVDIYNSTVATRQSTADLSPTTVAEREMWFAAHTDKRPIYALYDADGTV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
+ R AY + E ++YV H + G+G L H+L+ + +V+A++
Sbjct: 65 LAWGSFSDYHPRYAYHISAEVSIYVRHDMRGAGVGKILLRHMLERAPSLDIHNVIALVFG 124

Query: 129 PNDPSVRLHEALGYTARGTL 148
N PS+ L G+ G L
Sbjct: 125 HNYPSLNLFRFGFEWGR 144

>ref|ZP_07082756.1| phosphinothricin N-acetyltransferase [Sphingobacterium spiritivorum
ATCC 33861]
gb|EFK55885.1| phosphinothricin N-acetyltransferase [Sphingobacterium spiritivorum
ATCC 33861]
Length = 163

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 35/137 (25%), Positives = 63/137 (45%), Gaps = 2/137 (1%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER--LQDRYPWLVAEVE 65
++ R A +D+ + +I N + + V TEP + I E+ + R W++ E
Sbjct: 1 MQFRHAILSDLIRIVEIYNSTVASRVVTADTEPVSTNSRIPWFEKHDTEKRPLWVLENEE 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G + G + R AY TVE ++Y+ ++ GLG + ++ A G K+++
Sbjct: 61 QQIIGWISFQSFYGRPAYQATVEISYLDAYRGQGLGLAIDYAIQQAPAYGIKTLGLF 120

Query: 126 IGLPNDPSVRLHEALGY 142
I N S+ L E G+
Sbjct: 121 IFAHNTASLHLFEHFGF 137

>gb|ADC86037.1| Phosphinothricin N-acetyltransferase [Bifidobacterium animalis
subsp. lactis BB-12]
Length = 196

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 46/164 (28%), Positives = 63/164 (38%), Gaps = 6/164 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV-----E 65
R AT D+A + DI N + T P T + +E D Y V E E
Sbjct: 18 RLATVDDVAVITDIYNEAVMAGGSTADTVPVTYEARRRWIESHVDPYAVFVFETIAGDGE 77

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G + R YD + YV+ R QR G+G LL A+ + A+
Sbjct: 78 AEEVGFGAISVIFYDRPGYDGVCDLAYVYTARWQRRGVGRFALRTLLNECRARAMRKACAI 137

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGY-KHGGWHDVGFWRQDF 168
I N S L E+ G+ G + A Y G HD+ +W D
Sbjct: 138 IFSDNTASNALVESFGFEPFGEMPEAAAYDSRGVLHDMSYWCLDL 181

>ref|ZP_03945194.1| phosphinothricin N-acetyltransferase [Lactobacillus fermentum
ATCC
14931]
gb|EEI21789.1| phosphinothricin N-acetyltransferase [Lactobacillus fermentum ATCC
14931]
Length = 176

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 40/141 (28%), Positives = 54/141 (38%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ R AT AD+ + I N I V EP T ++ D +P V E G
Sbjct: 9 INFRQATLADLPTIVAIYNQTIAPHAVTADMEPVTVEQRRGWFNFSDDHPLWVVEDGGQ 68

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G P+ R AY T E +Y + GLG+ + + A +VVA I
Sbjct: 69 VIGWVGLEPFYGRAAYRHTAEVAIYFDQAVRHQGLGTKALAFMESQLACEITAVVAYIF 128

Query: 128 LPNDPSVRLHEALGYTARGTL 148
N S L + GY G
Sbjct: 129 GTNQASQALFKKFGYQKWGAF 149

>ref|YP_001843725.1| phosphinothricin N-acetyltransferase [Lactobacillus fermentum
IFO
3956]
ref|ZP_05862998.1| phosphinothricin N-acetyltransferase [Lactobacillus fermentum
28-3-CHN]
dbj|BAG27245.1| phosphinothricin N-acetyltransferase [Lactobacillus fermentum IFO
3956]
gb|EEX26377.1| phosphinothricin N-acetyltransferase [Lactobacillus fermentum
28-3-CHN]
Length = 169

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
Identities = 40/141 (28%), Positives = 54/141 (38%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ R AT AD+ + I N I V EP T ++ D +P V E G
Sbjct: 2 INFRQATLADLPTIVAIYNQTIAPHAVTADMEPVTVEQRRGWFNFSDDHPLWVVEDGGQ 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

V G P+ R AY T E +Y + GLG+ + + A +VVA I
 Sbjct: 62 VIGWVGLEPFYGRAAYRHTAEVAIYFDQAVRHQGLGTKALAFMESQLAAACEITAVVAYIF 121

Query: 128 LPNDPSVRLHEALGYTARGTL 148

N S L + GY G
 Sbjct: 122 GTNQASQALFKKFGYQKWGAF 142

>ref|YP_004096812.1| GCN5-related N-acetyltransferase [Bacillus cellulosilyticus DSM
 2522]
 gb|ADU32081.1| GCN5-related N-acetyltransferase [Bacillus cellulosilyticus DSM
 2522]
 Length = 189

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 44/177 (24%), Positives = 79/177 (44%), Gaps = 17/177 (9%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAG 70

RP D+A++ +I + Y++ S+ +F + T ++ + ++ + Y + E +G V G
 Sbjct: 10 RPMQKKDIASIVEINHYLDYSSNSFLLKLTKEQVLATMKNVNEYVVEFEDKGTVVG 69

Query: 71 IAYAGPWKARNAYD---WTVESTV--YVSHRHQ-----RLGLGSTLYTHLLKSMEAQ 117

P RN D W + V + R+Q R LGS + T L +S+ +
 Sbjct: 70 YIEIAPQIERNILDEVSWKKDVQVNPLKTKRYQYIEQVATHRDYLGSGVGTFLYRSLSS 129

Query: 118 GFKSVVAVIG---LPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGFWRQDFEL 170

K A + + N+ S+ HE LG+ GT A + H + + +WQ +L
 Sbjct: 130 ATKPTAAFVATKPIKNEASIHFEKLGFKRIGTYTADTFLHFKNYESILYWQTGTDL 186

>ref|YP_001104201.1| hypothetical protein SACE_1966 [Saccharopolyspora erythraea NRRL
 2338]
 ref|ZP_06561217.1| hypothetical protein SeryN2_01814 [Saccharopolyspora erythraea
 NRRL
 2338]
 emb|CAM01276.1| hypothetical protein SACE_1966 [Saccharopolyspora erythraea NRRL
 2338]
 Length = 270

Score = 53.1 bits (126), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 47/164 (28%), Positives = 68/164 (41%), Gaps = 14/164 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL-----VA 62

V +R +D V I IET F TE + D L+ + WL VA
 Sbjct: 108 VVVRALRPSPDWPGVRRRIYAEGIETGNATFETE-----VPDHGTLEAK--WLPGHRWVA 158

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122

E G +AG A +R Y VE++VYV + G+G+ L +++ +A G ++
 Sbjct: 159 EAGGRIAGWGAATAVSSRPCYSGVETSVYVGADARGRGVGNALLRKQIEAADADGLWTL 218

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQ 166

I N S+ LH A G+ G HG W D +R
 Sbjct: 219 QTAIFPENVASLALHRAAGFRTVGVRRERIARHHGVWRDVTILER 262

>ref|YP_004082619.1| gcn5-related n-acetyltransferase [Micromonospora sp. L5]
 gb|ADU08468.1| GCN5-related N-acetyltransferase [Micromonospora sp. L5]
 Length = 163

Score = 52.8 bits (125), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 42/148 (28%), Positives = 58/148 (39%), Gaps = 3/148 (2%)

Query: 19 AAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWK 78

AV +I I F TEP +W + W+ + G V G
 Sbjct: 14 GAVLEIYRLGIAEGNATFETEPP--DWTRFTAARLPGHRWVALDENGVDLGWVACSAVS 70
 Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHE 138
 R Y VE +VYV + G+G L L+ S EA G ++ + + N S+ LH
 Sbjct: 71 DRCVYAGVVEHSVYVHPGTRGRGVGRALLEALIASTEAGIWTIQSGVFPENTASLALHA 130
 Query: 139 ALGYTARGTLRAAGYKHGGWHDVGFQWQR 166
 G+ GT G HG W DV +R
 Sbjct: 131 TCGFRVVGTRERVRHGHGTWRDVTLIER 158

>ref|ZP_05868293.1| LOW QUALITY PROTEIN: conserved hypothetical protein [Brucella
 abortus bv. 6 str. 870]
 ref|ZP_05873237.1| LOW QUALITY PROTEIN: conserved hypothetical protein [Brucella
 abortus bv. 2 str. 86/8/59]
 ref|ZP_05929502.1| LOW QUALITY PROTEIN: conserved hypothetical protein [Brucella
 abortus bv. 3 str. Tulya]
 gb|EEX58147.1| LOW QUALITY PROTEIN: conserved hypothetical protein [Brucella
 abortus bv. 2 str. 86/8/59]
 gb|EEX62874.1| LOW QUALITY PROTEIN: conserved hypothetical protein [Brucella
 abortus bv. 6 str. 870]
 gb|EEX83689.1| LOW QUALITY PROTEIN: conserved hypothetical protein [Brucella
 abortus bv. 3 str. Tulya]
 Length = 148

Score = 52.8 bits (125), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 28/67 (41%), Positives = 40/67 (59%), Gaps = 2/67 (2%)

Query: 101 GLGSTLYTHLLKSMEAQGFKSVVAVIGLP--NDPSVRLHEALGYTARGTLRAAGYKHGGW 158
 G+G L L+ + A GF+ ++AVIG N SV+LHE+LG+T G + +G+KHG W
 Sbjct: 65 GIGKLLRLRELIARISALGFRQLLAVIGDGEHNIGSVKLHESLGFTHCGRIEGSGFKHGRW 124
 Query: 159 HDVGFQWQ 165
 D Q
 Sbjct: 125 LDTVLMQ 131

>ref|XP_002486528.1| GNAT family N-acetyltransferase, putative [Talaromyces
 stipitatus
 ATCC 10500]
 gb|EED14290.1| GNAT family N-acetyltransferase, putative [Talaromyces stipitatus
 ATCC 10500]
 Length = 250

Score = 52.8 bits (125), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 50/193 (25%), Positives = 80/193 (41%), Gaps = 47/193 (24%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA----- 62
 IR AT AD+ + I HYI + + F P P + ++ P+ VA
 Sbjct: 2 IRNATPADLPQIRAINTHYILNTVLTFMQTPPPPGAILTKYNEIKTHGLPYFVAVDDELK 61
 Query: 63 --EVEGVVAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 + G++ G AY P++ +Y TVE T++V HQ +GS L +LK+ E+ GF
 Sbjct: 62 YEDSSGLILGYAYLSPYRGHMLSASTVELTLFVHPEHQSKAVGSKLLAAILKAAES-GF 120
 Query: 120 -----KSVVAVIGL-PNDPS-----VRLHEALGYT 143
 ++++AV+ + PN P R + G+
 Sbjct: 121 LYHCHVYESTGSDEDQRTVFAGDNEMGVVVRNLAVMVDPNGPDGDLRRWYITRGFV 180
 Query: 144 ARGTLRAAGYKHG 156
 RG L G+K+G
 Sbjct: 181 ERGRLEKIGFKNG 193

>ref|ZP_02148288.1| phosphinothricin N-acetyltransferase, putative [Phaeobacter gallaeciensis 2.10]
 gb|EDQ10262.1| phosphinothricin N-acetyltransferase, putative [Phaeobacter gallaeciensis 2.10]
 Length = 174

Score = 52.8 bits (125), Expect = 2e-05, Method: Compositional matrix adjust.
 Identities = 38/155 (24%), Positives = 66/155 (42%), Gaps = 8/155 (5%)

Query: 26 NHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL-VAEVEGVVAGIAYAGPWKARNAYD 84
 N I + + F T +T + D++ ++ P++ VAE G + G G ++ Y
 Sbjct: 19 NQIIRDTLITFTTAEKTSAQVRDEI---AEKGPYVQVAEEAGQILGYISLGGFRTGPGYA 75

Query: 85 WTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTA 144
 + E +Y++ + G G L + A G +VA I N + H A+G+
 Sbjct: 76 RSECHAIYLAETARGRGAGRALIAAIEAVARADGIHVLVAGISAVNAGGLAFHAAMGFVE 135

Query: 145 RGTLLRAAGYKHGGWHDVGFWQDRDFELPAPPRPVRP 179
 G + G+K G W D+ Q+ P+ V P
 Sbjct: 136 VGRMPEVGHKAGQWLDLVLQMOKILS----PKGVP 166

>ref|YP_003489765.1| N-acetyltransferase [Streptomyces scabiei 87.22]
 emb|CBG71217.1| Putative N-acetyltransferase [Streptomyces scabiei 87.22]
 Length = 167

Score = 52.4 bits (124), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 45/146 (30%), Positives = 66/146 (45%), Gaps = 3/146 (2%)

Query: 21 VCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKAR 80
 V I I+ F T T +E+ D+ + RY L + G+V G A P R
 Sbjct: 20 VLTIIYQLGIDEGRATFETTAPTWEFF-DETKLPHHRYVAL--DGAGMVLGWAAVPVSDR 76

Query: 81 NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEAL 140
 AY VE +VYV + G+G+ L L++S EA G ++ + I N S+ +H+
 Sbjct: 77 CAYAGVVEHSVYVHPDARGHGIGAALLRELIRSTEAAGIWTIQSGIFPDNTASLAVHQKT 136

Query: 141 GYTARGTLRAAGYKHGGWHDVGFWQR 166
 G+ GT G G W DV +R
 Sbjct: 137 GFRVVGTRERLGRHRGVWRDVVLIER 162

>ref|YP_003136446.1| GCN5-related N-acetyltransferase [Cyanotheca sp. PCC 8802]
 gb|ACU99610.1| GCN5-related N-acetyltransferase [Cyanotheca sp. PCC 8802]
 Length = 165

Score = 52.4 bits (124), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 35/132 (26%), Positives = 61/132 (46%), Gaps = 6/132 (4%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAEVE 65
 +IR AT +D+A + +I N I + P T + +W E P V E++
 Sbjct: 3 KIRDATESDLATIVNIYNASIPSRIATGDLNPITVESRLKWF--YEHSPHHRPLWVMEID 60

Query: 66 GVVAG-IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 +AG + + + R AYD T E ++Y+ +QR G+G L ++ + +++
 Sbjct: 61 DTIAGWLGFQSFYYGRAAYDKTAEISLYICPNYQRQGIGKLLKQAIEKAPSLDLNTLLG 120

Query: 125 VIGLPNDPSVRL 136
 I N PS+ L
 Sbjct: 121 FIFAHNQPSLNL 132

>ref|YP_726072.1| sortase or related acyltransferase [Ralstonia eutropha H16]
 emb|CAJ92704.1| sortase or related acyltransferase [Ralstonia eutropha H16]
 Length = 166

Score = 52.4 bits (124), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 63/143 (44%), Gaps = 4/143 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWDLLERLQDRYPWLVAEVE 65
 +R A D+ + I N + + V TEP T Q W D + + R W+ + +
 Sbjct: 4 SLRIAEPRLPGIVAIYNSTVPSRMVTADTEPVTVASRQAWFDS-HQPERRPLWVCEDAD 62

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G +AG + R AY T E ++Y+ + + GLG L + G +++
 Sbjct: 63 GRMAGWMSFSDFYGRPAYGATAEVSIIYLDQRRGQGLGRYLLQQAIDHAPRVGVNTLLGF 122

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148
 I N PS+ L +LG+T G L
 Sbjct: 123 IFGHNAPSLGLFASLGFTRWGD 145

>ref|ZP_06753129.1| phosphinothricin N-acetyltransferase [Simonsiella muelleri ATCC
 29453]
 gb|EFG31861.1| phosphinothricin N-acetyltransferase [Simonsiella muelleri ATCC
 29453]
 Length = 168

Score = 52.4 bits (124), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 39/142 (27%), Positives = 62/142 (43%), Gaps = 3/142 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE--QTPQEWDLLERLQDRYPWLVAEVEG 66
 IR AT D+A + +I N + + EP + + W ++ L +++
 Sbjct: 5 IRLATHEDLAQIVEIYNSTVASRQSTADLEPVSVASREAWFQAHQKPNRPIYVLANQLDN 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V A + AR AYD T E ++YV H + +G G L ++L + K+VV VI
 Sbjct: 65 SVLAWASFSDYYARMAYDMTAEISLYVRHDSRGVGTGKDLLAYMLMKAPSLHIKNVVGVI 124

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
 N S+ L G+ G L
 Sbjct: 125 FAHNHASLHLFAKFGFVEWGRL 146

>ref|YP_001224775.1| fused glutathione synthetase/acetyltransferase domain-containing
 protein [Synechococcus sp. WH 7803]
 emb|CAK23478.1| Putative glutathione synthetase fused with a acetyltransferase
 domain [Synechococcus sp. WH 7803]
 Length = 502

Score = 52.0 bits (123), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 40/156 (25%), Positives = 61/156 (39%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWDLLERLQDRYPWLVAEVEGVVA 69
 I PA AA+ I ++ V T + + L +R + V V G V
 Sbjct: 343 IAPAREHHAAAMAIIYQQSVDQGGVTMDAGLMTAECFRQLSACGERSGFWVLSVAGEVL 402

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G + R Y +T E++ YV + G GS L ++ ++ +VA +
 Sbjct: 403 GWTELRAISPRWGYRFTAETSTYVHASARGRGFGSKLQRFVIGQAREMYRHLVAKVVS 462

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
 ND SV H G+ G + G+ WHDV Q
 Sbjct: 463 NDQSVAFHLRHGFERVGIQKEVGFLGNSWHDVVILQ 498

>ref|ZP_05054348.1| acetyltransferase, GNAT family [Octadecabacter antarcticus 307]
 gb|EDY75248.1| acetyltransferase, GNAT family [Octadecabacter antarcticus 307]
 Length = 158

Score = 52.0 bits (123), Expect = 3e-05, Method: Compositional matrix adjust.
 Identities = 39/157 (24%), Positives = 69/157 (43%), Gaps = 3/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 +R AT+AD A + I N I + V F + P++ + D + R +L+ E++ VA
 Sbjct: 3 VRTATSADAAKIAAIWNPQILETVVTFNSVPKSVE---DVAVMIAQRPCFLILEIDEKVA 59

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A ++ Y T+E T+ ++ G G L ++ A ++ A +
 Sbjct: 60 GFASYDQFRGGIGYANTMEHTIILAPDASQGAGRALMLAVMDHARAAVHTLWAGVSAE 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
 N V H+++G+ L G K W D+ Q+
 Sbjct: 120 NLVGVAFHKSMGFKTVAVLPDVGRKFDRWMDLVLMO 156

>ref|ZP_01076405.1| GCN5-related N-acetyltransferase [Marinomonas sp. MED121]
 gb|EAQ65425.1| GCN5-related N-acetyltransferase [Marinomonas sp. MED121]
 Length = 169

Score = 52.0 bits (123), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 44/148 (29%), Positives = 61/148 (41%), Gaps = 1/148 (0%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 MSP + IR A D A+ I N I T P + +D LE P+
 Sbjct: 1 MSPTKSG-RIRLALEDAPAILSIYNQAIATGLATGHLSPIKLLDVLDWLEEGHLERPF 59

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
 V E + V A A + A+ VE VYVS + R G+G L L + M G
 Sbjct: 60 VFESDSEVIWANADDFHGLPAFSDCEVGVYVSPKFHRQGVGKALLNKLEEDMILLGVT 119

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTL 148
 ++A + L N S+ L + G+ G L
 Sbjct: 120 HLMAFVFLQNLSSLGLFQQHGFNEWGLL 147

>ref|ZP_06381746.1| GCN5-related N-acetyltransferase [Arthrospira platensis str.
 Paraca]
 dbj|BAI91856.1| hypothetical protein [Arthrospira platensis NIES-39]
 Length = 167

Score = 51.6 bits (122), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 36/144 (25%), Positives = 66/144 (45%), Gaps = 5/144 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
 ++IR A D+ + +I N + EP + + W + + Q P V E+
 Sbjct: 5 LKIRDALENDLPQIIIEIYNLAVPQKIATADLEPISVESRLGWYRECQSAQR--PLWVVEI 62

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 + G +K R AYD T E ++Y+ +Q G+G L ++ G ++++A
 Sbjct: 63 GDRIIGWLSFQAFKKRAAYDATAELSIYIHTDYQGQGIGKLLHQAIEEGPKFGCETLLA 122

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
 +I N PS++L ++ G+ G L
 Sbjct: 123 LIFAHNQPSLKLFDSEFGFQQWGYL 146

>ref|YP_003561921.1| GNAT family acetyltransferase [Bacillus megaterium QM B1551]
 gb|ADE68487.1| acetyltransferase, GNAT family [Bacillus megaterium QM B1551]
 Length = 180

Score = 51.6 bits (122), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 39/156 (25%), Positives = 70/156 (44%), Gaps = 2/156 (1%)

Query: 6 RPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEV 64
 R V IRPA A+D + V IE + EP+T QE D + ++ + + ++VAEV
 Sbjct: 17 REVITIRPAQASDAEHITTAVREIIEAGEFIQKDEPRTVQEEQDFIASVEKNNHMYVVAEV 76

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 EG V GIA + + + T +S + Q +G+G + L + +
 Sbjct: 77 EGEVLGIARVLRGEIKMKRHTGLFRTWLIS-KAQGMGIGKQFMNYTLNWCKENNLHKLSL 135

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 + N + L++ +G+ G ++ Y + + D
 Sbjct: 136 TVFASNKVAYELYKKVGFEQEGVMKEQAYFNNEYVD 171

>ref|YP_003356174.1| GCN5-related N-acetyltransferase family protein [Methanocella
 paludicola SANAЕ]
 dbj|BAI61191.1| GCN5-related N-acetyltransferase family protein [Methanocella
 paludicola SANAЕ]
 Length = 162

Score = 51.6 bits (122), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 39/144 (27%), Positives = 58/144 (40%), Gaps = 21/144 (14%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL----- 60
 +R A D+ A+ I N + V EP T ++ R PW
 Sbjct: 3 VRDAVEGDLPAIIAIYNSTVPGRMVTADIEPVT-----VESRLPWFREHSPGFRP 52

Query: 61 --VAEEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 118
 V E +G + + R AY T E +VYVS ++ G+GS L + G
 Sbjct: 53 LWVVEDDGRILAWLSFQSFYGRPAYRATAEVSVYVSEAYRCKGIGSMLLERAIAQGPGLG 112

Query: 119 FKSVVAVIGLPNDPSVRLHEALGY 142
 K+++ I N PS+RL E G+
 Sbjct: 113 LKTLMGFIFAHNVPSLRLFEKFGF 136

>ref|ZP_00962754.1| phosphinothricin N-acetyltransferase, putative [Sulfitobacter sp.
 NAS-14.1]
 gb|EAP80241.1| phosphinothricin N-acetyltransferase, putative [Sulfitobacter sp.
 NAS-14.1]
 Length = 161

Score = 51.6 bits (122), Expect = 4e-05, Method: Compositional matrix adjust.
 Identities = 47/157 (29%), Positives = 72/157 (45%), Gaps = 3/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGVVA 69
 IRPA +D V + N I + F ++P+T E ++ L + W VA+ EGV
 Sbjct: 3 IRPAKGS DAGVVAALWNVMITQTLFTFTSQPKTGAE-VEALIAGRAGQFW-VADAEGVAG 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 I Y G +++ Y VE ++ + Q G G L + A QG + +VA I
 Sbjct: 61 FITY-GAFRSGVGYRDAVEHSIVLDAAAQGAGAGRALMQTACDAVAQGRVMVA AISGA 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 N +V H ALG+ G + G K+G D+ Q+
 Sbjct: 120 NPGAVGFHAALGFDHVGMRPRIGQKNGQQQLDLILMQK 156

>gb|EEH06992.1| conserved hypothetical protein [Ajellomyces capsulatus G186AR]
Length = 194

Score = 51.6 bits (122), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 54/197 (27%), Positives = 82/197 (41%), Gaps = 51/197 (25%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWI-DDLERLQDR-YPWLVA--- 62
++IR AT +D+ + I HY++ + V FR + P +I Q+R P+LVA
Sbjct: 3 LKIRSATESDLHQIHSIFTHYVQNTVTVFRVN-KPPFSYIARRFHEAQERGLPYLVAVEK 61

Query: 63 -----EVEG----VVAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
EG V G A ++ AY TVE ++ V +Q G+GS L + L+
Sbjct: 62 SNQDNPSHEGNTTEKVCGYTLASAFRGYMLAYAPTVMESLLVHPDYQSQGIGSALLSSLV 121

Query: 112 KSM-EAQGFKSVVAVIGLPNDPSVRLHEAL-----G 141
+++ EA+ V D RLHEA+ G
Sbjct: 122 EALSEAKHLSYEVG---DADSEARLHEAVNVKNILAVMAVNPEGKNGGGLRDWYVQRG 177

Query: 142 YTARGTLRAAGYKHGGW 158
+ RG +R G+KHG W
Sbjct: 178 FIERGRMREVGFKHGGW 194

>ref|YP_002323294.1| GCN5-related N-acetyltransferase [Bifidobacterium longum subsp.
infantis ATCC 15697]
gb|ACJ52916.1| GCN5-related N-acetyltransferase [Bifidobacterium longum subsp.
infantis ATCC 15697]
dbj|BAJ69485.1| putative acetyltransferase [Bifidobacterium longum subsp. infantis
JCM 1222]
Length = 165

Score = 51.6 bits (122), Expect = 4e-05, Method: Compositional matrix adjust.
Identities = 41/164 (25%), Positives = 63/164 (38%), Gaps = 2/164 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE- 65
P RPA +D+ A+ DI N + P+T + +E Y V E E
Sbjct: 2 PYTFRPAVESDIQAITDIYNASVMAGGATADLTPTLDQRRRAWVESHTPPYGVFVVESED 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G + G + R YD + Y+ Q G+G+ + LL A+ + +
Sbjct: 62 GSIIGFGALSVFYDRAGYDGVTDLAYYIDPAWQGRGVGTFMLDRLLTEARARHMRKACGI 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGFWRQDF 168
I N S+ L G+T G + AA G D+ +W D
Sbjct: 122 IFADNAGSIALMHRFGFTQFGLMPAAATDSTGTMRDMSYWYLDL 165

>ref|ZP_05614148.1| acetyltransferase, GNAT family [Faecalibacterium prausnitzii
A2-165]
gb|EEU97508.1| acetyltransferase, GNAT family [Faecalibacterium prausnitzii
A2-165]
Length = 172

Score = 51.6 bits (122), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 48/167 (28%), Positives = 65/167 (38%), Gaps = 5/167 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ +RP D AV I I T F+T W + R LV +GV
Sbjct: 4 ITVRPMPMPEDWTAVSKIYLEGIATEHATFQTNCPPYTAW---DASHTRECRLVVLDDGV 59

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
VAG A R Y E ++YV + + GLG L T L + E G+ ++ + +

Sbjct: 60 VAGWAALHRVDPRWCYRGVAEVSIIYVGEKFRGKGLGYHLLTALCREAEQAGYWTLQSTVL 119

Query: 128 LPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFQWQDFELPAP 173

N PS LH G+ G R A HG W D +R P

Sbjct: 120 QDNAPSRGLHLKCGFRVVGRRERIARDCHGRWLDTYLMERRCAADEP 166

>ref|ZP_03718257.1| hypothetical protein NEIFLAOT_00057 [Neisseria flavescens

NRL30031/H210]

gb|EEG34751.1| hypothetical protein NEIFLAOT_00057 [Neisseria flavescens

NRL30031/H210]

Length = 166

Score = 51.6 bits (122), Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 37/140 (26%), Positives = 62/140 (44%), Gaps = 1/140 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68

IRPA D+ A+ DI N + T P T E D+ P + + + +G V

Sbjct: 5 IRPALRQDLPAIVDIYNSTVATRQSTADLSPTTVAEREIWFAAHTDKRPIYALYDTDGTV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAVIGL 128

+ R AY + E ++YV H + G+G L ++L+ + ++V+A++

Sbjct: 65 LAWGSFSDYHPRYAYHISAEVSIYVRHDMRGAGVGKILLRNMLERAPSLDIRNVIALVFG 124

Query: 129 PNDPSVRLHEALGYTARGTL 148

N PS+ L G+ G L

Sbjct: 125 HNYPSLNLFHRFGFEWGRL 144

>ref|ZP_04665228.1| phosphinothricin N-acetyltransferase [Bifidobacterium longum subsp.

infantis CCUG 52486]

ref|YP_004220356.1| acetyltransferase [Bifidobacterium longum subsp. longum JCM 1217]

gb|EEQ54061.1| phosphinothricin N-acetyltransferase [Bifidobacterium longum subsp.

infantis CCUG 52486]

dbj|BAJ66264.1| putative acetyltransferase [Bifidobacterium longum subsp. longum JCM 1217]

Length = 177

Score = 51.6 bits (122), Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 41/165 (24%), Positives = 64/165 (38%), Gaps = 2/165 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE- 65

P RPA +D+ A+ DI N + P+T + +E Y V E E

Sbjct: 2 PYTFRPAVESDVQAIADIYNASVMAGGATADLTPTFTDQRRRAWVESHTPPYGVFVVESED 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125

G + G + R YD + Y+ Q G+G+ + LL A+ + +

Sbjct: 62 GSIIGFGALSVFYDRAGYDGVTDLAYYYIDPAWQGRGVGTFLDRLLTEALARHMRKACGI 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGFQWQDFE 169

I N S+ L G+T G + AA G D+ +W D +

Sbjct: 122 IFADNAGSIALMHRFGFTQFGLMPAAATDSTGTMRDMSYWYLDLQ 166

>ref|ZP_05101405.1| phosphinothricin acetyltransferase [Roseobacter sp. GAI101]

gb|EEB85707.1| phosphinothricin acetyltransferase [Roseobacter sp. GAI101]

Length = 149

Score = 51.6 bits (122), Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 41/154 (26%), Positives = 67/154 (43%), Gaps = 9/154 (5%)

Query: 21 VCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP---WLVAEVEGVVAGIAYAGPW 77

```

      + I N I + F T+ +T + +E + + P W VAE +GV+ + YA +
Sbjct: 2 IAGIWNAMIRDTLFTFTTDEKT---VAGIEAMIAQRPGACW-VAEADGVLGFVTYA-QF 55

Query: 78 KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLH 137
      + Y +VE ++ ++ + G G L L++ QG +VA I N V H
Sbjct: 56 RTGPGYATSVEHSIVLTEAARGQGAGRALMQRALQTAADQGLHVMVAGISAANPGGVAFH 115

Query: 138 EALGYTARGTLRAAGYKHGGWHDVGFQWQDFELP 171
      ALG+ G + K G W D+ Q+ P
Sbjct: 116 SALGFEHVGRMPQIARKQGQWLDLILMQKLLSAP 149

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>ref|YP_001319533.1| GCN5-related N-acetyltransferase [Alkaliphilus metalliredigens
QYMF]
gb|ABR47874.1| GCN5-related N-acetyltransferase [Alkaliphilus metalliredigens
QYMF]
Length = 168

```

Score = 51.6 bits (122), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 39/158 (24%), Positives = 73/158 (46%), Gaps = 1/158 (0%)

```

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68
      +R A D+ ++ +I N IE T+ ++ E I L++ +++ + E E V
Sbjct: 5 VRIAEQLDKSITEIYNIEGIEDRIATLETKIKSEAEMIPWLQQRSEKHKVITIENERDEV 64

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
      G A P+ +R YD + ++Y+ + + +GLG L L++ Q +V
Sbjct: 65 LGWASLNPFSNRCCYDGVADFSIYIKRQMRGMGLGKLLKALIEVAREQDIHKLVLSTFK 124

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQ 166
      N+ RL+E+ G+ GT + G G + DV ++
Sbjct: 125 SNEAGQRLYESGFGFREVGTYNQGILDGKFVDVTIMEK 162

```

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>ref|ZP_07921530.1| phosphinothricin N-acetyltransferase [Pseudoramibacter
alactolyticus ATCC 23263]
gb|EFV01190.1| phosphinothricin N-acetyltransferase [Pseudoramibacter
alactolyticus ATCC 23263]
Length = 172

```

Score = 51.2 bits (121), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 37/143 (25%), Positives = 62/143 (43%), Gaps = 6/143 (4%)

```

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE--WIDDLERLQDRYPWL 60
      E V +R D + DI+N I V P T ++ W E +R+P
Sbjct: 6 ENTKVRVRLFEEKDEQRILDILNMAIADRRVTALLTPVTRKKRVPWF--AEHRTERHPIF 63

Query: 61 VAEVEG-VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
      VAEV+G VV+ +A R + E + Y+ +Q G+G+ L ++ G+
Sbjct: 64 VAEVDGRVVSWMMAVTAYRSRGREGFSKACELSYLDKAYQHGGIGTVLMDRVITRCRTLG 123

Query: 120 KSVVAVIGLPNDPSVRLHEALGY 142
      + ++ +I N PS+ L G+
Sbjct: 124 RHLMLIIFEDNLPSLSLARKFGF 146

```

```

>gb|EFR93939.1| gnat family acetyltransferase [Listeria innocua FSL J1-023]
Length = 165

```

Score = 51.2 bits (121), Expect = 5e-05, Method: Compositional matrix adjust.
Identities = 38/158 (24%), Positives = 71/158 (44%), Gaps = 4/158 (2%)

```

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68

```

```

      +I P      + V +      I+T      F+ + + + W D + L+      LV EG V
Sbjct: 5 KILPMLKEHYSGVARVHQEGIDTGNATFQEKTLSFEAW--DEKYLKT--CRLVVLTEGQV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
      G A P+ + +AY E ++Y++ + G+G L ++++ E GF ++ ++I
Sbjct: 61 IGWAALLPFSSMHAYRGVAELSIYIAKSARGKGIGKALMQAIIQTSEENGFWTLQSLIFP 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
      N+ S+ LH G+ G +G + DV +R
Sbjct: 121 ENEASITLHHTYGFQTLCTIHEKLGEMNGVFRDVALER 158

```

>ref|ZP_04601883.1| hypothetical protein GCWU000324_01357 [Kingella oralis ATCC 51147]
 gb|EEP69443.1| hypothetical protein GCWU000324_01357 [Kingella oralis ATCC 51147]
 Length = 165

Score = 51.2 bits (121), Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 39/139 (28%), Positives = 64/139 (46%), Gaps = 4/139 (2%)

```

Query: 13 ATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE--WIDDLERLQDRYPWLVAEEGVVA 69
      A D+ + I N I + V +P + E W +R ++R ++V +V G +
Sbjct: 8 AQCEDLPEIVAIYNSTIASRQVTADLPQVSVTEREAWFVAHQ--ENRPLYVVRDVSGLM 66

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
      A + R AY T E ++Y+ +H+ GLG L +++ A G +VAVI +
Sbjct: 67 AWASLSDYYPRAAYHRTAEVSIYIHAQHRGAGLGKWLLEGMIRRAPALGVHKLVAIVFVH 126

Query: 130 NDPSVRLHEALGYTARGTL 148
      N S+ L LG+ G L
Sbjct: 127 NTASMALFRGLGFEIWGRL 145

```

>ref|YP_002370892.1| GCN5-like N-acetyltransferase [Cyanotheca sp. PCC 8801]
 gb|ACK64736.1| GCN5-related N-acetyltransferase [Cyanotheca sp. PCC 8801]
 Length = 165

Score = 51.2 bits (121), Expect = 5e-05, Method: Compositional matrix adjust.
 Identities = 35/132 (26%), Positives = 60/132 (45%), Gaps = 6/132 (4%)

```

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAEEV 65
      +IR AT +D+A + +I N I + P T + +W E P V E++
Sbjct: 3 KIRDATESDLATIVNIYNASIPSRIATGDLNPITVESRLKWF--YEHSPPHRPLWVMEID 60

Query: 66 GVVAG-IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
      +AG + + + R AYD T E ++Y+ +QR G+G L ++ +++
Sbjct: 61 DTIAGWLGFQSFYYGRAAYDKTAEISLYICPNYQRQGIGKLLKQAIEKAPNLDLNTLLG 120

Query: 125 VIGLPNDPSVRL 136
      I N PS+ L
Sbjct: 121 FIFAHNQPSLNL 132

```

>ref|ZP_03612047.1| hypothetical protein AM202_0459 [Actinobacillus minor 202]
 gb|EEF15775.1| hypothetical protein AM202_0459 [Actinobacillus minor 202]
 Length = 167

Score = 51.2 bits (121), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 39/142 (27%), Positives = 60/142 (42%), Gaps = 4/142 (2%)

```

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWDLLERLQDRYPWLVAEEV 66
      R A A D+A + +I N IE TV EP T Q W +YP V E++G
Sbjct: 2 FRFAQADDLARILEIYNQVIERRRTVTADLEPATTESRQTWFHQ--HLNHHKYPWVYELDG 60

```

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V + +R AYD + E + Y+ G+G L++ M +++A +
 Sbjct: 61 KVVAWCSYSQFYSRAAYDGSSEISFYLDKAVHGKGIGKACVNFLIEQMPNYQLHTLLAFV 120

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
 N S+ L +G+ G L
 Sbjct: 121 FGNNAQSLGLLNKMFGFEIWGKL 142

>ref|ZP_04151343.1| Phosphinothricin N-acetyltransferase [Bacillus pseudomycoides DSM 12442]
 gb|EEM16926.1| Phosphinothricin N-acetyltransferase [Bacillus pseudomycoides DSM 12442]
 Length = 167

Score = 51.2 bits (121), Expect = 6e-05, Method: Compositional matrix adjust.
 Identities = 32/141 (22%), Positives = 66/141 (46%), Gaps = 5/141 (3%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVI 61
 + ++IR A +D++++ DI N I + V TEP ++ ++W + E P +
 Sbjct: 2 KEDIKIRDAEISDLSSIVDIYNSTISSRMVTADTEPVTVKSRQWFN--EHSPSFRPLWI 59

Query: 62 AEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 E +G + G + R AY+ T E ++Y+ ++ +G + +L + K+
 Sbjct: 60 IESQGEICGWVSFQSFYGRPAYNGTAEISIIYIHQMYRGREIGKHILHRVLDTCPKLKIKT 119

Query: 122 VVAVIGLPNDPSVRLHEALGY 142
 ++A I N S++L +
 Sbjct: 120 LLAFIFAHNKASLQLFSCFDF 140

>ref|ZP_03236003.1| acetyltransferase, gnat family protein [Bacillus cereus H3081.97]
 gb|EDZ57903.1| acetyltransferase, gnat family protein [Bacillus cereus H3081.97]
 Length = 164

Score = 51.2 bits (121), Expect = 7e-05, Method: Compositional matrix adjust.
 Identities = 42/151 (27%), Positives = 64/151 (42%), Gaps = 4/151 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 I T D V DI I T T F TE +W + +D +VA+V+ ++
 Sbjct: 5 IVQLTEKDWPQVSDIYLGISTKTATFETECPDWYKW---KMNRLDKTCIVAKVDQIIII 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A +R AY E++VYV + +G L L+ E + ++ A I
 Sbjct: 61 GWASVSKISSRCAYVGGETSVYVHPNYIGNNVGFRLKELVDLSEENNYWTLQANIFAE 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 N S+++HE G+ G G +G W D
 Sbjct: 121 NISSIKIHEKNGFRIVGIREKIGQVNGIWKD 151

>ref|YP_003488051.1| acetyltransferase [Streptomyces scabiei 87.22]
 emb|CBG69491.1| putative acetyltransferase [Streptomyces scabiei 87.22]
 Length = 164

Score = 51.2 bits (121), Expect = 7e-05, Method: Compositional matrix adjust.
 Identities = 48/160 (30%), Positives = 68/160 (42%), Gaps = 3/160 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 + I P T A V I I+ F T T Q + + +L + VA+ +G
 Sbjct: 2 SITITPITEAHAEVLAIYQAGIDEGNATFETTAPTQW--VFEAGKLPEHRFAAVAD-DG 58

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

V G A R AY VE +VYV + G+ L T L+ S E+ G ++ + I
 Sbjct: 59 KVLGWIAASAVSDRCAYAGVVEHSVYVHPAARGQGVAMQLLTALIGSTESAGIWTIQSGI 118

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

N S+ LH+ G+ GT G HG W DV +R
 Sbjct: 119 FPENRASLALHQRAGFRVIGTRERIGRHHGVWRDVLLER 158

>ref|ZP_05258358.1| acetyltransferase, gnat family protein [Listeria monocytogenes J0161]

ref|ZP_05262087.1| conserved hypothetical protein [Listeria monocytogenes J2818]

gb|EFF98377.1| conserved hypothetical protein [Listeria monocytogenes J2818]

Length = 165

Score = 51.2 bits (121), Expect = 7e-05, Method: Compositional matrix adjust.

Identities = 40/161 (24%), Positives = 68/161 (42%), Gaps = 10/161 (6%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY---PWLVAEVE 65

+I P + V + IET F QE LE ++Y LV +
 Sbjct: 5 KILPMQKEHYSGVAHVHGEIETGNATF-----QEKTLSEAFDEKYLNTCRLVVVMN 57

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125

G V G A P+ + +AY E ++Y++ + G+G L ++++ E GF ++ ++
 Sbjct: 58 GEVIGWAALLPFSSMHAYRGVAELSIYIAKSARGKGIGKALMHEIIQTSEQNGFWTLQSL 117

Query: 126 IGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

I N S+ LH G+ G +G + DV +R
 Sbjct: 118 IFPENKASIALHHTYGFQTLCIHEKLGEMNGIFRDVALLER 158

>ref|ZP_03960042.1| acetyltransferase [Lactobacillus vaginalis ATCC 49540]

gb|EEJ40385.1| acetyltransferase [Lactobacillus vaginalis ATCC 49540]

Length = 165

Score = 50.8 bits (120), Expect = 7e-05, Method: Compositional matrix adjust.

Identities = 39/167 (23%), Positives = 68/167 (40%), Gaps = 7/167 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAEV 64

+ R AT D+ + I N + + + P T QEW L DR+P V
 Sbjct: 2 LSFRRATPNDLPRIVTIYNSAVPSHDITDDEMPITVDSRQEW---LNHFNDRFPIWVVIS 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM-EAQGFKSVMV 123

+ + G G + AY ++ E ++Y++ Q G G + + + + + K+V+
 Sbjct: 59 DSTIIGWCSLGGFYPHQAYQFSAEISYIYLASDTQGRGYGKQILNFIDQQITDNLDIKTVI 118

Query: 124 AVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQWQDFEL 170

A + N PS +L + GY G L G + + + F L
 Sbjct: 119 AYVYENNLPSQKLFQKCGYQQCGVLPQISIIDGELRTLKIFVKHFN 165

>ref|YP_003212786.1| hypothetical protein Ctu_3p00420 [Cronobacter turicensis z3032]

emb|CBA34747.1| hypothetical protein Ctu_3p00420 [Cronobacter turicensis z3032]

Length = 144

Score = 50.8 bits (120), Expect = 7e-05, Method: Compositional matrix adjust.

Identities = 32/84 (38%), Positives = 41/84 (48%), Gaps = 6/84 (7%)

Query: 101 GLGSTLYTHLLKSMEAQGFKSVMVAVIG-LPNDPSPVRLHEALGYTARGTLRAAGYKHGGWH 159

G G L H L +QG++ ++AV+G N SV LH G+T GTL+ G+KHG W
 Sbjct: 61 GGGKALLDHALTWARSQGYRQMIYVGDCCANVASVALHLRSGFTEIGTLKDIFKHKRW 120

Query: 160 DVGFWQWQDF-----ELPAPPRPVR 178

D Q LP P P R

Sbjct: 121 DTVLLQCQLGKGSCSLPDSPVPGR 144

>ref|ZP_03959265.1| acetyltransferase [Lactobacillus vaginalis ATCC 49540]
gb|EEJ41153.1| acetyltransferase [Lactobacillus vaginalis ATCC 49540]
Length = 170

Score = 50.8 bits (120), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 41/162 (25%), Positives = 64/162 (39%), Gaps = 1/162 (0%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP-WLVAEEVEGV 67

E A D+ + DI N I + EP T E +P W++ E

Sbjct: 9 EFSLANEKDLPRIVDIYNQIIPSLATADLEPVTVAEREAWYHSFTKTHPLWVIKNEQK 68

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

V G P+ R AY+ T E +Y+ + GLG+ ++ + G ++VA I

Sbjct: 69 VVGWVGLEPFYGRAAYEHTCEIAIYIDKSVRHHGLGTQAINFVISQLPQLGITAIVAYIF 128

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169

N PS+ L ++ +T G L G D+ R F+

Sbjct: 129 GHNLPGLFLFKSFHFTWGRLLPRVAELDGVQRDLIIMGRRFD 170

>ref|ZP_04268014.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-ST26]
gb|EEL00251.1| Phosphinothricin N-acetyltransferase [Bacillus cereus BDRD-ST26]
Length = 68

Score = 50.8 bits (120), Expect = 8e-05, Method: Compositional matrix adjust.
Identities = 22/60 (36%), Positives = 34/60 (56%), Gaps = 2/60 (3%)

Query: 119 FKSVAVIGLPLNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVR 178

+ +++A I N+ S+ LHE G+ GT++ AGYK W D+ F+Q EL P P+

Sbjct: 10 YMTLIAGIDAENEKSIALHENYGFVHAGTIKKAGYKFNKWLDAFYQ--LELCGPKNPLE 67

>ref|ZP_03272313.1| GCN5-related N-acetyltransferase [Arthrospira maxima CS-328]
gb|EDZ96094.1| GCN5-related N-acetyltransferase [Arthrospira maxima CS-328]
Length = 167

Score = 50.8 bits (120), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 35/144 (24%), Positives = 66/144 (45%), Gaps = 5/144 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEV 64

++IR A D+ + +I N + EP + + W + + Q P V E+

Sbjct: 5 LKIRDALENDLPQIIEIYNLAVPQKIATADLEPISVESRLGWYRECQSAQR--PLWVVEI 62

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124

+ G +K R AYD + E ++Y+ +Q G+G L ++ G ++++A

Sbjct: 63 GDRIIGWLSFQAFKKRAAYDASAELSIYIHTDYQGQGIGKKLLYQAIEEGPKFGCETLLA 122

Query: 125 VIGLPLNDPSVRLHEALGYTARGTL 148

+I N PS++L ++ G+ G L

Sbjct: 123 LIFAHNQPSLKLFDSEFGFQQWGYL 146

>ref|YP_002378285.1| GCN5-related N-acetyltransferase [Cyanotheca sp. PCC 7424]
gb|ACK71417.1| GCN5-related N-acetyltransferase [Cyanotheca sp. PCC 7424]
Length = 163

Score = 50.8 bits (120), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 41/157 (26%), Positives = 65/157 (41%), Gaps = 5/157 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQ---EWIDDLERLQDRYPWLVAEV 64

```

+ IR AT D+ + +I N I + P + + W D Q R W V E+
Sbjct: 1 MNIREATEGDLPTIVEIYNASIPSLATADINPISVESRINWFYD-HPPQSRPIW-VMEI 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+ V G + R AY T E ++YVS ++RLG+G L + + G +++
Sbjct: 59 DNKVVGWLSFQSFLGRPAYHCTAELSIVSPDYKRLGIGQKLLQQAIDKSPSLGLNTLIG 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
I N PS++L + G L G D+
Sbjct: 119 YIFAHNKPSLQLFTKYEFQQWGFLLPKVAVLDGIERDL 155

```

```

>ref|NP_470773.1| hypothetical protein lin1437 [Listeria innocua Clip11262]
emb|CAC96668.1| lin1437 [Listeria innocua Clip11262]
Length = 165

```

Score = 50.8 bits (120), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 38/158 (24%), Positives = 71/158 (44%), Gaps = 4/158 (2%)

```

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+I P + V + I+T F+ + + + W D + L + LV EG V
Sbjct: 5 KILPMLKEHYSGVARVHQEGIDTGNATFQEKTLSFEAW--DEKYL--KTCRLVVLTEGQV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A P+ + +AY E ++Y++ + G+G L ++++ E GF ++ ++I
Sbjct: 61 IGWAALLPFSSMHAYRGVAELSIYIAKSARGKGIGKALMQAIIQTSEQNGFWTLQSLIFP 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVWQR 166
N+ S+ LH G+ G +G + DV +R
Sbjct: 121 ENEASIILHHTYGFQTLCTIHEKLGEMNGVFRDVALLER 158

```

```

>ref|YP_003605073.1| GCN5-related N-acetyltransferase [Burkholderia sp. CCGE1002]
gb|ADG15562.1| GCN5-related N-acetyltransferase [Burkholderia sp. CCGE1002]
Length = 171

```

Score = 50.4 bits (119), Expect = 9e-05, Method: Compositional matrix adjust.
Identities = 42/144 (29%), Positives = 65/144 (45%), Gaps = 8/144 (5%)

```

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLV---AEV 64
R AT D+ A+ I N I + V EP ++ W D Q R W+V +
Sbjct: 6 R DATLDDLPAIVAIYNSTIPSRQVTADLEPVSVESRHAWFD-AHGPQKRPLWVVEDPKQA 64

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
V+A ++++ + R AY T E ++Y+ + GLG L L + G +V+
Sbjct: 65 GRVIAWLSFS-DFYGRPAYQRTAEVSIYLDDESARGQGLGKQLLAASLDAAPGLGIDTVLG 123

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
+ N+ SVRL G+ A GTL
Sbjct: 124 FVFGHNEASVRLFRGFGFDAGWTL 147

```

```

>ref|ZP_05822107.1| conserved hypothetical protein [Brucella abortus NCTC 8038]
ref|ZP_05871518.1| conserved hypothetical protein [Brucella abortus bv. 4 str. 292]
ref|ZP_05896583.1| conserved hypothetical protein [Brucella abortus bv. 9 str. C68]
gb|EEW80350.1| conserved hypothetical protein [Brucella abortus NCTC 8038]
gb|EEX56428.1| conserved hypothetical protein [Brucella abortus bv. 4 str. 292]
gb|EEX81566.1| conserved hypothetical protein [Brucella abortus bv. 9 str. C68]
Length = 119

```

Score = 50.4 bits (119), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 33/114 (28%), Positives = 48/114 (42%), Gaps = 1/114 (0%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEGVV 68
IR AD+ + I + T T ++ EP T E D+ +P LVAE +G V
Sbjct: 4 IRDFQPADIETITAIYTQAVLTGTGSYEIEPPTMDEMAKRFAAFADQGFILVAEADGRV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
G AYA ++ R AY W E ++ + L S + + GF S
Sbjct: 64 LGYAYASYFRVRPAYRWLAEDSILSPPMRRGRALASFCCANSSRGFPPLGFASC 117

>ref|YP_003172350.1| phosphinothricin N-acetyltransferase [Lactobacillus rhamnosus GG]
emb|CAR88499.1| Phosphinothricin N-acetyltransferase [Lactobacillus rhamnosus GG]
dbj|BAI43027.1| N-acetyltransferase [Lactobacillus rhamnosus GG]
Length = 164

Score = 50.4 bits (119), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 41/162 (25%), Positives = 68/162 (41%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E PAT AD+ + I N I T +PQT + D +P + +V+
Sbjct: 2 IEFVPATTADLPKIVAIYNETIPTHQATADLQPQTVDQKAAWFAAHNDHFFAWMIQVDHH 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
G + R AYD T E ++Y+ + +GS+ + + A+G +++A I
Sbjct: 62 NVGWLTLAYSADRAAYDQTAEISLYLDITARGHHIGSSALAFVDQEAPARGLTITIIARIF 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFE 169
N S RL + Y G L A G D+ + + F+
Sbjct: 122 GHNQASRRLFKKFNYDHWGHLPAIADLPEGKADLEIYGKHF 163

>ref|ZP_07902166.1| GCN5-related N-acetyltransferase [Paenibacillus vortex V453]
gb|EFU38863.1| GCN5-related N-acetyltransferase [Paenibacillus vortex V453]
Length = 166

Score = 50.4 bits (119), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 39/143 (27%), Positives = 68/143 (47%), Gaps = 7/143 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYP-WLVAEVE 65
I A D+ A+ DI N I V EP T + W + E D P W++ +
Sbjct: 7 IDYAVKEDLPAIVDIYNSTISGRKVTADLEPVTVESRIRWFE--EHSSDFRPLWVMHSD 64

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G+VA +++ + R AY+ T E ++YV+ +++ G GS L ++ ++V
Sbjct: 65 GMVAWMSFQ-SFYGRPAYNGTAEISIVNEKYRG TGAGSILIEKAIEESPRLKVSNLVGF 123

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148
+ N+PS++L + G+ G L
Sbjct: 124 VFGHNEPSMKLLKKYGFQWGLL 146

>ref|YP_562118.1| GCN5-related N-acetyltransferase [Shewanella denitrificans OS217]
gb|ABE54395.1| GCN5-related N-acetyltransferase [Shewanella denitrificans OS217]
Length = 162

Score = 50.4 bits (119), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 41/161 (25%), Positives = 66/161 (40%), Gaps = 4/161 (2%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
+R D V I I+T F+T + EW + + LVA + ++
Sbjct: 4 VRTFNQQDYDPVKRIYQQGIDTGNATFQTVAKDWLEWDSSMLKCCR----LVAVQDKLIL 59

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G A P +R Y E +VY++ Q G+G L + L+ E+ ++ A I

Sbjct: 60 GWAALSPISSRQVYSGVAEVSIVYLAKSAQKGIGHLLLSKLITDSESNHIWTLQAGIFPE 119

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQRFEL 170

N+ S+ LH+ G+ G G W DV +R +L

Sbjct: 120 NEASIELHKKNGFRIIGVREKFGQMGPLWRDVVLMERRSKL 160

>ref|ZP_00120498.1| COG1247: Sortase and related acyltransferases [Bifidobacterium longum DJ010A]

ref|YP_001954723.1| sortase [Bifidobacterium longum DJ010A]

ref|ZP_03976243.1| possible Phosphinothricin acetyltransferase [Bifidobacterium longum

subsp. infantis ATCC 55813]

ref|YP_004000379.1| sortase [Bifidobacterium longum subsp. longum BBMN68]

ref|ZP_07940882.1| acetyltransferase [Bifidobacterium sp. 12_1_47BFAA]

ref|YP_004208530.1| acetyltransferase [Bifidobacterium longum subsp. infantis 157F]

gb|ACD98225.1| Sortase [Bifidobacterium longum DJ010A]

gb|EEI81047.1| possible Phosphinothricin acetyltransferase [Bifidobacterium longum subsp. infantis ATCC 55813]

emb|CBK70752.1| Sortase and related acyltransferases [Bifidobacterium longum subsp. longum F8]

gb|ADQ03517.1| Sortase [Bifidobacterium longum subsp. longum BBMN68]

gb|EFV38041.1| acetyltransferase [Bifidobacterium sp. 12_1_47BFAA]

dbj|BAJ70752.1| putative acetyltransferase [Bifidobacterium longum subsp. infantis 157F]

Length = 165

Score = 50.4 bits (119), Expect = 1e-04, Method: Compositional matrix adjust.

Identities = 41/164 (25%), Positives = 63/164 (38%), Gaps = 2/164 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE- 65

P RPA +D+ A+ DI N + P+T + +E Y V E E

Sbjct: 2 PYTFRPAVESDVQAIADIYNASVMAGGATADLTPTFTDQRRRAWVESHTPPYGVFVVESED 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125

G + G + R YD + Y+ Q G+G+ + LL A+ + +

Sbjct: 62 GSIIGFGALSVFYDRAGYDGVTDLAYIYIDPAWQGRGVGTFMLDRLLTEALARHMRKACGI 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGVFWQRF 168

I N S+ L G+T G + AA G D+ +W D

Sbjct: 122 IFADNAGSIALMHRFGFTQFGLMPAAATDSTGTMRDMSYWYLDL 165

>ref|YP_002350131.1| acetyltransferase, gnat family [Listeria monocytogenes HCC23]

gb|ACK39517.1| acetyltransferase, gnat family [Listeria monocytogenes HCC23]

emb|CAR84161.1| acetyltransferase, GNAT family [Listeria monocytogenes L99]

gb|EFR84638.1| acetyltransferase [Listeria monocytogenes FSL F2-208]

Length = 165

Score = 50.1 bits (118), Expect = 1e-04, Method: Compositional matrix adjust.

Identities = 40/161 (24%), Positives = 67/161 (41%), Gaps = 10/161 (6%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY---PWLVAEVE 65

+I P V + IET F QE LE ++Y LV +

Sbjct: 5 KILPMQKEHYPGVAHVQEGIETGNATF-----QEKTLSLEAFDEKYLKTCRLVVVMN 57

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125

G V G A P+ + +AY E ++Y++ + G+G L ++++ E GF ++ ++

Sbjct: 58 GEVIGWAALLPFSSMHAYRGVAELSIYIAKSARGKGIGKALMHEIIQTSEQNGFWTLQSL 117

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFWQR 166

I N S+ LH G+ G +G + DV +R

Sbjct: 118 IFPENKASIALHHTYGFQTLCTHEKLGEMNGIFRDVALLER 158

```
>ref|ZP_04242914.1| Acetyltransferase, GNAT [Bacillus cereus Rock1-15]
ref|ZP_04254542.1| Acetyltransferase, GNAT [Bacillus cereus 95/8201]
ref|ZP_04292578.1| Acetyltransferase, GNAT [Bacillus cereus R309803]
gb|EEK75756.1| Acetyltransferase, GNAT [Bacillus cereus R309803]
gb|EEL13755.1| Acetyltransferase, GNAT [Bacillus cereus 95/8201]
gb|EEL25375.1| Acetyltransferase, GNAT [Bacillus cereus Rock1-15]
Length = 167
```

Score = 50.1 bits (118), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 42/151 (27%), Positives = 64/151 (42%), Gaps = 4/151 (2%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          I T D V DI I T T F TE +W + +D +VA+V+ ++
Sbjct: 8 IVQLTEKDWPQVSDIYLKGILTKTATFETECPDWYKW---KMNRLKTCIVAKVDQIII 63

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
          G A +R AY E++VYV + +G L L+ E + ++ A I
Sbjct: 64 GWASVSKISSRCAYVGVGETSVYVHPNYIGNNVGFRLLKELVDLSEENSYWTLQANIFAE 123

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
          N S+++HE G+ G G +G W D
Sbjct: 124 NISSIKIHEKNGFRIVGVREKIGQVNGIWKD 154
```

```
>ref|NP_982169.1| acetyltransferase, GNAT family protein [Bacillus cereus ATCC 10987]
ref|YP_001966790.1| acetyltransferase, GNAT family protein [Bacillus cereus]
ref|YP_001967114.1| acetyltransferase, GNAT family protein [Bacillus cereus]
ref|YP_002455182.1| acetyltransferase, gnat family protein [Bacillus cereus AH820]
ref|YP_003667816.1| acetyltransferase, GNAT [Bacillus thuringiensis BMB171]
gb|AAS45012.1| acetyltransferase, GNAT family protein [Bacillus cereus ATCC 10987]
gb|ABK00846.1| acetyltransferase, GNAT family protein [Bacillus cereus]
gb|ABK01111.1| acetyltransferase, GNAT family protein [Bacillus cereus]
gb|ACK92826.1| acetyltransferase, gnat family protein [Bacillus cereus AH820]
gb|ADH10096.1| Acetyltransferase, GNAT [Bacillus thuringiensis BMB171]
Length = 164
```

Score = 50.1 bits (118), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 42/151 (27%), Positives = 64/151 (42%), Gaps = 4/151 (2%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
          I T D V DI I T T F TE +W + +D +VA+V+ ++
Sbjct: 5 IVQLTEKDWPQVSDIYLKGILTKTATFETECPDWYKW---KMNRLKTCIVAKVDQIII 60

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
          G A +R AY E++VYV + +G L L+ E + ++ A I
Sbjct: 61 GWASVSKISSRCAYVGVGETSVYVHPNYIGNNVGFRLLKELVDLSEENSYWTLQANIFAE 120

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
          N S+++HE G+ G G +G W D
Sbjct: 121 NISSIKIHEKNGFRIVGVREKIGQVNGIWKD 151
```

```
>ref|ZP_06557427.1| acetyltransferase [Listeria monocytogenes FSL J2-071]
gb|EFD89540.1| acetyltransferase [Listeria monocytogenes FSL J2-071]
Length = 157
```

Score = 50.1 bits (118), Expect = 1e-04, Method: Compositional matrix adjust.
Identities = 35/132 (26%), Positives = 60/132 (45%), Gaps = 3/132 (2%)

```
Query: 38 TEPQTPQEWIDDLERLQDRY---PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVS 94
          T T QE LE ++Y LV + G V G A P+ + +AY E ++Y++
```

Sbjct: 19 TGNATFQEKTLSEAFDEKYLKTCRLVVVMNGEVIGWAALLPFSSMHAYRGVAELSIYIA 78

Query: 95 HRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYK 154

+ G+G L +++ E GF ++ ++I N S+ LH G+ G
Sbjct: 79 KSARGKGIGKALMHEIIQTSEQNGFWTLQSLIFPENKASIALHHTYGFQTLCTIHEKLGEM 138

Query: 155 HGGWHDVGFQWR 166

+G + DV +R

Sbjct: 139 NGIFRDVALLER 150

>ref|ZP_06981307.1| phosphinothricin N-acetyltransferase [Neisseria sp. oral taxon 014

str. F0314]

gb|EF122940.1| phosphinothricin N-acetyltransferase [Neisseria sp. oral taxon 014

str. F0314]

Length = 209

Score = 50.1 bits (118), Expect = 1e-04, Method: Compositional matrix adjust.

Identities = 38/142 (26%), Positives = 63/142 (44%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEG 66

+ A D+ A+ I N +ET P Q Q W + DR +++ G
Sbjct: 48 VSQAVRQDLPAIVAIYNSAVETRQSTADLAPVGTQDRQAWFE--THTGDRPLYVLKNQTG 105

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

V + R AY + E ++YV H + G+G L ++L+ + G ++V+AVI
Sbjct: 106 EVLAWGSFSDYYP RRAYHISAEISIIYVRHDMRGAGMGKILLRNMLERAPSLGIRNVLAVI 165

Query: 127 GLPNDPSVRLHEALGYTARGTL 148

N S+RL ++G+ G L

Sbjct: 166 FGHNHVSLRLFHSMGFQEWGRL 187

>emb|CBK99284.1| Sortase and related acyltransferases [Faecalibacterium prausnitzii L2-6]

Length = 172

Score = 50.1 bits (118), Expect = 1e-04, Method: Compositional matrix adjust.

Identities = 48/167 (28%), Positives = 69/167 (41%), Gaps = 5/167 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+ IRP D AV +I + I T F+T W D + R LV G
Sbjct: 4 ITIRPMEPEDWDAVSEIYSEGIATEHATFQTACPPYTAW-DAFHKECR---LVILDGGE 59

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+AG A R Y E ++YV + + GLGS L T L + E +G+ ++ + +
Sbjct: 60 LAGWAALRRIDPRWCYRGVAEVSIIYVGEKFRGRGLSRLLTALCEESEKEGYWTLHSTVL 119

Query: 128 LPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFQWQDFELPAP 173

N S+ LH G+ G R A HG W D +R + P

Sbjct: 120 QDNTASLGLHTKCGFRVVGRRERIARDCHGRWLDTYLMERRAKADEP 166

>ref|YP_001099698.1| putative acetyltransferase [Herminiimonas arsenicoxydans]

emb|CAL61571.1| Phosphinothricin N-acetyltransferase [Herminiimonas arsenicoxydans]

Length = 153

Score = 50.1 bits (118), Expect = 1e-04, Method: Compositional matrix adjust.

Identities = 38/129 (29%), Positives = 60/129 (46%), Gaps = 7/129 (5%)

Query: 18 MAAVCDIVNHYIETSTVNFRTEPQTPQ---EWIDDLERLQDRYPWLVAEVEGVVAG-IAV 73

M A+ I N I + V EP T EW + E D+ P V E +G + G +AY

Sbjct: 1 MPAIVAIYNSTIASRQVTADIEPVTVASRLEWFN--EHSADKRPIWVLENDGKILGWLAY 58

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133

+ + R AY T E ++Y++ + GLG T + ++V +I N+PS

Sbjct: 59 SN-FNPRAAYIHTAEISIIYAQDARGKGLGGYFLTEAIAASTLNIHTLVGLIFAHNEPS 117

Query: 134 VRLHEALGY 142

++L E G+

Sbjct: 118 LKLFERFGF 126

>ref|YP_002758108.1| N-acetyltransferase [Listeria monocytogenes Clip81459]
 ref|ZP_05274162.1| N-acetyltransferase [Listeria monocytogenes FSL J2-064]
 ref|ZP_05389685.1| N-acetyltransferase [Listeria monocytogenes FSL J1-175]
 emb|CAS05172.1| Putative N-acetyltransferase [Listeria monocytogenes serotype 4b
 str. CLIP 80459]
 Length = 165

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 34/132 (25%), Positives = 60/132 (45%), Gaps = 3/132 (2%)

Query: 38 TEPQTPQEWDLLERLQDRY---PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVS 94

T T QE +E ++Y LV + G V G A P+ + +AY E ++Y++

Sbjct: 27 TGNATFQEKTLSEAFDEKYLNTCRLVLMNGKVIGWAALLPFSSMHAYRGVAELSIYIA 86

Query: 95 HRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYK 154

+ G+G L ++++ E GF ++ ++I N S+ LH G+ G

Sbjct: 87 KSARGKGIGKALMHEIIQTSEQNGFWTLQSLIFPENKASIALHHTYGFQTL CVHEKLGEM 146

Query: 155 HGGWHDVGFQWR 166

+G + DV +R

Sbjct: 147 NGVFRDVALLER 158

>ref|ZP_04253227.1| GCN5-related N-acetyltransferase [Bacillus cereus 95/8201]
 gb|EEL14985.1| GCN5-related N-acetyltransferase [Bacillus cereus 95/8201]
 Length = 166

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 38/164 (23%), Positives = 65/164 (39%), Gaps = 6/164 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWDLLERLQDRYPWLVAEVEG 66

IR A A D+ + I N I+ + +EW + +R+ LVAE+EG

Sbjct: 6 IRNAKAQDIERIKLIYNQGIQDRIATLEENEKNTADMEEFWSNR---SERHEVLVAEIEG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

+ G P+ R AY + ++Y+ + G+G L + + GF +V

Sbjct: 63 QIVGWVSLNPYSHRCAYSGVADLSIYIDRDQRGKGIGKRLQGIIEVARQHGFYKIVLFT 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFEL 170

N L+ ++ Y G G G + DV +++ L

Sbjct: 123 FPFNALGQGLYRSMDYREVGIFEKQKLDGEFVDVMAMEKNIGL 166

>ref|YP_001820434.1| GCN5-related N-acetyltransferase [Opitutus terrae PB90-1]
 gb|ACB76834.1| GCN5-related N-acetyltransferase [Opitutus terrae PB90-1]
 Length = 176

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
 Identities = 42/155 (27%), Positives = 63/155 (40%), Gaps = 23/155 (14%)

Query: 1 MSPERRP--VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWDLLERLQDRYP 58

+ PE P + +R A A+D+ A+ I N I V DL ++ R P

Sbjct: 4 VDPEVLPPGIIVRDAQASDLPAIVSIYNEIIPGRMVTADL-----DLVTVESRLP 53

Query: 59 WL-----VAEEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLY 107

WL V E G V + R AYD T +YV+ + GLG L

Sbjct: 54 WLQLHNPAHHPVWVVEENGAVIAWLSFDTFYPRPAYDGTAMLAIYVTKARRGSGGLGRMLL 113

Query: 108 THLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGY 142

T ++ G ++ I N+PS++L A G+

Sbjct: 114 TRAMRHAPKLGIRVLLGYIFAHNEPSLKLFAAHGF 148

>ref|ZP_05620974.1| phosphinothricin N-acetyltransferase [Enhydrobacter aerosaccus SK60]

gb|EEV21889.1| phosphinothricin N-acetyltransferase [Enhydrobacter aerosaccus SK60]

Length = 174

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 44/169 (26%), Positives = 71/169 (42%), Gaps = 11/169 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWDLLERLQDRY 57

MS + IR A D+ + +I N I +P + Q W D +R

Sbjct: 1 MSASHHNLSIRLAAIDDLPRIVEIYNQSIAGKQATADLQPVSVVDRQAWFD--AHTGNR- 57

Query: 58 PWLVAEVE-----GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112

P +VA+ G + G AR AY + E ++YV+ + G+G L +L++

Sbjct: 58 PLVVAQTSSSENSLGEIVGWGSLSDLYARPAYHISTEISIVVADEAKGQGVGKALVNYLIQ 117

Query: 113 SMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

+ G + VVA+I N PS+ + LG+ G + +G DV

Sbjct: 118 VAPSCGVQQVVALIFAHNTPSLAMFGKLGFEWPWGKFKQVCDMNGFIADV 166

>ref|YP_004067627.1| acetyltransferase [Pseudoalteromonas sp. SM9913]

gb|ADT67475.1| acetyltransferase [Pseudoalteromonas sp. SM9913]

Length = 162

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 40/144 (27%), Positives = 64/144 (44%), Gaps = 6/144 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---PQEWIDDLERLQDRYPWLVAEV 64

+ IR A D+ A+ I N I + V TE T Q W D R ++ E

Sbjct: 1 MTIRLAKPDDLTAIVAIYNETIPSRMVTADTEEVTVADKQPWFD--SHTAQRPIFVYCEN 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124

V+A ++Y + R AYD TVE ++Y++ Q GLG L + + + ++

Sbjct: 59 NQVLAWLSYKS-FYGRPAYDGTVELSIYITAAQKGLGKKLMQFAQQQAKQLNIEVLLG 117

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148

I N+PS++L + + G L

Sbjct: 118 FIFSHNEPSIKLKFHFDFAVWGEL 141

>ref|YP_014017.1| acetyltransferase [Listeria monocytogenes str. 4b F2365]

ref|ZP_00231172.1| acetyltransferase, GNAT family [Listeria monocytogenes str. 4b H7858]

ref|ZP_05241902.2| acetyltransferase [Listeria monocytogenes FSL R2-503]

ref|ZP_05229541.2| acetyltransferase [Listeria monocytogenes FSL J1-194]

ref|ZP_07075730.1| GNAT family acetyltransferase [Listeria monocytogenes FSL N1-017]

gb|AAT04194.1| acetyltransferase, GNAT family [Listeria monocytogenes serotype 4b str. F2365]

gb|EAL09000.1| acetyltransferase, GNAT family [Listeria monocytogenes str. 4b H7858]

gb|EEW18473.1| acetyltransferase [Listeria monocytogenes FSL R2-503]
gb|EFG01540.1| acetyltransferase [Listeria monocytogenes FSL J1-194]
gb|EFK40600.1| GNAT family acetyltransferase [Listeria monocytogenes FSL N1-017]
Length = 157

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 34/132 (25%), Positives = 60/132 (45%), Gaps = 3/132 (2%)

Query: 38 TEPQTPQEWIDDLERLQDRY---PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVS 94
T T QE +E ++Y LV + G V G A P+ + +AY E ++Y++
Sbjct: 19 TGNATFQEKTLSEAFDEKYLNTCRLVLMNGKVIGWAALLPFSSMHAYRGVAELSIYIA 78

Query: 95 HRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYK 154
+ G+G L ++++ E GF ++ ++I N S+ LH G+ G
Sbjct: 79 KSARGKGIGKALMHEIIQTSEQNGFWTLQSLIFPENKASIALHHTYGFQTLCVHEKLGEM 138

Query: 155 HGGWHDVGFWQR 166
+G + DV +R
Sbjct: 139 NGVFRDVALLER 150

>ref|YP_003014556.1| GCN5-related N-acetyltransferase [Paenibacillus sp. JDR-2]
gb|ACT04470.1| GCN5-related N-acetyltransferase [Paenibacillus sp. JDR-2]
Length = 166

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 35/136 (25%), Positives = 61/136 (44%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEG 66
IR A D+ + +I N I + V EP ++ W D E D P V E +G
Sbjct: 7 IRDARVEDLPRIVEIYNSTIASRRVTADLEFPVSVESRMRWYD--EHSPDFRPLWVLEEDG 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVAI 126
+ + R AY+ T E ++Y+ ++ G+GS L L++ G ++++ +
Sbjct: 65 KMLAWLSFQSFYGRPAYNATAEISIIYIDQEYRARGIGSFLIQKSLEASPLGLRLTLLGFV 124

Query: 127 GLPNDPSVRLHEALGY 142
N+PS+ L G+
Sbjct: 125 FGHNEPSLALLRKFGF 140

>ref|ZP_00232961.1| acetyltransferase, GNAT family [Listeria monocytogenes str. 1/2a
F6854]
ref|ZP_05268099.2| acetyltransferase [Listeria monocytogenes F6900]
gb|EAL07095.1| acetyltransferase, GNAT family [Listeria monocytogenes str. 1/2a
F6854]
gb|EEW21602.1| acetyltransferase [Listeria monocytogenes F6900]
Length = 157

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 35/132 (26%), Positives = 60/132 (45%), Gaps = 3/132 (2%)

Query: 38 TEPQTPQEWIDDLERLQDRY---PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVS 94
T T QE LE ++Y LV + G V G A P+ + +AY E ++Y++
Sbjct: 19 TGNATFQEKTLSEAFDEKYLNTCRLVVVMNGEVIGWAALLPFSSMHAYRGVAELSIYIA 78

Query: 95 HRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYK 154
+ G+G L ++++ E GF ++ ++I N S+ LH G+ G
Sbjct: 79 KSARGKGIGKALMHEIIQTSEQNGFWTLQSLIFPENKASIALHHTYGFQTLCIHEKLGEM 138

Query: 155 HGGWHDVGFWQR 166
+G + DV +R
Sbjct: 139 NGIFRDVALLER 150

>ref|ZP_01743299.1| putative acetyltransferase, GNAT family protein [Rhodobacterales
bacterium HTCC2150]
gb|EBA02344.1| putative acetyltransferase, GNAT family protein [Rhodobacterales
bacterium HTCC2150]
Length = 166

Score = 49.7 bits (117), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 41/160 (25%), Positives = 67/160 (41%), Gaps = 3/160 (1%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL--ERLQDRYPWLVAEVEG 66
+I PA D A + I + S F ++ + I+ + ++ + +LVA+
Sbjct: 6 QICPAKTTDAAEIAAIWKPILAGSLATFNPVVKSTTD-IETMITDKADAGFAFLVAKDAD 64

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G A G ++ Y T+E T+ ++ R Q GLG L + G S+ A +
Sbjct: 65 GVLGFATYGGFRGGVGYARTMEHTIILADRAQGCGLGRQLMHAIEDHARTGGAHSIFAGV 124

Query: 127 GLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N V H LGY L + GYK + D+ Q+
Sbjct: 125 SAANQQGVAFHARLGYYEEVARLPVSGYKFDKYL DLVLMQK 164

>ref|ZP_04384226.1| transcriptional regulator, ArsR family [Rhodococcus erythropolis
SK121]
gb|EEN88455.1| transcriptional regulator, ArsR family [Rhodococcus erythropolis
SK121]
Length = 294

Score = 49.3 bits (116), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 44/164 (26%), Positives = 65/164 (39%), Gaps = 14/164 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL----VA 62
V +R D AV I I+T F E + E L +R WL VA
Sbjct: 133 VSVRAMVDDWDVAVRRIYGEIGIDTRNATFAAE-----VPSREHLHER--WLPQHRWVA 183

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
+ GVV G A P R+ Y E++VYV+ + G+G L + + +A G ++
Sbjct: 184 TIGGVVVGWAALSPVSEDCYRGVAENSVYVADGMRGRGVGKALLRKQVMAADADGLWTL 243

Query: 123 VAVIGLPNDPSPVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+ N S+ LH + G+ G G W D +R
Sbjct: 244 QTSMPFENRASISLHHSAGFRTVGLREKIAELDGVRDVTLLER 287

>ref|YP_004214188.1| GCN5-related N-acetyltransferase [Rahnella sp. Y9602]
gb|ADW75061.1| GCN5-related N-acetyltransferase [Rahnella sp. Y9602]
Length = 177

Score = 49.3 bits (116), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 32/113 (28%), Positives = 47/113 (41%)

Query: 40 PQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQ 99
P+ W D D +AE +G AG A D +YVS +R
Sbjct: 44 PRRQAFWQDKFAHPADGQGIFIAETDGAFAGFCLASASSNPEFGDMAEIKFLYVSPAFKR 103

Query: 100 LGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSPVRLHEALGYTARGTLRAAG 152
G+G L K + A+GF+S + N+P++R ++ALG G AG
Sbjct: 104 RGIGRLLIAKAAKHLAEGFRSAGLGVEGNEPAIRFYQALGGREAGRYTDAG 156

>ref|YP_003192986.1| GCN5-related N-acetyltransferase [Desulfotomaculum acetoxidans DSM

771]
gb|ACV64363.1| GCN5-related N-acetyltransferase [Desulfotomaculum acetoxidans DSM
771]
Length = 163

Score = 49.3 bits (116), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 38/144 (26%), Positives = 60/144 (41%), Gaps = 5/144 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
+ IR AT D+ + DI N + + V T P T + W E D P V E
Sbjct: 1 MNIRLATENDLPPIVDIYNSTVPSRMVTADTTPVTIESRLAWFH--EHNPDNRPIWVVEE 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
G G + R AY+ T E ++Y++ +Q G+G L + G +++
Sbjct: 59 GGNALGWLSFSFFYNRPAYNSTAEVSIYIAEEYQKGIGKLLAKAIHESPKLGITTILG 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
I N+PS++L + G L
Sbjct: 119 FIFGHNEPSLQLFLKFNFEEKWGYL 142

>ref|ZP_06303809.1| GCN5-related N-acetyltransferase [Raphidiopsis brookii D9]
gb|EFA74243.1| GCN5-related N-acetyltransferase [Raphidiopsis brookii D9]
Length = 123

Score = 49.3 bits (116), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 37/123 (30%), Positives = 52/123 (42%), Gaps = 5/123 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
IR AT D+ A+ I N + T EP T + W ER+ R P V EV
Sbjct: 3 IRNATELDLPAIVAIYNAAVPTRMATADLEPVTLESRTWFQ--ERVPSRSPLWVVEVND 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
+ G + R AY T E ++Y+S R GLG TL + G K++++
Sbjct: 61 NIGGWLSFQSFYGRPAYHATAEISIIYISPSFHRRGLGKTLLKAIHESPNLGIKTLLSFY 120

Query: 127 GLP 129
P
Sbjct: 121 FCP 123

>ref|YP_001801960.1| putative GCN5-related N-acetyltransferase [Cyanotheca sp. ATCC
51142]
gb|ACB49894.1| putative GCN5-related N-acetyltransferase [Cyanotheca sp. ATCC
51142]
Length = 170

Score = 49.3 bits (116), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 36/143 (25%), Positives = 62/143 (43%), Gaps = 5/143 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVE 65
+IR AT D+ + +I N I + E ++ +W ER YP V E +
Sbjct: 3 KIRSATIEDLEEIVNIYNASIPSRLATGDLEKIQVESRLKWFQ--ERDHHKHYPIWVMEKD 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 125
V G + R AY T E ++Y++ H+ G+G L ++++ G +++
Sbjct: 61 NQVLGWISLQHFYGRPAYKSTAEISLYIAENHRQGIGKLLGYVIEESPKLGLTNLLGF 120

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148
I N PS+ L + + G L
Sbjct: 121 IFAHNQPSLNLFFKYNFQQWGYL 143

>ref|ZP_02355372.1| phosphinothricin acetyltransferase [Burkholderia oklahomensis
E0147]
ref|ZP_02362513.1| phosphinothricin acetyltransferase [Burkholderia oklahomensis
C6786]
Length = 168

Score = 49.3 bits (116), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 40/144 (27%), Positives = 64/144 (44%), Gaps = 5/144 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAEV 64
+ R AT D++ + I N + + V TEP T + W D R W+V E
Sbjct: 4 LACRDATPDDLSEIVAIYNSTVASRRVTADTEPVTVDSSRAWFD-AHNPHARPLWVVEEA 62

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
V+A ++++ + R AY T E ++Y+ + GLG L L G + +
Sbjct: 63 GRVIAWLSFS-DFYGRPAYGHTAEISIIYLDEAARGKGLGKLELALAKAPELGVHTALG 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
I N+PS+RL G++ G L
Sbjct: 122 FIFGHNEPSLRLFARYGFSTWGAL 145

>ref|ZP_07149324.1| putative acetyltransferase [Corynebacterium resistens DSM 45100]
Length = 176

Score = 49.3 bits (116), Expect = 2e-04, Method: Compositional matrix adjust.
Identities = 41/151 (27%), Positives = 71/151 (47%), Gaps = 11/151 (7%)

Query: 14 TAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVEGVVAGIA 72
T D V +I+ ++T F +E +W+ R+ D ++ E + V+ I
Sbjct: 2 TERDYPQVREILQAGMDTGEATFESEAP---DWLGFSHHRIMD-LAFVAVEGDKVLGWIT 57

Query: 73 YAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDP 132
A P R + +E ++YVS + G+ L HL++ E+QG+ ++ + I N+
Sbjct: 58 -ATPASHREVFVRGVIEDSIYVSADAKGRGVAGGLLDHLIRDAESQGYWAMHSSIFPENES 116

Query: 133 SVRLHEALGYTARGTLRAA-----GYKHGGW 158
SV+LHE+ G+ G L + G K G W
Sbjct: 117 SVKLHESRGFQKVGILHSMAMTYGPKQGW 147

>emb|CAK50857.1| putative phosphinothricin N-acetyltransferase [Streptomyces
ambofaciens]
emb|CAK51095.1| putative phosphinothricin N-acetyltransferase [Streptomyces
ambofaciens]
Length = 159

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 46/155 (29%), Positives = 64/155 (41%), Gaps = 3/155 (1%)

Query: 12 PATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGI 71
P A V I I+ F T T E D ++ + R+ L + G V G
Sbjct: 2 PLAAEHAEQVLAIIYQAGIDEGNATFETVAPT-WEAFDAVKLPEHRFSAL--DENGTVLGW 58

Query: 72 AYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPND 131
A R AY VE +VYV + G+ S L L+ S E G ++ + I N
Sbjct: 59 VAASRVSDRCAYQGVVEHSVYVHPAARGRGVASALLKTLVDSTEQAGIWTIQSEIFPENA 118

Query: 132 PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
S+ +HE G+ GT G +HG W DV +R
Sbjct: 119 ASLGVHERAGFRVIGTRERIGRQHGVRDVLVER 153

>ref|ZP_08124242.1| hypothetical protein PseP1_30385 [Pseudonocardia sp. P1]
Length = 281

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 45/159 (28%), Positives = 65/159 (40%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V +R T D AV I I T F T+ P D L++ + W VA ++G
Sbjct: 122 VTVRAMTDDDWDVAVLRIYEGITTGHATFETD--VPDRADLDAGWLRE-HRW-VAALDGQ 177

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G P R Y E+++YV+ + G+G L + + + G ++ I
Sbjct: 178 VVGWTAVRPVSNRPVYSGVGETSIYVADGFRGRGIGKALIRQQVCAADDAGLWTLQTSIF 237

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH A GY G G G W D F +R
Sbjct: 238 PENRASLALHRAAGYRTLGVRRERIGQHDGRWRD TVFLER 276

>ref|YP_849613.1| GNAT family acetyltransferase [Listeria welshimeri serovar 6b str. SLCC5334]
emb|CAK20834.1| GNAT family phosphinothricin N-acetyltransferase, putative [Listeria welshimeri serovar 6b str. SLCC5334]
Length = 165

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 38/158 (24%), Positives = 69/158 (43%), Gaps = 4/158 (2%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+I P + A V + I+T F+ + T + W D + L + LV + V
Sbjct: 5 KILPMSKEHYAGVA AVHQEGIDTGNATFQEKVLT FESW--DAKYL--KTCRLVLLNEQV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A P+ + AY E ++Y++ + G+G L + + + + E GF ++ ++I
Sbjct: 61 IGWAALLPFSSMYAYRGVAELSIYIAKSARGKGVGKALMQEI IQASEENGFWTLQSLIFP 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N S+ LH G+ G +G + DV +R
Sbjct: 121 ENKASISLHHTYGFQTL CIHEKLGEINGDFRDVALLER 158

>ref|YP_001812925.1| GCN5-related N-acetyltransferase [Exiguobacterium sibiricum 255-15]
gb|ACB59908.1| GCN5-related N-acetyltransferase [Exiguobacterium sibiricum 255-15]
Length = 169

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 37/152 (24%), Positives = 58/152 (38%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IRP D+ + I N IE T+ + D RY VA +
Sbjct: 3 IRPVKEDDLKDILAIYNEGIEDRIATLETDTKELSFMEDWYRERTPRYAGFVAYEGTTIL 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G P+ R Y E +VY++ H+ G+G L + + QGF ++
Sbjct: 63 GFISLDPYNRPVYQSVGELSVYITRTHRQGIGRQLLHVIEHAITQGFHKLILFTFPF 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N +L+ G+ GT + G +G + DV
Sbjct: 123 NKIGQKLYIRSGFRIVGTFKEQGMLNGYYVDV 154

>ref|ZP_02144841.1| phosphinothricin N-acetyltransferase, putative [Phaeobacter gallaeciensis BS107]
 gb|EDQ13302.1| phosphinothricin N-acetyltransferase, putative [Phaeobacter gallaeciensis BS107]
 Length = 174

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 37/155 (23%), Positives = 65/155 (41%), Gaps = 8/155 (5%)

Query: 26 NHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL-VAEVEGVVAGIAYAGPWKARNAYD 84
 N I + + F T +T ++ D++ ++ ++ VAE G + G G ++ Y
 Sbjct: 19 NQIIRDTLITFTTAEKTSEQVRDEI---AEKGAYVQVAEEAGQILGYISLGAFRTGPGYA 75

Query: 85 WTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTA 144
 T E +Y++ + G G L + A G +VA I N + H A+G+
 Sbjct: 76 RTCEHAIYLAETARGRGAGRALIAAIEAVARADGVHVLVAGISAVNAGGLAFHAAMGFVE 135

Query: 145 RGTLRAAGYKHGGWHDVGFQWQDFELPAPPRPVRP 179
 G + G+K W D+ Q+ P+ V P
 Sbjct: 136 VGRMPEVGHKADQWLDLVLQMOKIL---SPKGVGP 166

>ref|YP_003116235.1| GCN5-related N-acetyltransferase [Catenulispora acidiphila DSM 44928]
 gb|ACU74394.1| GCN5-related N-acetyltransferase [Catenulispora acidiphila DSM 44928]
 Length = 168

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 48/167 (28%), Positives = 67/167 (40%), Gaps = 6/167 (3%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
 M+P + I P TAA V I H I+ F T P + D +L +
 Sbjct: 1 MTPS---IVIAPMTAAHADDVLRIRYQHGHIDEGNATFET--AAPSWDVF DAGKLP EHRFVA 55

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 + + V G R Y VE +VYV + G+G+ L + L+ S EA G
 Sbjct: 56 LDPAPKPAVLGYVVVSANSKRACYAGVVEISVYVDPAAARGRGVGNRLLSALIASTEAGVW 115

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGG-WHDVGFQWR 166
 ++ A I N S+ LHE G+ G G G W DV +R
 Sbjct: 116 TINAGIFPENTASLALHERHGRFVLGRQERIGKTAAGVWRDVVLLER 162

>ref|ZP_05109686.1| conserved hypothetical protein [Legionella drancourtii LLAP12]
 gb|EET12646.1| conserved hypothetical protein [Legionella drancourtii LLAP12]
 Length = 164

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
 Identities = 34/115 (29%), Positives = 56/115 (48%), Gaps = 4/115 (3%)

Query: 44 QEWDIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVE-STVYVSHRHQRLGL 102
 Q+W D L+ L+ E++ G A P++ NA E S +Y+ + R+GL
 Sbjct: 41 QQWQD---LLKQEVNVLIEIDHQAVGFASICPFRGVNAEPLMGEISAIYLHPDYWRMGL 97

Query: 103 GSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGG 157
 G+ L L + A G+K V + N+ + R +EALG+TA + + + GG
 Sbjct: 98 GTKLCLTALSELTAALGYKKVGLWVLEANNQARRFYEALGFTATSSTKLEEFYEGG 152

>ref|YP_002766969.1| ArsR family transcriptional regulator [Rhodococcus erythropolis PR4]

dbj|BAH34230.1| putative ArsR family transcriptional regulator [Rhodococcus
erythropolis PR4]
Length = 294

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 42/159 (26%), Positives = 64/159 (40%), Gaps = 4/159 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V +R D V I I+T F TE + + ER ++ W VA +EGV
Sbjct: 133 VSVRAMIDDDWDEVRRYIYEGIDTRNATFATEVPSREHL---HERWLSQHRW-VATIEGV 188

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
V G A P R+ Y E++VYV+ + G+G L + + + ++ I
Sbjct: 189 VVGWAALSPVSEDCYRGVAENSVYVAGMRGRGVGKALLRKQVMAADVDDLWTLQTSIF 248

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
N S+ LH + G+ G G W D +R
Sbjct: 249 PENRASISLHHSAGFRTIGLREKIAQLDGVWRD TVLLER 287

>ref|ZP_03398367.1| sortase/acyltransferase [Pseudomonas syringae pv. tomato T1]
gb|EEB58681.1| sortase/acyltransferase [Pseudomonas syringae pv. tomato T1]
Length = 174

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 39/144 (27%), Positives = 63/144 (43%), Gaps = 6/144 (4%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAE-----V 64
R AT AD+ A+ +I N IE EP + + W ++ R P VAE
Sbjct: 10 RAATLADLPAIVEIYNCAIEAGNSTCDVEPVSVEAWKPWFIFKHSRRPIWVAEDPRDPK 69

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
GV+ ++ + R Y T + +Y+ HQ G+GS L +++S + +
Sbjct: 70 TGVIGYLSLSYFMNERPGYFRTADLGLYIHPLHQSQGVGSFLLRSIMESAALLDIEVIAT 129

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
+ N S+RL E G+T G +
Sbjct: 130 TVFAHNHKSRLRFENSGFTRWGFM 153

>ref|ZP_05316934.1| putative phosphinothricin N-acetyltransferase [Neisseria sicca
ATCC
29256]
gb|EET45964.1| putative phosphinothricin N-acetyltransferase [Neisseria sicca ATCC
29256]
Length = 166

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 43/161 (26%), Positives = 68/161 (42%), Gaps = 12/161 (7%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
I A D+ + +I N I P + E W D R +++ EG
Sbjct: 5 ITEAAKTDLDPDIVEIYNSTIAARQSTADLTPVSIAREPWFD--AHGGKRPLYVLKNHEG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V + R+AY + E ++YV H + +G+G L ++L+ + G K+++AVI
Sbjct: 63 TVLAWCSLSDYYPRHAYHISAEISLYVRHDARGIGVGKILLQNVLERAPSLGIKNILAVI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRD 167
N PS+ L G+T G L A D+G Q D
Sbjct: 123 FGHNYPSLHLFHQFGFTEWGRLPAVC-----DLGTQQAD 156

>ref|YP_003583021.1| GNAT family acetyltransferase [Zunongwangia profunda SM-A87]
gb|ADF50825.1| GNAT family acetyltransferase [Zunongwangia profunda SM-A87]
Length = 160

Score = 48.9 bits (115), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 42/144 (29%), Positives = 63/144 (43%), Gaps = 17/144 (11%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER--LQDR--YPWLVAE 63
+E+R AT DM AV ++N F EP + + DLE DR + VAE
Sbjct: 3 IEVRKATKQDMPAVLKLINEL----AKFENEPDAVEITVKDLENDGFGDRPLFECEFAE 57

Query: 64 VEGVAGIAYA---GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
+ G+A WK + + +E V VS + GLG LYT +++ + QG
Sbjct: 58 ANDTIEGMALFYRYSTWKGKTVH--LEDLV-VSEAFRGKGLGKALYTKVIQYSKQQGC 113

Query: 120 KSVVAVIGLPNDPSVRLHEALGYT 143
K V+ N +V ++ G T
Sbjct: 114 KRTEWVVDWNTNAVEFYKNSGAT 137

>ref|ZP_06811307.1| GCN5-related N-acetyltransferase [Geobacillus thermoglucosidasius
C56-YS93]
gb|EFG52158.1| GCN5-related N-acetyltransferase [Geobacillus thermoglucosidasius
C56-YS93]
Length = 162

Score = 48.5 bits (114), Expect = 3e-04, Method: Compositional matrix adjust.
Identities = 38/142 (26%), Positives = 62/142 (43%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE--WIDDLERLQDRYPWLVAEVEG 66
IR A D+ A+ I N I + V EP T + W + + P V E++G
Sbjct: 2 IRNANIEDLPAIVQIYNETIPSRMVTADLEPVTVESRKAWFFNHD--PHTRPLWVVELDG 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126
V + R AY T E ++Y+S ++ G+G L ++ + K+++ I
Sbjct: 60 HVRWLSFQSFYGRPAYRHTAEISIIYISGAYRGKGIGKQLLQKAVEEAPSLDIKTLLGFI 119

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
N+PS+RL G+ G L
Sbjct: 120 FAHNEPSLRLFTRFGFETWGHL 141

>ref|ZP_07089105.1| phosphinothricin acetyltransferase [Chryseobacterium gleum ATCC
35910]
gb|EFK35897.1| phosphinothricin acetyltransferase [Chryseobacterium gleum ATCC
35910]
Length = 163

Score = 48.5 bits (114), Expect = 4e-04, Method: Compositional matrix adjust.
Identities = 34/153 (22%), Positives = 65/153 (42%), Gaps = 4/153 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
++I+P T + + + +I + + T+ F+ + Q+W ++ + +
Sbjct: 1 MKIKPITKDNFSELVEIYSQGLATNIATFQNDLPLWQDW---DKGHLDFCRISIYENNE 56

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
+ G P R Y E ++YV+ + G+G L L+K E ++ + I
Sbjct: 57 MLGWTALSPVSNRCVYSGLAEVSIYVATIARGKGIGEMLLNELIKQSELNEIWTLSQGIF 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
N S++LHE G+ G G K+G W D
Sbjct: 117 AENRGSIKLHEKCGFRIVGYREKIGKNGVWWD 149

>ref|ZP_04860080.1| polyprenyl synthetase [Fusobacterium varium ATCC 27725]

gb|EES63611.1| polyprenyl synthetase [Fusobacterium varium ATCC 27725]

Length = 165

Score = 48.5 bits (114), Expect = 4e-04, Method: Compositional matrix adjust.

Identities = 35/146 (23%), Positives = 60/146 (41%), Gaps = 9/146 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

IR D V I IE+ FR + + W + ++ +++ +G V

Sbjct: 5 IREMEDKDWEDVLKIYKQIESGISTFRKDLDPQKSWENSHLKI--CRFVLCNNDGTVV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129

G A P +R Y E ++Y+ HQ LG L + + E G ++ + I

Sbjct: 62 GWAALSPTSSRIDYCGVTEVSIYIDKAHQGKKGFLNKNVKEEAENGIWTLQSSIFQV 121

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKH 155

N+ S++LH+ G+ R GY+

Sbjct: 122 NEASIKLHKKCGF-----REVGYRE 141

>ref|ZP_04851039.1| phosphinothricin acetyltransferase [Paenibacillus sp. oral taxon

786 str. D14]

gb|EES75229.1| phosphinothricin acetyltransferase [Paenibacillus sp. oral taxon

786 str. D14]

Length = 171

Score = 48.5 bits (114), Expect = 4e-04, Method: Compositional matrix adjust.

Identities = 36/136 (26%), Positives = 58/136 (42%), Gaps = 5/136 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP--QEWDLLERLQDRYPWLVAEVEG 66

I AT D+ A+ I N I V EP T ++W D E D P LV + G

Sbjct: 9 IEDATLEDLPAIVAIYNETIAGRMVTADLEPVTVDARKWFD--EHSPDFRPLLVMKSGG 66

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVI 126

V + R AY+ T E ++Y++ ++ G+G L G +++ +

Sbjct: 67 KVIAWLSFQSFYGRPAYNGTAEISYITEAYRSRGIGGILLNRSFAICPEIGVHTLLGFV 126

Query: 127 GLPNDPSVRLHEALGY 142

N+PS++L G+

Sbjct: 127 FGHNEPSLKLKSKFGF 142

>ref|YP_003861768.1| phosphinothricin N-acetyltransferase [Maribacter sp. HTCC2170]

gb|EAR02469.1| phosphinothricin N-acetyltransferase [Maribacter sp. HTCC2170]

Length = 163

Score = 48.5 bits (114), Expect = 4e-04, Method: Compositional matrix adjust.

Identities = 38/150 (25%), Positives = 59/150 (39%), Gaps = 4/150 (2%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGP 76

D +V I I T F + + ++W ++ +V + V G A

Sbjct: 10 DWESVSKIYKAGINTGCATFEKKVPSYEDW---DKAHISSCRIVIKENDKVIGWAALST 65

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRL 136

+R Y E +VYV H G G L HL+ E GF ++ + I N+ S+ L

Sbjct: 66 VSSRCVYGGVAEVS VYVGQDHSKGKAGKLLMMHLIAQSEKDGFWTLQSGIFPENEASIAL 125

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFQWR 166

H+ G+ G G G W D ++R

Sbjct: 126 HKKAGFRYIGKREKVGQLDGVWKNLLFER 155

>ref|YP_003988012.1| Phosphinothricin acetyltransferase [Geobacillus sp. Y4.1MC1]
 gb|ADP73401.1| Phosphinothricin acetyltransferase [Geobacillus sp. Y4.1MC1]
 Length = 162

Score = 48.5 bits (114), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 38/142 (26%), Positives = 62/142 (43%), Gaps = 5/142 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IR A D+ A+ I N I + V EP T + W + + P V E++G
 Sbjct: 2 IRNANIEDLPAIVQIYNETIPSRMVTADLEPVTVESRKAWFFNHD--PHTRPLWVVELD 59

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 V + R AY T E ++Y+S ++ G+G L ++ + K+++ I
 Sbjct: 60 HVRAWLSFQSFYGRPAYRHTAEISIIYISGAYRGKGIGKQLLQKAVEEAPSLDIKTLLGFI 119

Query: 127 GLPNDPVRLHEALGYTARGTL 148
 N+PS+RL G+ G L
 Sbjct: 120 FAHNEPSLRLFMRFGFETWGHL 141

>ref|YP_345546.1| ArsR family transcriptional regulator [Rhodococcus erythropolis PR4]
 ref|ZP_04387110.1| transcriptional regulator, ArsR family [Rhodococcus erythropolis SK121]
 dbj|BAE46054.1| putative ArsR family transcriptional regulator [Rhodococcus erythropolis PR4]
 gb|EEN85651.1| transcriptional regulator, ArsR family [Rhodococcus erythropolis SK121]
 Length = 306

Score = 48.5 bits (114), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 44/164 (26%), Positives = 66/164 (40%), Gaps = 14/164 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL-----VA 62
 V +R + D AV I I T F TE + +E++D WL VA
 Sbjct: 146 VAVRMSDDDDAVLRIYEGEATRNATFTTEVPS-REYLD-----AQWLPNHRWVA 196

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 ++ VV G A R+ Y E++VYV+ + G+G L + + +A G ++
 Sbjct: 197 TIDVVVGVAAALSSTSGRDCYRGVAENSVYVADGMRGRGVGKALLRKQVMAADADGLWTL 256

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 I N SV LH + G+ G G W D +R
 Sbjct: 257 QTSIFPENRASVSLHHSAGFRTIGIREKIAQLDGIWRDVTLLER 300

>ref|ZP_06882616.1| GCN5-related N-acetyltransferase [Clostridium lentocellum DSM 5427]
 gb|EFG99887.1| GCN5-related N-acetyltransferase [Clostridium lentocellum DSM 5427]
 gb|ADZ83378.1| GCN5-related N-acetyltransferase [Clostridium lentocellum DSM 5427]
 Length = 165

Score = 48.5 bits (114), Expect = 4e-04, Method: Compositional matrix adjust.
 Identities = 42/160 (26%), Positives = 68/160 (42%), Gaps = 5/160 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 V +R T D V I I + F+TE + + W + R LVA V+
 Sbjct: 3 VMMRCMTEKDWPNVRCIYEQGISSGIATFQTEVPSYEVW-NAAHLTTGR---LVAVVDEE 58

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G P +R Y E ++Y+ QR G+ + L L++ E +G ++ + I
 Sbjct: 59 VVGWVALSPTSSRCVYKGVAELSIYIVQNAQRKGVATKLLNELIQLSEQEGIWTLQSSII 118

Query: 128 LPNDPSVRLHEALGYTARG-TLRAAGYKHGGWHDVGFWQR 166
 N S+ LH+ G+ G + A + G WH+ +R
 Sbjct: 119 EENKASLALHQQKCGFRQVGYREKIARDQKGDWHNTILMER 158

>ref|NP_696198.1| N-acetyl transferase [Bifidobacterium longum NCC2705]
 gb|AAN24834.1| possible N-acetyl transferase [Bifidobacterium longum NCC2705]
 Length = 165

Score = 48.1 bits (113), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 40/164 (24%), Positives = 62/164 (37%), Gaps = 2/164 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE- 65
 P PA +D+ A+ DI N + P+T + +E Y V E E
 Sbjct: 2 PYTFHPAVESDIQAITDIYNAAVVAGGATADLTPTLDQRRRAWVESHTPPYGVFVVESED 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + G + R YD + Y+ Q G+G+ + LL A+ + +
 Sbjct: 62 GSIIGFGLSVFYDRAGYDGVTDLAYIYIDPAWQGRGVGTFLDRLLTEARARHMRKACGI 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGFWQRDF 168
 I N S+ L G+T G + AA G D+ +W D
 Sbjct: 122 IFADNVGSIALMRRFGFTQFGLMPAAATDSTGTMRDMSYWYLDL 165

>ref|YP_003885733.1| GCN5-like N-acetyltransferase [Cyanotheca sp. PCC 7822]
 gb|ADN12458.1| GCN5-related N-acetyltransferase [Cyanotheca sp. PCC 7822]
 Length = 172

Score = 48.1 bits (113), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 38/157 (24%), Positives = 64/157 (40%), Gaps = 5/157 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAEV 64
 ++IR A D+A + +I N I + P T + W D + P V E+
 Sbjct: 1 MKIRDARETDLATIVEIYNASIPSRLATADLNPTITVESRLNWFYD--HPPETRPVWVMEI 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 + +V G + R AY T E ++YV+ ++R G+G L + G +++
 Sbjct: 59 DNIVVGWLSFQSFGLRPAYQCTAELSIVAPNYKRQGIGQKLLQAIKSPRLGLNTLIG 118

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 I N PS++L + G L G D+
 Sbjct: 119 YIFAHNKPSLQLFTKYDFQQWGFLPNVAVLDGVERDL 155

>gb|ADI17869.1| sortase and related acyltransferases [uncultured Chloroflexi
 bacterium HF0200_06I16]
 Length = 97

Score = 48.1 bits (113), Expect = 5e-04, Method: Compositional matrix adjust.
 Identities = 26/87 (29%), Positives = 43/87 (49%)

Query: 80 RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEA 139
 R AY E +VYV+ + +G G L L+ S E+ G ++ A+I + N+ S+ LH +
 Sbjct: 4 REAYSGVAEVSIVYVAEESRGIGAGKLLLECLISSESAGIWTQAMIFVENEASIALHTS 63

Query: 140 LGYTARGTLRAAGYKHGGWHDVGFWQR 166
 + + GT G G W + +R
 Sbjct: 64 CAFRSVGTRERIGRLSGRWRNTLLMER 90

>ref|NP_464925.1| hypothetical protein lmo1400 [Listeria monocytogenes EGD-e]
 ref|ZP_03668093.1| hypothetical protein LmonF1_08659 [Listeria monocytogenes Finland]

1988]
 ref|ZP_03669964.1| hypothetical protein LmonFR_03932 [Listeria monocytogenes FSL
 R2-561]
 ref|ZP_05234496.1| hypothetical protein Lmon1_00730 [Listeria monocytogenes 10403S]
 ref|YP_003413651.1| hypothetical protein LM5578_1541 [Listeria monocytogenes 08-5578]
 ref|YP_003416696.1| hypothetical protein LM5923_1493 [Listeria monocytogenes 08-5923]
 emb|CAC99478.1| lmo1400 [Listeria monocytogenes EGD-e]
 gb|ADB68289.1| hypothetical protein LM5578_1541 [Listeria monocytogenes 08-5578]
 gb|ADB71334.1| hypothetical protein LM5923_1493 [Listeria monocytogenes 08-5923]
 Length = 165

Score = 47.8 bits (112), Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 39/161 (24%), Positives = 67/161 (41%), Gaps = 10/161 (6%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY---PWLVAEVE 65
 +I P + V + IET F QE LE ++Y LV +
 Sbjct: 5 KILPMQKEHYSGVAHVHGEIETGNATF-----QEKTLSEAFDEKYLNTCRLVVLMMN 57

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G A P+ + +AY E ++Y++ + G+G L ++++ E F ++ ++
 Sbjct: 58 GEVIGWAALLPFSSMHAYRGVAELSIYIAKSARGKGVGKALMHEIIQTSEQNDFWTLQSL 117

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 I N S+ LH G+ G +G+ DV +R
 Sbjct: 118 IFPENKASIALHHTYGFQTLCEIHEKLGEMNGVFRDVALER 158

>ref|NP_691376.1| phosphinothricin N-acetyltransferase [Oceanobacillus iheyensis
 HTE831]
 dbj|BAC12411.1| phosphinothricin N-acetyltransferase [Oceanobacillus iheyensis
 HTE831]
 Length = 169

Score = 47.8 bits (112), Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 43/164 (26%), Positives = 64/164 (39%), Gaps = 6/164 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVEGVV 68
 I +D V DI +ET F T + W D D + L++ LV + +
 Sbjct: 4 IEKMKKSDWNQVLDIYIQGMETKNATFETTKPEWESWEDWSDHLENCR--LVVKEGTKL 61

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G A P R Y E ++Y+ G+GS L L++ E GF + + I
 Sbjct: 62 LGWAALLPISTRKYYSVGAEVSIYLDKESLGKIGSMLMKSLIEHSEKNGFWMLQSEIFP 121

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKHGG---WHDVGFWQRDFE 169
 N S++LH+ + G G G W DV +R E
 Sbjct: 122 ENIGSIKLHDKFAFRKVGIREKIGKMEGTKNEWRDVVLMERRE 165

>ref|YP_003660980.1| GCN5-like N-acetyltransferase [Bifidobacterium longum subsp.
 longum
 JDM301]
 gb|ADH00150.1| GCN5-related N-acetyltransferase [Bifidobacterium longum subsp.
 longum JDM301]
 Length = 165

Score = 47.8 bits (112), Expect = 6e-04, Method: Compositional matrix adjust.
 Identities = 40/164 (24%), Positives = 62/164 (37%), Gaps = 2/164 (1%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE- 65
 P PA +D+ A+ DI N + P+T + +E Y V E E
 Sbjct: 2 PYTFHPAVESDIQAITDIYNVAVVAGGATADLTPTLDQRRRAWVESHTPPYGVFVVESED 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + G + R YD + Y+ Q G+G+ + LL A+ + +
 Sbjct: 62 GSIIGFGALSVFYDRAGYDGVTDLAYIIDPAWQGRGVGTFLDRLLEARARHMRKACGI 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGFWRQDF 168
 I N S+ L G+T G + AA G D+ +W D
 Sbjct: 122 IFADNVGSIALMRRFGFTQFGLMPAAATDSTGTMRDMSYWYLDL 165

>ref|YP_003486909.1| acetyltransferase [Streptomyces scabiei 87.22]
 emb|CBG68339.1| putative acetyltransferase [Streptomyces scabiei 87.22]
 Length = 160

Score = 47.8 bits (112), Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 42/146 (28%), Positives = 67/146 (45%), Gaps = 12/146 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR ATA D + H + + +P T +E L + ++V + G
 Sbjct: 1 MQIREATADDWPGIWPFW-HRVVAAGDTYTWDPTSEEARALWMAPAKRIVYVVEDETGA 59

Query: 68 VAGIA-----YAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
 + G A Y GP AR A + V H G+G L +H+L AQQF+ +
 Sbjct: 60 LTGSAFLTPNYGGP-AARVA-----NAGFMVDPAHGGRGIGRALASHVLAEARAQGFGRM 113

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTL 148
 V + +P+VRL +LG+T GT+
 Sbjct: 114 VFNAVETNPVRLWTSLGFTVLGTV 139

>ref|YP_003428574.1| GCN5-related N-acetyltransferase [Bacillus pseudofirmus OF4]
 gb|ADC51682.1| GCN5-related N-acetyltransferase [Bacillus pseudofirmus OF4]
 Length = 163

Score = 47.8 bits (112), Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 46/154 (29%), Positives = 68/154 (44%), Gaps = 4/154 (2%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGP 76
 D V I I F+TE + +EW +R D LVA ++G +AG A P
 Sbjct: 10 DWTEVKGIYCEGIADGNATFQTEAPSWEW---DRSHDNECRLVARIDGELAGWAALSP 65

Query: 77 WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRL 136
 R Y E +VYVSH+ GLGS L + L+ E + ++ + I N S+ +
 Sbjct: 66 VSNRRVYAGVAEVSIVYVSHKWSGKGLGSLLSALVDLSENNDIWTLOQSSIFPENTASLFI 125

Query: 137 HEALGYTARGTLRAAGYKHGGWHDVGFWRQDFEL 170
 H+ G+ G G +G W D +R +L
 Sbjct: 126 HKKCGFREVGKRERIGKMNGVWRDTILLERRSQL 159

>ref|YP_721385.1| GCN5-related N-acetyltransferase [Trichodesmium erythraeum IMS101]
 gb|ABG50912.1| GCN5-related N-acetyltransferase [Trichodesmium erythraeum IMS101]
 Length = 178

Score = 47.8 bits (112), Expect = 7e-04, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 66/143 (46%), Gaps = 3/143 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVEG 66
 ++IR A A D+ + I N I + E + + I E D P LV E++G
 Sbjct: 1 MKIRNAEAKDLTVIVKIYNSSIPSRIATGDLELISIENRISWYQEHSPDSRPILVVELDG 60

Query: 67 -VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 V+A +++ + R AY T E ++YV+ ++ G+G L + + G K+++
 Sbjct: 61 QVIAWLSFQSFYD-RPAYQATAEISIVAPEYKQGIGKKLLSEAIYRSPQLGIKTLLGF 119

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148
I N PS+ L G+ G L
Sbjct: 120 IFAHNIPSLSLFNKFGFQHWGYL 142

>gb|EFW18117.1| GNAT family N-acetyltransferase [Coccidioides posadasii str.
Silveira]
Length = 182

Score = 47.8 bits (112), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 46/174 (26%), Positives = 78/174 (44%), Gaps = 23/174 (13%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDR-YPWLVAEVE 65
V IRPAT +D+ + I +HY+ S + F + P +I + + R P+ VA ++
Sbjct: 4 VSIRPATLSDLPGIHAIYSHYVHNSVLTFILH-EPPLSYIAGIYNSTRSRGLPFYVAHID 62

Query: 66 GV-----VAGIAYAGPWKAR-NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
+ + G A A P++ Y TVE T+++ HQ G + EA G
Sbjct: 63 QLRESKEKIIGYACASPFGRNLLGYASTVELTLFIHPEHQSQGFEDDPTREV--RYEADG 120

Query: 119 -----FKSVVAVIGLPNDPSVR-----LHEALGYTARGTLRAAGYKHGGWHDV 161
K+++A++ + D + + G+T G L+ G+K G W DV
Sbjct: 121 GQGARVKTLLAIMAVDIDGKAKGMGLRDWYVQRGFTEVGRLEKVGFKKGRWIDV 174

>ref|ZP_03058612.1| phosphinothricin acetyltransferase [Escherichia coli B171]
gb|EDX32377.1| phosphinothricin acetyltransferase [Escherichia coli B171]
Length = 121

Score = 47.8 bits (112), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 34/98 (34%), Positives = 48/98 (48%), Gaps = 1/98 (1%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-RLQDRYPWLVAE 63
R + IR A AD AA+ +I NH + + + + I E R YP LV+E
Sbjct: 20 RPDMSIRFARKADCAIAEYINHAVLYTAAIWNQTVADNRIAWFEARTIAGYPVLVSE 79

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLG 101
+ VV G A G W++ + + TVE +VYV HQ G
Sbjct: 80 EDSVVTGYASFQDWRSDGFRHTVEHSVYVHPDHQKG 117

>ref|ZP_03963018.1| acetyltransferase [Lactobacillus paracasei subsp. paracasei ATCC
25302]
gb|EEI69437.1| acetyltransferase [Lactobacillus paracasei subsp. paracasei ATCC
25302]
Length = 166

Score = 47.8 bits (112), Expect = 7e-04, Method: Compositional matrix adjust.
Identities = 40/162 (24%), Positives = 66/162 (40%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E PATA+D+ + I N I T +PQT E + +P + +V+
Sbjct: 2 IEFTPATASDLPKIVAIYNETIPTHQATADLQPQTVAEKQTFWAAHNNHFFAWMIQVDHK 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G + R+AYD T E ++Y+ + +GS + + +V+A I
Sbjct: 62 IVGWLTLAYSRSAYDQTAEISLYLDVAARGHHVGSAAALAFVDREAPKHDLTTVLARIF 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169
N S L GY G L A G D+ + + F+
Sbjct: 122 GHNQASRNLFTKFGYDHWGHLPAIAILPEGEADLEVYKGKHF 163

>ref|XP_001218368.1| predicted protein [Aspergillus terreus NIH2624]

gb|EAU29937.1| predicted protein [Aspergillus terreus NIH2624]

Length = 217

Score = 47.8 bits (112), Expect = 7e-04, Method: Compositional matrix adjust.

Identities = 37/117 (31%), Positives = 55/117 (47%), Gaps = 10/117 (8%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL-ERLQDRYPWLVAEVEG-- 66

IRPAT +D+ V I +YI +++ F P P + L P+LVA E

Sbjct: 3 IRPATESDLPQVRHINTYYILHTSLTFAQHPLPPPSYAKTYHHNLAKGLPYLVATDEAQK 62

Query: 67 -----VVAGIAYAGPWKA-RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116

+V G AY P++ R +Y TVE T++V + +GS L + LL + A

Sbjct: 63 WEDDSPLVLGYAYLSPYRGDRLSYAPTVELTLFVHPEYHSQSIGSQLLSALLDKVRA 119

>ref|YP_306013.1| putative acetyltransferase [Methanosarcina barkeri str. Fusaro]

ref|YP_306432.1| putative acetyltransferase [Methanosarcina barkeri str. Fusaro]

gb|AAZ71433.1| putative acetyltransferase [Methanosarcina barkeri str. Fusaro]

gb|AAZ71852.1| putative acetyltransferase [Methanosarcina barkeri str. Fusaro]

Length = 165

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.

Identities = 35/146 (23%), Positives = 58/146 (39%)

Query: 21 VCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKAR 80

V +I HY+ + V F + E + + +Y V + + G +K R

Sbjct: 17 VLEIYTHYVLNTNVTFAHAFAFSKDEMRELVFENPKYKTFVIKSADKINGYVILTQYKKR 76

Query: 81 NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEAL 140

AYD T E TVY+ + G+G + + Q ++A I N S+ L

Sbjct: 77 EAYDGTAEVTYVLKPDYIGKGIGIQAQVFIEDVAKKQNIHVLIATICGENSKSINLFVRN 136

Query: 141 GYTARGTLRAAGYKHGGWHDVGFWR 166

G++ + G K G DV +Q+

Sbjct: 137 GFSKCAHYKEVGEKFGQLLDVMAYQK 162

>gb|ADZ78327.1| Phosphinothricin acetyltransferase [Sphingobacterium sp. 21]

Length = 170

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.

Identities = 36/141 (25%), Positives = 59/141 (41%), Gaps = 4/141 (2%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRY 57

M+ ++ + R A D+ + I N ++ V TE T + W + L R

Sbjct: 1 MNIQKDILVYRDAQLVLDPTIVSIYNSTVASRMVTADTEAVTVESRLPWFNQHNPLT-RP 59

Query: 58 PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117

W+V G G + R AYD TVE ++Y+ ++ G G + +K

Sbjct: 60 LWMVETTGGETIGWLSFQSFYGRPAYDGTVEISYIDESQRKKGYGKMILREAIKRAPDL 119

Query: 118 GFKSVVAVIGLPNDPSVRLHE 138

+++A I N PS+RL E

Sbjct: 120 QVSTILAFIFAHNIPSIRLFE 140

>ref|ZP_00134886.2| COG1247: Sortase and related acyltransferases [Actinobacillus pleuropneumoniae serovar 1 str. 4074]

ref|YP_001053172.1| sortase and related acyltransferases [Actinobacillus

pleuropneumoniae L20]

gb|ABN73567.1| predicted sortase and related acyltransferases [Actinobacillus

pleuropneumoniae serovar 5b str. L20]
Length = 172

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 36/142 (25%), Positives = 59/142 (41%), Gaps = 4/142 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEV 64
++IR +T AD + +I N I T + E TP + W D ++YP E
Sbjct: 1 MQIRKSTEADFETILNIYNQAIPHTQITADLELATPINRRAWFD-FHLTSEQYPIWTVED 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
E +AG P+ R A+ T E ++Y+ + G GS + + M +++A
Sbjct: 60 ENGIAGWFSFSPFYERPAFVHTSEISIYLDSSAKGKGYSKIIIEFMQTEMLKHNIHTLMA 119

Query: 125 VIGLPNDPSVRLHEALGYTARG 146
+ N S L G+ G
Sbjct: 120 YVFELNQVSQNLMRKHGFEQWG 141

>ref|ZP_03742864.1| hypothetical protein BIFPSEUDO_03442 [Bifidobacterium
pseudocatenulatum DSM 20438]
gb|EEG70427.1| hypothetical protein BIFPSEUDO_03442 [Bifidobacterium
pseudocatenulatum DSM 20438]
Length = 179

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 40/164 (24%), Positives = 66/164 (40%), Gaps = 6/164 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEV-----E 65
R AT D+ A+ DI N + + P+T ++ +E D Y V E E
Sbjct: 16 RIATQNDIQAITDIYNAAVIRGGSSADITPRTYEQRKAWVESHHPYAVFVTETVDDDDGE 75

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
+ G + + R YD + Y+ + Q G+G+ T LL+ + + +
Sbjct: 76 RRIIGFSALSVFYDRAGYDGVTDLAYIDPQWQGRGVGTYYTLTKLLEECRKRNMKACGI 135

Query: 126 IGLPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFWRQDF 168
I N S+ L + G+T G + AA G D+ +W D
Sbjct: 136 IFADNAGSIALMKRFGFTQFGLMPTAATDSTGTMRDMSYWYLDL 179

>ref|ZP_02212214.1| hypothetical protein CLOBAR_01831 [Clostridium bartlettii DSM
16795]
gb|EDQ96064.1| hypothetical protein CLOBAR_01831 [Clostridium bartlettii DSM
16795]
Length = 162

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 32/131 (24%), Positives = 57/131 (43%), Gaps = 5/131 (3%)

Query: 21 VCDIVNHYIETSTVNF--RTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWK 78
V +I N+YIE + F P E I LE ++D YP +++ + G Y +K
Sbjct: 16 VMEIYNYIEHTFAAFPQTKLPSNFYEKI--LEDIKD-YPAYAVKLDDKIVGFCYLCYSYK 72

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHE 138
T E Y+S+ + G+G L G K+++A++ N S + +
Sbjct: 73 NYKTLRETAEVICYLSYDAKGKIGYNCLKKLEDDAREMGLKNLIALSTKNKISTKIFY 132

Query: 139 ALGYTARGTLR 149
G+ + G ++
Sbjct: 133 KYGFKSCGIIQ 143

>ref|ZP_05265944.2| acetyltransferase [Listeria monocytogenes HPB2262]
 gb|EFF96176.1| acetyltransferase [Listeria monocytogenes HPB2262]
 Length = 157

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 33/132 (25%), Positives = 60/132 (45%), Gaps = 3/132 (2%)

Query: 38 TEPQTPQEWIDDLERLQDRY---PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVS 94
 T T QE +E ++Y LV + G V G A P+ + +AY E ++Y++
 Sbjct: 19 TGNATFQEKTLSIEAFDEKYLNTCRLVLMNGKVIGWAALLPFSSMHAYRGVAELSIYIA 78

Query: 95 HRHQRLGLGSTLYTHLLKSMEAQGFKSVAIVIGLPNDPSVRLHEALGYTARGTLRAAGYK 154
 + G+G L ++++ E GF ++ ++I N S+ LH G+ G
 Sbjct: 79 KSARGKGVGKALMHEIIQTSEQNGFWTLQSLIFPENKASIALHHTYGFQTLCVHEKLGEM 138

Query: 155 HGGWHDVGFWQR 166
 +G + +V +R
 Sbjct: 139 NGVFRNVALER 150

>ref|YP_177262.1| phosphinothricin N-acetyltransferase [Bacillus clausii KSM-K16]
 dbj|BAD66301.1| phosphinothricin N-acetyltransferase [Bacillus clausii KSM-K16]
 Length = 165

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 45/159 (28%), Positives = 62/159 (38%), Gaps = 8/159 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP--WLVAEVEGV 67
 +R D V I I T F T+ T ++W +P VA+
 Sbjct: 5 VRQMIKDDWEQVKFIYEAGIATGNATFETQAPTYEKW-----RTSAHPECCFVADDGTS 58

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAIVIG 127
 V G R Y E +VYV + G+G L +KS E QGF ++ A I
 Sbjct: 59 VLGWCKVTSVSDRCVYAGVGEVSVYVHPEARGKGIGDVLLGESIKSSEQQGFWTQAGIF 118

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWQR 166
 N PS+ LH+ G+ G G +G W DV +R
 Sbjct: 119 PENAPSLHLHKKHGFRELGRRRERIGKMNGIWRDVLLEL 157

>ref|ZP_07544750.1| Predicted sortase and acyltransferase [Actinobacillus
 pleuropneumoniae serovar 13 str. N273]
 gb|EFN03214.1| Predicted sortase and acyltransferase [Actinobacillus
 pleuropneumoniae serovar 13 str. N273]
 Length = 172

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
 Identities = 36/142 (25%), Positives = 59/142 (41%), Gaps = 4/142 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEV 64
 ++IR +T AD + +I N I T + E TP + W D ++YP E
 Sbjct: 1 MQIRKSTEADFETILNIYNQAIPHTQITADLELATPINRRRAWFD-FHLTSEQYPIWTVED 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 E +AG P+ R A+ T E ++Y+ + G GS + + M +++A
 Sbjct: 60 ENGIAGWFSFSPFYERPAFVHTSEISIYLDSSAKGKGYSKIIIEFMQAEMLKHNHTLMA 119

Query: 125 VIGLPNDPSVRLHEALGYTARG 146
 + N S L G+ G
 Sbjct: 120 YVFELNQVSQNLMRKHGFEQWG 141

>ref|ZP_05978211.1| putative phosphinothricin N-acetyltransferase [Neisseria mucosa

ATCC 25996]
gb|EFC87822.1| putative phosphinothricin N-acetyltransferase [Neisseria mucosa
ATCC 25996]
Length = 165

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 37/144 (25%), Positives = 64/144 (44%), Gaps = 5/144 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEG 66
I A D+ + I N IE P +T + W + R +++ G
Sbjct: 5 ITLAKTEDLPDIVEIYNSTIEARQSTADLSPVSIETRKPFWE--AHSGKRPLYVLKNHSG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+ + R+AY + E ++YV H + +G+G L ++L+ + G K+V+AVI
Sbjct: 63 ELLAWGSFSDYYPRHAYHISAEISIVVRHNMGRGVGVGKILLRNMLERAPSLGIKNVLAVI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRA 150
N PS+ L + G+ G L A
Sbjct: 123 FGHNHPSLHLFHSFGFQEWGRLPA 146

>ref|ZP_04673483.1| phosphinothricin N-acetyltransferase [Lactobacillus paracasei
subsp. paracasei 8700:2]
gb|EEQ65736.1| phosphinothricin N-acetyltransferase [Lactobacillus paracasei
subsp. paracasei 8700:2]
Length = 164

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 40/162 (24%), Positives = 66/162 (40%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E PATA+D+ + I N I T +PQT E + +P + +V+
Sbjct: 2 IEFTPATASDLPKIVAIYNETIPTHQATADLQPQTVAEKQAWFAAHNNHFPAAWMIQVDHK 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G + R+AYD T E ++Y+ + +GS + + +V+A I
Sbjct: 62 IVGWLTLAYSARDSAYDQTAEISLYLDVAARGHHVGSAAALAFVDREAPKHDLTTVLARIF 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFE 169
N S L GY G L A G D+ + + F+
Sbjct: 122 GHNQASRNLFTKFGYDHWGHLPAIAILPEGEADLEVYKGKHF 163

>ref|ZP_02883607.1| GCN5-related N-acetyltransferase [Burkholderia graminis C4D1M]
gb|EDT11039.1| GCN5-related N-acetyltransferase [Burkholderia graminis C4D1M]
Length = 201

Score = 47.4 bits (111), Expect = 8e-04, Method: Compositional matrix adjust.
Identities = 43/146 (29%), Positives = 63/146 (43%), Gaps = 6/146 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVEG 62
+ R AT D+ A+ I N + + V EP + + W Q R W+V A
Sbjct: 30 LSYRDATLDDLPAIVAIYNSTVASRQVTADLEPVSVESRLAWFH-AHGPQKRPLWVVD 88

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
E G + G + R AY T E ++Y+ R + GLG L L + A G +V
Sbjct: 89 EAPGRLLGWLSFSDFYGRPAYQRTAEVSIYLDERARGKGLGKQLLAASLAAAPALGIDTV 148

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTL 148
+ I ND S+RL G+ G+L
Sbjct: 149 LGFIFGHNDASLRLFRGFGFDTWGSL 174


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>ref|YP_807782.1| sortase related acyltransferase [Lactobacillus casei ATCC 334]
ref|YP_001988695.1| Phosphinothricin N-acetyltransferase [Lactobacillus casei BL23]
ref|YP_003789626.1| sortase-like acyltransferase [Lactobacillus casei str. Zhang]
gb|ABJ71340.1| Sortase related acyltransferase [Lactobacillus casei ATCC 334]
emb|CAQ67837.1| Phosphinothricin N-acetyltransferase [Lactobacillus casei BL23]
gb|ADK19776.1| Sortase related acyltransferase [Lactobacillus casei str. Zhang]
Length = 166
```

Score = 47.4 bits (111), Expect = 9e-04, Method: Compositional matrix adjust.
Identities = 40/162 (24%), Positives = 66/162 (40%)

```
Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+E PATA+D+ + I N I T +PQT E + +P + +V+
Sbjct: 2 IEFTPATASDLPKIVAIYNETIPTHQATADLQPTVAEKQAWFAAHNNHFPAAWMIQVDHK 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G + R+AYD T E ++Y+ + +GS + + +V+A I
Sbjct: 62 IVGWLTLAYSYSRSDYDQTAEISLYLDVAARGHHVGSAAALAFVDREAPKHDLTTVLARIF 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWRDFE 169
N S L GY G L A G D+ + + F+
Sbjct: 122 GHNQASRNLFTKFGYDHWGHLPAIAAILPEGEADLEVYKGKHF 163
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>ref|ZP_03265871.1| GCN5-related N-acetyltransferase [Burkholderia sp. H160]
gb|EEA02562.1| GCN5-related N-acetyltransferase [Burkholderia sp. H160]
Length = 171
```

Score = 47.4 bits (111), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 42/146 (28%), Positives = 64/146 (43%), Gaps = 6/146 (4%)

```
Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEV 64
+ R AT D+ A+ I N + + V EP ++ W Q R W+V +
Sbjct: 3 LSYRDATFDDLPAIVAINSTVPSRQVTADLEPVSVESRHAWFH-AHGPQKRPLWVVEDP 61

Query: 65 E--GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
+ G V G + R AY T E ++Y+ + GLG L L++ G +V
Sbjct: 62 KQAGRVIGWLSFSDFYGRPAYQRTAEVSIYLDSTRGQGLKQLLAAALEAAPGLGIDTV 121

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTL 148
+ + N+PSVRL G+ A GTL
Sbjct: 122 LGFVFGHNEPSVRLFRGFGFDAWGTL 147
```

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>ref|YP_001651515.1| sortase and related acyltransferase [Actinobacillus
pleuropneumoniae serovar 3 str. JL03]
ref|ZP_07336455.1| sortase and related acyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
ref|ZP_07338301.1| sortase and related acyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. 4226]
ref|ZP_07527390.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 1 str. 4074]
ref|ZP_07529514.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. S1536]
ref|ZP_07531677.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 4 str. M62]
ref|ZP_07533920.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
ref|ZP_07536092.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 9 str. CVJ13261]
ref|ZP_07538299.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 10 str. D13039]
ref|ZP_07540445.1| Predicted sortase and acyltransferase [Actinobacillus
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pleuropneumoniae serovar 11 str. 56153]
gb|ABY69071.1| sortase and related acyltransferase [Actinobacillus
pleuropneumoniae serovar 3 str. JL03]
gb|EFL79104.1| sortase and related acyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. 4226]
gb|EFL81027.1| sortase and related acyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
gb|EFM85860.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 1 str. 4074]
gb|EFM88130.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 2 str. S1536]
gb|EFM90339.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 4 str. M62]
gb|EFM92502.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 6 str. Femo]
gb|EFM94751.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 9 str. CVJ13261]
gb|EFM96830.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 10 str. D13039]
gb|EFM98920.1| Predicted sortase and acyltransferase [Actinobacillus
pleuropneumoniae serovar 11 str. 56153]
Length = 172

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 36/142 (25%), Positives = 59/142 (41%), Gaps = 4/142 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWDLLERLQDRYPWLVAEV 64
++IR +T AD + +I N I T + E TP + W D ++YP E
Sbjct: 1 MQIRKSTEDFETILNIYNQAIPHTQITADLELATPINRRRAWFD-FHLTSEQYPIWTVED 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
E +AG P+ R A+ T E ++Y+ + G GS + + M +++A
Sbjct: 60 ENGIAGWFSFPFYERPAFVHTSEISIIYLDGSAKGKGYGSKIIFKMQAEMLKHNHITLMA 119

Query: 125 VIGLPNDPSVRLHEALGYTARG 146
+ N S L G+ G
Sbjct: 120 YVFELNQISQNLMRKHGFEQWG 141

>ref|ZP_07714682.1| phosphinothricin acetyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
gb|EFQ80451.1| phosphinothricin acetyltransferase [Corynebacterium
pseudogenitalium ATCC 33035]
Length = 166

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 46/167 (27%), Positives = 73/167 (43%), Gaps = 7/167 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIET---STVNFRTPEQTPQEWDLLERLQDRYPWLVAE 63
+ IRPA AD A+ I N + V ++ + +EW+ E + P VA
Sbjct: 1 MHIRPAELADAPALTAIYNAGSAAKPAANLVTWQEDVSDREEWLK--EMFKAGSPVFAV 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF-KSV 122
+ V G A + Y TVE +VY++ Q G+GS L L+ + +++
Sbjct: 59 HDDEVIGWAAAYFQFVTPAIYGTVEDSVYIAPSAQKGKGVGSELLDALMDVAADDAYVQTM 118

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDFE 169
+ I N+ S+ LH+ G+T G + K G + QRDQFE
Sbjct: 119 ITYIVDTNEGSIALHKKFGFTETGRMPNIHTKDGVRGLVHLQRDQFE 165

>ref|ZP_03324286.1| hypothetical protein BIFCAT_01074 [Bifidobacterium catenulatum
DSM

16992]
gb|EEB22100.1| hypothetical protein BIFCAT_01074 [Bifidobacterium catenulatum DSM
16992]
Length = 186

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 40/164 (24%), Positives = 66/164 (40%), Gaps = 6/164 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEV----E 65
R AT D+ A+ DI N + + P+T ++ +E D Y V E E
Sbjct: 23 RIATQNDIQAITDIYNAAVIRGGSSADITPRTYEQRKAWVESHHPYAVFVTETADDDGE 82

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
+ G + + R YD + Y+ + Q G+G+ T LL+ + + +
Sbjct: 83 RQIIGFSALSVFYDRAGYDGVTDLAYYIDPQWQGRGVGTYYTLTKLLEECRKRNMKACGI 142

Query: 126 IGLPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFWRQDF 168
I N S+ L + G+T G + AA G D+ +W D
Sbjct: 143 IFADNAGSIALMKWFGFTQFGLMPTAATDSTGTMRDMSYWYLDL 186

>ref|YP_796138.1| sortase related acyltransferase [Lactobacillus brevis ATCC 367]
gb|ABJ65107.1| Sortase related acyltransferase [Lactobacillus brevis ATCC 367]
Length = 165

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 45/153 (29%), Positives = 57/153 (37%), Gaps = 5/153 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAE 63
P R TAAD A V I N I T P T Q W + D +P V E
Sbjct: 2 PATFRLITAADAEQVVAIYNQAIATKGSTADLTPLTVAQRQPWFQEFSP--DHFPLWVIE 59

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMV 123
+ G P+ R AY T E +Y+S Q LG+ + A +++
Sbjct: 60 TTAGIVGYVGLPEYSDRQAYAQTAETIAIYLSAAAQGHGTQAVNWVEAQAPALHVTII 119

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHG 156
+ I N S L E LGY G L A G
Sbjct: 120 SRIFGHNQASRHLFEKLG YDHWGHLPAIADMQG 152

>ref|YP_004228168.1| phosphinothricin acetyltransferase [Burkholderia sp. CCGE1001]
gb|ADX55108.1| Phosphinothricin acetyltransferase [Burkholderia sp. CCGE1001]
Length = 174

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 40/143 (27%), Positives = 66/143 (46%), Gaps = 6/143 (4%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL--QDRYPWLVAEVEG-- 66
R AT D+ A+ I N I + V EP + + + Q R W+V + E
Sbjct: 6 RDATLDDLPAIVAIYNSTIASRQVTADLEPVSVESRVAVFHAHGPQKRPLWVVEDAEERG 65

Query: 67 -VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVMVAV 125
V+A ++++ + R AY T E ++Y+ R + GLG + L + A G +V+
Sbjct: 66 RVIAWLSFS-DFYGRPAYQRTAEVSIYLLDERARGKGLGKQMLAASLAAAPALGIDTVLGF 124

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148
I N+ S+RL G+ G+L
Sbjct: 125 IFGHNEASLRLFRGFGFDTWGSL 147

>ref|ZP_05704697.1| GNAT family toxin-antitoxin system, toxin component
[Cardiobacterium hominis ATCC 15826]

gb|EEV89130.1| GNAT family toxin-antitoxin system, toxin component
[Cardiobacterium hominis ATCC 15826]
Length = 167

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 39/145 (26%), Positives = 65/145 (44%), Gaps = 5/145 (3%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAE 63
P +R A A D+ A+ I N I + P + Q W + +R ++V +
Sbjct: 2 PETRLRLARADDLPAIVAIYNSTIASREATADLAPVSVAARQAWFAAHQ--GNRPLYVVED 59

Query: 64 VEGVVGAIYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
+G +A + R AY + E ++YV+ + GLG L +L+ A ++V+
Sbjct: 60 ADGAIAAWGSFSDYYPREAYRISAEISIVAPDQGRGLGKRLQLDMLRRAPALDIENVL 119

Query: 124 AVIGLPNDPSVRLHEALGYTARGTL 148
AVI N S+ L +A G+ G L
Sbjct: 120 AVIFAHNAASLALFQAQGFAEWGRL 144

>ref|YP_002549278.1| acetyltransferase [Agrobacterium vitis S4]
gb|ACM36272.1| acetyltransferase [Agrobacterium vitis S4]
Length = 159

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 28/83 (33%), Positives = 44/83 (53%), Gaps = 7/83 (8%)

Query: 60 LVAEEVGVVAGIYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
+VAEEVG +AG W AR A + V S +++S HQR G+G +L H ++M +G
Sbjct: 57 IVAEEVGTIAG-----WGAREA-ERDVISDIWISPDHQRRGIGRSLVLHFCETMRCEGV 109

Query: 120 KSVVAVIGLPNDPSVRLHEALGY 142
K N + L+++ G+
Sbjct: 110 KQARISTHQNNFAAQALYKSCGF 132

>ref|ZP_01135619.1| putative acetyltransferase [Pseudoalteromonas tunicata D2]
gb|EAR26732.1| putative acetyltransferase [Pseudoalteromonas tunicata D2]
Length = 184

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 40/142 (28%), Positives = 57/142 (40%), Gaps = 6/142 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEEVG 66
IR A A D+AAV DI N I + V P + QE W D L+ P V +
Sbjct: 21 IRKAIATDLAAVVDIYNETIASRIVTADLTPVSYQERQAWFDGHTDLR---PLFVYQSGS 77

Query: 67 VVAGIYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
+ G + R AY TVE ++YV+ + G+ L + + +A I
Sbjct: 78 EILGWVSFKTFYGRPAYQGTVEISIVVASHARGQGIKQLLDYAEHYAQTIAVNVFLAFI 137

Query: 127 GLPNDPSVRLHEALGYTARGTL 148
N PS+ G+ G L
Sbjct: 138 FSHNIPSITFFSRYGFANWGQL 159

>ref|ZP_08067122.1| phosphinothricin N-acetyltransferase [Actinobacillus ureae ATCC 25976]
gb|EFX92039.1| phosphinothricin N-acetyltransferase [Actinobacillus ureae ATCC 25976]
Length = 172

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.

Identities = 36/142 (25%), Positives = 59/142 (41%), Gaps = 4/142 (2%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAEV 64
          ++IR +T AD  + +I N I T +   E TP  + W D      ++YP   E
Sbjct: 1   MQIRKSTEADFETILNIYNQAIPTHQITADLELATPINRRRAWFD-FHLTSEQYPIWTVED 59

Query: 65   EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
          E  +AG      P+ R A+ T E ++Y+      + G GS +   + M      +++A
Sbjct: 60   ENGIAGWFSFSPFYERPAFVHTSEIISIYLDSSAKGKGYSKIIIEFMQAEMLKHNITLMA 119

Query: 125  VIGLPNDPSVRLHEALGYTARG 146
          +   N S L      G+   G
Sbjct: 120  YVFELNQVSQNLMRKHGFEQWG 141
```

>ref|ZP_03073379.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri 100-23]
gb|EDX43325.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri 100-23]
Length = 165

Score = 47.0 bits (110), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 39/144 (27%), Positives = 63/144 (43%), Gaps = 8/144 (5%)

```
Query: 9   EIRPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVE 65
          +IR AT D+ A+ DI N I   VN + P      +EW      +   +P VA ++
Sbjct: 4   QIRLATINDLPAIVDIFNQAIPLQ-VNDESAPIEVADRREW---FMQFDSTHPIWVATID 59

Query: 66   GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVA 124
          V      +   AYD + +   +Y+   ++R LG L T+ K +E      ++V+A
Sbjct: 60   DQVIAWCALEYFYPHPAYDHSQAIAIYIHEDYRRQHLGHDLLTYAQKQIEDHLDIRTVIA 119

Query: 125  VIGLPNDPSVRLHEALGYTARGTL 148
          + + N S L + GY   G L
Sbjct: 120  YVYIENQASYHLFTSCGYKEWGKL 143
```

>ref|XP_002563497.1| Pc20g10030 [Penicillium chrysogenum Wisconsin 54-1255]
emb|CAP86332.1| Pc20g10030 [Penicillium chrysogenum Wisconsin 54-1255]
Length = 227

Score = 46.6 bits (109), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 49/199 (24%), Positives = 78/199 (39%), Gaps = 44/199 (22%)

```
Query: 11   RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVE---- 65
          RPAT AD+ V DI + YI S   F T P      + D L L R P+ V +
Sbjct: 5   RPATLADIPQVRDINHWHYIVNSCSTFATTPPPISHYEDILRDLMRRNLFPYVIVSDTRKT 64

Query: 66   ----GVVAGIAYAGPWKAR-NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ--- 117
          ++ G AY P++      +Y TVE +++++ + Q+ G G+ +   LL+ ++
Sbjct: 65   PDGADLILGYAYLSPFRGHLLSYAPTVELSIFMRDQQQFGYGTIILRKLLRLVQEGEVE 124

Query: 118  -----GFKSVVAVIG-----LPNDPSV-----RLHEALGYTARG 146
          GF S + V+      +P D      + +   G+ +G
Sbjct: 125  HRCEERVGDIPRIGFGSSMGVMKTSLVQNIIAIIPYDTEAPTDGERLRKWMKMGFIEKG 184

Query: 147  TLRAAGYKHGGWHDVGFQW 165
          L   G K G W D + Q
Sbjct: 185  QLENVGRKMGGHWIDTVYLQ 203
```

>gb|ABX10632.1| phosphinothricin N-acetyltransferase [uncultured planctomycete 3FN]
Length = 243

Score = 46.6 bits (109), Expect = 0.001, Method: Compositional matrix adjust.

Identities = 36/138 (26%), Positives = 64/138 (46%), Gaps = 5/138 (3%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV 64
          + +R AT D+ + +I N I          TEP          EW + + R W++ +
Sbjct: 76  MTLRDATREDLPQIVEIYNASIPGRLATADTEPINVDDRSEWFQRHDPAR-RPLWVLKQE 134

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
          + +VA +          + R AY T E VY++ Q GLG+ L L+ + G ++++
Sbjct: 135 DRIVAWVDLRD-FYGRPAYHATAEIAVYIADDFQGRGLGTLLKRELMDACPRLGVTTL 193

Query: 125 VIGLPNDPSVRLHEALGY 142
          + N S+R++E LG+
Sbjct: 194 FVFGQNAASIRVNEKLG 211
```

```
>ref|ZP_07801142.1| acetyltransferase, GNAT family [Faecalibacterium cf. prausnitzii
KLE1255]
gb|EFQ05514.1| acetyltransferase, GNAT family [Faecalibacterium cf. prausnitzii
KLE1255]
Length = 172
```

Score = 46.6 bits (109), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 46/155 (29%), Positives = 62/155 (40%), Gaps = 5/155 (3%)

```
Query: 8   VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
          +EIRP D +AV I I T F+T W D + R LV +GV
Sbjct: 4   IEIRPMEPEDWSAVSRIYLEGIATEHATFQTTCPPYSAW-DASHAKECR---LVLLADGV 59

Query: 68  VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127
          +AG R Y E ++YV + + GLG L T L E G+ ++ + +
Sbjct: 60  IAGWTALRRVDPRWCYRGVAEVSIIYVGEQFRGHGLGYHLLTELCHQAEKAGYWTLQSTVL 119

Query: 128 LPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDV 161
          N S LH G+ G R A HG W D
Sbjct: 120 QDNAASRALHTKCGFRLVGRRERIARDCHGRWLD 154
```

```
>ref|ZP_05232348.2| acetyltransferase [Listeria monocytogenes FSL N3-165]
gb|EEW13365.1| acetyltransferase [Listeria monocytogenes FSL N3-165]
Length = 157
```

Score = 46.6 bits (109), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 34/132 (25%), Positives = 59/132 (44%), Gaps = 3/132 (2%)

```
Query: 38  TEPQTPQEWIDDLERLQDRY---PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVS 94
          T T QE LE ++Y LV + G V G A P+ + +AY E ++Y++
Sbjct: 19  TGNATFQEKTLSEAFDEKYLNTCRLVLMNGEVIGWAALLPFSSMHAYRGVAELSIYIA 78

Query: 95  HRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYK 154
          + G+G L ++++ E F ++ ++I N S+ LH G+ G
Sbjct: 79  KSARGKGVGKALMHEIIQTSEQNDFWTLQSLIFPENKASIALHHTYGFQTLCIHEKLGEM 138

Query: 155 HGGWHDVGFQWQR 166
          +G + DV +R
Sbjct: 139 NGVFRDVALER 150
```

```
>ref|ZP_01724099.1| phosphinothricin N-acetyltransferase [Bacillus sp. B14905]
gb|EAZ85474.1| phosphinothricin N-acetyltransferase [Bacillus sp. B14905]
Length = 114
```

Score = 46.6 bits (109), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 34/113 (30%), Positives = 53/113 (46%), Gaps = 4/113 (3%)

Query: 36 FRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSH 95
 F+TE + + W D R+ VAE V G P R Y E +VY+S
 Sbjct: 4 FQTEVPSEVRW-DGGHHTALRF--VAEEHNRVVGWIVISPVSTRAVYSGVGEVSVYISI 59

Query: 96 RHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTL 148
 ++ G+ S L+ L++ E +GF +V + I N S+ LH+ +G+ G L
 Sbjct: 60 DNKGKGIASKLFEILIEESEKEGFWTVQSSIFAINTSSIHLLHKKMGFKIVGKL 112

>ref|YP_001968334.1| predicted sortase--related acyltransferase [Actinobacillus
 pleuropneumoniae serovar 7 str. AP76]
 gb|ACE61192.1| predicted sortase--related acyltransferase [Actinobacillus
 pleuropneumoniae serovar 7 str. AP76]
 Length = 137

Score = 46.6 bits (109), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 35/138 (25%), Positives = 58/138 (42%), Gaps = 4/138 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEV 64
 ++IR +T AD + +I N I T + E TP + W D ++YP E
 Sbjct: 1 MQIRKSTEDFETILNIYNQAIPHTQITADLELATPINRAWFD-FHLTSEQYPIWTVED 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 E +AG P+ R A+ T E ++Y+ + G GS + + M +++A
 Sbjct: 60 ENGIAGWFSFSPFYERPAFVHTSEISIIYLDSSAKGKGYSKIIIEFMQAEMLKHNIHTLMA 119

Query: 125 VIGLPNDPSVRLHEALGY 142
 + N S L G+
 Sbjct: 120 YVFELNQVSQNLMRKHGF 137

>ref|YP_002834382.1| putative N-acetyltransferase [Corynebacterium aurimucosum ATCC
 700975]
 ref|ZP_06042261.1| putative N-acetyltransferase [Corynebacterium aurimucosum ATCC
 700975]
 gb|ACP32444.1| putative N-acetyltransferase [Corynebacterium aurimucosum ATCC
 700975]
 Length = 167

Score = 46.6 bits (109), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 39/165 (23%), Positives = 75/165 (45%), Gaps = 7/165 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIE---TSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE 65
 +RPA AD A+ I N T+ V ++ + ++W+ +E ++ +P VA +
 Sbjct: 3 VRPAELADAPAIYNAASAAPATNLVTWQESVEDREKWLQME--EEGFPVYVAVDD 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF-KSVVA 124
 + G A + Y T E ++Y++ + G+GS L L+ + + ++++
 Sbjct: 61 DEIVGWATYFQFVTPAIYYGTAEDSIYIAESARGKGVGSELMDTLMDHAKENDYVETMIT 120

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDFE 169
 I N+ S+ LH+ G+ G + K G + QRDF+
 Sbjct: 121 YIVDTNESSIALHQKFGFVETGRMPNIHTKDGVRGLVHLQRDFD 165

>ref|YP_001272503.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri DSM
 20016]
 ref|YP_001842806.1| putative phosphinothricin N-acetyltransferase [Lactobacillus
 reuteri JCM 1112]
 ref|ZP_03848389.1| acetyltransferase [Lactobacillus reuteri MM2-3]
 ref|ZP_08163011.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri MM4-
 1A]

gb|ABQ84166.1| GCN5-related N-acetyltransferase [Lactobacillus reuteri DSM 20016]
 dbj|BAG26326.1| putative phosphinothricin N-acetyltransferase [Lactobacillus
 reuteri JCM 1112]
 gb|EEI08939.1| acetyltransferase [Lactobacillus reuteri MM2-3]
 gb|EGC14796.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri MM4-1A]
 Length = 165

Score = 46.2 bits (108), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 40/144 (27%), Positives = 63/144 (43%), Gaps = 8/144 (5%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEP---QTPQEWIDDLERLQDRYPWLVAEVE 65
 +IR AT D+ A+ DI N I VN + P +EW + +P VA ++
 Sbjct: 4 QIRLATINDLPAIVDIFNQAIPLO-VNDESAPIEVADRREW---FMQFDSTHPIWVATMD 59

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVA 124
 V + AYD + + +Y+ ++R LG L T+ K +E ++V+A
 Sbjct: 60 DQVIAWCALEYFYPPAYDHSQAIAIYIHEDYRRQHLGRDLLTYAQKRIEDHLDIRTVIA 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
 I + N S L + GY G L
 Sbjct: 120 YIYIENQASYHLFTSCGYKEWGKL 143

>ref|ZP_05366550.1| acetyltransferase, gnat family [Corynebacterium
 tuberculoostearicum
 SK141]
 gb|EET76845.1| acetyltransferase, gnat family [Corynebacterium tuberculoostearicum
 SK141]
 Length = 166

Score = 46.2 bits (108), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 46/167 (27%), Positives = 73/167 (43%), Gaps = 7/167 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIET---STVNFRTPEPQTPQEWIDDLERLQDRYPWLVAE 63
 + IRPA AD A+ I N + V ++ + +EW+ E + P VA
 Sbjct: 1 MHIRPAELADAPALTAIYNAGSAAKPAANLVTWQEDVSDREEWLK--EMFKAGSPVFAV 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF-KSV 122
 + V G A + Y TVE +VY++ Q G+GS L L+ + +++
 Sbjct: 59 HDDEVIGWAAYFQFVTPAIYYGTVEDSVYIAPSAQKGKGVGSELLDALMDVAADDTYVQTM 118

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDFE 169
 + I N+ S+ LH+ G+T G + K G + QRDQFE
 Sbjct: 119 ITYIVDTNEGSIALHKKFGFTETGRMPNIHTKDGVRLLGLVHLQRDQFE 165

>ref|ZP_07542630.1| Predicted sortase and acyltransferase [Actinobacillus
 pleuropneumoniae serovar 12 str. 1096]
 gb|EFN01153.1| Predicted sortase and acyltransferase [Actinobacillus
 pleuropneumoniae serovar 12 str. 1096]
 Length = 172

Score = 46.2 bits (108), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 36/142 (25%), Positives = 59/142 (41%), Gaps = 4/142 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTP---QEWIDDLERLQDRYPWLVAEV 64
 ++IR +T AD + +I N I T + E TP + W D ++YP E
 Sbjct: 1 MQIRKSTEADFEITLNIYNQAIPHTQITADLELATPINRRRAWFDS-HLTSEQYPIWTVED 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF-KSVVA 124
 E +AG P+ R A+ T E ++Y+ + G GS + + M +++A
 Sbjct: 60 ENGIAGWFSFSPFYERPAFVHTSEISIYLDGSAKKGYSKIIKFMQAEMLKHNIHTLMA 119

Query: 125 VIGLPNDPSVRLHEALGYTARG 146
+ N S L G+ G
Sbjct: 120 YVFELNQISQNLMRKHGFEQWG 141

>ref|YP_003321282.1| GCN5-like N-acetyltransferase [Sphaerobacter thermophilus DSM 20745]
gb|ACZ40460.1| GCN5-related N-acetyltransferase [Sphaerobacter thermophilus DSM 20745]
Length = 182

Score = 46.2 bits (108), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 49/165 (29%), Positives = 70/165 (42%), Gaps = 4/165 (2%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA-- 62
R V +RPA D AA+ +I N I F TE +T +E L +P LVA
Sbjct: 6 RAAVIVRPAELRDAAAIAEYINQGI RGRMATFETEERTAEERARWLAHDKHHPVLVAVD 65

Query: 63 -EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
E + V AG A +++R Y E +VYV ++ G+G+ L L + E G
Sbjct: 66 PETDQV-AGWISADHYRSRWCYRGVAEFSVYVHEDYRGRGVGAALMEAFLPACEQAGLWK 124

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
+++ I N S L G+ G G W DV +R
Sbjct: 125 LLSRIFPENKASRALCARFGFREVGIIYEKHAQLDGVWKDVVIVER 169

>ref|ZP_07296419.1| GNAT family acetyltransferase [Streptomyces hygroscopicus ATCC 53653]
gb|EFL24788.1| GNAT family acetyltransferase [Streptomyces hygroscopicus ATCC 53653]
Length = 169

Score = 46.2 bits (108), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 34/102 (33%), Positives = 46/102 (45%)

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
+G V G A R AY VE +VYV + G+G L L+ S EA G ++ +
Sbjct: 62 DGRVLGWVAATKVS DRCAYAGVVEHSVYVHPAARNRGVGLALLNALIASTEAGIWTIQS 121

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFVQR 166
I N S+ LH+ G+ GT G H W DV +R
Sbjct: 122 GIFPENATSLGLHQ RAGFRVIGTRERIGRHHDVWRDVVLIER 163

>emb|CBL03028.1| Sortase and related acyltransferases [Faecalibacterium prausnitzii SL3/3]
Length = 172

Score = 45.8 bits (107), Expect = 0.002, Method: Compositional matrix adjust.
Identities = 47/158 (29%), Positives = 63/158 (39%), Gaps = 5/158 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IRP T D AV I I T F+TE W D + R LV GV+A
Sbjct: 6 IRPMTPEDWGA VSRIYVEGIATEYATFQTECPPYTAW-DASHTKECR---LVILSGGVLA 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIGLP 129
G R Y E ++YV ++ GLG L + L + E G+ ++ + +
Sbjct: 62 GWCALHRVDPRWCYRGVAEVSIIYVGEQFRGHGLGFQLLSALCAA AEKAGYWT LQSTVLQD 121

Query: 130 NDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFVQR 166
N S LH G+ G R A HG W D +R
Sbjct: 122 NTASRALHAKCGFRLVGRRERIARDCHGHWLD TYLMER 159

>ref|ZP_06500010.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae

FF5]
 Length = 104

Score = 45.8 bits (107), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 31/89 (34%), Positives = 43/89 (48%), Gaps = 7/89 (7%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER----LQDRYPWLVAEV 64
 ++R A DM AV I ++ +F EP E L+R L P+LVAE
 Sbjct: 19 DLRDARDDMPAVQAIYADHVLHGISSFELEPPDLAEL---LQRRRMVLAKGLPYLVAER 75

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYV 93
 G + G Y P++ R Y +TVE +VYV
 Sbjct: 76 GGEIVGYGYVTPYRPRPGYRFTVEDSVYV 104

>ref|ZP_03463681.1| hypothetical protein BACPEC_02780 [Bacteroides pectinophilus ATCC 43243]

gb|EEC56273.1| hypothetical protein BACPEC_02780 [Bacteroides pectinophilus ATCC 43243]
 Length = 117

Score = 45.8 bits (107), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 24/75 (32%), Positives = 38/75 (50%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63
 E+ + IR AT D + I Y+E + V F + E+ +E +YP+LVA
 Sbjct: 2 EKLDISIRTATPDDAEGLLAIYAQYVENTAVTFEYSVPSEAEFRRIENTLKKYPYLVAV 61

Query: 64 VEGVVAGIAYAGPWK 78
 +G + G AYAG ++
 Sbjct: 62 SQGEIVGYAYAGEFR 76

>ref|YP_581302.1| GCN5-related N-acetyltransferase [Psychrobacter cryohalolentis K5]
 gb|ABE75818.1| GCN5-related N-acetyltransferase [Psychrobacter cryohalolentis K5]

Length = 211

Score = 45.8 bits (107), Expect = 0.002, Method: Compositional matrix adjust.
 Identities = 40/154 (25%), Positives = 70/154 (45%), Gaps = 16/154 (10%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEVE- 65
 ++ ATA D++ V I N I EP T +E W + R ++V ++
 Sbjct: 32 VQYATANDLSEVLAIYNQSIAGKQATANLEPVTYEERAAWFVEHIESATRPIYVVRMIDI 91

Query: 66 -----GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 +VA +++ + AR AY + E ++Y+ + + GLGS L +L+
 Sbjct: 92 AVEDDMHKKHPSIVAWGSFSDLY-ARPAYHISSEISYIHNNYHSRGLGSLLLRWMLQQA 150

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTL 148
 + G ++V A+I N PS+ L LG+ G +
 Sbjct: 151 PSLGIRNVAALIFAHNQPSLGLFRKLGFEQWGLM 184

>ref|YP_001125715.1| phosphinothricin N-acetyltransferase [Geobacillus thermodenitrificans NG80-2]

gb|ABO66970.1| Phosphinothricin N-acetyltransferase [Geobacillus thermodenitrificans NG80-2]
 Length = 93

Score = 45.8 bits (107), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 27/84 (32%), Positives = 43/84 (51%)

Query: 83 YDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGY 142
Y E +VYV + G+G L ++K E +GF ++ A I N PS+RLH+++G+
Sbjct: 2 YKGVGEVSVYVRDVSRGKGVGKQLLQAIKESEEKGFWTLTAGIFPENIPSLRLHQSVGF 61

Query: 143 TARGTLRAAGYKHGGWHDVGFWR 166
G + G + W DV +R
Sbjct: 62 RVVGIRQRIKLNVRVWRDVVILER 85

>ref|YP_003783135.1| hypothetical protein cpfrc_00734 [Corynebacterium
pseudotuberculosis FRC41]
gb|ADK28528.1| hypothetical protein cpfrc_00734 [Corynebacterium
pseudotuberculosis FRC41]
gb|ADL10216.1| Putative phosphinothricin N-acetyltransferase [Corynebacterium
pseudotuberculosis C231]
gb|ADL20626.1| Putative phosphinothricin N-acetyltransferase [Corynebacterium
pseudotuberculosis 1002]
gb|ADO26008.1| Putative phosphinothricin N-acetyltransferase [Corynebacterium
pseudotuberculosis I19]
Length = 186

Score = 45.8 bits (107), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 32/116 (27%), Positives = 51/116 (43%), Gaps = 7/116 (6%)

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
E + + G A P +R+ + VE ++Y+ + G+ L L+ + G S+
Sbjct: 60 ENDSKILGWVSAAPISSRSVFRGVVEDSIYIHPDARGRGVAGALLDKLIDVCQGLGMWSI 119

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTL-----RAAGYKHGGWHDVGFWRDFELPAP 173
+ I N+ S RLHE+ G+ GTL G G W D W++ LP P
Sbjct: 120 HSWIFPENEGSARLHESRGFEKVGTLGHLAKMTYGEMAGQWRDIDIWEK--LLPKP 173

>ref|ZP_03973757.1| acetyltransferase [Lactobacillus reuteri CF48-3A]
ref|ZP_07126236.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri
SD2112]
gb|EEI66347.1| acetyltransferase [Lactobacillus reuteri CF48-3A]
gb|EFK87538.1| phosphinothricin N-acetyltransferase [Lactobacillus reuteri SD2112]
Length = 165

Score = 45.8 bits (107), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 39/144 (27%), Positives = 64/144 (44%), Gaps = 8/144 (5%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVE 65
+IR AT D+ A+ DI N I VN + P +EW + + +P VA ++
Sbjct: 4 QIRLATINDLPAIVDIFNQAIPQLQ-VNDESAPIEVADRREW---FMQFDNTHPIWVATMD 59

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVA 124
V + AYD + + +Y+ +++ LG L T+ K +E ++V+A
Sbjct: 60 DQVIAWCALEYFYPPHAYDHSQAIAIYIHEDYRQQHLGRDLLTYAQKQIEDHLDIRTVIA 119

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
I + N S L + GY G L
Sbjct: 120 YIYIENQASYHLFTSCGYKEWGKL 143

>ref|ZP_04609105.1| GCN5 N-acetyltransferase [Micromonospora sp. ATCC 39149]
gb|EEP75035.1| GCN5 N-acetyltransferase [Micromonospora sp. ATCC 39149]
Length = 165

Score = 45.8 bits (107), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 43/157 (27%), Positives = 62/157 (39%), Gaps = 3/157 (1%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
IRP AAD V I ++ +F T T E+ D R + + + G V
Sbjct: 6 IRPMVAADADRVLAIYRAGLDGGDASFETVAPTWAEF--DATR-SAAHRLVAVDDTGAVL 62

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
G P R Y VE +VYV + G+ L L+ + EA ++ + +
Sbjct: 63 GWVAVSPTSTRPVYAGVVEHSVYVDPAAARGRGVARLLLLDALIAATEAARIWTIQSGVFPE 122

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
N S+ LH G+ G G HG W DV +R
Sbjct: 123 NVASLALHARAGFRVVGVRERVGRHHGRWRDVLLER 159

>ref|YP_518100.1| hypothetical protein DSY1867 [Desulfitobacterium hafniense Y51]
ref|YP_002459481.1| GCN5-related N-acetyltransferase [Desulfitobacterium hafniense
DCB-2]
dbj|BAE83656.1| hypothetical protein [Desulfitobacterium hafniense Y51]
gb|ACL21045.1| GCN5-related N-acetyltransferase [Desulfitobacterium hafniense
DCB-2]
Length = 166

Score = 45.8 bits (107), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 40/163 (24%), Positives = 67/163 (41%), Gaps = 7/163 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQT---PQEWIDDLERLQD-RYPWLVAEVE 65
+R A D+ + I N + + F E ++ + W + QD YP V E +
Sbjct: 7 LRQAQVKDLERINAIYNWAVLNTVATFDLEERSLAAAEVWFGNH---QDPYYPVYVVENQ 63

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125
G V G P+ R AY + E ++Y++ +G L L + + G+ +++
Sbjct: 64 GQVTGWGSLSPFHPRAAYKQSGEFSIYIAPEWTQSMGDALLKVLCQEAKKLGHTLLGR 123

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDF 168
I N+ S+ L + G+ G G K G DV Q F
Sbjct: 124 ITSTNEKSISLAKKHGFWEAGKYHEVGTKFGQCLDVMIMQIIF 166

>ref|YP_004095829.1| GCN5-related N-acetyltransferase [Bacillus cellulosilyticus DSM
2522]
gb|ADU31098.1| GCN5-related N-acetyltransferase [Bacillus cellulosilyticus DSM
2522]
Length = 170

Score = 45.8 bits (107), Expect = 0.003, Method: Compositional matrix adjust.
Identities = 28/113 (24%), Positives = 55/113 (48%), Gaps = 12/113 (10%)

Query: 42 TPQEWIDDLERLQ-----DRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVES-T 90
P+E+++ L Q D P VAE G + G A G ++ ++ E
Sbjct: 30 VP EEYLN T LSYEQREVMWKRG IADNNPIFVAEDFGSIVGFATGGKERSAKYEEYEGEVYA 89

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYT 143
+Y+ ++ G+G L+ ++ + G S++ ++ L ++PS++ +EALG T
Sbjct: 90 IYILKEYEGRGIGKRLFNQVNEIVGYGMNSMIVLV-LEDNPSIQFYEALGGT 141

>ref|ZP_08042081.1| GNAT family acetyltransferase [Streptococcus equinus ATCC 9812]
gb|EFW88316.1| GNAT family acetyltransferase [Streptococcus equinus ATCC 9812]
Length = 164

Score = 45.4 bits (106), Expect = 0.003, Method: Compositional matrix adjust.

Identities = 40/158 (25%), Positives = 67/158 (42%), Gaps = 13/158 (8%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQ-EWIDDLERLQDRYPWLVAEVEG 66
      ++IRP  D+  V  +  N      +  NF  T    P      ++  Q+  +LVAE  G
Sbjct: 1  MQIRPMKLEDIEQVVAMEN----KTWDNFNTPASLPAVNKHKIIQAFQNHSHYLVAEENG 56

Query: 67  VVAGI-----AYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
      V+  G+    AY    AR+  +  +    V    Q  G+G  +L      ++  +K  V
Sbjct: 57  VILGVLDYHAYYPFPSARHVVSFIIA---VDKDTQKGIGHSLIQAFFTVAKSDNYKKV 112

Query: 123  VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
      V  +    N  +  R  +E  +G+T  TL+    Y  +G  +  D
Sbjct: 113  VIHVLSSNKNACRFYENIGFTLEATLKNQFYLNQTYVD 150

```

>gb|EEH23616.1| conserved hypothetical protein [Paracoccidioides brasiliensis Pb03]
 gb|EEH50090.1| conserved hypothetical protein [Paracoccidioides brasiliensis Pb18]
 Length = 183

Score = 45.4 bits (106), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 34/124 (27%), Positives = 62/124 (50%), Gaps = 17/124 (13%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWI-DDLERLQDR-YPWLVA--- 62
      ++IRPAT  +D+  +  I  HY+  +  +  F    +  P  ++  D  L    +DR  P+LVA
Sbjct: 3  IKIRPATESDIPQMHSIFTHYVLNTVITFLIN-KPPLSYVADKLYATRDRGLPFLVAVER 61

Query: 63  -----EVEGVVAGIAYAGPWKAR-NAYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
      +  +  V  G    P++  +  AY  TVE  +++V  +Q  G+GS  L  +  L+
Sbjct: 62  PEGANTSNEVDAQEKVCGYTQVSPFRGQLLAYGPTVELSLFVHPDYQSQGIGSKLLSSLI 121

Query: 112  KSME 115
      +  ++
Sbjct: 122  ELLK 125

```

>ref|ZP_07870722.1| gnat family acetyltransferase [Listeria marthii FSL S4-120]
 gb|EFR87765.1| gnat family acetyltransferase [Listeria marthii FSL S4-120]
 Length = 165

Score = 45.4 bits (106), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 34/138 (24%), Positives = 62/138 (44%), Gaps = 4/138 (2%)

```

Query: 29  IETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVE 88
      I+T  F+  +  T  +  W  D  +  L+    LV  +  V  G  A  P+  +  AY  E
Sbjct: 25  IDTGNATFQEKTLTLEAW--DEKYLKS--CRLVVLMDQVIGWAALLPFSSMYAYRGVAE 80

Query: 89  STVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTL 148
      ++Y++  +  G+G  L  ++++  E  GF  ++  ++I  N  S+  LH  G+
Sbjct: 81  LSIYIAKSARGKGVGKALMHEIIQTSEQNGFWTLQSLIFPENKASIALHHTYGFRTL CVH 140

Query: 149  RAAGYKHGGWHDVGFQWR 166
      G  +G  +  DV  +R
Sbjct: 141  EKL GEMNGVFRDVALER 158

```

>ref|ZP_04753113.1| sortase and related acyltransferase [Actinobacillus minor NM305]
 gb|EER47535.1| sortase and related acyltransferase [Actinobacillus minor NM305]
 Length = 170

Score = 45.4 bits (106), Expect = 0.003, Method: Compositional matrix adjust.
 Identities = 36/142 (25%), Positives = 60/142 (42%), Gaps = 4/142 (2%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTP---QEWIDDLERLQDRYPWLVAEV 64

```

```

      + IR +T AD  + I N I T +   E T   + W D   ++YP   E
Sbjct: 1  MRIRKSTEDFETILAIYNQAIPHTQITADLELATTNRRRAWFD-FHLSSEKYPITWVED 59

Query: 65  EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
      E +AG      P+  R A+  T E ++Y+  + +  G GS +  +  M  G  +++A
Sbjct: 60  EEGIAGWFSFSPFYERPAFIHTSEISIIYLDGKAKGKGYGSVIIQFMQAEMLNHGIHTLMA 119

Query: 125  VIGLPNDPSVRLHEALGYTARG 146
      +  N+ S +L   G+   G
Sbjct: 120  YVFEMNEVSQKLMYKHGFQWQ 141

```

```

>ref|NP_104417.1| hypothetical protein mlr3271 [Mesorhizobium loti MAFF303099]
dbj|BAB50203.1| mlr3271 [Mesorhizobium loti MAFF303099]
      Length = 174

```

Score = 45.1 bits (105), Expect = 0.004, Method: Compositional matrix adjust.
Identities = 43/170 (25%), Positives = 74/170 (43%), Gaps = 21/170 (12%)

```

Query: 2  SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFR-TEPQTPQEWIDDLERLQDRY--- 57
      SPE+  +IR      +D  A+C I N          FR      + P E ++++ER  +
Sbjct: 8  SPEKIQPQIRSVRPSDAEALCAIFN-----MPGFRWGTLRMPFERVEEVERRIAKSGQE 61

Query: 58  -PWLVAEVEGVVAG---IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112
      W+VAE++G V G      +  P ++          E  +  +      G+GS +  LL
Sbjct: 62  TTWIVAELDGKVVGHGSLVVQGSPPRRSHIG-----EINIGLDDAFVKGIGSAILGALLD 116

Query: 113  SMEA-QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
      +  +  K V          N+P++RL+ + G+  G      AG+  G +HD+
Sbjct: 117  VADNWRALKRVELTAYADNEPAIRLYTSHGFVEVGRHVKAGFTDQGYHDL 166

```

```

>ref|YP_561875.1| GCN5-related N-acetyltransferase [Shewanella denitrificans OS217]
gb|ABE54152.1| GCN5-related N-acetyltransferase [Shewanella denitrificans OS217]
      Length = 147

```

Score = 45.1 bits (105), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 38/139 (27%), Positives = 67/139 (48%), Gaps = 9/139 (6%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
      ++IR      D+ A+ +  N  +  T N + + +T   +  L   D+  +LVAE++G
Sbjct: 1  MKIRTGQHTDLIALVNF-NQAMALETENLQLDSETLTGLVSTLLAHPDKGCYLVAEIDGE 59

Query: 68  VAGIAYA----GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSV 122
      +AG          W+A+N Y W      +VY+  +++R G+ + LY  +      + Q G  S
Sbjct: 60  IAGSLMVTFEWSDWRAKNYY-WI--QSVYILPQYRRQGIYAKLYQAVKDLAKEQGGAASF 116

Query: 123  VAVIGLPNDPSVRLHEALG 141
      +  N P+ R +EALG
Sbjct: 117  RLYVENENTPAQRTYEALG 135

```

```

>ref|YP_002138059.1| GNAT family acetyltransferase [Geobacter bemidjensis Bem]
gb|ACH38263.1| acetyltransferase, GNAT family [Geobacter bemidjensis Bem]
      Length = 177

```

Score = 45.1 bits (105), Expect = 0.005, Method: Compositional matrix adjust.
Identities = 43/156 (27%), Positives = 64/156 (41%), Gaps = 20/156 (12%)

```

Query: 8  VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID---DLERLQ---DRYPWLW 61
      + IRPA  ++  + DIV          E  +  +W D  D  LQ  D  V
Sbjct: 2  ILIRPAKMTELDITLLDIVQ-----AATRHEAKGIHQWDDIYPDRAILQSDVDSQMHMV 55

```

Query: 62 AEVEGVVAGIAYAGPWKARNAYD--WTVESTVYVSHR-----HQRLGLGSTLYTHLLKS 113
 EV+G + G+ ++ D W V V HR HQR G+ + L K+
 Sbjct: 56 IEVDGRIVGMISINDSQSPEYQDVKWQYSGRVLVIHRLTIDPSHQRQGMATRLMDFAEKT 115

Query: 114 MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLR 149
 E QG++++ N + L+E LGY GT+R
 Sbjct: 116 AEKQGYETIRFDAFTQNP GATALYEHLGYEKAGTVR 151

>ref|YP_004044624.1| acetyltransferase [Halogeometricum borinquense DSM 11551]
 gb|ADQ69268.1| acetyltransferase [Halogeometricum borinquense DSM 11551]
 Length = 170

Score = 44.7 bits (104), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 37/143 (25%), Positives = 63/143 (44%), Gaps = 12/143 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDD-----LERLQDRYPW 59
 + IR AT +D A+ I +T T +T +E + D E +++
 Sbjct: 1 MNIRTATESDTHAILRIAEQSWKTDYPEILTR-ETAEEAVTDWYTSEQIEAELNEEQTMI 59

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 LVAE EG V G A+A W + + +YV H+R +G L ++ QG
 Sbjct: 60 LVAEREGAVVGFAHAA--WNDSEEDGYILR--IYVHPEHRRENIGRELLERTCTNLAEQGI 116

Query: 120 KSVVAVIGLPNDPSVRLHEALGY 142
 + + A++ + NDP ++ G+
 Sbjct: 117 ERINAMVLVENDPGNAFYKRFGF 139

>ref|ZP_03931540.1| possible Phosphinothricin acetyltransferase [Corynebacterium
 accolens ATCC 49725]
 gb|EEI15479.1| possible Phosphinothricin acetyltransferase [Corynebacterium
 accolens ATCC 49725]
 Length = 166

Score = 44.7 bits (104), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 44/166 (26%), Positives = 72/166 (43%), Gaps = 7/166 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVN---FRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 + IRPA AD ++ I N N ++ E ++W+ +L + P LVA
 Sbjct: 1 MHIRPAELADAPSISAIYNAASAAPANNLITWQEEVSEREDWLKELSKAGS--PVLVAV 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSV 122
 + + G A + Y TVE +VY+S Q G+GS L L+ + + +++
 Sbjct: 59 DDDEIIIGWAAYFQFVTPAIYYGTVEDSVYISPAAQKGVGSELLDALMDIAADDSYIETM 118

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQRDF 168
 + I N S+ LH+ G+ G + K G + QRDF
 Sbjct: 119 ITYIVDTNAGSIALHKKFGFIETGRMPNIHTKDGVRGLVHLQRDF 164

>ref|YP_089481.1| hypothetical protein MS2289 [Mannheimia succiniciproducens MBEL55E]
 gb|AAU38896.1| unknown [Mannheimia succiniciproducens MBEL55E]
 Length = 176

Score = 44.7 bits (104), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 36/147 (24%), Positives = 63/147 (42%), Gaps = 10/147 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID--DLERLQDRYPWLVAEV--- 64
 IR A D + DI N I + + EP T + D + +R+P V E
 Sbjct: 3 IRIAKKQDYPQIIDIIYNQAIPSRITADLEFVTMESRKDWFEFHLHSEHPHPIWVLENSII 62

Query: 65 -----EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119

E + G P+ R A+D TVE ++Y+ ++ + G GS + + + M +
 Sbjct: 63 KNNQEEKQILGWCTFSPFYPRAAFNTVEISYLDNKAAGNGYGSKILQFMKEQMMCRDI 122

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARG 146

 +++A + N+ S + E G+ G
 Sbjct: 123 NTLMAYVIEENNISRKAFAFEKQGFKLWG 149

>ref|YP_004260817.1| GCN5-like N-acetyltransferase [Cellulophaga lytica DSM 7489]
 gb|ADY27946.1| GCN5-related N-acetyltransferase [Cellulophaga lytica DSM 7489]
 Length = 163

Score = 44.7 bits (104), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 39/156 (25%), Positives = 61/156 (39%), Gaps = 9/156 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV--- 64

 +E +P + A+ ++V I I T F T+ T W + P+ +
 Sbjct: 1 MEFKPISKANYSSVAKIYQDGISTGVATFETKVPTWDVW-----SKAHLFPFGCIALFTN 54

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124

 EG + G A +R Y E +VYV+ + G G L L+ E ++ A
 Sbjct: 55 EGTMQGWASLAAVSSRCVYGGVAEVSVYVAANARGKGYGKLLLKQLITISEQNNIWTLQA 114

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

 I N S+ LH+ G+ G G +G W D
 Sbjct: 115 GIMRANKASLHLHKECGFREIGYREKIGRLNGKWLD 150

>ref|ZP_02092539.1| hypothetical protein FAEPRAM212_02833 [Faecalibacterium
 prausnitzii

 M21/2]

gb|EDP20049.1| hypothetical protein FAEPRAM212_02833 [Faecalibacterium prausnitzii
 M21/2]

Length = 202

Score = 44.7 bits (104), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 47/158 (29%), Positives = 62/158 (39%), Gaps = 5/158 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69

 IRP T D AV I I T F+TE W D + R LV GV+A
 Sbjct: 36 IRPMTPEWGAVSRIYVEGIATEYATFQTECPPYTAW-DASHTKECR---LVILSGGVLA 91

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129

 G R Y E ++YV + + GLG L L + E G+ ++ + +
 Sbjct: 92 GWCALHRVDPWCYRGVAEVSIVYVGEQFRGHGLGFQLLNALCAAEEKAGYWTLQSTVLQD 151

Query: 130 NDPSVRLHEALGYTARG-TLRAAGYKHGGWHDVGFQWR 166

 N S LH G+ G R A HG W D +R
 Sbjct: 152 NAASRALHAKCGFRLVGHREIRIARDCHGHWLDTYLMER 189

>ref|YP_233975.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae
 B728a]

gb|AA35937.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae
 B728a]

Length = 161

Score = 44.7 bits (104), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 32/125 (25%), Positives = 59/125 (47%), Gaps = 7/125 (5%)

Query: 41 QTPQEWIDDLERLQDRYPW----LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHR 96

 + P + I+D+++L + LVAE +G+V G A ++ R + + + V+
 Sbjct: 31 RMPHQSIINDVKKLVESRSASGLSLVAECDGMVVGACAMLYRFQGRQH--VADFWMGVADS 88

Query: 97 HQRLGLGSTLYTHLLKSMEA-QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKH 155
 H R G+G L + L + K + + + N P++ L+E G+ GT R Y+
 Sbjct: 89 HHRQGIGDLLLLSELTATASRWMLKRLLELTVFVDNKPAIALYEKNGFVIEGTHRKFAIRD 148

Query: 156 GGWHD 160
 G + D
 Sbjct: 149 GEYID 153

>ref|YP_002941961.1| GCN5-related N-acetyltransferase [Variovorax paradoxus S110]
 gb|ACS16695.1| GCN5-related N-acetyltransferase [Variovorax paradoxus S110]
 Length = 160

Score = 44.7 bits (104), Expect = 0.005, Method: Compositional matrix adjust.
 Identities = 45/153 (29%), Positives = 65/153 (42%), Gaps = 10/153 (6%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRT-EPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 R AT D+ AV I Y+ S V F +P E+ + L D + + E EG VA
 Sbjct: 3 RLATPQDLEAVFTI---YMHEVVPFLGYDPMPLDEFRAIYKELVDSRSFYLYEAEGRVA 59

Query: 70 GIAYAG--PWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 G A P +AR+ T+ V G+ + + ++A+G K +
 Sbjct: 60 GFYRATRYPGRARHV---ACFGTLAVDPSLHGKGIAQAMVNDIAIARLKAEGVKRIELYAE 116

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 N P +R +E LG+ GTLR YK G D
 Sbjct: 117 SDNAPGLRFYEKLGFEYEGTLRRF-YKRAGEAD 148

>ref|YP_003936999.1| GNAT family acetyltransferase [Clostridium sticklandii DSM 519]
 emb|CBH22094.1| putative Acetyltransferase, GNAT family protein [Clostridium
 sticklandii]
 Length = 165

Score = 44.7 bits (104), Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 32/110 (29%), Positives = 50/110 (45%), Gaps = 15/110 (13%)

Query: 59 WLVAEVEGVVAGIAYA---GPWKARNAYDWTVES-----TVYVSHRHQRLGLGSTL 106
 + V EV+G VA A P+ + N Y W +++ V VS +Q +G+G +
 Sbjct: 47 FKVVEVDGKVAFLIARENKPYASVN-YKWFLDNYDKFLYVDRVVVSEDIYQHMIGIRLI 105

Query: 107 YTHLLKSMEAQGFKSVVAVIGL--PNDPSVRLHEALGYTARGTLRAAGYK 154
 Y + + G + A I + PN S++ HEA G+ G AG K
 Sbjct: 106 YNEVFNHANSTGVDRITAEIDIKPPNPVSLKFHEAFGFKEVGKQMVAGGK 155

>ref|NP_939298.1| putative phosphinothricin N-acetyltransferase [Corynebacterium
 diphtheriae NCTC 13129]
 emb|CAE49454.1| Putative phosphinothricin N-acetyltransferase [Corynebacterium
 diphtheriae]
 Length = 188

Score = 44.7 bits (104), Expect = 0.006, Method: Compositional matrix adjust.
 Identities = 43/186 (23%), Positives = 69/186 (37%), Gaps = 26/186 (13%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRT-----PQTPQEWIDDLER 52
 +P + IRP D V I +ET ++ E + P+ +E+
 Sbjct: 3 APSQPDFVIRPLRRTDFGQVQQIYLLGLETHGASYEIEAPSWEKFFSTSKIPETLFFAVEK 62

Query: 53 LQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112
 D V G A P +R + VE ++Y+ + G+ L L+
 Sbjct: 63 TDDSK-----VLGWVSAAPISSRTVFRGVVEDSIYIHPDARGRGVAGALVDKLIID 112

Query: 113 SMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLR-----AAGYKHGGWHDVGFQWQRD 167
 + GF ++ + I N+ S RLH + G+ GT G G W D W++
 Sbjct: 113 VCQHLGFWAIHSHWIFPENEGSARLHASRGFEKVGTFSHLAKMTYGEMAGQWRDIDIWEK- 171

Query: 168 FELPAP 173
 LP P
 Sbjct: 172 -LLPKP 176

>ref|NP_046564.1| hypothetical protein SPBc2p012 [Bacillus phage SPBc2]
 ref|NP_390038.1| acetyl-transferase [Bacillus subtilis subsp. subtilis str. 168]
 ref|ZP_03591913.1| hypothetical protein Bsubs1_11866 [Bacillus subtilis subsp. subtilis str. 168]
 ref|ZP_03596192.1| hypothetical protein BsubsN3_11782 [Bacillus subtilis subsp. subtilis str. NCIB 3610]
 ref|ZP_03600604.1| hypothetical protein BsubsJ_11713 [Bacillus subtilis subsp. subtilis str. JH642]
 ref|ZP_03604880.1| hypothetical protein BsubsS_11842 [Bacillus subtilis subsp. subtilis str. SMY]
 sp|O31995.1|YOKL_BACSU RecName: Full=SPBc2 prophage-derived uncharacterized N-acetyltransferase YokL
 emb|CAB14073.1| putative acetyltransferase; phage SPbeta [Bacillus subtilis subsp. subtilis str. 168]
 gb|AAC12985.1| unknown [Bacillus phage SPbeta]
 Length = 177

Score = 44.3 bits (103), Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 32/144 (22%), Positives = 65/144 (45%), Gaps = 10/144 (6%)

Query: 32 STVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVEST 90
 +++F +EW+++ LE+ D + ++ E + + G+ +N T
 Sbjct: 36 DSLHFPRSANMREWVEEQLEK--DEFRFIAVESDNNIVGMIETFDCCRKNG---TFGGY 90

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVAVIGLPNDPSVRLHEALGYTARGTLR 149
 + V ++ G + +L+ + ++ V + N+PS+RLHE LG+ G LR
 Sbjct: 91 LAVFEPYRGKGFAGKEMILMVLRFFFLELAYQKVNTTVYSFNNPSIRLHEKLGFMKEGQLR 150

Query: 150 AAGYKHGGWHD---VGFQWQDFEL 170
 + G ++D G + +FEL
 Sbjct: 151 KIIFTKGAYYDGICFGMTREEFEL 174

>dbj|BAI85559.1| hypothetical protein BSNT_03093 [Bacillus subtilis subsp. natto BEST195]
 Length = 177

Score = 44.3 bits (103), Expect = 0.007, Method: Compositional matrix adjust.
 Identities = 32/144 (22%), Positives = 65/144 (45%), Gaps = 10/144 (6%)

Query: 32 STVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVEST 90
 +++F +EW+++ LE+ D + ++ + + + GI +N T
 Sbjct: 36 DSLHFPRSANMREWVEEQLEK--DEFRFIAVSDNNIVGIIETFDCCRKNG---TFGGY 90

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVAVIGLPNDPSVRLHEALGYTARGTLR 149
 + V ++ G + +L+ + ++ V + N+PS+RLHE LG+ G LR
 Sbjct: 91 LAVFEPYRGKGFAGKEMILMVLRFFFLELAYQKVNTTVYSFNNPSIRLHEKLGFMKEGQLR 150

Query: 150 AAGYKHGGWHD---VGFQWQDFEL 170
 + G ++D G + +FEL
 Sbjct: 151 KIIFTKGAYYDGICFGMTREEFEL 174

>ref|ZP_07990096.1| putative acetyltransferase [Corynebacterium variabile DSM 44702]
Length = 188

Score = 44.3 bits (103), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 37/130 (28%), Positives = 58/130 (44%), Gaps = 10/130 (7%)

Query: 60 LVAEEVGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
VA+ +G + G + R+ + VE +VYVS G+ L HL++ G

Sbjct: 44 FVADEDEGEILGWVTGSWYSHRSVFSGVVEDSVYVSPDATGRGVAGALLDHLIEKSTEAGC 103

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTLRAA----GYKHGGWHDVGFQWQDFE-LPAP 173
S+ AV+ N S++LH + G+ GT G G W D+ +++ E PA

Sbjct: 104 WSIHAVVFPENPGSMKLRSGFKEIGTAHTMAKMTYGP MKGNWRDIVSFEKVLEGGPAH 163

Query: 174 P----RPVRP 179

P R V+P

Sbjct: 164 PEYHERVVKP 173

>ref|ZP_07468657.1| phosphinothricin acetyltransferase [Corynebacterium accolens ATCC 49726]

gb|EFM44048.1| phosphinothricin acetyltransferase [Corynebacterium accolens ATCC 49726]
Length = 166

Score = 44.3 bits (103), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 43/166 (25%), Positives = 72/166 (43%), Gaps = 7/166 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVN----FRTEPQTPQEWIDDLERLQDRYPWLVAE 63

+ IRPA AD ++ I N N ++ E ++W+ ++ + P LVA

Sbjct: 1 MHIRPAELADAPSISAIYNAASAAPANNLITWQEEVSDREDWLKEMSKAGS--PVLVAV 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSV 122

+ + G A + Y TVE +VY+S Q G+GS L L+ + + +++

Sbjct: 59 DDDEIIGWAAAYFQFVTPAIYYGTVEDSVYISPAAQKGKGVGSELLDALMDIAADDSYIETM 118

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDF 168

+ I N S+ LH+ G+ G + K G + Q RDF

Sbjct: 119 ITYIVDTNAGSIALHKKFGFIETGRMPNIHTKDGVRGLVHLQ RDF 164

>ref|ZP_04588131.1| acetyltransferase [Pseudomonas syringae pv. oryzae str. 1_6]
Length = 161

Score = 43.9 bits (102), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 28/102 (27%), Positives = 50/102 (49%), Gaps = 3/102 (2%)

Query: 60 LVAEEVGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QG 118

LVAE +G V G A ++ R + + + V+ H R G+G + L+++ Q

Sbjct: 54 LVAEQDGAVVGCAMLYRFQGRRH--AADFWMGVADGHHRQGIGGLMLKELIETASRWQN 111

Query: 119 FKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

K + + + N+P++ L+E G+ GT R Y+ G + D

Sbjct: 112 IKRLELTVFIDNEPAIALYEKHGFVVEGTHREFAYRDGEYID 153

>ref|ZP_01059497.1| N-acetyltransferase [Leeuwenhoekiella blandensis MED217]

gb|EAQ51329.1| N-acetyltransferase [Leeuwenhoekiella blandensis MED217]
Length = 162

Score = 43.9 bits (102), Expect = 0.008, Method: Compositional matrix adjust.
Identities = 42/140 (30%), Positives = 60/140 (42%), Gaps = 17/140 (12%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERL----QDRYPWLVAEVE 65
 IR A A DMA V ++ + EP + +DDL + VAE E
 Sbjct: 5 IRKAEADMAQVLRLIKE-----LAIYEKPDAVEVTVDLLIAYGTGSNADFTCFVAERE 59

Query: 66 GVVAGIAYA----GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 G + GIA WK R + +E + V +++ GLG LYT ++K G K
 Sbjct: 60 GEILGIALVYYRFSTWKGRTVH--LEDLI-VREQYRGEGLGMALYTEVIKYTYELGLKR 115

Query: 122 VVAVIGLPNDPSVRLHEALG 141
 V V+ N +V +EA G
 Sbjct: 116 VEWVLDWNTSAVDFYEASG 135

>ref|YP_804838.1| sortase related acyltransferase [Pediococcus pentosaceus ATCC 25745]
 gb|ABJ68396.1| Sortase related acyltransferase [Pediococcus pentosaceus ATCC 25745]
 Length = 165

Score = 43.9 bits (102), Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 39/155 (25%), Positives = 64/155 (41%), Gaps = 1/155 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-RYPWLVAEVEG 66
 VE A D+ + I N I++ T+ T +E + + Q+ P V +V G
 Sbjct: 3 VEFELAKEDLPEIVKIYNETIDSRMATADTKYVTVEERQEWFAQHEPTRPLWVIKVRG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVI 126
 V+AG + R AY TVE ++Y+ + + LG + ++A I
 Sbjct: 63 VIAGWISFSSFYGRPAYLHTVEISIIYIDQSRFGMHLGRKAIFAEEQAPKLEINRIMAFI 122

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 N PS+ L ++ Y GTL G +D+
 Sbjct: 123 FAHNLPISIGLFKSENYEKWGTL PQIAEMDGQLYDL 157

>ref|NP_828437.1| acetyltransferase [Streptomyces avermitilis MA-4680]
 dbj|BAC74972.1| putative acetyltransferase [Streptomyces avermitilis MA-4680]
 Length = 160

Score = 43.9 bits (102), Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 35/129 (27%), Positives = 60/129 (46%), Gaps = 2/129 (1%)

Query: 27 HYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWT 86
 H I + + +P T +E L + ++V + G V G AY P A
 Sbjct: 19 HRIVAAGETYAWDPATSEEQARALWMAPGKR VYVVEDETGA VVG SAYVTPNYGGPAAR-V 77

Query: 87 VESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIGLPNDPSVRLHEALGYTARG 146
 + V H G+G L H+L + +A G+++V + +P+V+L +LG+T G
 Sbjct: 78 ANAGFMVDPDHAGRGIGRALADHVLATAKADGYRAMVFNAV VETNPAVQLWTS LGFTV LG 137

Query: 147 TLRAAGYKH 155
 T+ A Y+H
 Sbjct: 138 TVPDA-YEH 145

>ref|YP_265042.1| phosphinothricin acetyltransferase [Psychrobacter arcticus 273-4]
 gb|AAZ19608.1| probable phosphinothricin acetyltransferase [Psychrobacter arcticus 273-4]
 Length = 216

Score = 43.9 bits (102), Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 41/153 (26%), Positives = 67/153 (43%), Gaps = 14/153 (9%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLV----- 61
 ++ A A+D+ V I N I EP T +E W + R ++V
 Sbjct: 32 VQFAVASDLVEVLAIYNKSIAGKQATANLEPVTYEERAVWFAEHINSATRIYVVRMANM 91

Query: 62 ---AEVEGVVAGIAYAGPWK---ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
 +E+E ++ I G + AR AY + E ++Y+ + + GLGS L +L
 Sbjct: 92 AMESEMEKQLSSIIAWGSFSDLYARPAYHISSEISIIYHNDYHGQGLGSLLVRWMLHQAP 151

Query: 116 AQGFKSVVAVIGLPNDPSVRLHEALGYTARGTL 148
 + G +V A+I N PS+ L LG+ G +
 Sbjct: 152 SLGIYNVAALIFAHNQPSLGLFRKLGFEQWGLM 184

>ref|XP_002538119.1| conserved hypothetical protein [Ricinus communis]
 gb|EEF24265.1| conserved hypothetical protein [Ricinus communis]
 Length = 151

Score = 43.9 bits (102), Expect = 0.009, Method: Compositional matrix adjust.
 Identities = 40/147 (27%), Positives = 70/147 (47%), Gaps = 26/147 (17%)

Query: 9 EIRPATAADMAAVCDIVNHYI-ETSTVNFR-----TEPQTPQEWIDDLERLQDRYPWL 60
 EIRPA+ AD A+ ++ + E++ ++ E +P + RL L
 Sbjct: 4 EIRPASEADAEAISGVILAAALRESNATDYSPDIIARVAESFSPA----GMRRLLSNRTVL 59

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFK 120
 VA +G + G A + D V TV+VS QR G+G++L + ++ +A G
 Sbjct: 60 VAIDDGSLVGTA-----SLDGAVVRTVFVSPSAQRRGIGASLMAAIERAAQASG-- 108

Query: 121 SVVAVIGLPNDPSVR-LHEALGYTARG 146
 +AV+ +P+ + + +E LG+ A G
 Sbjct: 109 --IAVLSVPSSITAQGFYERLGFNAVG 133

>ref|YP_703758.1| phosphinothricin N-acetyltransferase [Rhodococcus jostii RHA1]
 gb|ABG95600.1| possible phosphinothricin N-acetyltransferase [Rhodococcus jostii
 RHA1]
 Length = 156

Score = 43.9 bits (102), Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 42/153 (27%), Positives = 61/153 (39%), Gaps = 4/153 (2%)

Query: 14 TAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAY 73
 T D V I I T F TE T Q +D L R+ VAE++ VV G A
 Sbjct: 2 TDQDWDVRRRIYGEIATRNATFTTEVPT-QATLDGLWLPGHRW--VAEIDDVVVGWAA 57

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133
 P R Y E+++YV+ + G+G L + + + G ++ I N S
 Sbjct: 58 LSPVSGRACYAGVAENSIYVADGMRGRGVGKALLRSQVIAADEAGLWTLQTSIFPENRAS 117

Query: 134 VRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
 + LH + G+ G W D F +R
 Sbjct: 118 IALHHSAGFRTLGVRRERIALDDIWRDVFLE 150

>ref|ZP_01727450.1| GCN5-related N-acetyltransferase [Cyanotheca sp. CCY0110]
 gb|EAZ93052.1| GCN5-related N-acetyltransferase [Cyanotheca sp. CCY0110]
 Length = 168

Score = 43.9 bits (102), Expect = 0.010, Method: Compositional matrix adjust.
 Identities = 34/143 (23%), Positives = 60/143 (41%), Gaps = 5/143 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAEVE 65
 +IR A D+ + +I N I + + T + +W ER YP V E +

Sbjct: 3 KIRLAEELEDLEDIVEIYNSSIPSRIATGDLQKITVESRLKWFQ--ERDSKHYPWVIEND 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
V G + R AY T E ++Y++ H+ G+G L ++++ +++

Sbjct: 61 NKVIGWISLQHFYGRPAYKSTAEISLYIAQSHRSKGIGKKLLEYVIQESPKLELTTLGLF 120

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148
I N PS+ L + + G L

Sbjct: 121 IFAHNQPSLNLFFKKYNFQQWGYL 143

>gb|EER38620.1| GNAT family N-acetyltransferase [Ajellomyces capsulatus H143]
gb|EGC47772.1| GNAT family N-acetyltransferase [Ajellomyces capsulatus H88]
Length = 182

Score = 43.9 bits (102), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 43/150 (28%), Positives = 67/150 (44%), Gaps = 22/150 (14%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDD-LERLQDR-YPWLVA---- 62
+IR AT +D+ + I HY++ + V FR + P +I Q+R P+LVA

Sbjct: 4 KIRSATESDLHQIHSIFTHYVQNTVTVFRVN-KPPFSYIAKRFHEAQERGLPYLVAVEKS 62

Query: 63 -----EVEGVVAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112
V G A ++ AY TVE ++ V +Q G+GS L + L++

Sbjct: 63 NQDNPSHEGNTTEKVCGYTLASAFRGYMLAYAPTVEMSLLVHPDYQSQGIGSALLSSIVE 122

Query: 113 SM-EAQGFKSVVAVIGLPNDPSVRLHEALG 141
++ EA+ V D RLHEA+

Sbjct: 123 ALREAKHLSYEVG----DADSEARLHEAVN 148

>ref|YP_684288.1| acetyltransferase, putative [Roseobacter denitrificans OCh 114]
gb|ABG33602.1| acetyltransferase, putative [Roseobacter denitrificans OCh 114]
Length = 160

Score = 43.9 bits (102), Expect = 0.010, Method: Compositional matrix adjust.
Identities = 39/167 (23%), Positives = 71/167 (42%), Gaps = 12/167 (7%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
M + +P++IRP D+AA+ ++++ T F +E P D L Q WL

Sbjct: 1 MKKDEKPMKIRPTMHDDIAALQEVLDR-----TALFPSE-MLPDMMRDFLSDTQSSDIWL 54

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
E +G G YA P + W + + + V Q G GS + HL +++ + +

Sbjct: 55 TCEADGKAVGFCYAVPEELAEV-WNMRA-IAVQPTQGGCGSAIVAHLEAALKERSQR 112

Query: 121 SVVAVIGLPN--DPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQ 165
++A + +P+ + GY +R + G + FW+

Sbjct: 113 ILIADTSGADAFEPTRAFYRKNGYIEEACIR--DFWAEGDDKIVFWK 157

>ref|ZP_05635004.1| GCN5-related N-acetyltransferase [Fusobacterium ulcerans ATCC 49185]
ref|ZP_07929600.1| polyprenyl synthetase [Fusobacterium ulcerans ATCC 49185]
gb|EFS27626.1| polyprenyl synthetase [Fusobacterium ulcerans ATCC 49185]
Length = 165

Score = 43.5 bits (101), Expect = 0.011, Method: Compositional matrix adjust.
Identities = 36/147 (24%), Positives = 57/147 (38%), Gaps = 11/147 (7%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLERLQDRYPWLVAEVEGVV 68
IR D V I IE+ FR + + W LE + + + +G +

Sbjct: 5 IRDMKDGWDKDVARIYEQGIIESGIATFRKDLPDQESWKKAHLEICR----FTLCNKDGI 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G P +R Y E ++Y+ HQ LG L + + E G ++ + I
 Sbjct: 61 VGWTALSPTSSRIDYCGVTEVSIYIDKAHQGKKLGFEFLNKKVKEEAENGVWTLQSSIFQ 120

Query: 129 PNDPSVRLHEALGYTARGTLRAAGYKH 155
 N SV+LH+ G+ R GY+
 Sbjct: 121 VNKASVKLHKKCGF-----REVGyre 141

>ref|ZP_01862614.1| putative acetyltransferase [Erythrobacter sp. SD-21]
 gb|EDL50049.1| putative acetyltransferase [Erythrobacter sp. SD-21]
 Length = 158

Score = 43.5 bits (101), Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 31/107 (28%), Positives = 45/107 (42%), Gaps = 5/107 (4%)

Query: 59 WLVAEEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM-EAQ 117
 W+ + EG VAG A P + E V QR G+ L++ + E +
 Sbjct: 47 WIAEDAEGRVAGRFVAVPGLDKG---VAEIGYVVCMDRQREGVAHKCTAALVRHLIEG 102

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF 164
 G + + A + + N PSVRL E LG+T R G DV +
 Sbjct: 103 GLRKLTAEDIENVPSVRLLERLGFTREALFRQHEISQKGLCDVAVY 149

>ref|YP_003973202.1| putative acetyltransferase; phage SPbeta [Bacillus atrophaeus 1942]
 gb|ADP32271.1| putative acetyltransferase; phage SPbeta [Bacillus atrophaeus 1942]
 Length = 143

Score = 43.5 bits (101), Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 33/145 (22%), Positives = 69/145 (47%), Gaps = 12/145 (8%)

Query: 32 STVNFRTEPQTPQEWIDD-LERLQDRYPWLVAEEGVVAGIAYAGPWKARNA-YDWTVES 89
 +++F +EWI++ LE+ D + ++ + + + G+ +N +D+ +
 Sbjct: 2 DSLHFPRSANKMREWIEEQLEK--DDFRFIAVDRDNNIVGMIETFDCCRKNGTFDYLL-- 57

Query: 90 TVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVAVIGLPNDPSVRLHEALGYTARGTL 148
 V+ +R + G + +L+ + ++ V + N+PS+RLHE LG+ G L
 Sbjct: 58 AVFEPYRDK--GFAKEMILMVLRRFFLELAYQKVNIITVYSFNNPSMRLHEKLGFMKEGQL 115

Query: 149 RAAGYKHGGWHD---VGFWQRDFEL 170
 R + G ++D G + +FEL
 Sbjct: 116 RNIIFTKGAYYDGICFGMTREEFEL 140

>ref|ZP_03931617.1| phosphinothricin N-acetyltransferase [Corynebacterium accolens ATCC 49725]
 ref|ZP_07468733.1| probable phosphinothricin N-acetyltransferase [Corynebacterium accolens ATCC 49726]
 gb|EEI15556.1| phosphinothricin N-acetyltransferase [Corynebacterium accolens ATCC 49725]
 gb|EFM43949.1| probable phosphinothricin N-acetyltransferase [Corynebacterium accolens ATCC 49726]
 Length = 192

Score = 43.5 bits (101), Expect = 0.011, Method: Compositional matrix adjust.
 Identities = 40/180 (22%), Positives = 76/180 (42%), Gaps = 8/180 (4%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAE 63
 +++ IRP T+AD + +I ++T + T T +E+ + + + + A+

Sbjct: 16 KKKDFRIRPFTSADYPQMREIYEQGLQTHATYETRSLTYEFTNS-KIMASVHVAVEAD 74

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
+ V G A P +R + VE ++Y+ Q G+ L L++ + ++

Sbjct: 75 DDSKVLGWVSAAPISSRTVFHGVVEDSIYLGSDAQGRGIAGALLDCLIEVCKDLHKWAIH 134

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLR-----AAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
+ I N+ S LH++ G+ GT G G W D ++ LP P R

Sbjct: 135 SWIFPENEGSAGLHKSFGFEKVGTYSHMAKMTYAGELAGQWRDQVYE--LLLPKPEEKNR 192

>ref|XP_002623155.1| GNAT family N-acetyltransferase [Ajellomyces dermatitidis SLH14081]
gb|EEQ71403.1| GNAT family N-acetyltransferase [Ajellomyces dermatitidis SLH14081]
Length = 195

Score = 43.5 bits (101), Expect = 0.011, Method: Compositional matrix adjust.
Identities = 45/195 (23%), Positives = 82/195 (42%), Gaps = 46/195 (23%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVAEVEG 66
+++R AT +D+ + I HY+ + + + Q+R P+LVA VE

Sbjct: 3 LKVRTATESDIPQIYSIFTHYVRNTVITLFANTPPFSYMTKRFHKTQERGLPFLVA-VEQ 61

Query: 67 V-----VAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
+ V G A P++ +Y TVE +++V + G+GSTL + L+

Sbjct: 62 LEQDDTCHGGNMAEKVCYTLASPFRGYMLSYAPTVMESLFFVHPEYHSRGIGSTLLSSLI 121

Query: 112 KSM-EAQGF-----KSVVAVIGLPNDPSVRLHEAL-----GYT 143
+++ EA+ KS++A++ + N E L G+

Sbjct: 122 EALQEAKHLSYQVTGHAGSEARVHAEAKVKSILAIMTV-NPEGKNGGEGLRDWYVQRGFV 180

Query: 144 ARGTLRAAGYKHGGW 158
RG ++ G+K+G W

Sbjct: 181 ERGRMKEVGFKYKWK 195

>ref|NP_440374.1| hypothetical protein sll1647 [Synechocystis sp. PCC 6803]
dbj|BAA17054.1| sll1647 [Synechocystis sp. PCC 6803]
Length = 172

Score = 43.5 bits (101), Expect = 0.012, Method: Compositional matrix adjust.
Identities = 40/144 (27%), Positives = 63/144 (43%), Gaps = 8/144 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYP-W-LVAEV 64
+R AT D+ ++ I N I + T+ T+ +W D D YP W LV E

Sbjct: 8 LRDATITDLDSIVAIYNANIPQNVATGDTDAITVESRRQWFAD--HGPDTYPLWVLVTEH 65

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
+ +V + + + R AY T E ++Y+ GLG L + G K+++

Sbjct: 66 KQIVGWLGFQ-RFYGRPAYHRTAELSIYLDPLWHHRGLGQYLLKTAIAKAPQLGLKTLTG 124

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
I N PS+RL + G+ G L

Sbjct: 125 YIFAHNQPSIRLFQRHGFEQWGLL 148

>ref|ZP_02919047.1| hypothetical protein BIFDEN_02369 [Bifidobacterium dentium ATCC 27678]
ref|YP_003360346.1| N-acetyl transferase [Bifidobacterium dentium Bd1]
ref|ZP_07456553.1| GNAT family acetyltransferase [Bifidobacterium dentium ATCC 27679]
ref|ZP_07695745.1| acetyltransferase, GNAT family [Bifidobacterium dentium JCVIHM022]
gb|EDT46515.1| hypothetical protein BIFDEN_02369 [Bifidobacterium dentium ATCC

27678]

gb|ADB09522.1| N-acetyl transferase [Bifidobacterium dentium Bd1]
 gb|EFM41720.1| GNAT family acetyltransferase [Bifidobacterium dentium ATCC 27679]
 gb|EFO78047.1| acetyltransferase, GNAT family [Bifidobacterium dentium JCVIHMP022]
 Length = 170

Score = 43.5 bits (101), Expect = 0.014, Method: Compositional matrix adjust.
 Identities = 40/164 (24%), Positives = 61/164 (37%), Gaps = 6/164 (3%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG---- 66
 R A D+ A+ DI N + + P+T ++ +E QD Y V E
 Sbjct: 7 RIAGEHDLRAITDIYNAAVIAGSSADLSPTLEQRKVVVESHQDPYAVFVVEAADDDGN 66

Query: 67 -VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G + R YD + YV Q G+G+ T LL+ + + +
 Sbjct: 67 PQTVGFGALSVFYDRAGYDGVTDLAYYYVDPAAWQKGVGTYTLTKLLEECRKRNMKACGI 126

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHDVGFWRQDF 168
 I N S+ L G+T G + AA G D+ +W D
 Sbjct: 127 IFADNAGSIALMRRFGFTQFGLMPAAATDSTGTMRDMSYWYLDL 170

>ref|YP_001343476.1| GCN5-related N-acetyltransferase [Actinobacillus succinogenes 130Z]
 gb|ABR73541.1| GCN5-related N-acetyltransferase [Actinobacillus succinogenes 130Z]
 Length = 169

Score = 43.1 bits (100), Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 37/141 (26%), Positives = 60/141 (42%), Gaps = 7/141 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLVAEV 64
 ++IR A D+ + I N I + + +P T Q W + R+P V E
 Sbjct: 1 MKIRTAKEQDLQPQIVAIYNQAIPSRITADLQPVTEQARRPWFE-AHLNSSRHPIWVLES 59

Query: 65 ---EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 + + G P+ R A+D TVE +VY+ + G GS L M A +
 Sbjct: 60 AVEKNKILGWCSFSPFYDRAAFDQTVEISVYLDQSAKGRGYGSQAIRFLQAQMTALDVHT 119

Query: 122 VVAVIGLPNDPSVRLHEALGY 142
 ++A + N S ++ E LG+
 Sbjct: 120 LMAYVIEENHISRKMFEKLG 140

>ref|YP_003736550.1| GCN5-related N-acetyltransferase [Halalkalicoccus jeotgali B3]
 gb|ADJ14758.1| GCN5-related N-acetyltransferase [Halalkalicoccus jeotgali B3]
 Length = 253

Score = 43.1 bits (100), Expect = 0.015, Method: Compositional matrix adjust.
 Identities = 40/147 (27%), Positives = 63/147 (42%), Gaps = 17/147 (11%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRT---PQTPQEWIDD--LERL----QDRYPWL 60
 IR AT +D+AA+ ++ + TS +F E ++W D LE L D
 Sbjct: 3 IRDATRSDVAAIREVARQSLRTSYAHFLEEQTIDDAVEQWYGDGRLEELISDEADDVSIP 62

Query: 61 VAEVEGVVAGIA--YAGPWKAR-NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
 V EV+G + A Y + R W ++V H+ G GS LY H+ ++ E +
 Sbjct: 63 VLEVDGEIVAFACQCYLVEFFPERVGEIHW-----LHVDPEHRGEGYGSQLYEHVRETFFEE 117

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTA 144
 G + N+P +E GY +
 Sbjct: 118 GIDRFKGFVFAENEPGNEFYERRGYES 144

Query: 123 VAVIGLPNDPSVRLHEALGYTARG 146
+ + N+ + RL+ LG+ RG

Sbjct: 107 TLEVRVSNEGAQRLYRRLGFMPRG 130

>ref|YP_002834468.1| putative acetyltransferase [Corynebacterium aurimucosum ATCC 700975]
 ref|ZP_06042169.1| putative acetyltransferase [Corynebacterium aurimucosum ATCC 700975]
 gb|ACP32530.1| putative acetyltransferase [Corynebacterium aurimucosum ATCC 700975]
 Length = 191

Score = 43.1 bits (100), Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 40/184 (21%), Positives = 73/184 (39%), Gaps = 8/184 (4%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63
 +++ IRP AAD + +I + T + T T +E+ +++ + + + +
 Sbjct: 8 KKKDFRIRPFNAADYPQMREIYEQGLNTGHATYETRSLTFEEF-KNVKIMSSVFVAVEED 66

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 + V G A R + VE ++Y+S Q G+G L L++ ++
 Sbjct: 67 DDSKVLGWVCAAQASTRTVFHGVVEDSIYLSKEAQGRGIGGALLDQLIEVCRDLHKWAIH 126

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLR-----AAGYKHGGWHDVGFWRDFELPAPPRPVR 178
 + I N+ S LH++ G+ GT G G W D ++ LP P
 Sbjct: 127 SWIFPENEGSAGLHKSRGFVKVGTYSMAKMTYGELAGQWRDTDVYE--LLLPKPEEKKA 184

Query: 179 PVTQ 182
 Q
 Sbjct: 185 EANQ 188

>ref|YP_003264892.1| GCN5-related N-acetyltransferase [Haliangium ochraceum DSM 14365]
 gb|ACY12999.1| GCN5-related N-acetyltransferase [Haliangium ochraceum DSM 14365]
 Length = 225

Score = 43.1 bits (100), Expect = 0.017, Method: Compositional matrix adjust.
 Identities = 34/122 (27%), Positives = 56/122 (45%), Gaps = 3/122 (2%)

Query: 28 YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTV 87
 Y+E+ +V+ + W + L R + W++ E G VAG A GP + ++
 Sbjct: 68 YLESLSVHDLAGRWNQRIWAEPLRRPEACNIWVI-EDGGEVAGFALLGPCRDQDEEPGFA 126

Query: 88 EST--VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTAR 145
 +YV R GLGSTL+ H + + +G+ V + N + R +E +G A
 Sbjct: 127 GEVLMIIYVHPRRTGRGLGSTLFAHAFELLAQRGYFWGVVWVLEGNRSARRFYEGMGLEAD 186

Query: 146 GT 147
 GT
 Sbjct: 187 GT 188

>ref|ZP_05117902.1| acetyltransferase, gnat family [Vibrio parahaemolyticus 16]
 gb|EED28388.1| acetyltransferase, gnat family [Vibrio parahaemolyticus 16]
 Length = 163

Score = 43.1 bits (100), Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 42/163 (25%), Positives = 70/163 (42%), Gaps = 13/163 (7%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ----EWIDDLERLQDRYPWLVAEVE 65
 IRP D AA+CDI Y + S R Q P+ W LE + VAEV+
 Sbjct: 5 IRPTLVNDAACDI---YSQPSAQ--RETLQLPKPSVAMWTQRLENIPAGVYSFVAEVD 59

Query: 66 G-VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QGFKSVV 123

G V V I + + R ++ T V+ +Q +G+GS L +L + K +
 Sbjct: 60 GKVVGNIGFEHNQRPRISHCATFGLGVH--DEYQGIGVGSKLIETVLDLADNWLQVKRIQ 117

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166

+ N+ ++ ++ G+ G +A ++ G + D + R
 Sbjct: 118 IEVNTDNEKAIACYKKFGFEIEGEAKARSFRDGEYIDTYMAR 160

>ref|ZP_07263169.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae

642]

Length = 161

Score = 43.1 bits (100), Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 32/125 (25%), Positives = 59/125 (47%), Gaps = 7/125 (5%)

Query: 41 QTPQEWIDDLERLQDRYPW----LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHR 96
 + P + I+D+++L + LVAE +G+V G A ++ R + + + V+

Sbjct: 31 RMPYQSINDIKKLVESRNASGLSLVAEQDGMVVCAMLYRFQGRQRH--VADFWMGVADS 88

Query: 97 HQRLGLGSTLYTHLLKS-MEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKH 155
 H R G+G +L L + K + + + N P++ L+E G+ GT R Y+

Sbjct: 89 HHRQGIGDSLLKELTATACRWMNLKRLELTVFVDNKPAIALYEKNGFVIEGTHRKFAIRD 148

Query: 156 GGWHD 160

G + D

Sbjct: 149 GEYID 153

>ref|YP_002828185.1| putative acyl-CoA N-acyltransferase, GNAT family protein
 [Sinorhizobium fredii NGR234]

gb|ACP27432.1| putative acyl-CoA N-acyltransferase, GNAT family protein
 [Sinorhizobium fredii NGR234]

Length = 167

Score = 43.1 bits (100), Expect = 0.018, Method: Compositional matrix adjust.
 Identities = 40/165 (24%), Positives = 74/165 (44%), Gaps = 10/165 (6%)

Query: 1 MSPERRPVEIRPATAAD---MAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRY 57
 M+ IR A+ AD +A + D+ T + F P+ + W LE L +

Sbjct: 1 MTASSNAFHIRAASVADWEALAVLRDLPGVRSGLRLPF-APPEQTRRW---LEGLTEND 56

Query: 58 PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA- 116
 +VAE+EG + G+A K R + + +V+ +R R G+G L L+++ +

Sbjct: 57 LIIVAELEGRIVGLAGLHRHKGRRQHAADLGMSVHDDYR--RRGIGKALLEALLETADRW 114

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

G + + N+ ++ L+ G+ G L++ + G + DV

Sbjct: 115 LGISRLLELTVFTDNEAAIGLYRNAGFVTEGILKSYALRDGAYADV 159

>ref|ZP_04977988.1| acyltransferase [Mannheimia haemolytica PHL213]

gb|EDN74384.1| acyltransferase [Mannheimia haemolytica PHL213]

Length = 172

Score = 42.7 bits (99), Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 58/143 (40%), Gaps = 6/143 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQ---EWID-DLERLQDRYPWLVAE 63
 ++ R A AD + I N I T + E T Q +W D LE Q YP V E

Sbjct: 1 MQFRKAVEADFETILAIYNQAIPHTQITADLELATTQNRKWFDFHLETAQ--YPIWVVE 58

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 123

E +AG P+ R A+ T E ++Y+ + G GS + + M +++
 Sbjct: 59 DEKGIAGWFSFSPFYERPAFLHTSEISIYLD RYSGKGYGSKIIEFMQAEMLNHNHTLM 118

Query: 124 AVIGLPNDPSVRLHEALGYTARG 146

A + N S L G+ G

Sbjct: 119 AYVFELNNTVSQNLMRKHGFEQWG 141

>emb|CBL03517.1| Sortase and related acyltransferases [Gordonibacter pamelaee
 7-10-1-b]
 Length = 178

Score = 42.7 bits (99), Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 44/164 (26%), Positives = 73/164 (44%), Gaps = 10/164 (6%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+EIRP D+A + + N +E + EP T ++ E + +VA+++G

Sbjct: 13 LEIRPYREEDLAGMLKVWNEVVEGGEAFQIEPLTLEKAA---EFFAAQTL SVVADLDGK 69

Query: 68 VAGIAYAGPWK-ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV-VAV 125

V G+ P R A+ V S R LGLG L L +GF+ +

Sbjct: 70 VMGLYVLHPNNGVGRCAHVNASYAVASSVRG--LGLGRALVEDSLAQAARKGFRGLQFNA 127

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKH--GGWHDVGFWRD 167

+ N ++ L+E LG+ GT+ G+ + GG+ D+ + RD

Sbjct: 128 VVAGNAGAIHLYEDLGFVRVGTGTV-PGGFVNFMGGYEDIHIYYRD 170

>gb|ADZ92302.1| GCN5-related N-acetyltransferase [Marinomonas mediterranea MMB-1]
 Length = 164

Score = 42.7 bits (99), Expect = 0.019, Method: Compositional matrix adjust.
 Identities = 30/141 (21%), Positives = 59/141 (41%), Gaps = 7/141 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67

+++R A D A+ +I +I +N + WI E+ P VA ++G

Sbjct: 9 IKVRYAVLDDAPAILEIYQQHIPFDDINLLSAVH---WI---EQANSHRPMWVATIDG 61

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G + D E ++Y++ +R G+G L ++ + ++V +

Sbjct: 62 LIGWCSLESYYGLKVLDMHMAELSLYIAKSWRRKGIGRQLMAEVMANALCINLTNLVVNVF 121

Query: 128 LPNDPSVRLHEALGYTARGTL 148

N+ S+R E+L + G L

Sbjct: 122 SGNESIRFFESLNFQRYGAL 142

>ref|YP_003640603.1| GCN5-related N-acetyltransferase [Thermincola sp. JR]
 gb|ADG82702.1| GCN5-related N-acetyltransferase [Thermincola potens JR]
 Length = 174

Score = 42.7 bits (99), Expect = 0.020, Method: Compositional matrix adjust.
 Identities = 34/139 (24%), Positives = 63/139 (45%), Gaps = 4/139 (2%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE--WIDDLERLQDR-YPWLVAE 63

P IRPAT D+ + ++ I + EP QE I LE++++R + WLVA

Sbjct: 10 PFVIRPATNTDLTDIAYVITR-IAREENSLGAEPMLTQEPATITMLEKMRERPHCWVAL 68

Query: 64 VEGV VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123

V+ + GIA A + T + V H+ +GS L +++ + +

Sbjct: 69 VDNKIIGIACAVKFFETGNSGSTAVLGIGVLKEHRNRSVGSALIHVRVIEWCISNNISKIR 128

Query: 124 AVIGLPNDPSVRLHEALGY 142

+ N+ +++L++ G+
 Sbjct: 129 LTVWEHNNAALQLYKKFGF 147

>ref|ZP_05989200.1| acyltransferase [Mannheimia haemolytica serotype A2 str. BOVINE]
 ref|ZP_05991085.1| acyltransferase [Mannheimia haemolytica serotype A2 str. OVINE]
 gb|EEY10938.1| acyltransferase [Mannheimia haemolytica serotype A2 str. OVINE]
 gb|EEY12956.1| acyltransferase [Mannheimia haemolytica serotype A2 str. BOVINE]
 Length = 172

Score = 42.7 bits (99), Expect = 0.022, Method: Compositional matrix adjust.
 Identities = 39/143 (27%), Positives = 58/143 (40%), Gaps = 6/143 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWID-DLERLQDRYPWLVAE 63
 ++ R A AD + I N I T + E T Q +W D LE Q YP V E
 Sbjct: 1 MQFRKAVEADFETILAIYNQAIPHTQITADLELATTQNRKWFDFHLETAQ--YPIWVVE 58

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
 E +AG P+ R A+ T E ++Y+ + G GS + + M +++
 Sbjct: 59 DEQGIAGWFSFSPFYERPAFLHTSEISYILDYRSGKGYGSKIIEFMQAEMLNHNHITLM 118

Query: 124 AVIGLPNDPSVRLHEALGYTARG 146
 A + N S L G+ G
 Sbjct: 119 AYVFELNNTVSQNLMRKHGFEQWG 141

>ref|YP_003411640.1| GCN5-related N-acetyltransferase [Geodermatophilus obscurus DSM
 43160]
 gb|ADB77269.1| GCN5-related N-acetyltransferase [Geodermatophilus obscurus DSM
 43160]
 Length = 154

Score = 42.7 bits (99), Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 40/138 (28%), Positives = 59/138 (42%), Gaps = 5/138 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + + P TA D AV +I I T F +P P + D RL D + + + G
 Sbjct: 12 IAVAPLTAEDWPAVREIYAQGIATGHATFEADP--PSWEVFDASRLPD-HRLIALDGGGR 68

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V G A P AR Y VE + YV+ + G+G L L+ S EA ++ + +
 Sbjct: 69 VVGWAAVSPVPARAVYAGVVEHSAYVAPAGRGHGIGRLLMEELIVSTEAAADIWTIQSSVF 128

Query: 128 LPNDPSVRLH--EALGYT 143
 P+ ALGY+
 Sbjct: 129 PRTSPASACTRPSALGYS 146

>ref|YP_002507954.1| SSU ribosomal protein S18P alanine acetyltransferase
 [Halothermothrix orenii H 168]
 gb|ACL68959.1| SSU ribosomal protein S18P alanine acetyltransferase
 [Halothermothrix orenii H 168]
 Length = 151

Score = 42.4 bits (98), Expect = 0.024, Method: Compositional matrix adjust.
 Identities = 34/139 (24%), Positives = 64/139 (46%), Gaps = 16/139 (11%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
 IRP +D+ V +I + P + + ++ +L+ ++Y +L ++G +
 Sbjct: 5 IRPMEESDLPRVLEIEGKCFQA-----PWSKKAFLRELQ--DNKYSLYLSGWLDGRL 54

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
 G Y G W ++ T + V ++R GL + L +L+ E QG K V + +

Sbjct: 55 VG--YIGSWIIKDELHIT---NLAVDPGYRRRGLATRLINLMNFAEDQGLKEVTLEVRV 109

Query: 129 PNDPSVRLHEALGYTARGET 147

N ++RL+E LG+ G

Sbjct: 110 SNKAAIRLYEKLGFPIGIC 128

>ref|YP_002016217.1| GCN5-related N-acetyltransferase [Prosthecochloris aestuarii DSM 271]

gb|ACF46570.1| GCN5-related N-acetyltransferase [Prosthecochloris aestuarii DSM 271]

Length = 172

Score = 42.4 bits (98), Expect = 0.024, Method: Compositional matrix adjust.
Identities = 39/126 (30%), Positives = 55/126 (43%), Gaps = 8/126 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60

M+PE + IR D+A +CD+ E+ ++ TE Q ID L L

Sbjct: 2 MTPE---ILIRDEVPDDVADICDVTVAAFESMEISNHTE----QFVIDALRAANALTLSL 54

Query: 61 VAEVEGVVAG-IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119

VAEV G V G IA++ + +W V V +QR G+GS L L ++ G

Sbjct: 55 VAEVNGQVVGHIASFPTISDGTDNWYGLGPVSVLPVYQRKGIGSALIEKGLSRLKDLGA 114

Query: 120 KSVVAV 125

K V

Sbjct: 115 KGCCLV 120

>ref|XP_002540679.1| predicted protein [Uncinocarpus reesii 1704]

gb|EEP75346.1| predicted protein [Uncinocarpus reesii 1704]

Length = 179

Score = 42.4 bits (98), Expect = 0.026, Method: Compositional matrix adjust.
Identities = 35/105 (33%), Positives = 44/105 (41%), Gaps = 12/105 (11%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-YPWLVA---- 62

+ IRPATA D+ A+ I HY+ S + F D + Q R P+ VA

Sbjct: 3 ISIRPATATDLPAIHTIYTHYVRNSVLTFLVNDPALSAITDKYDATQARGLPFHVACLND 62

Query: 63 ----EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLG 103

EV G AY G Y TVE T++V HQ G G

Sbjct: 63 GGSEEVVGYACASAYRGYLL---GYAPTVELTLFVHPGHQSNGAG 104

>ref|YP_003327372.1| GCN5-related N-acetyltransferase [Xylanimonas cellulositytica DSM 15894]

gb|ACZ31814.1| GCN5-related N-acetyltransferase [Xylanimonas cellulositytica DSM 15894]

Length = 177

Score = 42.4 bits (98), Expect = 0.027, Method: Compositional matrix adjust.
Identities = 42/138 (30%), Positives = 61/138 (44%), Gaps = 8/138 (5%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL--VAEVEGVV 68

R AD +AV I I T F P T +E+ ++P L VA ++G V

Sbjct: 17 RALVRADWSAVEAIYREGIATGHATFEAAPPTWEEFD-----AGKHPALRLVATLDGDV 70

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAIVIGL 128

G A P +R Y VE +VYV+ Q G+G L L+ + + ++ + I

Sbjct: 71 VGWAAGAPVSSRAVYRGVVEHSVYVAESAQGRGVGGLLLAALIVAADDDEVWTLQSGIFP 130

Query: 129 PNDPSVRLHEALGYTARG 146

N S+RLHE G+ G

Sbjct: 131 ENTASLRLHEQHGFVRVVG 148

>ref|ZP_07714579.1| probable phosphinothricin N-acetyltransferase [Corynebacterium pseudogenitalium ATCC 33035]

gb|EFQ80348.1| probable phosphinothricin N-acetyltransferase [Corynebacterium pseudogenitalium ATCC 33035]

Length = 192

Score = 42.4 bits (98), Expect = 0.027, Method: Compositional matrix adjust.

Identities = 42/180 (23%), Positives = 73/180 (40%), Gaps = 8/180 (4%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63

+++ IRP TAAD + +I + T + T T +E+ + + + + A+

Sbjct: 16 KKKDFRIRPFTAADYPQMREIYEQGLNTGHATYETRSLTFEEFKAG-KIMPSVHVAVEAD 74

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123

+ V G A P R + VE ++Y+ Q G+G L L++ + ++

Sbjct: 75 DDSKVLGWVSAAPVSTRTVFHGVVEDSIYLGAEAQGRGIGGALLDRLIEVCKDLHKWAIH 134

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLR-----AAGYKHGGWHDVGFWRDFELPAPPRPVR 178

+ I N S LH++ G+ GT G G W D ++ LP P R

Sbjct: 135 SWIFPENAGSAGLHKS RGFVKVGTYSHMAKMTY GELAGQWRD TDVYE--LLLPKPEEKKR 192

>ref|ZP_05362847.1| phosphinothricin N-acetyltransferase [Campylobacter showae RM3277]

gb|EET80434.1| phosphinothricin N-acetyltransferase [Campylobacter showae RM3277]

Length = 208

Score = 42.4 bits (98), Expect = 0.028, Method: Compositional matrix adjust.

Identities = 33/125 (26%), Positives = 57/125 (45%), Gaps = 1/125 (0%)

Query: 24 IVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAY 83

++ E + N ++ +++ D E L ++ P + ++A + + + R Y

Sbjct: 64 VLREVEYANLTNKKDSKADCEKFKDS DGENLGEQKPSVTNPKSEILAWGSLS-DYHPREGY 122

Query: 84 DWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYT 143

T E +VYV+ + GLG L +LK G K+VVA+I N S+ L G+T

Sbjct: 123 RITAEISVYVAPDARGKGLGGRLVNFMLKLAPKFGIKNVVALIFSSNAASLNLFAKFGFT 182

Query: 144 ARGTL 148

G L

Sbjct: 183 RWGEL 187

>ref|YP_004171066.1| GCN5-like N-acetyltransferase [Deinococcus maricopenensis DSM 21211]

gb|ADV67401.1| GCN5-related N-acetyltransferase [Deinococcus maricopenensis DSM 21211]

Length = 191

Score = 42.4 bits (98), Expect = 0.030, Method: Compositional matrix adjust.

Identities = 47/183 (25%), Positives = 70/183 (38%), Gaps = 36/183 (19%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP-----QEWDLLERLQDRY 57

+ IRPA D A ++ I + EP QE +D RL R

Sbjct: 2 LTIRPAVPGDARACVPLIVDAIGDIALTLTVEPTVSRAAGALRAFFQEDEEDDNRLSYRN 61

Query: 58 PWLVAEVEGVVAGI--AYAGP-----WKARNAYDWTVE-----STVY 92

W VAEV+G +AG+ AY G W + + +E TV

Sbjct: 62 AW-VAEVDGHMAGVLVAYDGARARMLDWPFLRRRAWALTDNTHYVIEETEAGEFYVDTVS 120

Query: 93 VSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAG 152
V +Q G+G+ L + +GF V ++ N + RL+E LG+ GT G
Sbjct: 121 VRAAYQGRGVGTQLVQFAVALARERGFPRVTLVDEGNVGARRLYERLGFVAGTRSIGG 180

Query: 153 YKH 155
+ +
Sbjct: 181 HAY 183

>ref|YP_003479445.1| GCN5-related N-acetyltransferase [Natrialba magadii ATCC 43099]
gb|ADD04883.1| GCN5-related N-acetyltransferase [Natrialba magadii ATCC 43099]
Length = 187

Score = 42.4 bits (98), Expect = 0.030, Method: Compositional matrix adjust.
Identities = 22/68 (32%), Positives = 37/68 (54%), Gaps = 2/68 (2%)

Query: 80 RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEA 139
R+ +W E ++V +QR G+G+ L HLL G + V + N+P++ L+E
Sbjct: 110 RDEIEW--ELAIFVLQDYQRAGIGTHLLEHLLGHASDVGIERVWLTVERWNNPAIALYER 167

Query: 140 LGYTARGT 147
+G+ A GT
Sbjct: 168 VGFEASGT 175

>ref|YP_002550145.1| acetyltransferase protein [Agrobacterium vitis S4]
gb|ACM37136.1| acetyltransferase protein [Agrobacterium vitis S4]
Length = 160

Score = 42.0 bits (97), Expect = 0.032, Method: Compositional matrix adjust.
Identities = 36/138 (26%), Positives = 61/138 (44%), Gaps = 9/138 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEV-EGVV 68
IRP+T+ D + D +N E R PQ + + +DR VA+ EG +
Sbjct: 3 IRPSTSLDAQGMSDALN---EIFAAGLRKSAGDPQLVLANYIEHKDRIECSVAQDDEGRI 59

Query: 69 AGIAYAGPWKARNAYD---WTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
G N Y W + T ++S R G+GS L+ L++ ++ ++ A
Sbjct: 60 FGFQSLRFATVDNPNYGTPEGWGIIGT-HISPLAARRGIGSALFRATLQAAKSFPLDNIEA 118

Query: 125 VIGLPNDPSVRLHEALGY 142
IG N+ + +EA+G+
Sbjct: 119 AIGADNEAGLAYYEAMGF 136

>ref|YP_909505.1| N-acetyl transferase [Bifidobacterium adolescentis ATCC 15703]
dbj|BAF39423.1| possible N-acetyl transferase [Bifidobacterium adolescentis ATCC 15703]
Length = 174

Score = 42.0 bits (97), Expect = 0.033, Method: Compositional matrix adjust.
Identities = 39/170 (22%), Positives = 63/170 (37%), Gaps = 10/170 (5%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV- 67
R AT D+ A+ DI N + + T P+T + +E D Y V V
Sbjct: 5 SFRIATQDDIQAITDIYNAAVIRGGSSADTTPRTYAQRKAWVESHHDPYAVFVTTVPATD 64

Query: 68 -----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
+ G + + R YD + Y++ Q G G+ LL +
Sbjct: 65 AATEGGERIIGFSALSVFYDRAGYDGVTDLAYYIAPEWQGRGAGTFTLARLLDECRNRHM 124

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFWRQDF 168

+ +I N S+ L + G+T G + +AA G D+ +W D
 Sbjct: 125 RKACGIIFADNRGSIAlMKHFGFTQFGLMPQAATDSTGTMRDMSYWHLDL 174

>ref|ZP_04850775.1| conserved hypothetical protein [Paenibacillus sp. oral taxon 786
 str. D14]
 gb|EES74965.1| conserved hypothetical protein [Paenibacillus sp. oral taxon 786
 str. D14]
 Length = 169

Score = 42.0 bits (97), Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 27/105 (25%), Positives = 53/105 (50%), Gaps = 3/105 (2%)

Query: 38 TEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWK-ARNAYDWTVESTVYVSHR 96
 T+ + + W+D LQD +V + V A+ G + A Y+ + S +Y+
 Sbjct: 40 TQERRVKLWLDIFASLQDDDRIVVGKDGDCVVAFAHGGKCREAELGYEGELYS-IYILKE 98

Query: 97 HQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALG 141
 +Q +GLG L H++ + ++G S++A + L +PS+ + +G
 Sbjct: 99 YQGMGLGQQLLNHIINHLRSKGNTSMMAWV-LEGNPSIDFYLRMG 142

>ref|YP_003410975.1| GCN5-related N-acetyltransferase [Geodermatophilus obscurus DSM
 43160]
 gb|ADB76604.1| GCN5-related N-acetyltransferase [Geodermatophilus obscurus DSM
 43160]
 Length = 169

Score = 42.0 bits (97), Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 33/86 (38%), Positives = 45/86 (52%), Gaps = 4/86 (4%)

Query: 59 WLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 +LVAEV+GV AG G W+ V+ VYV+ +R GL L L +S A G
 Sbjct: 62 FLVAEVDGVPAGC---GGWRVHEPGVAEVKR-VYVAPGFRRQGLAQLLMGALEESAAAAG 117

Query: 119 FKSVAVIGLPNDPSVRLHEALGYTA 144
 +SVV G ++ L+ ALGYT+
 Sbjct: 118 VRSVVLNSGSRQPEALALYAALGYTS 143

>ref|ZP_07953439.1| ribosomal-protein-alanine acetyltransferase [Gemella moribillum
 M424]
 gb|EFV36313.1| ribosomal-protein-alanine acetyltransferase [Gemella moribillum
 M424]
 Length = 150

Score = 42.0 bits (97), Expect = 0.034, Method: Compositional matrix adjust.
 Identities = 20/87 (22%), Positives = 43/87 (49%), Gaps = 4/87 (4%)

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130
 I + G W + Y + + + HQ LG +T++++ ++ +G K + + + N
 Sbjct: 53 IGFCGGWLVSDEYQI---NKIVIDKPHQNKKLQGIFFTYIMQVLKLGKVKALVEVRVSN 109

Query: 131 DPSVRLHEALGYTARGTLRAAGYKHGG 157
 P++ ++E G+ A +R YK+ G
 Sbjct: 110 MPAITIEKSGF-ATIDIRKNYYKNNG 135

>ref|YP_003404965.1| GCN5-related N-acetyltransferase [Haloterrigena turkmenica DSM
 5511]
 gb|ADB62292.1| GCN5-related N-acetyltransferase [Haloterrigena turkmenica DSM
 5511]
 Length = 186

Score = 42.0 bits (97), Expect = 0.037, Method: Compositional matrix adjust.
Identities = 22/68 (32%), Positives = 37/68 (54%), Gaps = 2/68 (2%)

Query: 80 RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEA 139
R+ +W E ++V +QR G+G+ L HLL G + V + N+P++ L+E
Sbjct: 110 RSDVEW--ELAIFVLQAYQRAGIGTKLLEHLLGHAADIGIEQVWLTVERWNNPAIALYER 167

Query: 140 LGYTARGET 147
+G+ A GT
Sbjct: 168 VGFEATGT 175

>dbj|BAI77988.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
Length = 193

Score = 42.0 bits (97), Expect = 0.037, Method: Compositional matrix adjust.
Identities = 41/147 (27%), Positives = 64/147 (43%), Gaps = 18/147 (12%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLW 61
R P IR T D+ A+ +I N + + T P T +E +++ +R D P V
Sbjct: 12 RLPRGIREFTEDDLEAMNIFNETAGSGANSVPVTRPMTYEEVKFYVNLKYR--DGLPVYV 69

Query: 62 AEVEGVVAGIAYAGPWKARNAYDW-----TVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
E G V G W + N + W T E+ +YV H G+G L +
Sbjct: 70 YERRGEVLG-----WLSINRFSGWTQACYRTGETAIYVRGDHFGSGIGVLLCKATVILG 123

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALG 141
+ G +++VA I N PS ++ A+G
Sbjct: 124 QQAGLENLVAVIMAANTPSQKIVTAVG 150

>ref|YP_003476587.1| GCN5-related N-acetyltransferase [Thermoanaerobacter italicus Ab9]
gb|ADD02025.1| GCN5-related N-acetyltransferase [Thermoanaerobacter italicus Ab9]
Length = 178

Score = 42.0 bits (97), Expect = 0.040, Method: Compositional matrix adjust.
Identities = 34/158 (21%), Positives = 75/158 (47%), Gaps = 17/158 (10%)

Query: 3 PERRP-VEIRPATAADMAAVCDIVNH-----YIETSTVNFRTPEQTPQEWIDDLERLQD 55
P++ P + IR A D + ++N Y+ + T N+ E + ++ I +L+R +D
Sbjct: 8 PQKEPQLVIREAKIKDARGIIKLLNSVGREKLYMVSETFNWSEEEE--KQLIKNLDNRKD 65

Query: 56 RYPWLVAEVEGVVAG----IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
LVA+ G + G Y G ++ + E + + R + +G+G+ L+T +
Sbjct: 66 --LILVADYGGIEIVGCLTLFRYYGGRSSKVQH--VGEIGISIDARFRNMGIGTKLFTEAI 121

Query: 112 KSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGETLR 149
+++G++ + + N+ ++ L++ G+ G R
Sbjct: 122 GWAKSKGYEKLCLSVFSTNEVAIHLYKKFGFEEEGRRR 159

>dbj|BAI77987.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
Length = 193

Score = 42.0 bits (97), Expect = 0.040, Method: Compositional matrix adjust.
Identities = 41/147 (27%), Positives = 64/147 (43%), Gaps = 18/147 (12%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLW 61
R P IR T D+ A+ +I N + + T P T +E +++ +R D P V
Sbjct: 12 RLPRGIREFTENDLEAMNIFNETAGSGANSVPVTRPMTYEEVKFYVNLKYR--DGLPVYV 69

Query: 62 AEVEGVVAGIAYAGPWKARNAYDW-----TVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 E G V G W + N + W T E+ +YV H G+G L +
 Sbjct: 70 YERRGEVLG-----WLSINRFSWGTQACYRTGETAIYVRGDHFGSGIGVLLCKATVILG 123

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALG 141
 + G +++VA I N PS ++ A+G
 Sbjct: 124 KQAGLENLVAWIMAANTPSQKIVTAVG 150

>ref|YP_003194023.1| N-acetyltransferase [Robiginitalea biformata HTCC2501]
 gb|EAR16244.1| N-acetyltransferase [Robiginitalea biformata HTCC2501]
 Length = 162

Score = 41.6 bits (96), Expect = 0.041, Method: Compositional matrix adjust.
 Identities = 39/140 (27%), Positives = 63/140 (45%), Gaps = 17/140 (12%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQ---TPQEWIDDLERLQDRYPWLVAEVE 65
 IRPA ADM V ++ + EP T Q+ + D ++ VAE +
 Sbjct: 5 IRPAEEADMKVEYRLIRE-----LAVYEREPDAVEVTEQQLLRDGFGPDPKFRCFVAERD 59

Query: 66 GVVAGIAYAGP----WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 G + G+A P WK + +E + V+ + LG+GS L T +++ QG K
 Sbjct: 60 GGIVGMALIYPRYSTWKGPANH---LEDLI-VTEEARGLVGSALLTEVIRYASGQGVKR 115

Query: 122 VVAVIGLPNDPSVRLHEALG 141
 V + N+P++ +EA G
 Sbjct: 116 VCWEVLWDWNEPAIDFYEARG 135

>ref|YP_863525.1| GNAT family acetyltransferase [Gramella forsetii KT0803]
 emb|CAL68458.1| GNAT family acetyltransferase-possibly polyamine acetyltransferase
 [Gramella forsetii KT0803]
 Length = 162

Score = 41.6 bits (96), Expect = 0.043, Method: Compositional matrix adjust.
 Identities = 36/124 (29%), Positives = 55/124 (44%), Gaps = 21/124 (16%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQD-----RYPWL 60
 + IR AT DM AV +++N F EP+ ID+ + ++D +
 Sbjct: 2 EINIRKATKVDMAVLELINE-----LAVFEKEPEAV--IIDENDLIRDGFGENPAFHCF 54

Query: 61 VAEVEGVVAGIAYA---GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
 VAE G + G+A WK + + +E V V + + GLGS LYT ++K
 Sbjct: 55 VAEANGKIEGMALLYFRYSTWKGKTVH---LEDLV-VREKFRGKGLGSALYTKVIKFAAE 110

Query: 117 QGFK 120
 Q K
 Sbjct: 111 QKVK 114

>ref|ZP_02028574.1| hypothetical protein BIFADO_01007 [Bifidobacterium adolescentis
 L2-32]
 gb|EDN84075.1| hypothetical protein BIFADO_01007 [Bifidobacterium adolescentis
 L2-32]
 Length = 199

Score = 41.6 bits (96), Expect = 0.043, Method: Compositional matrix adjust.
 Identities = 41/170 (24%), Positives = 65/170 (38%), Gaps = 10/170 (5%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLV----- 61
 R AT D+ A+ DI N + + T P+T + +E D Y V
 Sbjct: 30 SFRIATQDDIQAITDIYNAAVIRGGSSADTTPRTYAQRKAWVESHHDPYAVFVTTVPATD 89

Query: 62 AEVEGV--VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
A EG + G + + R YD + Y++ Q G G+ LL +
Sbjct: 90 AATEGGERIIGFSALSVMFYDRAGYDGVTDLAYYIAPEWQGRGAGTFTLAKLLDECNRNHM 149

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFQWQDF 168
+ +I N S+ L + G+T G + +AA G D+ +W D
Sbjct: 150 RKACGIIIFADNRGSIAMKHFQFTQFGLMPQAATDSTGTMRDMSYWHLDL 199

>ref|YP_003859178.1| (SSU ribosomal protein S18P)-alanine acetyltransferase
[Ignisphaera
aggregans DSM 17230]
gb|ADM27298.1| (SSU ribosomal protein S18P)-alanine acetyltransferase [Ignisphaera
aggregans DSM 17230]
Length = 161

Score = 41.6 bits (96), Expect = 0.045, Method: Compositional matrix adjust.
Identities = 34/144 (23%), Positives = 68/144 (47%), Gaps = 20/144 (13%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQ--TPQEWIDDLERLQDRYPWLVAEVE 65
+ IRPA+ D+ +V +N P+ WI+ +E+ D + VAEV
Sbjct: 8 IRIRPASMDLDSVI-----AINIECLPEHYLKSFWIEHIEKWNDF--YVAEVN 55

Query: 66 GVVAGIAYA---GPWKARNAYDWTVES-TVYVSHRHQRLGLGSTLYTHLLKSMEA-QGF 119
+ G A A G +N + ++ V +++R G+ +L + L+ +++ G
Sbjct: 56 NEIVGYALARVENGSPITKNMFSKVGHVVSIAVREKYRRKGIATMLMSALIYTLKTIYGA 115

Query: 120 KSVVAVIGLPNDPSVRLHEALGYT 143
+ V + + N+P++RL++ LG+
Sbjct: 116 EEVYLEVRVSNEPAIRLYQKLGFEV 139

>ref|YP_002544534.1| N-acetyltransferase protein [Agrobacterium radiobacter K84]
gb|ACM26606.1| N-acetyltransferase protein [Agrobacterium radiobacter K84]
Length = 154

Score = 41.6 bits (96), Expect = 0.048, Method: Compositional matrix adjust.
Identities = 38/140 (27%), Positives = 61/140 (43%), Gaps = 9/140 (6%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-G 66
+ IRPA + D + +++N E R + + R VAE E G
Sbjct: 1 MNIRPAESIDAQGMNVLN---EIFDAGLRKSAGDVTLVLAQYIEHEHRIECSVAEDEQG 57

Query: 67 VVAGIAYAGPWKARNAY----DWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
+ G A N Y DW + T +VS R R G+GS L+ L++ + G +++
Sbjct: 58 QILGFQSLRYAVAGNPYGVSEWDGIIGT-HVSPRAGRQIGSALFQATLRAAKTFGLQNI 116

Query: 123 VAVIGLPNDPSVRLHEALGY 142
A IG N + +EA+G+
Sbjct: 117 DATIGEGNKMGLAYYEAMGF 136

>ref|YP_004152368.1| gcn5-related N-acetyltransferase [Variovorax paradoxus EPS]
gb|ADU34257.1| GCN5-related N-acetyltransferase [Variovorax paradoxus EPS]
Length = 160

Score = 41.6 bits (96), Expect = 0.050, Method: Compositional matrix adjust.
Identities = 33/139 (23%), Positives = 61/139 (43%), Gaps = 3/139 (2%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGVVAG 70
R AT D+ AV + H E +P +E+ + + + + V E++G VAG
Sbjct: 3 RLATLEDLHAVFTLYMH--EKVVPYLYGDPMPLEEFRIYQEMLESRRFFVYELDGRVAG 60

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130

A + R + ++ + H + G+ + + + ++A G K + + N

Sbjct: 61 FYRATRPYGRVQHVASLGLTAVDPTLHGK-GVALAMVSAIDELKAAGVKRIELCVESDN 119

Query: 131 DPSVRLHEALGYTARGTLR 149

P +R +E LG+ GTLR

Sbjct: 120 APGLRFYEKLGFGQREGTLR 138

>ref|YP_038811.1| acetyltransferase [Bacillus thuringiensis serovar konkukian str. 97-27]

ref|ZP_03238213.1| acetyltransferase, gnat family [Bacillus cereus H3081.97]

ref|YP_002340826.1| acetyltransferase, gnat family [Bacillus cereus AH187]

ref|YP_002532296.1| acetyltransferase, gnat family [Bacillus cereus Q1]

gb|AAT60954.1| possible acetyltransferase, GNAT family [Bacillus thuringiensis serovar konkukian str. 97-27]

gb|EDZ55877.1| acetyltransferase, gnat family [Bacillus cereus H3081.97]

gb|ACJ79527.1| acetyltransferase, gnat family [Bacillus cereus AH187]

gb|ACM15007.1| possible acetyltransferase, GNAT family [Bacillus cereus Q1]

Length = 174

Score = 41.6 bits (96), Expect = 0.050, Method: Compositional matrix adjust.

Identities = 15/42 (35%), Positives = 30/42 (71%), Gaps = 3/42 (7%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF---WQRDF 168

ND +++L+++LG+ GT + A +++G WHD+ F +QR++

Sbjct: 132 NDRAIKLYKSLGFGHEGTCKEAI FRNGTWH DIEFFALFQRNY 173

>ref|ZP_06499389.1| GCN5-related N-acetyltransferase [Pseudomonas syringae pv. syringae

FF5]

Length = 161

Score = 41.6 bits (96), Expect = 0.050, Method: Compositional matrix adjust.

Identities = 28/102 (27%), Positives = 47/102 (46%), Gaps = 3/102 (2%)

Query: 60 LVAEEVGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QG 118

LVAE +G+V G A ++ R + + + V+ H R G+G L L +

Sbjct: 54 LVAERDGMVVGCMALYRFQGRQH--VADFWMGVADSHHRQGIGDLLLLNELTATASRWMM 111

Query: 119 FKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160

K + + + N P++ L+E G+ GT R Y+ G + D

Sbjct: 112 LKRLLETVFVDNKPALALYEKNGFVIEGTHRKFA YRDGEYID 153

>ref|ZP_05365511.1| phosphinothricin N-acetyltransferase [Corynebacterium tuberculoostearicum SK141]

gb|EET77600.1| phosphinothricin N-acetyltransferase [Corynebacterium tuberculoostearicum SK141]

Length = 189

Score = 41.6 bits (96), Expect = 0.051, Method: Compositional matrix adjust.

Identities = 42/180 (23%), Positives = 72/180 (40%), Gaps = 8/180 (4%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63

+++ IRP TAAD + +I + T + T T +E+ + + + + A

Sbjct: 13 KKKDFRIRPFTAADYPQMREIYEQGLNTGHATYETRSLTFEEFKAG-KIMPSVHVAVEAN 71

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123

+ V G A P R + VE ++Y+ Q G+G L L++ + ++

Sbjct: 72 DDSKVLGWVSAAPVSTRTVFHGVVEDSIYLGAEAQGRGIGGALLDRLEVCCKDLHKWAIH 131

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLR-----AAGYKHGGWHDVGFQWQDFELPAPPRPVR 178
 + I N S LH++ G+ GT G G W D ++ LP P R
 Sbjct: 132 SWIFPENAGSAGLHKS RGFVKVGTYSMAKMTYGELAGQWRD TDVYE--LLLPKPEEK R 189

>ref|ZP_00518247.1| GCN5-related N-acetyltransferase [Crocospaera watsonii WH 8501]
 gb|EAM48673.1| GCN5-related N-acetyltransferase [Crocospaera watsonii WH 8501]
 Length = 179

Score = 41.6 bits (96), Expect = 0.052, Method: Compositional matrix adjust.
 Identities = 35/152 (23%), Positives = 64/152 (42%), Gaps = 14/152 (9%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAE-- 63
 +IR A D+ + +I N I + + T + +W ER + YP V E
 Sbjct: 3 KIRLANLEDLEKIVNIYND SIPSRIATGDLQKITVESRLK WFK--ERDTNHYPIWVMEDH 60

Query: 64 -----VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA 116
 V+ V G + R AY T E ++Y++ +++ G+G L +++
 Sbjct: 61 NQSSTTGKVNQVVGWISLQHFYCRPAYKSTAEISLYIAEKYRGQGIGKKLLEYVIEESPK 120

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGYTARGTL 148
 G +++ I N PS+ L + + G L
 Sbjct: 121 LGLTNLLGFIFAHNKPSLNLFKKYNFQQWGYL 152

>ref|ZP_01040135.1| YnaD [Erythrobacter sp. NAP1]
 gb|EAQ30606.1| YnaD [Erythrobacter sp. NAP1]
 Length = 180

Score = 41.2 bits (95), Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 33/109 (30%), Positives = 51/109 (46%), Gaps = 11/109 (10%)

Query: 59 WLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQ-RLGLGSTLYTHLLK----- 112
 W+ + G VAG A P A++ VE Y++ H+ R G+ L++
 Sbjct: 63 WIAEDAGGDVAGRFVAFP-----AHEKGVEEVGYITAIHRTREGVARECMEALIRHLFTA 117

Query: 113 SMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
 ++E +G + + A + N SVRL EALG+T LR H G D+
 Sbjct: 118 AIEDEGARKLTA EVDTRNAASVRLLEALGFTREAH LREHETTHAGLCDI 166

>ref|YP_001525754.1| acetyltransferase [Azorhizobium caulinodans ORS 571]
 dbj|BAF88836.1| acetyltransferase [Azorhizobium caulinodans ORS 571]
 Length = 173

Score = 41.2 bits (95), Expect = 0.054, Method: Compositional matrix adjust.
 Identities = 47/168 (27%), Positives = 71/168 (42%), Gaps = 11/168 (6%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV 64
 RRPV+ A A M + N + +V RT+ +EWI ++AE
 Sbjct: 13 RRPVDADFAVLAQMRRDSRLQNMLL---SVPERTDDDAVREWIARRSSAPGGLFRVIAET 69

Query: 65 EGVVAG-IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK-SMEAQGFKSV 122
 +G G I + + AY + ++ ++ G+G+ + LL + E G S+
 Sbjct: 70 DGAAVGFIQISRVDEPPKAY-----GGIALAEGYRGRGVGAVALSALLMIAREELGLISL 124

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW-HDVGFQWQDFE 169
 +A I N S+RLHE GY G + G HDV QR FE
 Sbjct: 125 LAEIRTDNPSSIRLHERFGYRRVGVMD EHF LGTDGQRH DVLQMQRFE 172

>ref|ZP_05629105.1| sortase and related acyltransferase [Actinobacillus minor 202]
 gb|EEV24437.1| sortase and related acyltransferase [Actinobacillus minor 202]

Length = 170

Score = 41.2 bits (95), Expect = 0.055, Method: Compositional matrix adjust.
Identities = 34/142 (23%), Positives = 58/142 (40%), Gaps = 4/142 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP---QEWIDDLERLQDRYPWLVAEV 64
+ IR + D + I N I T + E T + W D ++YP E
Sbjct: 1 MRIRKSIEDTFETILAIYNQAIPHTQITADLELATTNRRRAWFD-FHLSSEKYPITWVED 59

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
E +AG P+ R A+ T E ++Y+ + + G GS + + M G +++A
Sbjct: 60 EEGIAGWFSFSPFYERPAFIHTSEISIYLDGKAKGKGYSSEIIQFMQAEMLNHGIHTLMA 119

Query: 125 VIGLPNDPSVRLHEALGYTARG 146
+ N+ S +L G+ G
Sbjct: 120 YVFEMNEVSQKLMFKHGFQWQ 141

>ref|ZP_05784948.1| putative phosphinothricin N-acetyltransferase [Silicibacter
lacuscaerulensis ITI-1157]
gb|EEX08064.1| putative phosphinothricin N-acetyltransferase [Silicibacter
lacuscaerulensis ITI-1157]
Length = 96

Score = 41.2 bits (95), Expect = 0.057, Method: Compositional matrix adjust.
Identities = 28/94 (29%), Positives = 44/94 (46%), Gaps = 4/94 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYP-WLVAEVEGVV 68
+RPA D A+ I N + + V F T+ ++P +D+ R P + VAE V
Sbjct: 3 VRPARTQDAVAIAAITNQVVRDTLVTFTTQERSPASIAEDIAA---RGPAFQVAERGNQV 59

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGL 102
G A G ++ YD T E T+ + + Q G+
Sbjct: 60 VGFATYGRFRTGPGYDATREHTIMLDPQAQGRGV 93

>ref|ZP_07326841.1| GCN5-related N-acetyltransferase [Acetivibrio cellulolyticus CD2]
gb|EFL61961.1| GCN5-related N-acetyltransferase [Acetivibrio cellulolyticus CD2]
Length = 144

Score = 41.2 bits (95), Expect = 0.057, Method: Compositional matrix adjust.
Identities = 27/104 (25%), Positives = 47/104 (45%), Gaps = 7/104 (6%)

Query: 48 DDLERLQDRYP--WLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGST 105
D +ER R P V E++G + G G R+ Y + VS +Q +G+
Sbjct: 33 DGMERFLRRNPNTSFVVEIDGKIVGSILCGN-DGRSGYIYHA----CVSREYQNKIGTR 87

Query: 106 LYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLR 149
L + ++++A+G + + + ND R E +G+ R LR
Sbjct: 88 LVEKVFEALKAEGISDITLAVYINNDGGRFWRMGFRDRDFLR 131

>ref|YP_786135.1| acetyltransferase [Bordetella avium 197N]
emb|CAJ49224.1| putative acetyltransferase [Bordetella avium 197N]
Length = 152

Score = 41.2 bits (95), Expect = 0.058, Method: Compositional matrix adjust.
Identities = 40/146 (27%), Positives = 66/146 (45%), Gaps = 10/146 (6%)

Query: 1 MSPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL 60
MS E +++R A D+ + D+ +E V Q + DD+ + RY W
Sbjct: 1 MSKESPELQRTAGEDDVPFLDLRRRTMEPHLV-----QDHVPFDDDIHMQRIRYHWE 54

Query: 61 VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
 A + V+ AG +K + + ++ Q LGLG+ L +L +AQ
 Sbjct: 55 DARI--VLIDQQPAGLFKVHLDEEGLYVIQIQLAPAWQGLGLGARLLNTVLRADAQKLA 112

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARG 146
 +AV L N+P+ RL+E LG+ +G
 Sbjct: 113 VRLAV--LKNNPARRLYERLGF LTQG 136

>ref|ZP_04148126.1| hypothetical protein bthur0001_46870 [Bacillus thuringiensis
 serovar tochiensis BGSC 4Y1]
 gb|EEM20171.1| hypothetical protein bthur0001_46870 [Bacillus thuringiensis
 serovar tochiensis BGSC 4Y1]
 Length = 174

Score = 41.2 bits (95), Expect = 0.060, Method: Compositional matrix adjust.
 Identities = 15/42 (35%), Positives = 30/42 (71%), Gaps = 3/42 (7%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGF---WQRDF 168
 ND +++L+++LG+ GT + A +++G WHD+ F +QR++
 Sbjct: 132 NDRAIKLYKSLGFQHEGTCKEAI FRNGTWH DIEFFALFQRNY 173

>ref|ZP_05075392.1| acetyltransferase, gnat family [Rhodobacterales bacterium
 HTCC2083]
 gb|EDZ43052.1| acetyltransferase, gnat family [Rhodobacteraceae bacterium
 HTCC2083]
 Length = 162

Score = 41.2 bits (95), Expect = 0.060, Method: Compositional matrix adjust.
 Identities = 33/136 (24%), Positives = 59/136 (43%), Gaps = 3/136 (2%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVE-G 66
 + IRP +D+ + +++N IE P E + R +R W +AE + G
 Sbjct: 3 ITIRPLQMSDIRLMTTELLNEIIEIGGTTAYLNPLPEAELACWVARGTERTSWTIAEDDTG 62

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + G +A P ++ + V V + G+G L+ K M+ GF+ + A I
 Sbjct: 63 KLVGFQWAEPHALLPPEAASIATFVRVGVVGR--GIGKRLFAETSKHMKRFGFEWINASI 120

Query: 127 GLPNDPSVRLHEALGY 142
 ND +R + +G+
 Sbjct: 121 RSDNDSGLRYYAKMGF 136

>emb|CBG92007.1| phosphinothricin acetyltransferase [Streptomyces hygroscopicus]
 Length = 20

Score = 41.2 bits (95), Expect = 0.061, Method: Compositional matrix adjust.
 Identities = 18/20 (90%), Positives = 18/20 (90%)

Query: 31 TSTVNFRTEPQTPQEWIDDL 50
 TSTVNFRTEPQ PQEW DDL
 Sbjct: 1 TSTVNFRTEPQEPQEWTDLL 20

>ref|ZP_01154999.1| acetyltransferase, GNAT family protein [Oceanicola granulosus
 HTCC2516]
 gb|EAR53109.1| acetyltransferase, GNAT family protein [Oceanicola granulosus
 HTCC2516]
 Length = 158

Score = 41.2 bits (95), Expect = 0.062, Method: Compositional matrix adjust.

Identities = 36/140 (25%), Positives = 59/140 (42%), Gaps = 10/140 (7%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE-GVV 68
          +RPA+ AD A +C ++N I          P TP +          D          +AE E G V
Sbjct: 3   LRPASDADAAGLCVINPLIAAGGTTAHRFPFTPARMVAHYIAPPDGCCTLAEDEAGTV 62

Query: 69  AGIAYAGPWKARNAY-----DWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
          G +          +A A+          W + +T +V   H R G+GS L+          ++ A G ++
Sbjct: 63  LG--FQSLVRADPAFGDGIPAGWGIIAT-FVRAGHGRGGIGSALFAVTREAAARAAGLVAI 119

Query: 123  VAVIGLPNDPSVRLHEALGY 142
          A I   N   +   +   +G+
Sbjct: 120  DATIRRENAGGLAYYGRMGF 139
```

>gb|ADZ81183.1| GCN5-related N-acetyltransferase [Sphingobacterium sp. 21]
Length = 146

Score = 41.2 bits (95), Expect = 0.064, Method: Compositional matrix adjust.
Identities = 31/140 (22%), Positives = 64/140 (45%), Gaps = 23/140 (16%)

```
Query: 10  IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDR-----YPWLVA 62
          IR A   D + + ++++          + P+E   LE ++D          +   VA
Sbjct: 2   IRKAQKEDCSRILELIHE-----LALYERAPEEVTVSLEEMEDAGFGANPVWEAFVA 53

Query: 63  EVEGVVAGIAYA---GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 118
          E++GV+ GIA          WK R Y   +E + V+   + G+G L+   +++ M+ +G
Sbjct: 54  EIDGVIQIGIALYYTRYSTWKGRRLY---LEDLI-VTQEMRGRGIGKLLFDKVIEEMQNKG 109

Query: 119  FKSVVAVIGLPNDPSVRLHE 138
          + +V +   N+P++ ++
Sbjct: 110  YSGMVWQVLEWNEPAINFYK 129
```

>ref|YP_003388727.1| GCN5-related N-acetyltransferase [Spirosoma linguale DSM 74]
gb|ADB39928.1| GCN5-related N-acetyltransferase [Spirosoma linguale DSM 74]
Length = 150

Score = 41.2 bits (95), Expect = 0.066, Method: Compositional matrix adjust.
Identities = 35/146 (23%), Positives = 56/146 (38%), Gaps = 10/146 (6%)

```
Query: 24  IVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY---PWLVAEVEGVVAGIAYAGPWKAR 80
          I   I+T          T+ +P          E +   Y   P LVA          V G A          R
Sbjct: 4   IYQQGIDTGNATMETQAPSP-----ETMAASYMASPQLVAVDGDTVIGYALLTAVSGR 56

Query: 81  NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEAL 140
          +   E ++Y+   ++ G+G L   L+   E +   ++ A I   N S+ LH+
Sbjct: 57  CIFAGVAEVSLEYIGAAYRGKGVGQQLLNRLIADSEEKNLWTLQASILRENTASIALHKRC 116

Query: 141  GYTARGTLRAAGYKHGGWHDVGFWR 166
          G+   G          G + G W D+   +R
Sbjct: 117  GFREIGYHERIGKRAGIWRDILLER 142
```

>gb|EFW82027.1| acetyltransferase [Pseudomonas syringae pv. glycinea str. B076]
Length = 161

Score = 41.2 bits (95), Expect = 0.067, Method: Compositional matrix adjust.
Identities = 31/125 (24%), Positives = 60/125 (48%), Gaps = 7/125 (5%)

```
Query: 41  QTPQEWIDDLERLQDRYPW----LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHR 96
          +TP + ++D+++L +          LVAE +G+V G A          ++ R +   + + V+
Sbjct: 31  RTPYQSVNDIKKLVEGRSASGLSLVAERDGI VVGCAMLYRFQGRRH--VADFWMGVADG 88
```

Query: 97 HQRLGLGSTLYTHL-LKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKH 155
 H R G+G L L + K + + + N+P++ L++ G+ GT R Y+
 Sbjct: 89 HHRQGIGDELLKELSATACRWMNVKRLELTVFVDNEPAIALYKKNGFVIEGTHRKFAIRD 148

Query: 156 GGWHD 160
 G + D
 Sbjct: 149 GEYID 153

>ref|ZP_04776977.1| ribosomal-protein-alanine acetyltransferase [Gemella haemolysans
 ATCC 10379]
 gb|EER67685.1| ribosomal-protein-alanine acetyltransferase [Gemella haemolysans
 ATCC 10379]
 Length = 150

Score = 40.8 bits (94), Expect = 0.073, Method: Compositional matrix adjust.
 Identities = 19/87 (21%), Positives = 43/87 (49%), Gaps = 4/87 (4%)

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130
 I + G W + Y + + + HQ LG +T++++ ++ +G K + + + N
 Sbjct: 53 IGFCGGWLVADEYQV---NKIVIDKPHQNKKLGGQIFFTYVMQLLKLKGKKAIVEVRVS 109

Query: 131 DPSVRLHEALGYTARGTLRAAGYKHGG 157
 P++ ++E G++ +R YK+ G
 Sbjct: 110 MPAITVYEKAGFSTI-DIRKNYYKNNG 135

>ref|YP_076248.1| putative acetyltransferase [Symbiobacterium thermophilum IAM 14863]
 dbj|BAD41404.1| putative acetyltransferase [Symbiobacterium thermophilum IAM 14863]
 Length = 165

Score = 40.8 bits (94), Expect = 0.075, Method: Compositional matrix adjust.
 Identities = 33/121 (27%), Positives = 55/121 (45%), Gaps = 3/121 (2%)

Query: 42 TPQEWIDDLERLQDRYPW-LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRL 100
 TP+ W LE + RY + LVAEV+G V G + ++ T + V Q
 Sbjct: 37 TPESWRKKLEGIDPRYDYLVAEVDGKVVGNVWLQRYRNSRTLH-TASLGIMVHDAWQGR 95

Query: 101 GLGSTLYTHLLKSMEAQGFKSVVAVIGLP-NDPSVRLHEALGYTARGTLRAAGYKHGGWH 159
 G+G L + + V + P N+ +++L+E+ G+ A G R A ++ G +
 Sbjct: 96 GIGRALMAAIDVADRWLNLVRLVELEVFPDNERAIKLYESFGFVAEGRKRMAAFRDGQYV 155

Query: 160 D 160
 D
 Sbjct: 156 D 156

>ref|ZP_03754730.1| hypothetical protein ROSEINA2194_03159 [Roseburia inulinivorans
 DSM 16841]
 gb|EEG93001.1| hypothetical protein ROSEINA2194_03159 [Roseburia inulinivorans DSM
 16841]
 Length = 145

Score = 40.8 bits (94), Expect = 0.077, Method: Compositional matrix adjust.
 Identities = 39/147 (26%), Positives = 64/147 (43%), Gaps = 16/147 (10%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 ++IR D AV +I ++P + Q ++D + +LVAE
 Sbjct: 2 IQIREMQVRDITNAVAEIERQIF-----SQPWSRQGFDAVN--LGNTVFLVAEENNR 51

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127

+ G Y G + A + + T + V H G+G L T LLK E +G +V +
 Sbjct: 52 IIG--YIGMYLAMDEGEITNVAVAPVERCH---GVGGMLLTTELLKIAENKGVARIVLEVR 106

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYK 154
 ND ++RL+E G+ G +R Y+

Sbjct: 107 ASNDSAIRLYERNGFVQCG-MRKGFYE 132

>ref|YP_002905889.1| putative acetyltransferase [Corynebacterium kroppenstedtii DSM
 44385]
 gb|ACR17346.1| putative acetyltransferase [Corynebacterium kroppenstedtii DSM
 44385]
 Length = 157

Score = 40.8 bits (94), Expect = 0.077, Method: Compositional matrix adjust.
 Identities = 41/154 (26%), Positives = 62/154 (40%), Gaps = 13/154 (8%)

Query: 14 TAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWL--VAEVEGVVAGI 71
 T D V I + T + P T +E++D + P L VAE EG + G
 Sbjct: 2 TRDDYPDVARIHQAGLNTGNGAYEASPTWEEFVDK-----KIPELCFVAEDEGTILGW 55

Query: 72 AYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPND 131
 P+ R + +E ++Y+ G+G+ L H + G ++ I N
 Sbjct: 56 VALMPFPHYRPSLTGFLEDSIYIDPAASGRGVGTALLEHSAAKAKEWGAWTITGWIFEDNS 115

Query: 132 PSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQW 165
 S LH G+ GTL+ +H GW D G W
 Sbjct: 116 ASQALHAKAGFRKVGTLQ----RH-GWMDYGPWS 144

>ref|ZP_04783922.1| phosphinothricin N-acetyltransferase [Weissella paramesenteroides
 ATCC 33313]
 gb|EER73858.1| phosphinothricin N-acetyltransferase [Weissella paramesenteroides
 ATCC 33313]
 Length = 137

Score = 40.8 bits (94), Expect = 0.079, Method: Compositional matrix adjust.
 Identities = 26/106 (24%), Positives = 52/106 (49%), Gaps = 4/106 (3%)

Query: 44 QEWIDDLERLQDRYP-WLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGL 102
 ++W D ++YP W++A+ + V+ G G + R AY T E ++Y+ + +
 Sbjct: 14 KKWFD--ASSHEKYPIWIIADDDQVI-GWCSLGAFYGRAAYQHTAEISYIDETTRGKHV 70

Query: 103 GSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTL 148
 G+ L ++ + +++VA + N PS+ L + G+ G L
 Sbjct: 71 GTQTIQFLATQLKQRDQLNIVAYVFRQNTPSMTLFKKQGFEQWGLL 116

>ref|ZP_04241767.1| hypothetical protein bcere0018_44690 [Bacillus cereus Rock1-15]
 gb|EEL26515.1| hypothetical protein bcere0018_44690 [Bacillus cereus Rock1-15]
 Length = 174

Score = 40.8 bits (94), Expect = 0.079, Method: Compositional matrix adjust.
 Identities = 14/43 (32%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWRQDFE 169
 ND +++L+++LG+ GT + A +++G WHD+ +QR+++
 Sbjct: 132 NDRAIKLYKSLGFQHEGTCKEAIFRNGNWHDIELFALFQRNYK 174

>ref|ZP_02613950.1| acetyltransferase [Clostridium botulinum NCTC 2916]
 gb|EDT81799.1| acetyltransferase [Clostridium botulinum NCTC 2916]
 Length = 179

Score = 40.8 bits (94), Expect = 0.082, Method: Compositional matrix adjust.
Identities = 13/32 (40%), Positives = 22/32 (68%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161

N+ +++L+E +G+ G LR A Y+ G WHD+

Sbjct: 132 NERAIKLYEKMGFICEGILRQALYRAGNWHDI 163

>ref|YP_001895573.1| GCN5-related N-acetyltransferase [Burkholderia phytofirmans PsJN]
gb|ACD16349.1| GCN5-related N-acetyltransferase [Burkholderia phytofirmans PsJN]
Length = 174

Score = 40.8 bits (94), Expect = 0.083, Method: Compositional matrix adjust.
Identities = 40/144 (27%), Positives = 64/144 (44%), Gaps = 8/144 (5%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEG- 66

R AT D+ A+ I N + + V +P ++ W Q R W+V E

Sbjct: 6 R DATLDDLPAIVAIYNSTVPSRQVTADLDPVSVESRMGWFH-AHGPQKRPLWVVEATEQP 64

Query: 67 --VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124

V+A ++++ + R AY T E ++Y+ + GLG L L + A G SV+

Sbjct: 65 GRVIAWLSFS-DFYGRPAYQRTAEVSIYLDSEARGRLGKQLLAASLAAPALGIDSVLG 123

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148

I N+ S+RL G+ G+L

Sbjct: 124 FIFGHNEASLRLFRGFGFDTWGSL 147

>ref|ZP_08132925.1| phosphinothricin N-acetyltransferase [Kingella denitrificans ATCC
33394]
gb|EGC17841.1| phosphinothricin N-acetyltransferase [Kingella denitrificans ATCC
33394]
Length = 166

Score = 40.8 bits (94), Expect = 0.083, Method: Compositional matrix adjust.
Identities = 36/143 (25%), Positives = 62/143 (43%), Gaps = 8/143 (5%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVE 65

R A D+A + I N + + +P + Q W D Q P V + +

Sbjct: 4 RRARQGD LAEIVAIYNSTVASGQSTADLQPIRIEQRQAWFD--AHRQPHRPLYVVRDDQQ 61

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 125

+VA +++ + R AY + E ++Y+ ++ GLG + +L G ++V+AV

Sbjct: 62 NMVAWASFSD-YPREAYRISAEISYIHESYRGRGLGREILAFMLALAPDLGIRNVLA 120

Query: 126 IGLPNDPSVRLHEALGYTARGTL 148

I N S+ L E G+ G L

Sbjct: 121 IFAHNAASLHLFERFGFETWGRL 143

>emb|CBG92010.1| pat [Streptomyces viridochromogenes]
Length = 19

Score = 40.8 bits (94), Expect = 0.085, Method: Compositional matrix adjust.
Identities = 19/19 (100%), Positives = 19/19 (100%)

Query: 1 MSPERRPVEIRPATAADMA 19

MSPERRPVEIRPATAADMA

Sbjct: 1 MSPERRPVEIRPATAADMA 19

>ref|ZP_06604042.1| ribosomal-protein-alanine acetyltransferase [Selenomonas noxia ATCC

43541]
gb|EFF65754.1| ribosomal-protein-alanine acetyltransferase [Selenomonas noxia ATCC 43541]
Length = 155

Score = 40.8 bits (94), Expect = 0.085, Method: Compositional matrix adjust.
Identities = 20/79 (25%), Positives = 41/79 (51%), Gaps = 3/79 (3%)

Query: 71 IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130
I + G W + ++ + + + + GLG L L+ + A+G + + + + N
Sbjct: 46 IGFGGCWIS---FEEAQVTNIALTTAQRGRGLGRILMKKLMHAAAARGAECMTLEVRMSN 102

Query: 131 DPSVRLHEALGYTARGTLR 149
P++RL+E LG++A G R
Sbjct: 103 TPAIRLYEGLGFSAVGVRR 121

>ref|ZP_04448201.1| hypothetical protein BIFANG_03206 [Bifidobacterium angulatum DSM 20098]

gb|EEP20637.1| hypothetical protein BIFANG_03206 [Bifidobacterium angulatum DSM 20098]
Length = 222

Score = 40.8 bits (94), Expect = 0.086, Method: Compositional matrix adjust.
Identities = 38/169 (22%), Positives = 65/169 (38%), Gaps = 16/169 (9%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWLVAEVEGV 67
R A +D+ A+ DI N + + P+T ++ W+D + P+ V E V
Sbjct: 59 RQAAESDIQALTDIYNAAVVVGSSADIAPRTIEQRRWL D-----SHKAPYAVFVTEAV 113

Query: 68 -----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
V G + + R Y+ + Y++ Q G+G+ LL + +
Sbjct: 114 RGDGTRQVVGFSALS VFYDRAGYNGVTDLAYYIAPEWQGRGVGTFTLRSLLD EARKRHRM 173

Query: 121 SVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKH-GGWHVDVGFWRD 168
+I N S+ L G+T G + AA G D+ +W D
Sbjct: 174 KACGIIFADNAGSIALMHFHFGFTQFGLMPAAATDSTGTMRDMSYWYLDL 222

>ref|ZP_04281143.1| hypothetical protein bcere0011_44930 [Bacillus cereus m1550]
gb|EEK87221.1| hypothetical protein bcere0011_44930 [Bacillus cereus m1550]
Length = 174

Score = 40.8 bits (94), Expect = 0.087, Method: Compositional matrix adjust.
Identities = 14/43 (32%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
ND +++L+++LG+ GT + A +++G WHD+ +QR+++
Sbjct: 132 NDRAIKLYKSLGFQHEGTCKEAI FRNGNWHDIELFALFQRNYK 174

>ref|ZP_06860143.1| acetyltransferase, gnat family protein [Citromicrobium bathyomarinum JL354]

Length = 181

Score = 40.8 bits (94), Expect = 0.088, Method: Compositional matrix adjust.
Identities = 30/89 (33%), Positives = 41/89 (46%), Gaps = 3/89 (3%)

Query: 44 QE WIDDLERLQDRYPWLVAEV--EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLG 101
Q+ ID L R D LVA E V+ IA++ + DW + V QR G
Sbjct: 36 QDIIDTLRRDGLTSLVATNMDEAVIGHIAFSPVSMDSGTRDWYAAGPISVMPTRQRTG 95

Query: 102 LGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130
 +GS L L M A G K +V ++G P+
 Sbjct: 96 IGSQLAEESSLRMRALGAKGIV-LLGEPD 123

>ref|ZP_01622046.1| hypothetical protein L8106_22596 [Lyngbya sp. PCC 8106]
 gb|EAW36033.1| hypothetical protein L8106_22596 [Lyngbya sp. PCC 8106]
 Length = 175

Score = 40.8 bits (94), Expect = 0.088, Method: Compositional matrix adjust.
 Identities = 35/113 (30%), Positives = 51/113 (45%), Gaps = 8/113 (7%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEV-EGVV 68
 IR A+D+ A+ ++ E N QT Q I+ L + LVAE+ E VV
 Sbjct: 3 IRSEAASDIQAI AEVTIAAFE---NLEVSNQTEQFIETLRAAEMLTISLVAEIDERVV 58

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRQRLGLGSTLYTH---LLKSMEAQG 118
 IA++ + + DW V +QR +G+TL H LL+ M QG
 Sbjct: 59 GHIAFSPVTISDGSRDWYGIGPFSVLPEYQRSIGTTLMQHGLSLLREMGQG 111

>ref|NP_834464.1| acetyltransferase [Bacillus cereus ATCC 14579]
 ref|ZP_04259006.1| hypothetical protein bcere0015_44820 [Bacillus cereus BDRD-Cer4]
 ref|ZP_04275684.1| hypothetical protein bcere0012_44650 [Bacillus cereus BDRD-ST24]
 ref|YP_003666929.1| acetyltransferase [Bacillus thuringiensis BMB171]
 gb|AAP11665.1| Acetyltransferase [Bacillus cereus ATCC 14579]
 gb|EEK92646.1| hypothetical protein bcere0012_44650 [Bacillus cereus BDRD-ST24]
 gb|EEL09360.1| hypothetical protein bcere0015_44820 [Bacillus cereus BDRD-Cer4]
 gb|ADH09209.1| acetyltransferase [Bacillus thuringiensis BMB171]
 Length = 174

Score = 40.8 bits (94), Expect = 0.088, Method: Compositional matrix adjust.
 Identities = 14/43 (32%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
 ND +++L+++LG+ GT + A +++G WHD+ +QR+++
 Sbjct: 132 NDRAIKLYKSLGFGHEGTCKEAI FRNGNWHDIELFALFQRNYK 174

>ref|ZP_04194030.1| hypothetical protein bcere0027_44300 [Bacillus cereus AH676]
 gb|EEL74275.1| hypothetical protein bcere0027_44300 [Bacillus cereus AH676]
 Length = 174

Score = 40.8 bits (94), Expect = 0.090, Method: Compositional matrix adjust.
 Identities = 14/43 (32%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
 ND +++L+++LG+ GT + A +++G WHD+ +QR+++
 Sbjct: 132 NDRAIKLYKSLGFGHEGTCKEAI FRNGNWHDIELFALFQRNYK 174

>ref|YP_001815262.1| ribosomal-protein-alanine acetyltransferase [Exiguobacterium
 sibiricum 255-15]
 gb|ACB62245.1| ribosomal-protein-alanine acetyltransferase [Exiguobacterium
 sibiricum 255-15]
 Length = 151

Score = 40.4 bits (93), Expect = 0.090, Method: Compositional matrix adjust.
 Identities = 39/141 (27%), Positives = 64/141 (45%), Gaps = 15/141 (10%)

Query: 7 PVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG 66
 V IR T D V H +E + F T P T + +I ++ + + Y +LVAE E

Sbjct: 3 KVTIRKMTVVDAPGV-----HAVELES--FAT-PWTLESFIAEMTQNPAY-YLVAETEE 53

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
 + I +AG W + T V V + + G+G L L++ G +++ +

Sbjct: 54 I---IGFAGLWHIADEGHIT---NVAVKQKARGTGIGEALLVALIEQARQLGLRAMTLEV 107

Query: 127 GLPNDPSPVRLHEALGYTARGT 147
 + N P+ L+E LG+ GT

Sbjct: 108 RVSNTPARTLYEKLGLFLYAGT 128

>ref|YP_002967100.1| putative acetyltransferase [Methylobacterium extorquens AM1]
 gb|ACS43759.1| putative acetyltransferase [Methylobacterium extorquens AM1]
 Length = 193

Score = 40.4 bits (93), Expect = 0.093, Method: Compositional matrix adjust.
 Identities = 26/104 (25%), Positives = 47/104 (45%), Gaps = 1/104 (0%)

Query: 71 IAYAGPWKARNAYDWTVE-STVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 + +A + R+ +++ + S+VYV H+R G+ L + + +G + + +

Sbjct: 70 VGFAASTRKRHPFEFIKAVSSVYVQAGHRAGVAHALLALIEGAARGEVTKLTAVAVQ 129

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDFELPAP 173
 N + RL+EALGY G A G + D + LP P

Sbjct: 130 NAGARRLYEALGYETYGIEPCAMRVGGMFVDEELRAKFLALPDP 173

>ref|YP_079508.1| putative N-acetyltransferase [Bacillus licheniformis ATCC 14580]
 ref|YP_091919.1| hypothetical protein BLi02346 [Bacillus licheniformis ATCC 14580]
 ref|ZP_07999557.1| hypothetical protein HMPREF1012_00590 [Bacillus sp. BT1B_CT2]
 gb|AAU23870.1| putative N-acetyltransferase [Bacillus licheniformis ATCC 14580]
 gb|AAU41226.1| putative protein [Bacillus licheniformis ATCC 14580]
 gb|EFV73927.1| hypothetical protein HMPREF1012_00590 [Bacillus sp. BT1B_CT2]
 Length = 183

Score = 40.4 bits (93), Expect = 0.094, Method: Compositional matrix adjust.
 Identities = 35/156 (22%), Positives = 65/156 (41%), Gaps = 10/156 (6%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQE---WIDDLERLQDRYPWLVAEVEG 66
 IRP AD + + V I+T + P+T +E +I D+ + + Y E++G

Sbjct: 21 IRPVKMADAPDIIEAVKDVIQTGVYIQRKPRPTLEEERAFISDMMKKDNMYA--AVEIDG 78

Query: 67 VVAGIAYA--GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 V GIA G K + T ++ + Q LG+G + ++ LK +

Sbjct: 79 TVYGIARVIRGELKMKR---HTGLFRTWLHLSKAQGLGIGREIMSYTLKWCRHLRLHLKCL 135

Query: 125 VIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 + N+ ++ L++ G+ G + G + D

Sbjct: 136 TVFSENEAALSLYKKS GFIVEGVQKEQVLSDGKYED 171

>ref|YP_001445734.1| hypothetical protein VIBHAR_02546 [Vibrio harveyi ATCC BAA-1116]
 gb|ABU71507.1| hypothetical protein VIBHAR_02546 [Vibrio harveyi ATCC BAA-1116]
 Length = 159

Score = 40.4 bits (93), Expect = 0.094, Method: Compositional matrix adjust.
 Identities = 23/85 (27%), Positives = 41/85 (48%), Gaps = 11/85 (12%)

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
 VAE++GV+ G + P + + + H +Q G+G L TH+LK EA+G

Sbjct: 59 FVAELDGVIVGYSDVQPSGLVDHF-----FCHHEYQGQGVGRVLMTHVLKQAEAKGL 110

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTA 144

++++ P +E +G+T
Sbjct: 111 NRIDSEVSITARP---FYEHMGTFTV 132

>ref|ZP_04122658.1| hypothetical protein bthur0005_44820 [Bacillus thuringiensis
serovar pakistani str. T13001]
gb|EEM45648.1| hypothetical protein bthur0005_44820 [Bacillus thuringiensis
serovar pakistani str. T13001]
Length = 174

Score = 40.4 bits (93), Expect = 0.098, Method: Compositional matrix adjust.
Identities = 14/43 (32%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
ND +++L+++LG+ GT + A +++G WHD+ +QR+++
Sbjct: 132 NDRAIKLYKSLGFGHEGTCKEAI FRNGNWHDIELFALFQRNYK 174

>ref|ZP_04308421.1| hypothetical protein bcere0005_44320 [Bacillus cereus 172560W]
gb|EEK59904.1| hypothetical protein bcere0005_44320 [Bacillus cereus 172560W]
Length = 177

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 15/43 (34%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
ND +V+L+++LG+ GT + A +++G WHD+ +QR+++
Sbjct: 135 NDRAVKLYKSLGFGHEGTCKEAI FRNGTWHDIELFALFQRNYK 177

>ref|ZP_04320007.1| hypothetical protein bcere0002_47020 [Bacillus cereus ATCC 10876]
gb|EEK48361.1| hypothetical protein bcere0002_47020 [Bacillus cereus ATCC 10876]
Length = 177

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 15/43 (34%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
ND +V+L+++LG+ GT + A +++G WHD+ +QR+++
Sbjct: 135 NDRAVKLYKSLGFGHEGTCKEAI FRNGTWHDIELFALFQRNYK 177

>ref|ZP_03230810.1| acetyltransferase, gnat family [Bacillus cereus AH1134]
gb|EDZ52712.1| acetyltransferase, gnat family [Bacillus cereus AH1134]
Length = 174

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 15/43 (34%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
ND +V+L+++LG+ GT + A +++G WHD+ +QR+++
Sbjct: 132 NDRAVKLYKSLGFGHEGTCKEAI FRNGTWHDIELFALFQRNYK 174

>gb|ABA47270.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
Length = 193

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 40/147 (27%), Positives = 63/147 (42%), Gaps = 18/147 (12%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWLW 61
R P IR T D+ A+ +I N + + T P T +E +++ +R D P V
Sbjct: 12 RLPRGIREFTEDDLEAMNIFNETAGSGANSVPVTRPMTYEEVKFYVNLKYR--DGLPVVY 69

Query: 62 AEVEGVVAGIAYAGPWKARNAYDW-----TVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
E G + G W + N + W T E+ +YV H G+G L +
Sbjct: 70 YERRGEILG-----WLSINRFSGWTQACYRTGETAIYVRADHFGSGIGVLLCKATVILG 123

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALG 141
G +++VA I N PS ++ A+G
Sbjct: 124 RQAGLENLVAWIMAANTPSQKIVTAVG 150

>ref|YP_645273.1| CoA-binding protein [Rubrobacter xylanophilus DSM 9941]
gb|ABG05461.1| CoA-binding protein [Rubrobacter xylanophilus DSM 9941]
Length = 911

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 19/58 (32%), Positives = 33/58 (56%)

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTAR 145
E ++ +S ++QR GLG+ + LL+ A+G + V A I N P ++ LG++ R
Sbjct: 835 EFSMLISDKYQRRGLGTLMLRRLLEVGRAEGIRRVTTADILFENRPMQKICRKLGFSLR 892

>ref|ZP_04205474.1| hypothetical protein bcere0025_44320 [Bacillus cereus F65185]
gb|EEL62845.1| hypothetical protein bcere0025_44320 [Bacillus cereus F65185]
Length = 177

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 15/43 (34%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWRQDFE 169
ND +V+L+++LG+ GT + A +++G WHD+ +QR+++
Sbjct: 135 NDRAVKLYKSLGFQHEGTCKEAIFRNGTWHDIELFALFQRNYK 177

>ref|ZP_04117060.1| hypothetical protein bthur0006_44090 [Bacillus thuringiensis
serovar kurstaki str. T03a001]
gb|EEM51273.1| hypothetical protein bthur0006_44090 [Bacillus thuringiensis
serovar kurstaki str. T03a001]
Length = 177

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 15/43 (34%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWRQDFE 169
ND +V+L+++LG+ GT + A +++G WHD+ +QR+++
Sbjct: 135 NDRAVKLYKSLGFQHEGTCKEAIFRNGTWHDIELFALFQRNYK 177

>ref|ZP_05492640.1| GCN5-related N-acetyltransferase [Thermoanaerobacter ethanolicus
CCSD1]
gb|EEU62326.1| GCN5-related N-acetyltransferase [Thermoanaerobacter ethanolicus
CCSD1]
Length = 178

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 34/158 (21%), Positives = 74/158 (46%), Gaps = 17/158 (10%)

Query: 3 PERRP-VEIRPATAADMAAVCDIVNH-----YIETSTVNFRTPEQTPQEWIDDLERLQD 55
P++ P + IR A D + ++N Y+ + T N+ E + ++ I +L+R +D
Sbjct: 8 PKKEPQLVIREAKIKDARGIIKLLNSVGREKLYMVSETFNWSEEEE--KQLIKNLDRNKD 65

Query: 56 RYPWLVAEVEGVVAG----IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
LVA+ G + G Y G + + E + + R + +G+G+ L+T +

Sbjct: 66 --LILVADYGGGEIVGCLTLFRYYGGRSPKVQH--VGEIGISIDARFRNIGIGTKLFTETAI 121

Query: 112 KSMEAQGFKSVVAVIGLPLNDPSVRLHEALGYTARGTLR 149

+++G++ + + N+ ++ L++ G+ G R

Sbjct: 122 NWAKSKGYEKLCLSVFSTNEVAIHLYKKFGFEEEGRRR 159

>ref|XP_001246318.1| hypothetical protein CIMG_00089 [Coccidioides immitis RS]
Length = 205

Score = 40.4 bits (93), Expect = 0.11, Method: Compositional matrix adjust.
Identities = 44/180 (24%), Positives = 78/180 (43%), Gaps = 44/180 (24%)

Query: 24 IVNHYIETSTVNFRT-EPQTPQEWIDDL-ERLQDR-YPWLVAEVEGV-----VAGIAYA 74

++ HY+ S + F EP P +I + + R P+ VA ++ + + G A A

Sbjct: 20 LIVHYVHNSVLTLFLIHEP--PLSYIAGIYNSARSRLPFYVAHIDQLRESKEKIIGYACA 77

Query: 75 GPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM----- 114

P++ Y TVE T+++ HQ G+GS L++ ++ S+

Sbjct: 78 SPFRGNLLGYAPTVELTLFIHPEHQSQGVGSRLFSSIVSSIQGETRHLAREFEDDPTREV 137

Query: 115 --EAQG-----FKSVVAVIGLPLNDPSVRL-----HEALGYTARGTLRAAGYKHGGWHDV 161

EA G K+++A++ + D + + G+T G L+ G+K G W DV

Sbjct: 138 RYEADGGQGARVKTLLAIMAVDIDGKAKGMGLRDWYVQRGFTEVGRLEKVGFKKGRWIDV 197

>ref|YP_003901482.1| ribosomal-protein-alanine acetyltransferase [Vulcanisaeta
distributa DSM 14429]

gb|ADN50431.1| ribosomal-protein-alanine acetyltransferase [Vulcanisaeta
distributa DSM 14429]

Length = 169

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 18/61 (29%), Positives = 34/61 (55%)

Query: 90 TVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPLNDPSVRLHEALGYTARGTLR 149

+V V ++R+G+G+ L + SM +G V+ + + N P++ L+ LG+ G LR

Sbjct: 76 SVGVLSDYRRMGIGNALMCRSICSMERGIDHVILEVRVSNTPAITLYRKLGFVDVHGVLRL 135

Query: 150 A 150

+

Sbjct: 136 S 136

>ref|ZP_04214509.1| hypothetical protein bcere0023_46470 [Bacillus cereus Rock4-2]

gb|EEL53816.1| hypothetical protein bcere0023_46470 [Bacillus cereus Rock4-2]

Length = 177

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 15/43 (34%), Positives = 30/43 (69%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169

ND +V+L+++LG+ GT + A +++G WHD+ +QR+++

Sbjct: 135 NDRVAVLYKSLGFGHEGTCKEAIIFRNGTWHDIELFALFQRNYK 177

>gb|EGC44325.1| conserved hypothetical protein [Ajellomyces capsulatus H88]

Length = 741

Score = 40.0 bits (92), Expect = 0.12, Method: Composition-based stats.
Identities = 34/122 (27%), Positives = 54/122 (44%), Gaps = 24/122 (19%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQT---PQEWIDDLERLQDRYPWLVA---- 62

+RP D+ + + N YI+ + EP + QE ID+ E QD++P LVA
 Sbjct: 547 LRPIEKKDLQGLLKLFNWYIQNTVRCVDLEPLSFGNLQERIDECE--QDKFPALVAVEKK 604

Query: 63 -----EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110
 E+ G + + GP +T E ++V ++ RLG+GS L L

Sbjct: 605 PRLGHALNGEEEEIFGCILASDFTGPDATINR---YTAELELFVEPKYCRLGVGSCLVDKL 661

Query: 111 LK 112

 L+

Sbjct: 662 LE 663

>ref|YP_002940564.1| GCN5-related N-acetyltransferase [Kosmotoga olearia TBF 19.5.1]
 gb|ACR79560.1| GCN5-related N-acetyltransferase [Kosmotoga olearia TBF 19.5.1]
 Length = 160

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
 Identities = 19/43 (44%), Positives = 27/43 (62%), Gaps = 3/43 (6%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV---GFWQRDFE 169
 N+PS+RL E+LG+ G LR A Y G + D+ G +R+FE

Sbjct: 117 NEPSIRLMESLGFKLEGRLREARYVDGKYWDILRYGILREFE 159

>ref|YP_928642.1| GCN5-related N-acetyltransferase [Shewanella amazonensis SB2B]
 gb|ABM00973.1| GCN5-related N-acetyltransferase [Shewanella amazonensis SB2B]
 Length = 150

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
 Identities = 38/140 (27%), Positives = 65/140 (46%), Gaps = 11/140 (7%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + IR A AAD+ + + N + T + + T + + L + +LVA+++G

Sbjct: 1 MNIRKAVAADLTDIVNF-NQAMAMETERLQLDTATLTGKGVSTLLDNPAGFYLVADIDGE 59

Query: 68 VAGIAYA----GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ--GFKS 121
 +AG W+A++ Y W +VY+ H+R G+ + LY +K M A G S

Sbjct: 60 IAGSLMVTFEWSDWRAKDYY-WI--QSVYIRPEHRRKGIYTRLY-QAVKDMAAAEGGAAS 115

Query: 122 VVAVIGLPNDPSVRLHEALG 141

 + N + R +EALG

Sbjct: 116 FRLYVEQENANAQRTYEALG 135

>ref|ZP_08168265.1| acetyltransferase, GNAT family [Turicibacter sp. HGF1]
 gb|EGC91434.1| acetyltransferase, GNAT family [Turicibacter sp. HGF1]
 Length = 167

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
 Identities = 24/89 (26%), Positives = 43/89 (48%), Gaps = 1/89 (1%)

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHE 138
 +R+ ++ E ++Y+ G+G L +L+ E G S+++ I N S+RLH+

Sbjct: 72 SRSCFEGVAEVSIIYLDQHVIGQGIGEQLLNYLITSEQNGIWSLISGIFPENVASLRLHQ 131

Query: 139 ALGYTARGTLRAAGY-KHGGWHDVGFWR 166

 G+ G G + G + DV F +R

Sbjct: 132 KCGFRYVGYREKMGKTREGVFRDVLFMER 160

>gb|EEH09853.1| conserved hypothetical protein [Ajellomyces capsulatus G186AR]
 Length = 741

Score = 40.0 bits (92), Expect = 0.12, Method: Composition-based stats.
Identities = 34/122 (27%), Positives = 54/122 (44%), Gaps = 24/122 (19%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQT---PQEWIDDLERLQDRYPWLVA---- 62
+RP D+ + + N YI+ + EP + QE ID+ ER D++P LVA
Sbjct: 547 LRPIEKKDLQGLLKLNFNWIQNTVRCVDLEPLSFGNLQERIDECER--DKFPALVAVEQK 604

Query: 63 -----EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110
E+ G + + GP +T E ++V ++ RLG+GS L L
Sbjct: 605 PRLGHALNGEEEEIFGCILASDFTGPDATINR--YTAELELFVEPKYCRLGVGSCLVDKL 661

Query: 111 LK 112
L+
Sbjct: 662 LE 663

>ref|ZP_07665673.1| ribosomal-protein-alanine acetyltransferase [Gardnerella vaginalis ATCC 14018]
ref|YP_003985844.1| GNAT family acetyltransferase [Gardnerella vaginalis ATCC 14019]
gb|ADP38821.1| GNAT family acetyltransferase [Gardnerella vaginalis ATCC 14019]
Length = 202

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 15/57 (26%), Positives = 36/57 (63%)

Query: 90 TVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARG 146
T+ V+ +Q+ G+ S L +++++ ++ G K ++ + + N+P+++L+E G+T G
Sbjct: 94 TIGVAKEYQKRGIASNLLKTMENAKSIGAKRMLLEVRVNNNPALKLYEKFGFTKMG 150

>ref|YP_002940792.1| GCN5-related N-acetyltransferase [Kosmotoga olearia TBF 19.5.1]
gb|ACR79788.1| GCN5-related N-acetyltransferase [Kosmotoga olearia TBF 19.5.1]
Length = 167

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 30/119 (25%), Positives = 55/119 (46%), Gaps = 5/119 (4%)

Query: 49 DLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYT 108
DLE + R LVAEV+G V G A K R + + V+ + G+G+ L
Sbjct: 47 DLENRETR--TLVAEVDGKVVGFASIHFMKGRRRHIAGIGMMVHDDFHGK--GIGTKLME 102

Query: 109 HLLKSMEA-QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
L+ + + + + N+P+++L++ G+ G LR +++G + D R
Sbjct: 103 ALIDLADNWNIRRIQLEVYVDNEPAIKLYKKFGFEIEGRLRDFSRNGEYIDAYIMSR 161

>ref|YP_003676537.1| GCN5-related N-acetyltransferase [Thermoanaerobacter mathranii subsp. mathranii str. A3]
gb|ADH60526.1| GCN5-related N-acetyltransferase [Thermoanaerobacter mathranii subsp. mathranii str. A3]
Length = 178

Score = 40.0 bits (92), Expect = 0.12, Method: Compositional matrix adjust.
Identities = 35/158 (22%), Positives = 74/158 (46%), Gaps = 17/158 (10%)

Query: 3 PERRP-VEIRPATAADMAAVCDIVNH-----YIETSTVNFRTPEQTPQEWIDDLERLQD 55
P++ P + IR A D + ++N Y+ + T N+ E + ++ I +L+R +D
Sbjct: 8 PKKEPQLVIREAKIKDARGIIKLLNSVGREKLYMVSETFNWSEEEE--KQLIRNLDNRKD 65

Query: 56 RYPWLVAEVEGVVAG----IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
LVA+ G + G Y G + + E V + R + +G+G+ L+T +
Sbjct: 66 --LILVADYGGIEIVGCLTLFRYYGGRSPKVQH--VGEIGVSDARFRNIGIGTKLFTEAI 121

Query: 112 KSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLR 149

+++G++ + + N+ ++ L++ G+ G R

Sbjct: 122 NWAKSKGYEKLCLSVFSTNEVAIHLYKKFGFEEEGRRR 159

>ref|ZP_06622285.1| acetyltransferase, GNAT family [Turicibacter sanguinis PC909]

gb|EFF63390.1| acetyltransferase, GNAT family [Turicibacter sanguinis PC909]

Length = 167

Score = 40.0 bits (92), Expect = 0.13, Method: Compositional matrix adjust.

Identities = 24/89 (26%), Positives = 43/89 (48%), Gaps = 1/89 (1%)

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHE 138

+R+ ++ E ++Y+ G+G L +L+ E G S+++ I N S+RLH+

Sbjct: 72 SRSCFEGVAEVSIIYLDQHVGIGQIGEQLLNYLITESEQNGIWSLISGIFPENVASLRLHQ 131

Query: 139 ALGYTARGTLRAAGY-KHGGWHDVGFQWR 166

G+ G G + G + DV F +R

Sbjct: 132 KCGFRYVGyreKMGKTREGVFRDVLFMER 160

>ref|ZP_03702661.1| GCN5-related N-acetyltransferase [Flavobacteria bacterium MS024-2A]

gb|EEG41752.1| GCN5-related N-acetyltransferase [Flavobacteria bacterium MS024-2A]

Length = 160

Score = 40.0 bits (92), Expect = 0.13, Method: Compositional matrix adjust.

Identities = 37/140 (26%), Positives = 62/140 (44%), Gaps = 17/140 (12%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERL----QDRYPWLVAEVE 65

IRPA A+D A+ ++N F EP++ D+E+ + LVAE+E

Sbjct: 5 IRPAIASDSKAIISLINE-----LALFEKEPESVNLVELDIEKYGFGGAPLFECLVAELE 59

Query: 66 GVVAGIAYAGP---WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121

V G+A P WK + +E + VS + G G+ LYT ++ G +

Sbjct: 60 NEVIGMALFYPRFSTWKGPTEFH--LEDLI-VSEEFKKGFGTQLYTAFIRHALKTGVQR 115

Query: 122 VVAVIGLPNDPSVRLHEALG 141

+ + N P+++ +E G

Sbjct: 116 IEWNVLDWNTPAIKFYENSG 135

>ref|YP_003405120.1| ribosomal-protein-alanine acetyltransferase [Haloterrigena turkmenica DSM 5511]

gb|ADB62447.1| ribosomal-protein-alanine acetyltransferase [Haloterrigena turkmenica DSM 5511]

Length = 160

Score = 40.0 bits (92), Expect = 0.13, Method: Compositional matrix adjust.

Identities = 38/136 (27%), Positives = 54/136 (39%), Gaps = 15/136 (11%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEW-IDDLERLQDRYPWLVAEVEG 66

+ IRPA AD+ AV I N Q W D ER +LVA EG

Sbjct: 15 LSIRPAERADLLAVVRIENESFS-----QPWPYDAFERFLGNDGFLVALEEG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126

+AG A + + V H+ G+G+ L T + + A+G SV +

Sbjct: 62 TIAGYLVA-DVSTQFGRQLGHKIDIAVHPDHRDSGIGTALLTRGMAVLTARGADSVKLEV 120

Query: 127 GLPNDPSVRLHEALGY 142

ND + RL+ G+

Sbjct: 121 RRTNDGAKRLYRQFGF 136

>dbj|BAG24087.1| phosphinothricin N-acetyltransferase [*Pseudomonas cichorii*]
Length = 193

Score = 40.0 bits (92), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 41/147 (27%), Positives = 63/147 (42%), Gaps = 18/147 (12%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLERLQDRYPWL 61
R P IR T D+ A+ +I N + + T P T +E +++ +R D P V
Sbjct: 12 RLPRGIREFTEDDLEAMNIFNETAGSGANSPVTRPMTYEEVKFYVNLKYR--DGLPVYV 69

Query: 62 AEVEGVVAGIAYAGPWKARNAYDW-----TVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
E G V G W + N + W T E+ +YV H G+G L +
Sbjct: 70 YERRGEVLG-----WLSINRFSWGTQACYRTGETAIYVRGDHFGSGIGVLLCKATVILG 123

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALG 141
+ G ++ VA I N PS ++ A+G
Sbjct: 124 QQAGLENPVAWIMAANTPSQKIVTAVG 150

>ref|ZP_07290419.1| phosphinothricin N-acetyltransferase [*Streptomyces* sp. C]
gb|EFL18788.1| phosphinothricin N-acetyltransferase [*Streptomyces* sp. C]
Length = 168

Score = 40.0 bits (92), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 32/101 (31%), Positives = 42/101 (41%)

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G A R AY VE +VYV + G+ L L+ S E G ++ +
Sbjct: 62 GRVLGWVAASAVSDRCAYAGVVEHSVYVHPDARGRGVARALLEALIASTEEAGIWTIQSG 121

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWR 166
I N S+ LH G+ GT G G W DV +R
Sbjct: 122 IFPENTASLALHARAGFRVIGTRERIGRHRGVWRDVLLE 162

>ref|NP_981206.1| acetyltransferase [*Bacillus cereus* ATCC 10987]
gb|AAS43814.1| acetyltransferase, GNAT family [*Bacillus cereus* ATCC 10987]
Length = 174

Score = 40.0 bits (92), Expect = 0.13, Method: Compositional matrix adjust.
Identities = 21/74 (28%), Positives = 41/74 (55%), Gaps = 6/74 (8%)

Query: 101 GLGSTLYTHLLKS--MEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
G G +T LL +E + + V ND +++L+++LG+ GT + A +++G W
Sbjct: 102 GYGKEAFTLLLNAYAFLELNLHRLSLRVFSF-NDRAIKLYKSLGFGHEGTCKEAI FRNGTW 160

Query: 159 HDV---GFWRD 169
HD+ +QR+++
Sbjct: 161 HDIELFALFQRNYK 174

>ref|XP_002844551.1| conserved hypothetical protein [*Arthroderma otae* CBS 113480]
gb|EEQ33696.1| conserved hypothetical protein [*Arthroderma otae* CBS 113480]
Length = 719

Score = 40.0 bits (92), Expect = 0.14, Method: Compositional matrix adjust.
Identities = 32/120 (26%), Positives = 55/120 (45%), Gaps = 20/120 (16%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQ-DRYPWLVA----- 62
IRP D+AA+ ++ N Y+ + E T E + +E L+ DRYP+LVA
Sbjct: 507 IRPVEPKDIAALVELFNWYVRNTLRRADLEEITYDEMREHIEELRTDRYPFLVAVERHPK 566

Query: 63 -----EVE---GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112
 E E G ++GP + +T + ++V + +LG+GS L +++
 Sbjct: 567 AWHAMNHEAEMLHGFCCISDFSGPLSTQR---FTCDIELFVHFKRFLGVGSCLLDKLMVE 623

>ref|YP_317104.1| GCN5-related N-acetyltransferase [Nitrobacter winogradskyi Nb-255]
 gb|ABA03752.1| GCN5-related N-acetyltransferase [Nitrobacter winogradskyi Nb-255]
 Length = 183

Score = 40.0 bits (92), Expect = 0.14, Method: Compositional matrix adjust.
 Identities = 43/143 (30%), Positives = 61/143 (42%), Gaps = 13/143 (9%)

Query: 8 VEIRPATAADMAAVC-----DIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPW 59
 +E+RPA AD +AV I + + + PQ W D R R
 Sbjct: 20 IELRPAKVADASAVAATHDESWRSAYQGIIPGALEKLINRRGPQ-WWDSAIRKGSRSISV 78

Query: 60 LVAEEGVVAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 LV + VAG A G +AR+ YD V +Y+ Q LG G L+ + + G
 Sbjct: 79 LVFGEQ--VAGYANYGRNRARSLOYDGEVYE-LYLRPEFQGLGFRRLFAAARRDLVQSG 135

Query: 119 FKSVAVIGLPNDPSVRLHEALG 141
 KSVV N+P++ + ALG
 Sbjct: 136 LKSVVTWALSDNEPAMEFYCALG 158

>ref|YP_251248.1| putative acetyltransferase [Corynebacterium jeikeium K411]
 emb|CAI37630.1| putative acetyltransferase [Corynebacterium jeikeium K411]
 Length = 229

Score = 40.0 bits (92), Expect = 0.14, Method: Compositional matrix adjust.
 Identities = 42/175 (24%), Positives = 66/175 (37%), Gaps = 26/175 (14%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL---- 60
 ++ + IR D V I+ ++T F E P+ W D ++ R P L
 Sbjct: 21 KQAISIRLMEEKDYPQVQKILQTGMTDGEATF--EENAPEAWED---FMRHRLPELSFVA 75

Query: 61 -----VAEEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYT 108
 + E + G A R+ +D +E ++YV G+ +L
 Sbjct: 76 IDTDPAAAAAAGLGEDGEKILGWITATSASHRDVFDGVLEDSIYVHKDAAGKGVAGSLLD 135

Query: 109 HLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAA-----GYKHGGW 158
 LLK QG ++ + I N+ SVRLH + G+ G G K G W
 Sbjct: 136 RLLKDAAEQGHWAMHSSIFPENEGSVRLHVSRGFEVGVFHCMSHMNYGPKKGTW 190

>ref|NP_354328.2| acetyltransferase [Agrobacterium tumefaciens str. C58]
 gb|AAK87113.2| acetyltransferase [Agrobacterium tumefaciens str. C58]
 Length = 169

Score = 40.0 bits (92), Expect = 0.15, Method: Compositional matrix adjust.
 Identities = 29/93 (31%), Positives = 44/93 (47%), Gaps = 10/93 (10%)

Query: 56 RYPWL---VAEEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLK 112
 R WL VAE G VAG W AR +D T+ + ++ R G+GS L + +
 Sbjct: 49 RSSWLTMRAEFGGSVAG-----WAAREHFDETI-TDFWIDPDFHRRGIGSRLLGDVER 101

Query: 113 SMEAQGFKSVAVIGLPNDPSVRLHEALGYTAR 145
 +E +GF ++ N+P+V GY+ R
 Sbjct: 102 LIEEKGFDAIRLETHAQNEPAVAFFRRHGYSVR 134

>ref|ZP_06964844.1| GCN5-related N-acetyltransferase [Ktedonobacter racemifer DSM

44963]
gb|EFH87955.1| GCN5-related N-acetyltransferase [Ktedonobacter racemifer DSM
44963]
Length = 144

Score = 40.0 bits (92), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 35/141 (24%), Positives = 66/141 (46%), Gaps = 14/141 (9%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE----VE 65
+RPA+ +D +A+ ++ + + TE Q +E + L D Y LVAE +
Sbjct: 6 LRPASLSDASAIARLMEQ-----LGYPTETQEMEERLTGLLSQSD-YQTLVAERNRRIV 58

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G++ G+ ++ Y V V +H+ Q +G S+L + ++ +G + ++
Sbjct: 59 GMI-GLHVGHSEYKNGVYGGIIVALVVEQAHQGHIG--SSLVAEGERWLKTRGVQIIIVN 115

Query: 126 IGLPNDPSVRLHEALGYTARG 146
G+ + R +E LGY A G
Sbjct: 116 SGMHRQAAHRFYEHLGYQATG 136

>ref|ZP_03942033.1| acetyltransferase [Lactobacillus buchneri ATCC 11577]
gb|EEI20104.1| acetyltransferase [Lactobacillus buchneri ATCC 11577]
Length = 165

Score = 40.0 bits (92), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 33/139 (23%), Positives = 58/139 (41%), Gaps = 5/139 (3%)

Query: 13 ATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
A D+ + DI N I + V EP + + W + + R W + + +A
Sbjct: 8 ADITDLPKIVDIYNETIASRMVTADLEPVSIASKRSWFNAFNH-EHRPIWKII-LNDQIA 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G + R AY TVE ++Y+ + GLG + ++ ++V+ I
Sbjct: 66 GWVSLESFYGRPAYHHTVEISIIYDAEFRHHGLGQQALDFVATQLKDLEIDTIVSFIFAH 125

Query: 130 NDPSVRLHEALGYTARGTL 148
N PS+ L + G+ + G L
Sbjct: 126 NLPSLGLFKKNGFQSWGHL 144

>ref|YP_001972175.1| hypothetical protein Smlt2386 [Stenotrophomonas maltophilia
K279a]
emb|CAQ45875.1| conserved hypothetical protein [Stenotrophomonas maltophilia K279a]
Length = 159

Score = 40.0 bits (92), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 46/155 (29%), Positives = 66/155 (42%), Gaps = 16/155 (10%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLER--LQDRYPWLVAEVE 65
+EIRPA A D A+ + I T P ++ Q + P VA +E
Sbjct: 1 MEIRPARAGDFDAMWGMFKQAIATQD----ALPFAGSFAVETFRTHWFQAQAPH-VAVLE 55

Query: 66 GVVAGIAYAGPWKARNAYDW---TVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122
G V G+ GP N D +T V Q G+G L H L+ A+GF ++
Sbjct: 56 GRVVGMYKMGP---NFPDLGAHVASATYVVDAPAQQGVGRALVEHSLELRARAEGFLAM 111

Query: 123 -VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHG 156
+ N P+V L+ LG+ GTL A ++HG
Sbjct: 112 QFNYVVSTNRPAVALYRKLGFDDVVGTLPKA-FRHG 145

>ref|ZP_03939126.1| acetyltransferase [Lactobacillus brevis subsp. gravesensis ATCC

27305]
gb|EEI71531.1| acetyltransferase [Lactobacillus brevis subsp. gravesensis ATCC
27305]
Length = 165

Score = 39.7 bits (91), Expect = 0.15, Method: Compositional matrix adjust.
Identities = 33/139 (23%), Positives = 57/139 (41%), Gaps = 5/139 (3%)

Query: 13 ATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
A D+ + DI N I + V EP + + W + + R W + + +A
Sbjct: 8 AEITDLPKIVDIYNETIASRMVTADLEPVSIVASKRSWFNAFNH-EHRPIWKII-LNDQIA 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G + R AY TVE ++Y+ + GLG + ++ ++V+ I
Sbjct: 66 GWVSLESFYGRPAYHHTVEISIIYIGAEFRHHGLGQQALDFVATQLKDLKIDTIVSFIFAH 125

Query: 130 NDPSVRLHEALGYTARGTL 148
N PS+ L + G+ G L
Sbjct: 126 NLPSLGLFKKNGFQTWGH 144

>ref|YP_283420.1| GCN5-related N-acetyltransferase [Dechloromonas aromatica RCB]
gb|AAZ44950.1| GCN5-related N-acetyltransferase [Dechloromonas aromatica RCB]
Length = 168

Score = 39.7 bits (91), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 36/148 (24%), Positives = 61/148 (41%), Gaps = 18/148 (12%)

Query: 8 VEIRPATAADMAAVCDIVNHY-----IETSTVNFRTEPQTPQEWI-DDLERLQDRYP 58
VEIRP T D+ A+ + I ++F E + E + DDLE D +
Sbjct: 7 VEIRPVTPPDVPAIAALAREIWQATYPGIITQEIDFMLEQRYGHERLYDDLE---DLHK 63

Query: 59 WLVAEVEG-VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
WL G G A++ + D +Y+ QR G+G L H+ + + Q
Sbjct: 64 WLDQAFHGDRRVGFAFSEIYNDEFKLD-----KLYIHPDVQRQGVGGQLIAHVAERAKKQ 118

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTAR 145
G+ V+ + N ++ ++ G+ R
Sbjct: 119 GYPCVILQVKNRVNAINSYKKYGFVVR 146

>ref|ZP_03955019.1| acetyltransferase [Lactobacillus hilgardii ATCC 8290]
gb|EEI23194.1| acetyltransferase [Lactobacillus hilgardii ATCC 8290]
Length = 165

Score = 39.7 bits (91), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 33/139 (23%), Positives = 57/139 (41%), Gaps = 5/139 (3%)

Query: 13 ATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
A D+ + DI N I + V EP + + W + + R W + + +A
Sbjct: 8 ADITDLPKIVDIYNETIASRMVTADLEPVSIVASKRSWFNAFNH-EHRPIWKII-LNDQIA 65

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G + R AY TVE ++Y+ + GLG + ++ ++V+ I
Sbjct: 66 GWVSLESFYGRPAYHHTVEISIIYIDAEFRHHGLGQQALDFVATQLKDLEIDTIVSFIFAH 125

Query: 130 NDPSVRLHEALGYTARGTL 148
N PS+ L + G+ G L
Sbjct: 126 NLPSLGLFKKNGFQTWGH 144

>ref|ZP_08098391.1| putative acetyltransferase [Vibrio brasiliensis LMG 20546]
gb|EGA65628.1| putative acetyltransferase [Vibrio brasiliensis LMG 20546]

Length = 163

Score = 39.7 bits (91), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 37/165 (22%), Positives = 70/165 (42%), Gaps = 13/165 (7%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQ----EWIDDLERLQDRYPWLVAE 63
+ IRP +D AA+C+I Y + R Q P+ W + LE + + VAE
Sbjct: 3 IVIRPTQVSDAAAICEI---YAQPKAQ--RETLQLPKPSVAMWTNRLENMPEGVYSFVAE 57

Query: 64 VEG-VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QGFKS 121
V+G +V I + + R A+ + V+ LG+GS + +L + K
Sbjct: 58 VDGKIVGNIGFEQSQRPRTAHCGSFGLGVH--DDFHGLGIGSKMIETVLDLADNWLQIKR 115

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
+ + N ++ ++ G+ G + A ++ G + + + R
Sbjct: 116 IQIDVNSDNQTAIACYKKFGFEIEGEAKCASFRDGEYINTLYMAR 160

>ref|ZP_06177647.1| conserved hypothetical protein [Vibrio harveyi 1DA3]
gb|EEZ86083.1| conserved hypothetical protein [Vibrio harveyi 1DA3]
Length = 158

Score = 39.7 bits (91), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 25/101 (24%), Positives = 49/101 (48%), Gaps = 15/101 (14%)

Query: 44 QEWDIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLG 103
Q W+ + +Q P+ VAE++GV+ G + P + + + H +Q G+G
Sbjct: 46 QLWLKKMTAIQ---PF-VAELDGVIVGYSDVQPSGLVDHF-----FCHHEYQGGQGVG 93

Query: 104 STLYTHLLKSMEAQGFKS SVVAVIGLPNDPSVRLHEALGYTA 144
L TH++K +A+G + + + + P +E +G+T
Sbjct: 94 RALMTHVIKQAQAKGLDKIYSEVSITASP---FYEHMGFTV 131

>ref|YP_003958986.1| ribosomal-protein-alanine acetyltransferase [Eubacterium limosum KIST612]
gb|ADO36023.1| ribosomal-protein-alanine acetyltransferase [Eubacterium limosum KIST612]
Length = 147

Score = 39.7 bits (91), Expect = 0.17, Method: Compositional matrix adjust.
Identities = 25/87 (28%), Positives = 44/87 (50%), Gaps = 5/87 (5%)

Query: 58 PVLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
+LV E EG VAG +AG W D V + +++ GLG+ L LL + A+
Sbjct: 43 KYLVVEAEGQVAG--FAGIW---CVVDEAQMNVGILEKYRQNGLTLLMEALLSTARAR 97

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTA 144
G + + N ++ L++ +G++A
Sbjct: 98 GCSCMTLEVKETNTAAICLYKKMGFSA 124

>ref|YP_002805376.1| acetyltransferase [Clostridium botulinum A2 str. Kyoto]
gb|AC085347.1| acetyltransferase [Clostridium botulinum A2 str. Kyoto]
Length = 179

Score = 39.7 bits (91), Expect = 0.18, Method: Compositional matrix adjust.
Identities = 13/32 (40%), Positives = 22/32 (68%)

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDV 161
N+ +++L+E +G+ G LR A Y+ G WHD+
Sbjct: 132 NERAIKLYEKMGFIREGILRQALYRAGNWHDI 163

>ref|YP_004114156.1| GCN5-like N-acetyltransferase [Pantoea sp. At-9b]
 gb|ADU67600.1| GCN5-related N-acetyltransferase [Pantoea sp. At-9b]
 Length = 163

Score = 39.7 bits (91), Expect = 0.18, Method: Compositional matrix adjust.
 Identities = 38/161 (23%), Positives = 67/161 (41%), Gaps = 5/161 (3%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 + +R T AD AA+ + +H ET Q+P W + L+ ++ LVA +EG
 Sbjct: 4 ITVRHTTPADAAALFQLYSH-AETQADTLHLPLQSPALWQERLQNIRPGEQRLVACIEGQ 62

Query: 68 VAGIAYAGPWKA-RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QGFKSVVAV 125
 V G + R + T+ + V R G+GS L ++ + +
 Sbjct: 63 VVGQLTVSVLEVMMRRHTATI--GMGVDPAPFHRRGVGSALMAAMVDLCDNWLQVTRIELT 120

Query: 126 IGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGVFQWR 166
 + N ++ L++ G+ GT R ++G W D + R
 Sbjct: 121 VFTDNKAAIGLYQKFGFAVEGTARRHAMRNGEVDTHYMAR 161

>ref|YP_001267788.1| GCN5-related N-acetyltransferase [Pseudomonas putida F1]
 gb|ABQ78604.1| GCN5-related N-acetyltransferase [Pseudomonas putida F1]
 Length = 182

Score = 39.7 bits (91), Expect = 0.19, Method: Compositional matrix adjust.
 Identities = 23/59 (38%), Positives = 32/59 (54%)

Query: 87 VESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTAR 145
 E V VS QR GLG L HL+++ GF+ +V+ N RL +ALG+T+R
 Sbjct: 107 CECAVAVSEDWQRKGLGKRLMQHLIEAARRNGFQCMVSRDLASNYGMHRLVKALGFTSR 165

>ref|ZP_06190054.1| GCN5-related N-acetyltransferase [Serratia odorifera 4Rx13]
 gb|EFA18356.1| GCN5-related N-acetyltransferase [Serratia odorifera 4Rx13]
 Length = 175

Score = 39.7 bits (91), Expect = 0.19, Method: Compositional matrix adjust.
 Identities = 27/109 (24%), Positives = 50/109 (45%), Gaps = 1/109 (0%)

Query: 39 EPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQ 98
 EP+ +W + L++ + L+AE + G A + +++VS HQ
 Sbjct: 41 EPRRLAQWQEKLQQ-PGKAQVLLAESADQLVGFCLADAPSHPQFGEHAEIKSLFVSDEHQ 99

Query: 99 RLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGT 147
 R G+G L + M+ G++S+ + ND ++R ++ALG G
 Sbjct: 100 RQGIGRRLGAAAREMQKLGYSIALGVVDGNDNAMRFYQALGGAPAGN 148

>ref|ZP_04599568.1| hypothetical protein VEIDISOL_01005 [Veillonella dispar ATCC 17748]
 gb|EEP65131.1| hypothetical protein VEIDISOL_01005 [Veillonella dispar ATCC 17748]
 Length = 149

Score = 39.7 bits (91), Expect = 0.20, Method: Compositional matrix adjust.
 Identities = 32/139 (23%), Positives = 60/139 (43%), Gaps = 14/139 (10%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
 +EIR AT D ++ DI P + + + +LE ++ ++ E E +
 Sbjct: 1 MEIRLATVDDAQSIYDIEQQSFSV-----PWSLESVLAELEGADNKLYMVICEDHEI 52

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 V YAG W YD + + + + G GS L L++ +G + +

Sbjct: 53 VG---YAGAWLV---YDEGQITNIAILPSARGKGYGSKLTKELIEECLNRMHEIFLEVR 106

Query: 128 LPNDPSVRLHEALGYTARG 146
 + N P++ ++ LG+T +G

Sbjct: 107 ISNLPALAMYRNLGFTVKG 125

>dbj|BAI77986.1| phosphinothricin N-acetyltransferase [Pseudomonas cichorii]
 Length = 193

Score = 39.7 bits (91), Expect = 0.20, Method: Compositional matrix adjust.
 Identities = 40/147 (27%), Positives = 63/147 (42%), Gaps = 18/147 (12%)

Query: 5 RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQE---WIDDLERLQDRYPWL 61
 R P IR T D+ A+ +I N + + T P T +E +++ +R D P V
 Sbjct: 12 RLPRGIREFTEDDLEAMNIFNETAGSGANSPVTRPMTYEEVKFYVNLKYR--DGLPVYV 69

Query: 62 AEVEGVVAGIAYAGPWKARNAYDW-----TVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
 G V G W + N + W T E+ +YV H G+G L +
 Sbjct: 70 YXRRGEVLG-----WLSINRFSGWTQACYRTGETAIYVRGDHFGSGIGVLLCKATVILG 123

Query: 115 EAQGFKSVVAVIGLPNDPSVRLHEALG 141
 + G +++VA I N PS ++ A+G
 Sbjct: 124 QQAGLENLVAWIMAANTPSQKIVTAVG 150

>ref|ZP_05296504.1| hypothetical protein LmonocyFSL_15566 [Listeria monocytogenes FSL
 J1-208]
 Length = 135

Score = 39.3 bits (90), Expect = 0.20, Method: Compositional matrix adjust.
 Identities = 32/121 (26%), Positives = 54/121 (44%), Gaps = 10/121 (8%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY---PWLVAEVE 65
 +I P + V + IET F QE LE ++Y LV +
 Sbjct: 5 KILPMQKEHYSGVAHVHGEIETGNATF-----QEKTLSLEVFNEKYLNLCRLVVLNM 57

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
 G V G A P+ + +AY E ++Y++ + G+G L L+++ E QGF ++ ++
 Sbjct: 58 GEVIGWAALLPFSSMHAYRGVAELSIYIAKSARGKGVGKALMHELIQTSEQQGFWTQLSL 117

Query: 126 I 126
 I
 Sbjct: 118 I 118

>ref|YP_001547447.1| GCN5-related N-acetyltransferase [Herpetosiphon aurantiacus ATCC
 23779]
 gb|ABX07319.1| GCN5-related N-acetyltransferase [Herpetosiphon aurantiacus ATCC
 23779]
 Length = 169

Score = 39.3 bits (90), Expect = 0.20, Method: Compositional matrix adjust.
 Identities = 29/106 (27%), Positives = 48/106 (45%), Gaps = 7/106 (6%)

Query: 58 PWLVAEVEGVVAGIAY--AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSME 115
 P LVA ++ +V GI G + R+A D + V +Q G+G+ L ++ E
 Sbjct: 56 PRLVATIDAMVVGIISLEIGEGRRRHAGDLELA---VRDDYQGRGIGAAALMAAMIDLAE 111

Query: 116 A-QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD 160
 G + V+ N P++ L++ + GTLR Y+ G D
 Sbjct: 112 NWLGLSRLEIVVFTDNTPAITLYKRFDFAVEGTLRNYAYRGGKLS 157

>ref|YP_003647086.1| glycoside hydrolase family 38 [Tsukamurella paurometabola DSM
20162]
gb|ADG78747.1| glycoside hydrolase family 38 [Tsukamurella paurometabola DSM
20162]
Length = 1003

Score = 39.3 bits (90), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 24/65 (36%), Positives = 39/65 (60%), Gaps = 7/65 (10%)

Query: 111 LKSMEAQGFKS VVAVIGLPNDPS----VRLHEALGYTARGLRAAGYKHGGWHDVGVFWQR 166
L +++ +G V++ I L +D S VRL+EALG ARG+L + G+ HGG +V +
Sbjct: 921 LVTLDGEGI--VISAIKLADDRSGDVIVRLYEALGRRARGSL-SVGFSHGGIREVSLIED 977

Query: 167 DFELP 171
+ + P
Sbjct: 978 EIDDP 982

>ref|YP_002479907.1| GCN5-related N-acetyltransferase [Desulfovibrio desulfuricans
subsp. desulfuricans str. ATCC 27774]
gb|ACL49229.1| GCN5-related N-acetyltransferase [Desulfovibrio desulfuricans
subsp. desulfuricans str. ATCC 27774]
Length = 152

Score = 39.3 bits (90), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 33/110 (30%), Positives = 51/110 (46%), Gaps = 24/110 (21%)

Query: 58 PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
P +A V+G +AG +A R + + V + + RH+ GLG L T ++K M
Sbjct: 54 PGYIARVDGQMAGYCFA----DRESGEIMV---LALLPRHENQGLGRMLLTQMVKDMHHS 106

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGVFWQRD 167
GFK + + +D VR + G+ Y+H GW + G QRD
Sbjct: 107 GFKRL--FLACNSDSKVR---SYGF-----YRHLGWKETG--QRD 139

>ref|NP_745432.1| acetyltransferase [Pseudomonas putida KT2440]
gb|AAN68896.1|AE016521_5 acetyltransferase, GNAT family [Pseudomonas putida KT2440]
Length = 182

Score = 39.3 bits (90), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 23/59 (38%), Positives = 31/59 (52%)

Query: 87 VESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS VVAVIGLPNDPSVRLHEALGYTAR 145
E V VS QR GLG L HL+ + GF+ +V+ N RL +ALG+T+R
Sbjct: 107 CECAVAVSEDWQRKGLGKRLMQHLIAAARRNGFQCMVSRDLASNYAMHRLVKALGFTSR 165

>ref|YP_001833465.1| GCN5-related N-acetyltransferase [Beijerinckia indica subsp.
indica
ATCC 9039]
gb|ACB95976.1| GCN5-related N-acetyltransferase [Beijerinckia indica subsp. indica
ATCC 9039]
Length = 181

Score = 39.3 bits (90), Expect = 0.22, Method: Compositional matrix adjust.
Identities = 25/108 (23%), Positives = 54/108 (50%), Gaps = 3/108 (2%)

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QG 118
+VA +EG + G+A + R ++ E + V HQ+ G+G+ L ++ + + G
Sbjct: 73 IVAVLEGNIIGVAGFKCFPGRRSH--AAELGMGVHDDHQKRGVGTALLKEVIDAADNWFG 130

Query: 119 FKSVAVIGLPLNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQR 166

+ + + N+ ++ L++ G+ GTLRA ++ G + + + R

Sbjct: 131 VRRLELTVYTDNEQAIHLYKKFGFETEGTLRAYAFRAGCYANALYMAR 178

>ref|YP_003750846.1| hypothethical protein, acyl-CoA N-acyltransferase domain
[Ralstonia

solanacearum PSI07]

emb|CBJ49524.1| hypothethical protein, Acyl-CoA N-acyltransferase domain [Ralstonia
solanacearum PSI07]

Length = 56

Score = 39.3 bits (90), Expect = 0.23, Method: Composition-based stats.

Identities = 21/54 (38%), Positives = 25/54 (46%)

Query: 122 VVAVIGLPLNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPPR 175

++ I N S+RLHE LG+ G A K G W D F QR E P R

Sbjct: 1 MIGAIDGANAGSIRLHEKLGFKGRCPEAAIKRGQWLDVFMQRRLEAPGTVR 54

>ref|ZP_08212291.1| GCN5-related N-acetyltransferase [Thermoanaerobacter ethanolicus
JW

200]

gb|EGD51712.1| GCN5-related N-acetyltransferase [Thermoanaerobacter ethanolicus JW

200]

Length = 178

Score = 39.3 bits (90), Expect = 0.24, Method: Compositional matrix adjust.

Identities = 34/157 (21%), Positives = 72/157 (45%), Gaps = 17/157 (10%)

Query: 10 IRPATAADMAAVCDIVNH-----YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE 63

IR A D + ++N Y+ + T N+ E + ++ I +L+R +D LVA+

Sbjct: 16 IREAKVKDARGIIKLLNSVGREKLYMVSETFNWSEEEE--KQLIKNLDRNKD--LILVAD 71

Query: 64 VEGVVAG----IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119

G + G Y G + + E + + R + +G+G+ L+T + +++G+

Sbjct: 72 YGGEIVGCLTLFRYYGGRSPKVQH--VGEIGISIDARFRNIGIGTKLFTEAINWAKSKGY 129

Query: 120 KSVVAVIGLPLNDPSVRLHEALGYTARGTLRAAGYKHG 156

+ + + N+ ++ L++ G+ G R +K G

Sbjct: 130 EKLCLSVFSTNEVAIHLYKKFGFEEEGR-RKKQFKIG 165

>ref|ZP_01740397.1| GCN5-related N-acetyltransferase [Rhodobacterales bacterium
HTCC2150]

gb|EBA04808.1| GCN5-related N-acetyltransferase [Rhodobacterales bacterium
HTCC2150]

Length = 325

Score = 39.3 bits (90), Expect = 0.25, Method: Compositional matrix adjust.

Identities = 36/141 (25%), Positives = 61/141 (43%), Gaps = 15/141 (10%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQ---EWIDDLERLQDRYPWLVAE 64

+ IR A D + D++N I+ T+P +P+ EW+D D W +AE

Sbjct: 167 MHIRHAGPFDCRPLADLLNEIIDQGGTTALTDPVSPETIAEWMD-----TDNSSWHLAED 221

Query: 65 E-GVVAGIAYAGPWKA--RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121

E G V G + P ++A +V LG+GS L+ K+ + G+

Sbjct: 222 EKG NVLGYQWIDPHDLPKDA---AHIAITFVKLGKTGLGIGSALFEATKKTAKKLGYNH 277

Query: 122 VVAVIGLPLNDPSVRLHEALGY 142

+ AVI N + +++ G+

Sbjct: 278 IDAVIRTDNSGGLAYYQSRGF 298

```
>ref|YP_273193.1| acetyltransferase [Pseudomonas syringae pv. phaseolicola 1448A]
gb|AAZ37911.1| acetyltransferase, GNAT family [Pseudomonas syringae pv.
    phaseolicola 1448A]
gb|EFW86339.1| acetyltransferase [Pseudomonas syringae pv. glycinea str. race 4]
    Length = 161
```

Score = 39.3 bits (90), Expect = 0.25, Method: Compositional matrix adjust.
Identities = 30/125 (24%), Positives = 59/125 (47%), Gaps = 7/125 (5%)

```
Query: 41 QTPQEWIDDLERLQDRYPW----LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHR 96
    + P + ++D+++L + LVAE +G+V G A ++ R + + + V+
Sbjct: 31 RMPYQSVNDIKKLVEGRSASGLSLVAERDGI VVG CAMLYRFQRRQH--VADFWMGVADG 88

Query: 97 HQRLGLGSTLYTHL-LKSMEAQGFKS VVAVIGLPNDPSVRLHEALGYTARGLRAAGYKH 155
    H R G+G L L + K + + + N+P++ L++ G+ GT R Y+
Sbjct: 89 HHRQGIGDELLKELSATA CRWMNVKRL ELTVFVDNEPAIALYKKN GFVIEGTHRKFAYRD 148

Query: 156 GGWHD 160
    G + D
Sbjct: 149 GEYID 153
```

```
>ref|YP_001030055.1| hypothetical protein Mlab_0614 [Methanocorpusculum labreanum Z]
gb|ABN06788.1| GCN5-related N-acetyltransferase [Methanocorpusculum labreanum Z]
    Length = 181
```

Score = 39.3 bits (90), Expect = 0.26, Method: Compositional matrix adjust.
Identities = 27/111 (24%), Positives = 51/111 (45%), Gaps = 3/111 (2%)

```
Query: 59 WLVAEVEGVVAGIA-YAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
    W + + ++ G Y+ P R ++ T +Y+ + + +G+ HL + +
Sbjct: 61 WCMHYKDRIIGGAGFYSPPGTRL SHSATF--FLYIEPAYWGMSIGTKAIMHLEDEAKKR 118

Query: 118 GFKS VVAVIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFWRDF 168
    GF + ++ N +V L+E LGY GT + A Y G + D+ F + F
Sbjct: 119 GFIRMECLVADTNPRVCLYERLGYELEGTKKMAFYLDGKYTDLKF LGKIF 169
```

```
>gb|AAU82639.1| probable acetyltransferase [uncultured archaeon GZfos18H11]
    Length = 173
```

Score = 38.9 bits (89), Expect = 0.27, Method: Compositional matrix adjust.
Identities = 33/129 (25%), Positives = 61/129 (47%), Gaps = 17/129 (13%)

```
Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYP---WLVAEV 64
    + IR T D Y + +VN + Q + I + R ++Y +LVAE+
Sbjct: 3 INIRKETEKD-----YEDIKSVNDKAFGQENEGKIVENLRKNEKYISDLYLVAEI 52

Query: 65 EGVVAGIAYAGPWKAR---NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
    + + G P K R N Y+ + + V +Q++G+GS L + +K+ + G+ S
Sbjct: 53 DNKIVGHILFFPIKIRSQENEYETLSLAPMSVLPNYQKMIGIGSKLIEYGIKAAKAGYGS 112

Query: 122 VVAVIGLPN 130
    ++ V+G P+
Sbjct: 113 II-VVGHPD 120
```

```
>ref|ZP_05845618.1| acetyltransferase [Corynebacterium jeikeium ATCC 43734]
gb|EEW17320.1| acetyltransferase [Corynebacterium jeikeium ATCC 43734]
    Length = 245
```


Score = 38.9 bits (89), Expect = 0.27, Method: Compositional matrix adjust.
Identities = 42/175 (24%), Positives = 66/175 (37%), Gaps = 26/175 (14%)

```
Query: 5   RRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL---- 60
          ++ + IR      D   V   I+   ++T   F   E   P+ W D   ++ R P L
Sbjct: 37  KQAISIRLMEEKDYPQVQKILQTGMDTGEATF--EENAPEAWED---FMRHRLPELSFVA 91

Query: 61  -----VAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYT 108
          + E      + G   A      R+ +D +E ++YV      G+ +L
Sbjct: 92  IDTDPAAAAAAGLGEDGEKILGWITATSASHRDVFDGVLEDSIYVHKDAAGKGVAGSLLD 151

Query: 109 HLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAA-----GYKHGGW 158
          LLK   QG  ++ + I   N+ SVRLH + G+   G      G K G W
Sbjct: 152 RLLKDAAEQGHWAHSSIFPENEGSVRLHVSRGFEVGVFHCMSHMNYGPKKGTW 206
```

>ref|ZP_06976320.1| acetyltransferase [Gardnerella vaginalis 5-1]
gb|EFH71774.1| acetyltransferase [Gardnerella vaginalis 5-1]
Length = 176

Score = 38.9 bits (89), Expect = 0.28, Method: Compositional matrix adjust.
Identities = 22/76 (28%), Positives = 41/76 (53%), Gaps = 3/76 (3%)

```
Query: 71  IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPN 130
          YAG W   + D   + T+ V+ ++QR GL + L + ++K+ E G K ++ + + N
Sbjct: 75  CGYAGYW--FDGDDAQI-MTIGVAKKYQRKGLAAELLSTMIKTAEKIGAKRMLLEVRVDN 131

Query: 131 DPSVRLHEALGYTARG 146
          P++ L+E G+   G
Sbjct: 132 VPALALYERFGFKKMG 147
```

>ref|ZP_01616171.1| hypothetical protein GP2143_04500 [marine gamma proteobacterium
HTCC2143]
gb|EAW31680.1| hypothetical protein GP2143_04500 [marine gamma proteobacterium
HTCC2143]
Length = 197

Score = 38.9 bits (89), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 36/131 (27%), Positives = 56/131 (42%), Gaps = 17/131 (12%)

```
Query: 3   PERRPVEIRPATAADMAAVCDIVNHYIETSTVNFR---TEPQTPQEWIDDLERLQDRYPW 59
          P+   VE+R TAAD A+ +   +   + R   T+P+ EWID++E
Sbjct: 17  PDGASVELRIMTAADKNAILEFSQALPQEDLLFLRVDLTQPEVVDEWIDNIESGFSTSLV 76

Query: 60  LVAEVEGVVAGIAYA-----GPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKS 113
          + E E +V   YA      PW R      E V VS ++ GLG L + +
Sbjct: 77  VFDEDEHLV---GYATVHRNPAPWTRRVG-----ELRVNVSSSYRARGLGKNTSEIFDV 128

Query: 114 MEAQGFKSVVA 124
          ++ G K ++A
Sbjct: 129 AQSIGVKKLLA 139
```

>ref|YP_001435167.1| ribosomal-protein-alanine acetyltransferase [Ignicoccus
hospitalis
KIN4/I]
gb|ABU81760.1| ribosomal-protein-alanine acetyltransferase [Ignicoccus hospitalis
KIN4/I]
Length = 147

Score = 38.9 bits (89), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 28/92 (30%), Positives = 47/92 (51%), Gaps = 8/92 (8%)

Query: 60 LVAEVEGVVAGIAYAGPW--KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
LVAEV G V G A A K + ++ V+ +++ LG+GS L L K + +
Sbjct: 45 LVAEVNGKVVGYAIAAKEVDKLLHLLNFAVDP-----QYRGLGIGSALLESELEKLAKKK 98

Query: 118 GFKSVAVIGLPLNDPSVRLHEALGYTARGTLR 149
G KS+ + N ++RL++ +G+ G +R
Sbjct: 99 GLKSIYLEVEEDNYRAMRLYKKMGFVEVGRIR 130

>ref|ZP_07469914.1| acetyltransferase [Corynebacterium accolens ATCC 49726]
gb|EFM42762.1| acetyltransferase [Corynebacterium accolens ATCC 49726]
Length = 333

Score = 38.9 bits (89), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 23/79 (29%), Positives = 37/79 (46%)

Query: 64 VEGVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
++G I ++ + W S V V+ H+R GLG+ L H+L+ QG K
Sbjct: 242 IDGETVAITRGITITESGDTAWLGYSAVEVAPARRQGLGALLGQHMLRWGREQGAKHAY 301

Query: 124 AVIGLPLNDPSVRLHEALGY 142
+ N +RL+E LG+
Sbjct: 302 LDVLASNTAGIRLYEKLGF 320

>ref|YP_004093376.1| ribosomal-protein-alanine acetyltransferase [Bacillus
cellulosilyticus DSM 2522]
gb|ADU28645.1| ribosomal-protein-alanine acetyltransferase [Bacillus
cellulosilyticus DSM 2522]
Length = 150

Score = 38.9 bits (89), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 31/107 (28%), Positives = 51/107 (47%), Gaps = 6/107 (5%)

Query: 40 PQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQR 99
P + + +I++L Q Y ++VA VEG V G YAG W D + + V +QR
Sbjct: 29 PWSRKAFINELTTNQFAY-YIVAVVEGRVVG--YAGVWVV---IDEAHITNIAVHSAYQR 82

Query: 100 LGLGSTLYTHLLKSMEAQGFKSVVAVIGLPLNDPSVRLHEALGYTARG 146
+G+G L +L+ + G + + ND + L+E G+ G
Sbjct: 83 MGIGDLLLKGILEIAKMLGANKATLEVRVSNDKAKSLYEKHXGFENG 129

>ref|NP_558835.1| N-acyltransferase [Pyrobaculum aerophilum str. IM2]
gb|AAL63017.1| N-acyltransferase [Pyrobaculum aerophilum str. IM2]
Length = 176

Score = 38.9 bits (89), Expect = 0.29, Method: Compositional matrix adjust.
Identities = 39/153 (25%), Positives = 67/153 (43%), Gaps = 31/153 (20%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEW--IDDLERLQDRYPWLVAEVEGV 67
IR AT D+ DI+ ++N + P+ W ++ LE+ ++VAE+EG
Sbjct: 24 IREATLKDLN---DII-----SINRKVLPEYNPNWFFVEHLEQFPK--AFIVAEIEGK 71

Query: 68 VAGIAYAGPWKARNAYDWT-VESTVYVSHRH-----QRLGLGSTLYTHLLKSMEA 116
V G + R Y W+ + V H +RLG+ + + +K+M+
Sbjct: 72 VVGVM-----RVEYGWSNIHRGKAVRKGHIVSVGVLPARRLGIATAMMLRAMKAMKV 126

Query: 117 Q-GFKSVVAVIGLPLNDPSVRLHEALGYTARGTL 148
G V + + N P++ L+E LGY G +
Sbjct: 127 YYGASEVYLEVRVSNTPAISLYEKLGYKVGRI 159

>ref|YP_001191493.1| GCN5-related N-acetyltransferase [Metallosphaera sedula DSM 5348]
 gb|ABP95569.1| GCN5-related N-acetyltransferase [Metallosphaera sedula DSM 5348]
 Length = 147

Score = 38.9 bits (89), Expect = 0.30, Method: Compositional matrix adjust.
 Identities = 40/138 (28%), Positives = 63/138 (45%), Gaps = 13/138 (9%)

Query: 7 PVEIRPATAADMAAVCDIVNHYI-ETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVE 65
 P+ IR AT D+ V + E + F + + E I+ L QD + L+AE++
 Sbjct: 2 PLTIREATRGDIEGVYRLYQSLTPEDLYMRFFSFHRVSHEEIEQLFSRQD-HITLLAEID 60

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAV 125
 G + G A YD E +V V +R G+G+ L L++ + G S V
 Sbjct: 61 GEIVGEA-----TLYDDG-EFSVAVKPNQRRGGIGTELVAELIRRAKKMGI-SKVVF 110

Query: 126 IGLP-NDPSVRLHEALGY 142
 LP N P +R+ + LG+
 Sbjct: 111 YTLPENYPMIRIGKKLGF 128

>ref|YP_003938802.1| ribosomal-protein-alanine N-acetyltransferase [Bifidobacterium
 bifidum S17]
 gb|ADO53228.1| ribosomal-protein-alanine N-acetyltransferase [Bifidobacterium
 bifidum S17]
 Length = 194

Score = 38.9 bits (89), Expect = 0.30, Method: Compositional matrix adjust.
 Identities = 16/56 (28%), Positives = 29/56 (51%)

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARG 146
 + VS HQR G+ + HL+ QG + ++ + + NDP++ L+ G+ G
 Sbjct: 83 IGVSKTHQRQGIAMMMNHLISRARRQGARRMLLEVSVVNDPAIALYHRFGFQCIG 138

>ref|XP_001542255.1| predicted protein [Ajellomyces capsulatus NAM1]
 gb|EDN05823.1| predicted protein [Ajellomyces capsulatus NAM1]
 Length = 713

Score = 38.9 bits (89), Expect = 0.31, Method: Composition-based stats.
 Identities = 33/122 (27%), Positives = 54/122 (44%), Gaps = 24/122 (19%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQT---PQEWIDDLERLQDRYPWLVA---- 62
 +RP D+ + + N YI+ + EP + QE ID+ ER D++P LVA
 Sbjct: 491 LRPIEKKDLQGLLKLFNWYIQNTVRCVDLEPLSFGNLQERIDECER--DKFPALVAVEQK 548

Query: 63 -----EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110
 ++ G + + GP +T E ++V ++ RLG+GS L L
 Sbjct: 549 PRLGHALNGEEKIFGCILASDFTGPDATINR---YTAELELFVEPKYCRLGVGSCLVDKL 605

Query: 111 LK 112
 L+
 Sbjct: 606 LE 607

>ref|YP_003119106.1| GCN5-related N-acetyltransferase [Catenulispora acidiphila DSM
 44928]
 gb|ACU77265.1| GCN5-related N-acetyltransferase [Catenulispora acidiphila DSM
 44928]
 Length = 184

Score = 38.9 bits (89), Expect = 0.31, Method: Compositional matrix adjust.
 Identities = 31/109 (28%), Positives = 53/109 (48%), Gaps = 4/109 (3%)

Query: 50 LERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVES--TVYVSHRHQRLGLGSTLY 107
 ++R R LVAEV GVV+G A GP + + + +V +YV RLG+G+ L
 Sbjct: 65 VDRAARRVAVLVAEVGGVVSASFASVGPSPRDADESEGSVGELYAIYVDPAMWRLGVGARLQ 124

Query: 108 THLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHG 156
 L+ + +G++ + N S +E G+ G + +G++ G
 Sbjct: 125 DVALRRLRDEGYREATLWVLATNGASRAFYEHTGWRHDGGV--SGFEAG 171

>gb|EGC23553.1| acetyltransferase [Streptococcus sanguinis SK353]
 Length = 156

Score = 38.9 bits (89), Expect = 0.31, Method: Compositional matrix adjust.
 Identities = 26/85 (30%), Positives = 42/85 (49%), Gaps = 2/85 (2%)

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYD-WTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 L AEV+G + G + K YD T ++ + GLG L T +L ++A+G
 Sbjct: 58 LAAEVDGQLVGAVWVRIMKDYGYDDQTPSLSSISFLPEFRSQGLGQQLMTAMLDDLKAKG 117

Query: 119 FKSVAVIGLPNDPSVRLHEALGYT 143
 + SV + N P+VR ++ LG+
 Sbjct: 118 YPSVSLSVSKDN-PAVRFYQRLGFV 141

>ref|YP_001578082.1| GCN5-related N-acetyltransferase [Lactobacillus helveticus DPC
 4571]
 gb|ABX27777.1| GCN5-related N-acetyltransferase [Lactobacillus helveticus DPC
 4571]
 Length = 172

Score = 38.9 bits (89), Expect = 0.32, Method: Compositional matrix adjust.
 Identities = 35/160 (21%), Positives = 60/160 (37%), Gaps = 5/160 (3%)

Query: 13 ATAADMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 A A++ + I N I + EP + Q W + D P V + + +A
 Sbjct: 7 AKQAELPKIVAIYNETIPSRLATADLEPVSVASRQPWFESFN--PDSRPLWVIKDDDKIA 64

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G + R AY T E ++Y+ + G+G +++ + G ++VA I
 Sbjct: 65 GWVGLESFYGRPAYHKTAEISIIYIDKDFRHQIGIGQQAIAAYVISQLPRLGLDALVAFIFSH 124

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDFE 169
 N PS L + + G L G + R F+
 Sbjct: 125 NQPSQHLFKQNQFETWGHLPDVAIMDGQRRSLDILGRRFQ 164

>ref|ZP_04559314.1| conserved hypothetical protein [Citrobacter sp. 30_2]
 gb|EEH95373.1| conserved hypothetical protein [Citrobacter sp. 30_2]
 Length = 179

Score = 38.9 bits (89), Expect = 0.32, Method: Compositional matrix adjust.
 Identities = 19/57 (33%), Positives = 32/57 (56%), Gaps = 3/57 (5%)

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHD--VGFWQRDFELP 171
 G + + A + N+ S RL E +G+ GTLRA+ + H WHD G +++++ P
 Sbjct: 121 GLRRLTACVTAGNEASRRLLEKVGFIHEGTLRASYWLHHTWHDDWIFGLLKQEYQPP 177

>ref|ZP_03932074.1| histone acetyltransferase HPA2 family protein [Corynebacterium
 accolens ATCC 49725]
 gb|EEI15272.1| histone acetyltransferase HPA2 family protein [Corynebacterium
 accolens ATCC 49725]

Length = 333

Score = 38.9 bits (89), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 23/79 (29%), Positives = 37/79 (46%)

Query: 64 VEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVV 123
++G I ++ + W S V V+ H+R GLG+ L H+L+ QG K
Sbjct: 242 IDGETVAITRGTTITESGDTAWLGYSAVEVAPAHRRQGLGALLGQHMLRWGREQGAHAY 301

Query: 124 AVIGLPNDPSVRLHEALGY 142
+ N +RL+E LG+
Sbjct: 302 LDVLA SNTAGIRLYEKLGF 320

>ref|YP_575960.1| GCN5-related N-acetyltransferase [Nitrobacter hamburgensis X14]
gb|ABE61500.1| GCN5-related N-acetyltransferase [Nitrobacter hamburgensis X14]
Length = 183

Score = 38.9 bits (89), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 41/143 (28%), Positives = 60/143 (41%), Gaps = 13/143 (9%)

Query: 8 VEIRPATAADMAAVCDIVNH-----YIETSTVNFRTEPQTPQEWIDDLERLQDRYPW 59
+E+RPA AD +AV + I + + + P W D R R
Sbjct: 20 IELRPAKVADASAVAATHDEAWRSAYRGIIPGAEEKLINRRGPH-WWDSAIRKGSRSVS 78

Query: 60 LVAEEVGVVAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 118
LV VAG A G +AR+ YD + +Y+ Q LG G L+T + + G
Sbjct: 79 LV--FGDNVAGYANYGRNRARSLQYDGEIYE-LYLRPEFQGLGFRRRLFTAARRDLMQSG 135

Query: 119 FKSVVAVIGLPNDPSVRLHEALG 141
KS+V N+P+ + ALG
Sbjct: 136 LKSMVTWALSDNEPATEFYRALG 158

>gb|EGC25902.1| acetyltransferase [Streptococcus sanguinis SK405]
gb|EGC26611.1| acetyltransferase [Streptococcus sanguinis SK678]
Length = 156

Score = 38.9 bits (89), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 25/85 (29%), Positives = 43/85 (50%), Gaps = 2/85 (2%)

Query: 60 LVAEEVGVVAGIAYAGPWKARNAYD-WTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 118
L AEV+G + G + K YD T ++ + GLG L T +L ++A+G
Sbjct: 58 LAAEVDGQLVGAVWVRIMKDYGYDDQTPSL SISFLPEFRSQGLGQQLMTAML DLLKAG 117

Query: 119 FKSVVAVIGLPNDPSVRLHEALGYT 143
+ SV + ++P+VR ++ LG+
Sbjct: 118 YPSVLSVS-KDNPAVRFYQRLGFV 141

>ref|ZP_00788288.1| acetyltransferase, GNAT family [Streptococcus agalactiae CJB111]
gb|EA072965.1| acetyltransferase, GNAT family [Streptococcus agalactiae CJB111]
Length = 163

Score = 38.9 bits (89), Expect = 0.33, Method: Compositional matrix adjust.
Identities = 42/162 (25%), Positives = 71/162 (43%), Gaps = 7/162 (4%)

Query: 10 IRPATAADMAAVCDIVNH YIETSTVNFRTEPQTPQEWID-DLER-LQDRYPWLVAEEGV 67
IRP D AV + N + T P ++W + DLE+ L + + VAEV+
Sbjct: 3 IRPMQDCDRGAVLTLQN-----TGWTALTSPVYDRKWTESDLEKNLANGMSFFVAEVDK 57

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+AGI GP+ A + ++ +Q GLG L LL +AQG+ + +

Sbjct: 58 IAGILDFGPYPFPAGKHVATFGILIAEPYQGQGLGKALLKALLTEAKAQGYIKIAMHVM 117

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDDE 169

N ++ L++ G+T + A + + D + +D E

Sbjct: 118 GNNSRAISLYQKYGFTEEARITKAFFIENHYVDALIFAKDLE 159

>ref|ZP_02182565.1| GCN5-related N-acetyltransferase [Flavobacteriales bacterium ALC-1]

gb|EDP70497.1| GCN5-related N-acetyltransferase [Flavobacteriales bacterium ALC-1]

Length = 162

Score = 38.5 bits (88), Expect = 0.35, Method: Compositional matrix adjust.

Identities = 23/79 (29%), Positives = 35/79 (44%)

Query: 80 RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEA 139

R AY E +VYV+ G+G+ L L+K E ++ A I N S+++H

Sbjct: 69 RKAYRGVAEVSYYVAKNKSCKGIGTKLLKSLIKVSEVNNIWTQLQAGIMEANKISIKMHIN 128

Query: 140 LGYTARGTLRAAGYKHGGW 158

G+ G G +G W

Sbjct: 129 CGFRQIGYREKIGNLNGKW 147

>ref|XP_001374182.1| PREDICTED: hypothetical protein [Monodelphis domestica]

Length = 243

Score = 38.5 bits (88), Expect = 0.37, Method: Compositional matrix adjust.

Identities = 33/121 (27%), Positives = 52/121 (42%), Gaps = 12/121 (9%)

Query: 23 DIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNA 82

DIV+H + T + R + + + VAE EG V G+ A P +

Sbjct: 84 DIVDHALHTDMRDIRKSYLSARGSC-----FWVAESEGQVGMVCARPVEEAPE 132

Query: 83 YDWTVEST-VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALG 141

VE + V H+ G+ L L++ + QG+ +VV N P+ RL+E LG

Sbjct: 133 RQKNVELLHLSVDQDHRGQGIKCLIQTLIEFAQDQGYDNVVLSTHALNYPQRLYERLG 192

Query: 142 Y 142

+

Sbjct: 193 F 193

>ref|ZP_00208304.1| COG1670: Acetyltransferases, including N-acetylases of ribosomal proteins [Magnetospirillum magnetotacticum MS-1]

Length = 176

Score = 38.5 bits (88), Expect = 0.37, Method: Compositional matrix adjust.

Identities = 19/61 (31%), Positives = 29/61 (47%), Gaps = 1/61 (1%)

Query: 101 GLGSTLYTHLLK-SMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGWH 159

GLG + +L+ G + +V+ PN S R+HE G+ G R ++ GGW

Sbjct: 96 GLGEAVIRRVLEHGFHGLRLKIVSDFMAPNQGSRRRIHERAGFREEGCARDDSWRRGGWV 155

Query: 160 D 160

D

Sbjct: 156 D 156

>ref|ZP_01364096.1| hypothetical protein PaerPA_01001200 [Pseudomonas aeruginosa PACS2]

Length = 168

Score = 38.5 bits (88), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 35/108 (32%), Positives = 44/108 (40%), Gaps = 5/108 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR T D+ A+ + T + TE Q ID L R LVAE G
Sbjct: 3 ISIRAETPGDIEAIARLTEAAFRNETHSSHTTE---QYIIDALRRAGALTFFSLVAEANGQ 58

Query: 68 VAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
V G A P A DW + + V+ QR GLGS L LL +
Sbjct: 59 VIGHIAASPVITIDGEAGDWYGLAPLSVAPERQRQGLGSQLVRRLLAEL 106

>ref|YP_002935498.1| acetyltransferase [Eubacterium eligens ATCC 27750]
gb|ACR73364.1| acetyltransferase [Eubacterium eligens ATCC 27750]
Length = 79

Score = 38.5 bits (88), Expect = 0.38, Method: Compositional matrix adjust.
Identities = 19/68 (27%), Positives = 36/68 (52%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+EI+ T D + +I Y++ + + F + + +E+ + + DRYP++ A G
Sbjct: 1 MEIQNVITIEDAEELLEIYAPYVKNTAITFEYDVPSVEEFRQIRVNISDRYPYIKAVDNGQ 60

Query: 68 VAGIAYAG 75
+ G AYAG
Sbjct: 61 IVGYAYAG 68

>ref|YP_003382392.1| GCN5-related N-acetyltransferase [Kribbella flavida DSM 17836]
gb|ADB33593.1| GCN5-related N-acetyltransferase [Kribbella flavida DSM 17836]
Length = 371

Score = 38.5 bits (88), Expect = 0.39, Method: Compositional matrix adjust.
Identities = 28/86 (32%), Positives = 38/86 (44%), Gaps = 2/86 (2%)

Query: 60 LVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
+VA VE V G+A A PW +E V V QR GLGS L +++ G
Sbjct: 205 IVASVEDAVVGMATAAPWDELGG--GAMEVAVLVEDGWQRQGLGSQLLRLVIREARLLGA 262

Query: 120 KSVVAVIGLPNDPSVRLHEALGYTAR 145
VV ++ N +R E+L R
Sbjct: 263 DRVVCMVQPENAAMLRTVESLRMRTR 288

>ref|YP_136761.1| acetyltransferase [Haloarcula marismortui ATCC 43049]
gb|AAV47055.1| acetyltransferase (GNAT) family [Haloarcula marismortui ATCC 43049]
Length = 173

Score = 38.5 bits (88), Expect = 0.39, Method: Compositional matrix adjust.
Identities = 35/144 (24%), Positives = 65/144 (45%), Gaps = 15/144 (10%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFR-----TEPQTPQEWIDDLERLQDRYP 58
E R +++ PA AD + +V Y++ + + +EW+D + L
Sbjct: 24 EDRSIDVIPADDADTES---LVEMYLDFDPADRAQGIPPVKEEAIREWLDTI--LNGDCV 78

Query: 59 WLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
+VA+ + VAG A P E ++V +Q G+G+ L LL +++G
Sbjct: 79 NVVAKHDDTVAGHATLVPDNEDEH-----ELAIFVLQAYQGAGIGTALVETLLGQGQSKG 133

Query: 119 FKSVAVIGLPNDPSVRLHEALGY 142
V + NDP++ L+E +G+
Sbjct: 134 IDHVWLTVERWNPAPISLYEKVGF 157

>ref|YP_001538076.1| thioester reductase domain-containing protein [Salinispora arenicola

CNS-205]

gb|ABV99085.1| thioester reductase domain [Salinispora arenicola CNS-205]

Length = 2374

Score = 38.5 bits (88), Expect = 0.40, Method: Compositional matrix adjust.
 Identities = 53/188 (28%), Positives = 73/188 (38%), Gaps = 36/188 (19%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRY--PWLVAEVE 65
 + IRPAT AD+ + I E + + P+ P E E LQ R P V+EV
 Sbjct: 2072 LHIRPATTADLPQLARICYEAFEATNASLGLPPEWPSEQAVT-EMLQGRLTAPSCVSEV- 2129

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVY---VSHRHQRLGLGSTLYTHLLKSMEAQGFKS 121
 + AG N E + V+ Q G+G L ++ + E G S
 Sbjct: 2130 ---AVDAAGSVVGSNFLVLGEEVAAGPLSVAPDTQGSQVGRMLMESIVAASERLGRPS 2185

Query: 122 VVAVIGLPNDPSVRLHEALGYTARGLRAAGYKHGGWHDVGFQWQDFELPAPPRP----- 176
 V AV N + RL+ +LG+ R L VGF APP P
 Sbjct: 2186 VRAVQVTNNLRNYRLYSSLGFVPREQLSVM-----VGF-----APPTPRTMAG 2228

Query: 177 --VRPVTQ 182
 VRP+T+
 Sbjct: 2229 FEVRPMTE 2236

>ref|YP_003683239.1| GCN5-related N-acetyltransferase [Nocardiosis dassonvillei subsp.

dassonvillei DSM 43111]

gb|ADH70733.1| GCN5-related N-acetyltransferase [Nocardiosis dassonvillei subsp.

dassonvillei DSM 43111]

Length = 151

Score = 38.5 bits (88), Expect = 0.41, Method: Compositional matrix adjust.
 Identities = 29/89 (32%), Positives = 39/89 (43%), Gaps = 6/89 (6%)

Query: 60 LVAEVEGVVAG--IAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
 L+AE EG +AG I + P AY V+ H+R GL + LY +
 Sbjct: 46 LIAEAEAGELAGFLIGFSPSPVPEEAY---VHFAGVAPGHRRTGLANGLYRRFTDGARER 101

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARG 146
 G V AV N+ S+ H A G+T G
 Sbjct: 102 GCTVVRAVTSPANERSIAFHRAHGFTVTG 130

>ref|ZP_05663843.1| conserved hypothetical protein [Enterococcus faecium 1,231,501]

gb|EEV47176.1| conserved hypothetical protein [Enterococcus faecium 1,231,501]

Length = 164

Score = 38.5 bits (88), Expect = 0.42, Method: Compositional matrix adjust.
 Identities = 31/135 (22%), Positives = 58/135 (42%), Gaps = 5/135 (3%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAY 73
 D+ + +I N I T EP ++ + W D + ++R W V +++ +AG
 Sbjct: 11 DLPRIVEIYNQAIPTRLSTADLEPVTIESKKAQFD-AHQSKERPMW-VLKIDQNIAGWVS 68

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133
 + R AY T E ++Y+ +++ GLG + + +++A + N S
 Sbjct: 69 LSDFYGRPAYAKTAEISYIDSNYRKHGLGQKALSFAESQLLDCKIDTLLAFVFATNQAS 128

Query: 134 VRLHEALGYTARGTL 148
 + L GY G L

Sbjct: 129 INLFRKNGYEQWGH 143

>ref|YP_003680354.1| GCN5-related N-acetyltransferase [Nocardiopsis dassonvillei subsp.
dassonvillei DSM 43111]
gb|ADH67848.1| GCN5-related N-acetyltransferase [Nocardiopsis dassonvillei subsp.
dassonvillei DSM 43111]
Length = 178

Score = 38.5 bits (88), Expect = 0.43, Method: Compositional matrix adjust.
Identities = 29/86 (33%), Positives = 45/86 (52%), Gaps = 2/86 (2%)

Query: 59 WLVAEVEG-VVAGIAYAGPWKARNAYDWTVE-STVYVSHRHQRLGLGSTLYTHLLKSMEA 116
++AE++G +VAG A K R+A T E V+ S RH+RLGL S + T L ++
Sbjct: 69 LVLAEELDGEIVAGGAVRPYKDRSAMADTAEFKRVWTSGRHRLGLASRVMTALEEAARD 128

Query: 117 QGFKSVVAVIGLPNDPSVRLHEALGY 142
G+ V+ G +V + +GY
Sbjct: 129 LGYTRVLLFTGPAQPEAVAFYTRIGY 154

>ref|YP_001863614.1| aminotransferase class-III [Burkholderia phymatum STM815]
gb|ACC76564.1| aminotransferase class-III [Burkholderia phymatum STM815]
Length = 451

Score = 38.5 bits (88), Expect = 0.44, Method: Compositional matrix adjust.
Identities = 31/86 (36%), Positives = 41/86 (47%), Gaps = 17/86 (19%)

Query: 19 AAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEG-----VVA 69
AAVCD V HY+ + V E + Q + L RL R+PW+ A+V G V
Sbjct: 319 AAVCDAVIHYMRENDVLANVERRGAQ-LEEGLRRLSARFPWM-ADVRGRGLLWGFVFTD 376

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSH 95
I A P ARNA +T +V+H
Sbjct: 377 AITKAAPDPARNA-----NTEFVAH 396

>ref|YP_003297965.1| GCN5-related N-acetyltransferase [Thermomonospora curvata DSM 43183]
gb|ACY95927.1| GCN5-related N-acetyltransferase [Thermomonospora curvata DSM 43183]
Length = 156

Score = 38.5 bits (88), Expect = 0.45, Method: Compositional matrix adjust.
Identities = 43/167 (25%), Positives = 67/167 (40%), Gaps = 19/167 (11%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGV 67
V +RPA AD A+ +++ + P+ ++D R +VAE +G
Sbjct: 5 VRLRPAEPADYDAIVAVMDDWWRPV-----RAALPRLFLDHFHRTS-----IVAHDGD 54

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
+ G + P AY V V R + GL +Y + + G V A+
Sbjct: 55 LVG--FLSPSAPEVAY----IHFGVDPRFRGRGLARRMYRRFFELARSDGRSVVQAITS 108

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFELPAPP 174
N S+ H ALG+T G + GY G D ++ D + P PP
Sbjct: 109 PHNHGSIAFHTALGFTVTGPV--PGYN-GPSADRVVFRLLDDPRPP 152

>ref|YP_002882859.1| GCN5-related protein N-acetyltransferase [Beutenbergia cavernae DSM 12333]

gb|ACQ81097.1| GCN5-related protein N-acetyltransferase [Beutenbergia cavernae DSM 12333]

Length = 181

Score = 38.1 bits (87), Expect = 0.45, Method: Compositional matrix adjust.
Identities = 25/81 (30%), Positives = 41/81 (50%)

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G V G A +R Y VE ++YV + G+G+ L +HL+ + E GF ++ +
Sbjct: 70 GHVLGWAACSSSTSSRLVYVGVELSLYVDPAARGRGIGTLLMSHLVAASERAGFWTLQSA 129

Query: 126 IGLPNDPSVRLHEALGYTARG 146
+ N S+ LH+A G+ G
Sbjct: 130 VFPENTASLALHQAHGFRVTG 150

>ref|ZP_05752266.1| phosphinothricin N-acetyltransferase [Lactobacillus helveticus DSM

20075]

gb|EEW68289.1| phosphinothricin N-acetyltransferase [Lactobacillus helveticus DSM 20075]

Length = 189

Score = 38.1 bits (87), Expect = 0.46, Method: Compositional matrix adjust.
Identities = 35/160 (21%), Positives = 60/160 (37%), Gaps = 5/160 (3%)

Query: 13 ATAADMAAVCDIVNHYIETSTVNFRTPEP---QTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
A A++ + I N I + EP + Q W + D P V + + +A
Sbjct: 24 AKQAELPKIVAIIYNETIPSRLATADLEPVSVASRQPWFESFN--PDSRPLWVIKDDDKIA 81

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
G + R AY T E ++Y+ + G+G +++ + G ++VA I
Sbjct: 82 GWVGLESFYGRPAYHKTAEISIIYIDKDFRHQIGQQAIAVISQLPRLGLDALVAFIFSH 141

Query: 130 NDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRQDFE 169
N PS L + + G L G + R F+
Sbjct: 142 NQPSQHLFKQNQFETWGHLPDVAIMDGQRRSLDILGRRFQ 181

>gb|EEQ90903.1| GNAT family N-acetyltransferase [Ajellomyces dermatitidis ER-3]
Length = 183

Score = 38.1 bits (87), Expect = 0.46, Method: Compositional matrix adjust.
Identities = 30/124 (24%), Positives = 56/124 (45%), Gaps = 17/124 (13%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDR-YPWLVAEVEG 66
+++R AT +D+ + I HY+ + + Q+R P+LVA VE
Sbjct: 3 LKVRTATESDIPQIYSIFTHYVRNTVITL FANTPPFSYMTKRFHETQERGLPFLVA-VEQ 61

Query: 67 V-----VAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLL 111
+ V G A P++ +Y TVE +++V + G+GSTL + L+
Sbjct: 62 LEQDDTCHGGNMAEKVCGYTLASPFRGYMLSYAPTVEMSLVFVHPEYHSRGIGSTLLSSLI 121

Query: 112 KSME 115
++++
Sbjct: 122 EALQ 125

>ref|YP_001013176.1| acetyltransferase [Hyperthermus butylicus DSM 5456]
gb|ABM80831.1| predicted Acetyltransferase [Hyperthermus butylicus DSM 5456]
Length = 170

Score = 38.1 bits (87), Expect = 0.46, Method: Compositional matrix adjust.

Identities = 34/128 (26%), Positives = 63/128 (49%), Gaps = 17/128 (13%)

Query: 33 TVNFRTEPQTPQEWI--DDLRLQDRYPWLVAEVEGVVAG-----IAYAGPWKARNAYDW 85
 +N T P+ EW + LE+ + + VAEV+G V G + Y P+ A+
 Sbjct: 31 MINKVTLPPEHYPEWFWREHLEKWGE--AFFVAEVDGEVVGVMTRVEYGPFFVAKGL--- 85

Query: 86 TVES----TVYVSHRHQRLGLGSTLYTHLLKSMEAQ-GFKSVVAVIGLPNDPSVRLHEAL 140
 V+ ++ V ++R G+G L +++++ + G K V + + N+P++RL+E L
 Sbjct: 86 IVKKGHIVSIAVLEGYRRRGIGRALMEAAAMEALKTRYGCKEVYLEVRVSNNPAIRLYEKL 145

Query: 141 GYTARGTL 148
 G+ L
 Sbjct: 146 GFKKVKVL 153

>ref|YP_001645660.1| GCN5-related N-acetyltransferase [Bacillus weihenstephanensis KBAB4]
 gb|ABY44032.1| GCN5-related N-acetyltransferase [Bacillus weihenstephanensis KBAB4]
 Length = 156

Score = 38.1 bits (87), Expect = 0.46, Method: Compositional matrix adjust.
 Identities = 17/50 (34%), Positives = 28/50 (56%)

Query: 93 VSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGY 142
 V+ + +R G+ STLY++ S A K V A+ N S+R H+ +G+
 Sbjct: 75 VNPFRKRGIASTLYSYFFDSARANNRQVVKAITSSVNKKSIRFHQEIF 124

>ref|YP_558760.1| putative phosphinothricin N-acetyltransferase [Burkholderia xenovorans LB400]
 gb|ABE30708.1| Putative phosphinothricin N-acetyltransferase [Burkholderia xenovorans LB400]
 Length = 176

Score = 38.1 bits (87), Expect = 0.47, Method: Compositional matrix adjust.
 Identities = 39/144 (27%), Positives = 65/144 (45%), Gaps = 8/144 (5%)

Query: 11 RPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQE---WIDDLRLQDRYPWLVAEVEG- 66
 R AT D+ A+ I N + + V EP + + W Q R W+V + +
 Sbjct: 6 R DATLDDLPAIVAIYNSTVPSRQVTADLEPVSVESRLAWFH-AHGPQKRPLWVVEDPQQP 64

Query: 67 --VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVA 124
 V+A ++++ + R AY T E ++Y+ + GLG L L + A G +V+
 Sbjct: 65 GRVIAWLSFS-DFYGRPAYLRTAEVSIYLDDESARGRGLGRQLLAASLAAAPALGIDTVLG 123

Query: 125 VIGLPNDPSVRLHEALGYTARGTL 148
 I N+ S+RL G+ G+L
 Sbjct: 124 FIFGHNEASLRLFRGFGFDTWGSL 147

>ref|YP_001152298.1| ribosomal-protein-alanine acetyltransferase [Pyrobaculum arsenaticum DSM 13514]
 gb|ABP49646.1| SSU ribosomal protein S18P alanine acetyltransferase [Pyrobaculum arsenaticum DSM 13514]
 Length = 176

Score = 38.1 bits (87), Expect = 0.48, Method: Compositional matrix adjust.
 Identities = 41/162 (25%), Positives = 68/162 (41%), Gaps = 33/162 (20%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEW--IDDLRLQDRYPWLVAEVEGV 67
 IR AT D+ V +N + P+ W ++ LE+ ++VAE++G
 Sbjct: 24 IREATTDLNDVI-----MINRKVL PENYPTWFFVEHLEQFPK--AFIVAEIDGR 71

Query: 68 VAGIAYAGPWKARNAYDWT-VESTVYVSHRH-----QRLGLGSTLYTHLLKSMEA 116
 V G + R Y W+ ++ V H +RLG+ + + +K+M+
 Sbjct: 72 VVG YIMS-----RVEYGWSNIQKGKAVRKGHIVSVGVLPPEARRLGIATAMMLRAMKAMKV 126

Query: 117 -QGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGG 157
 G V + + N P++ L+E LGY G R GY G
 Sbjct: 127 FYGASEVYLEVRVSNTPAISLYEKLGYKVVG--RIPGYSDG 166

>ref|YP_004170058.1| GCN5-like N-acetyltransferase [Deinococcus maricopensis DSM 21211]
 gb|ADV66393.1| GCN5-related N-acetyltransferase [Deinococcus maricopensis DSM 21211]
 Length = 315

Score = 38.1 bits (87), Expect = 0.48, Method: Compositional matrix adjust.
 Identities = 38/138 (27%), Positives = 58/138 (42%), Gaps = 12/138 (8%)

Query: 8 VEIRPATAADMAAVCDIVNHYIE--TSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEV 64
 V IR AT D+ + ++ ++ T+ R E DDL + VAE
 Sbjct: 3 VTIRDATPDDLGVIAELYTRFLPDEPTTAEMLRAE-----DDLAPANMHWRRFVAEQ 54

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVA 124
 G V G ++AG + D + + + R R G+G L HL + + A+G S +A
 Sbjct: 55 NGRVVGTSWAGQFTGMYHPDKYLVNVIVDPERQGR-GVGRALTAHLDEHLGARGVLSTLA 113

Query: 125 VIGLPNDPSVRLHEALGY 142
 + SV EA GY
 Sbjct: 114 DAREDHARSVAFLARGY 131

>ref|YP_079920.1| GCN5-related N-acetyltransferase [Bacillus licheniformis ATCC 14580]
 ref|YP_092335.1| hypothetical protein BLi02771 [Bacillus licheniformis ATCC 14580]
 ref|ZP_07999140.1| hypothetical protein HMPREF1012_00173 [Bacillus sp. BT1B_CT2]
 gb|AAU24282.1| GCN5-related N-acetyltransferase [Bacillus licheniformis ATCC 14580]
 gb|AAU41642.1| hypothetical protein BLi02771 [Bacillus licheniformis ATCC 14580]
 gb|EFV73510.1| hypothetical protein HMPREF1012_00173 [Bacillus sp. BT1B_CT2]
 Length = 174

Score = 38.1 bits (87), Expect = 0.48, Method: Compositional matrix adjust.
 Identities = 23/84 (27%), Positives = 46/84 (54%), Gaps = 3/84 (3%)

Query: 59 WLVAEEVEGVVAGIAYAGPWKAR-NAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
 ++ E +G + G A GP + + Y V S +Y+ ++Q+ G+GS L +++ + +
 Sbjct: 62 YVAEETDGKIIGFASGGPNRDHLSKYKGEV-SAIYLLQLYQKKGIGSRLMKAIVEELVKK 120

Query: 118 GFKSVVAVIGLPNDPSVRLHEALG 141
 KS++ + L +PS+ +E LG
 Sbjct: 121 NIKSLVWV-LAGNPSINFYEKLK 143

>ref|YP_004288199.1| acetyltransferase [Streptococcus gallolyticus subsp. gallolyticus]
 ATCC BAA-2069]
 emb|CBZ48455.1| acetyltransferase [Streptococcus gallolyticus subsp. gallolyticus ATCC BAA-2069]
 Length = 169

Score = 38.1 bits (87), Expect = 0.49, Method: Compositional matrix adjust.
 Identities = 36/151 (23%), Positives = 72/151 (47%), Gaps = 14/151 (9%)

Query: 8 VEIRPATAADMAAV---CDIVNHYIETSTVNFRTPEQT-----PQEWIDDLERLQDRYPW 59
 V +R A A+D A+ C + ET +++ E T + + + + + + + +
 Sbjct: 2 VIVRNALASDAEAILAFCQQIGS--ETDNLSYGEEGLTISVADEEILLSEIQSKTSH-F 58

Query: 60 LVAEEGEGVAGIAYAGPW-KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 LVAE G + G + K R A+ + V ++ +Q G+G L T L+ + + G
 Sbjct: 59 LVAEEAGEIVGTCNCSAFRKKRLAHRAEIGIVVKAYWNQ--GIGRQLLTRLIAAAQQSG 116

Query: 119 FKSVMVAVIGLPNDPSVRLHEALGYTARGTLR 149
 K + + ND ++ L+++LG+ GT +
 Sbjct: 117 LKVL SLEVRSDNDRAIHL YDSLGLGFQKIGTFK 147

>ref|YP_003430715.1| acetyltransferase, GNAT family [Streptococcus gallolyticus UCN34]
 emb|CBI13784.1| putative acetyltransferase, GNAT family [Streptococcus gallolyticus UCN34]
 Length = 169

Score = 38.1 bits (87), Expect = 0.50, Method: Compositional matrix adjust.
 Identities = 36/151 (23%), Positives = 72/151 (47%), Gaps = 14/151 (9%)

Query: 8 VEIRPATAADMAAV---CDIVNHYIETSTVNFRTPEQT-----PQEWIDDLERLQDRYPW 59
 V +R A A+D A+ C + ET +++ E T + + + + + + + +
 Sbjct: 2 VIVRNALASDAEAILAFCQQIGS--ETDNLSYGEEGLTISVADEEILLSEIQSKTSH-F 58

Query: 60 LVAEEGEGVAGIAYAGPW-KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
 LVAE G + G + K R A+ + V ++ +Q G+G L T L+ + + G
 Sbjct: 59 LVAEEAGEIVGTCNCSAFRKKRLAHRAEIGIAVKKAYWNQ--GIGRQLLTRLIAAAQQSG 116

Query: 119 FKSVMVAVIGLPNDPSVRLHEALGYTARGTLR 149
 K + + ND ++ L+++LG+ GT +
 Sbjct: 117 LKVL SLEVRSDNDRAIHL YDSLGLGFQKIGTFK 147

>ref|YP_171992.1| putative acetyltransferase [Synechococcus elongatus PCC 6301]
 ref|YP_399250.1| putative acetyltransferase [Synechococcus elongatus PCC 7942]
 dbj|BAD79472.1| putative acetyltransferase [Synechococcus elongatus PCC 6301]
 gb|ABB56263.1| putative acetyltransferase [Synechococcus elongatus PCC 7942]
 Length = 174

Score = 38.1 bits (87), Expect = 0.52, Method: Compositional matrix adjust.
 Identities = 44/173 (25%), Positives = 71/173 (41%), Gaps = 22/173 (12%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEEGEGV- 68
 IRPA AAD A+ I+ T P P D+ + + W+ + V
 Sbjct: 6 IRPAIAADWPAILAILEPIFRAG---ETYPYPP-----DISETEAQTVMWTVPTQTFVF 56

Query: 69 -----AGIAYAGPWK-ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 120
 G Y P + ++ V + R Q G+G TL H L+ + GF+
 Sbjct: 57 ESGDRQILGTYYLKPNQPGLGSHVCNCGFAVAAAARGQ--GVGKTLGLHALQVASSFGFR 114

Query: 121 SV-VAVIGLPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFQWQDFELP 171
 ++ ++ N PS++L + LG+T G L +A + GW D + + E P
 Sbjct: 115 AMQFNLVVAATNTPSIQLWQQLGFTTIGRLPQAFRHPQQGWVDALIFYKLEELP 167

>ref|YP_920983.1| GCN5-related N-acetyltransferase [Thermofilum pendens Hrk 5]
 gb|ABL78980.1| GCN5-related N-acetyltransferase [Thermofilum pendens Hrk 5]
 Length = 161

Score = 38.1 bits (87), Expect = 0.52, Method: Compositional matrix adjust.
 Identities = 37/133 (27%), Positives = 53/133 (39%), Gaps = 13/133 (9%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR TA D+ A +++ E + + T RL LVAE++G V
 Sbjct: 10 IRWLTAGDLPAAAMEVLEEAFEGAERYWST-----RLLGYLETLVAEIDGRVV 56

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G+A +AR V S + V +R+G+G +L K +G V A
 Sbjct: 57 GVAEIYETEARGYGRLGVSYLAVKREFRRMGVGRSLVEAAEKIFRERGCAVVAASTRKS 116

Query: 130 NDPSVRLHEALGY 142
 N S L LGY
 Sbjct: 117 NKASQALFRKLG 129

>ref|ZP_03646501.1| ribosomal-protein-alanine N-acetyltransferase [Bifidobacterium
 bifidum NCIMB 41171]
 ref|ZP_07802522.1| conserved hypothetical protein [Bifidobacterium bifidum NCIMB
 41171]
 gb|EFR50456.1| conserved hypothetical protein [Bifidobacterium bifidum NCIMB
 41171]
 Length = 193

Score = 38.1 bits (87), Expect = 0.54, Method: Compositional matrix adjust.
 Identities = 15/52 (28%), Positives = 28/52 (53%)

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGY 142
 + VS HQR G+ + HL+ QG + ++ + + NDP++ L+ G+
 Sbjct: 82 IGVSKTHQRQGIAMMMNHLISRARRQGARRMLLEVSVVNDPAIALYHRFGF 133

>ref|ZP_01984676.1| hypothetical acetyltransferase YafP [Vibrio harveyi HY01]
 gb|EDL70830.1| hypothetical acetyltransferase YafP [Vibrio harveyi HY01]
 Length = 159

Score = 38.1 bits (87), Expect = 0.54, Method: Compositional matrix adjust.
 Identities = 28/117 (23%), Positives = 52/117 (44%), Gaps = 15/117 (12%)

Query: 28 YIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWT 87
 Y E + E Q W++ + +Q P+ VAE+ GV+ G + P + +
 Sbjct: 31 YTEQQVKAWAQEGFDSQLWLNKMISIQ---PF-VAELNGVIVGYSDVQPSGLVDHF---- 82

Query: 88 ESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTA 144
 + H +Q G+G L TH++K A+G + + + + P +E +G+T
 Sbjct: 83 ----FCHHEYQGGVGRVLMTHVIKQAAAKGLDRIYSEVSITARP---FYEHMGFTV 132

>ref|YP_330531.1| acetyltransferase [Streptococcus agalactiae A909]
 ref|ZP_00782160.1| acetyltransferase, GNAT family [Streptococcus agalactiae H36B]
 gb|ABA46325.1| acetyltransferase, GNAT family [Streptococcus agalactiae A909]
 gb|EAO79123.1| acetyltransferase, GNAT family [Streptococcus agalactiae H36B]
 Length = 193

Score = 38.1 bits (87), Expect = 0.54, Method: Compositional matrix adjust.
 Identities = 41/162 (25%), Positives = 71/162 (43%), Gaps = 7/162 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLER-LQDRYPWLVAEVEGV 67
 IRP D AV + N + T P ++W + DLE+ L + + VAEV+
 Sbjct: 33 IRPMQDCDREAVLTLQN-----TGWTALTSPVYDRKWTESDLEKNLANGMSFFVAEVDK 87

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 +AG+ GP+ A + ++ +Q GLG L LL +AQG+ + +
 Sbjct: 88 IAGVLDGFPYYPFAGKHVATFGILIAEYPQGGGLKALLKALLTEAKAQGYIKIAMHVM 147

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFFE 169
N ++ L++ G+T + A + + D + +D E
Sbjct: 148 GNNSRAISLYQKYGFTEEARITKAFFIENHYVDALIFAKDLE 189

>ref|ZP_07835149.1| GCN5-related N-acetyltransferase [Thermaerobacter subterraneus DSM

13965]
gb|EFR63493.1| GCN5-related N-acetyltransferase [Thermaerobacter subterraneus DSM
13965]
Length = 159

Score = 38.1 bits (87), Expect = 0.55, Method: Compositional matrix adjust.
Identities = 34/136 (25%), Positives = 56/136 (41%), Gaps = 8/136 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQD---RYPWLVAEVEG 66
+ PA AD V ++ + P P+ DDL R+QD R VA G
Sbjct: 4 VEPAAPADAVQVLEVTRRAFRRYEGKY---PVAPEPLQDDLARVQDDIGRGRVWVARNGG 60

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
V G+ A P R W + V + +L +G++L + + QG +++
Sbjct: 61 RVIGVVRARPLAGRQEA-WEIYGLA-VDPEYSQLDVGTSLVRAVEDRLRPQGVRAHLHLQT 118

Query: 127 GLPNDPSVRLHEALGY 142
GL + P++ +GY
Sbjct: 119 GLRDAPAIEFWYRVGY 134

>ref|NP_386563.2| hypothetical protein SMC01824 [Sinorhizobium meliloti 1021]
ref|ZP_07588263.1| GCN5-related N-acetyltransferase [Sinorhizobium meliloti BL225C]
ref|ZP_07596779.1| GCN5-related N-acetyltransferase [Sinorhizobium meliloti AK83]
emb|CAC47036.2| Conserved hypothetical protein [Sinorhizobium meliloti 1021]
gb|EFN27674.1| GCN5-related N-acetyltransferase [Sinorhizobium meliloti AK83]
gb|EFN31570.1| GCN5-related N-acetyltransferase [Sinorhizobium meliloti BL225C]
Length = 161

Score = 38.1 bits (87), Expect = 0.55, Method: Compositional matrix adjust.
Identities = 33/115 (28%), Positives = 54/115 (46%), Gaps = 19/115 (16%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLER-----LQDRYPWLVA 62
V R AT ADM A I+N +I+ + R PQ +D+ER + P +VA
Sbjct: 9 VSCRDATLADMPACAGILNRWIDATPWMPRVHPQ-----EDVERHYRESVFANGPVIVA 62

Query: 63 EVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
+ G +AG A +A + + +Y+ RH+ +G+G+TL K ++
Sbjct: 63 DCRGEIAGFL-----ALSADGFV--TALYLDERHRGVGIGTTLIREAKKRARSE 109

>ref|ZP_04932411.1| hypothetical protein PACG_05270 [Pseudomonas aeruginosa C3719]
gb|EAS56530.1| hypothetical protein PACG_05270 [Pseudomonas aeruginosa C3719]
Length = 168

Score = 38.1 bits (87), Expect = 0.55, Method: Compositional matrix adjust.
Identities = 35/108 (32%), Positives = 44/108 (40%), Gaps = 5/108 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEGV 67
+ IR T D+ A+ + T + TE Q ID L R LVAE G
Sbjct: 3 ISIRAETPGDIDAIARLTEAAFRNETHSSHT---QYIIDALRRAGALTFSLVAEANGQ 58

Query: 68 VAGIAYAGPWKARN-AYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSM 114
V G A P A DW + + V+ QR GLGS L LL +
Sbjct: 59 VIGHIAASPVTIDGEAGDWYGLAPLSVAPERQRQGLGSQVRRLLAEL 106

>ref|ZP_02445001.1| hypothetical protein ANACOL_04336 [Anaerotruncus colihominis DSM 17241]
 gb|EDS09011.1| hypothetical protein ANACOL_04336 [Anaerotruncus colihominis DSM 17241]
 Length = 162

Score = 38.1 bits (87), Expect = 0.57, Method: Compositional matrix adjust.
 Identities = 40/159 (25%), Positives = 64/159 (40%), Gaps = 6/159 (3%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IR T D+AAV I N + + P TP+E + VAE G +
 Sbjct: 5 IRQYTEKDLAAVTKIWNEVVAEGNAFPQDTPFTPEE---ARAFFASQFTTGVAESGGRIV 61

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV-VAVIGL 128
 G P A + ++ VS + G+G L H L+ GF + +
 Sbjct: 62 GFYILHPNNAGHC-AHIANASYGVSSEARGTGMGERLVRHSLEMCRKHGFVGLQFNAVVS 120

Query: 129 PNDPSVRLHEALGYTARGTLRAA-GYKHGGWHDVGFQWR 166
 N ++RL+E LG+ GT + +K G + D+ + +
 Sbjct: 121 SNTAAIRLYEKLGFVRIGTAKNGYRFKDGHYEDLFLFNK 159

>ref|ZP_03743073.1| hypothetical protein BIFPSEUDO_03658 [Bifidobacterium pseudocatenulatum DSM 20438]
 gb|EEG70636.1| hypothetical protein BIFPSEUDO_03658 [Bifidobacterium pseudocatenulatum DSM 20438]
 Length = 191

Score = 37.7 bits (86), Expect = 0.59, Method: Compositional matrix adjust.
 Identities = 22/74 (29%), Positives = 37/74 (50%), Gaps = 3/74 (4%)

Query: 73 YAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDP 132
 YAG W + D + T+ V R QR G+ ++L L+ QG K ++ + + N P
 Sbjct: 89 YAGFWY--DGDDAEI-MTIGVGRRFQRQGIASLMEALIARAREQGAKRMLLEVRVDNTP 145

Query: 133 SVRLHEALGYTARG 146
 ++ L+E G+ G
 Sbjct: 146 ALALYERFGFAKMG 159

>ref|ZP_05913840.1| N-acetyltransferase [Brevibacterium linens BL2]
 Length = 163

Score = 37.7 bits (86), Expect = 0.60, Method: Compositional matrix adjust.
 Identities = 37/148 (25%), Positives = 63/148 (42%), Gaps = 18/148 (12%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEPQTPQEWIDDLERLQ---DRYP---WLV 61
 + +R AT D+ + +V + + EP + DD + D +P LV
 Sbjct: 1 MNVREATKDDLDPDILRLVQ-----ALAVYEKEPDAVEATEDDFAAVMFPADGHPNTYGLV 55

Query: 62 AEVEGVVAGIAY---AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
 AEV+G + GIA W +N W ++V H+ G G L HL + + +
 Sbjct: 56 AEVDGQIIGIAIWFHSFSTWTGKNRI-WL--EDLFVDPDRGNGAGKALLGHQAQICQER 112

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTAR 145
 G + + N+PS+ + +LG A+
 Sbjct: 113 GLTRLEWCVLKWNPSIGFYRSLGAKAQ 140

>ref|ZP_08017910.1| ribosomal-protein-alanine acetyltransferase [Lautropia mirabilis ATCC 51599]
 gb|EFV95268.1| ribosomal-protein-alanine acetyltransferase [Lautropia mirabilis

ATCC 51599]
Length = 160

Score = 37.7 bits (86), Expect = 0.61, Method: Compositional matrix adjust.
Identities = 35/142 (24%), Positives = 61/142 (42%), Gaps = 10/142 (7%)

Query: 29 IETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAE-VEGVVAG-----IAYAG-PWK--- 78
++ ST+ FR + +D +E+ YPW +++ + + AG AG P+
Sbjct: 6 MDLSTIGFRPMTEADLPDAVDAIEQAVQYPWRISQFADSLKAGHQAWIFTEAGQPFQYAV 65

Query: 79 ARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHE 138
A D T+ ++ HQ GLG L + QG +S+ + N P++ L++
Sbjct: 66 LLAALDEVELLTLALARSHQGRGLGRHCLGWLQAQVRQQGRSLFLEVATANAPALALYQ 125

Query: 139 ALGYTARGTLRAAGYKHGGWHD 160
+G+ G R G HD
Sbjct: 126 RMGFETLGRRRNYRAADGRHD 147

>emb|CBJ28808.1| ribosomal-protein-alanine acetyltransferase-like protein
[Ectocarpus siliculosus]
Length = 227

Score = 37.7 bits (86), Expect = 0.63, Method: Compositional matrix adjust.
Identities = 18/48 (37%), Positives = 27/48 (56%)

Query: 97 HQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTA 144
H+ GLG+ LY K+++ +G V AV N SV H+A+G+ A
Sbjct: 115 HRGAGLGALLYDQFFKAVQTRGCTLVHAVTSPANTASVAFHKAIGFEA 162

>ref|YP_003971182.1| ribosomal-protein-S18-alanine acetyltransferase [Bifidobacterium
bifidum PRL2010]
gb|ADP36145.1| RimI Ribosomal-protein-S18-alanine acetyltransferase
[Bifidobacterium bifidum PRL2010]
Length = 193

Score = 37.7 bits (86), Expect = 0.64, Method: Compositional matrix adjust.
Identities = 15/52 (28%), Positives = 28/52 (53%)

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGY 142
+ VS HQR G+ + HL+ QG + ++ + + NDP++ L+ G+
Sbjct: 82 IGVSKTHQRQGIAMMNHLLISRAHRQGARRMLLEVSVVNDPAIALYHRFGF 133

>ref|ZP_02929682.1| hypothetical protein VspiD_23575 [Verrucomicrobium spinosum DSM
4136]
Length = 201

Score = 37.7 bits (86), Expect = 0.64, Method: Compositional matrix adjust.
Identities = 37/159 (23%), Positives = 64/159 (40%), Gaps = 16/159 (10%)

Query: 2 SPERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDL----- 51
+P + +EIR A +D + +I + + P E +D L+
Sbjct: 4 TPHQMMIEIRRANTSDATGIAEI-----QVAGWQAAYRGIVPDEVLDGLDVASRIPLWQR 58

Query: 52 -RLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHL 110
L + VA++EG VAG + P + A + +YV+ R G+G L T
Sbjct: 59 FSLDAKGDLYVADLEGGVAGFCHLIPSRDPGATGTAEIAAIYVNPLAWRTGIGRKLCTTA 118

Query: 111 LKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLR 149
L S + + V + N R +EA+G+ G ++
Sbjct: 119 LHASAVERSYLRVTLLWVLSGNHLGRRFYEAGFEHDAVK 157

```
>ref|YP_003868969.1| Histone acetyltransferase HPA2-like protein [Paenibacillus
polymyxa
      E681]
gb|ADM68431.1| Histone acetyltransferase HPA2-like protein [Paenibacillus polymyxa
      E681]
      Length = 170
```

Score = 37.7 bits (86), Expect = 0.68, Method: Compositional matrix adjust.
Identities = 32/103 (31%), Positives = 49/103 (47%), Gaps = 4/103 (3%)

```
Query: 41 QTPQEWIDDLERLQDRYPWLVAEVE-GVVAGIAYAGPWKARNAYDWTVEST-VYVSHRHQ 98
      Q + W +L +D + VAE E G + G GP K+ + E T +YV +
Sbjct: 42 QRTELWNANLSS-EDGHRVYVAENEKGEIIGFVSGGPEKSGEYPPYGGEITAIYVLSEYH 100

Query: 99 RLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALG 141
      LGLG LY LL+ + SV+ + L ++P+ +E LG
Sbjct: 101 SLGLGKRLYLRLQLHFNSMDIHSVIVVW-LADNPACTFYERLG 142
```

```
>ref|ZP_05784651.1| acetyltransferase, gnat family [Silicibacter lacuscaerulensis
ITI-1157]
gb|EEX11378.1| acetyltransferase, gnat family [Silicibacter lacuscaerulensis
ITI-1157]
      Length = 140
```

Score = 37.7 bits (86), Expect = 0.69, Method: Compositional matrix adjust.
Identities = 23/79 (29%), Positives = 34/79 (43%), Gaps = 2/79 (2%)

```
Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
      G G +Y W + T+++ H+R GLG L H +G S A +
Sbjct: 43 GAGRVGGLHGATSYGWLLIKTLWIDPAHRRRGLGRQLLDHAFAEARRRGCHS--AWLDTS 100

Query: 130 NDPSVRLHEALGYTARGTL 148
      N + R +EALG+ G L
Sbjct: 101 NPAAARFYEALGFEPFGRL 119
```

```
>ref|ZP_02194079.1| putative acetyltransferase [Vibrio sp. AND4]
gb|EDP60415.1| putative acetyltransferase [Vibrio sp. AND4]
      Length = 166
```

Score = 37.7 bits (86), Expect = 0.69, Method: Compositional matrix adjust.
Identities = 33/151 (21%), Positives = 67/151 (44%), Gaps = 5/151 (3%)

```
Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWIDDLERLQDRYPWLVAEVEG-VV 68
      +RP T D AA+ DI + + + W+D L + VAEV+G +V
Sbjct: 5 VRPTTVEDAAALVDIYSQP-KAQRETLLQPKPSLSMWVDRLSNMPTGVYSYVAEVDGKIV 63

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEA-QGFKSVVAVIG 127
      I + + R ++ T + V ++ LG+GS L + + + + + +
Sbjct: 64 GNIGFHHSQRPRTSH--TASFGIGVHDKYHGLGVGSALISTVTQLADNWLNVRRRIQIEVN 121

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158
      N+ ++ L++ G+ G L A ++ G +
Sbjct: 122 ADNETAIGLYKKHGFIEGELIDACFRDGEY 152
```

```
>ref|NP_688964.1| acetyltransferase [Streptococcus agalactiae 2603V/R]
ref|NP_736396.1| GNAT family acetyltransferase [Streptococcus agalactiae NEM316]
ref|ZP_00781511.1| acetyl transferase [Streptococcus agalactiae 18RS21]
ref|ZP_00789134.1| acetyltransferase, GNAT family [Streptococcus agalactiae 515]
```

gb|AAN00837.1|AE014281_6 acetyltransferase, GNAT family [Streptococcus agalactiae 2603V/R]

emb|CAD47622.1| Unknown [Streptococcus agalactiae NEM316]

gb|EAO61896.1| acetyl transferase [Streptococcus agalactiae 18RS21]

gb|EAO72177.1| acetyltransferase, GNAT family [Streptococcus agalactiae 515]

Length = 163

Score = 37.7 bits (86), Expect = 0.69, Method: Compositional matrix adjust.

Identities = 41/162 (25%), Positives = 71/162 (43%), Gaps = 7/162 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTEPQTPQEWID-DLER-LQDRYPWLVAEVEGV 67

IRP D AV + N + T P ++W + DLE+ L + + VAEV+

Sbjct: 3 IRPMQDCDREAVLTLQN-----TGWTALTSPVYDRKWTESDLEKNLANGMSFFVAEVDK 57

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIG 127

+AG+ GP+ A + ++ +Q GLG L LL +AQG+ + +

Sbjct: 58 IAGVLDFGPYPFPAGKHVATFGILIAEPYQGGGLGKALLKALLTEAKAQGYIKIAMHVM 117

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWQDFE 169

N ++ L++ G+T + A + + D + +D E

Sbjct: 118 GNNRAISLYQKYGFTEEARITKAFFIENHYVDALIFAKDLE 159

>ref|YP_347744.1| hypothetical protein Pfl01_2012 [Pseudomonas fluorescens Pf0-1]

gb|ABA73755.1| hypothetical protein Pfl01_2012 [Pseudomonas fluorescens Pf0-1]

Length = 229

Score = 37.7 bits (86), Expect = 0.69, Method: Compositional matrix adjust.

Identities = 21/57 (36%), Positives = 28/57 (49%)

Query: 102 LGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGGW 158

L L L K+M AQQ VV V N P+++LH +GYT +G + G W

Sbjct: 144 LSVDLQLELWKAMAAQGCCKVVDVCEFHNPALKLHLRMGYTEQGRIMNVYELFGRW 200

>ref|ZP_07464734.1| GNAT family acetyltransferase [Streptococcus gallolyticus subsp. gallolyticus TX20005]

gb|EFM29475.1| GNAT family acetyltransferase [Streptococcus gallolyticus subsp. gallolyticus TX20005]

Length = 169

Score = 37.7 bits (86), Expect = 0.75, Method: Compositional matrix adjust.

Identities = 25/92 (27%), Positives = 46/92 (50%), Gaps = 3/92 (3%)

Query: 59 WLVAEVEGVVAGIAYAGPW-KARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117

+LVAE G + G + K R A+ + V ++ +Q G+G L T L+ + +

Sbjct: 58 FLVAEEAGEIVGTCNCSAFRKKRLAHRAEIGIAVKKAYWNQ--GIGRQLLTRLIAAAQQS 115

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLR 149

G K + + ND ++ L+++LG+ GT +

Sbjct: 116 GLKVLSEVRSDNDRAIHLVDSLGFQKIGTFK 147

>ref|YP_384797.1| SSU ribosomal protein S18P alanine acetyltransferase [Geobacter metallireducens GS-15]

gb|ABB32072.1| [SSU ribosomal protein S18P]-alanine acetyltransferase [Geobacter metallireducens GS-15]

Length = 164

Score = 37.4 bits (85), Expect = 0.77, Method: Compositional matrix adjust.

Identities = 33/118 (27%), Positives = 55/118 (46%), Gaps = 8/118 (6%)

Query: 40 PQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQR 99

P T + +ID+L YP + +G+VAG Y P + + ++ V + R +
 Sbjct: 35 PWTREHFIDELNSPHS-YPLVARTADGIVAG--YICPLLVLDEGE-ILDVAVRLGSRGK- 89

Query: 100 LGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGYTARGTLRAAGYKHGG 157

G+G L + + AQG + V + + N P++ L+ LG+ R T R GY G
 Sbjct: 90 -GVGGALVRRAITELRAQGARVVCLEVRVSNLPALTLYRQLGF--RETGRRKGYENG 144

>ref|XP_001356126.2| GA16428 [Drosophila pseudoobscura pseudoobscura]

gb|EAL33186.2| GA16428 [Drosophila pseudoobscura pseudoobscura]

Length = 182

Score = 37.4 bits (85), Expect = 0.79, Method: Compositional matrix adjust.

Identities = 20/75 (26%), Positives = 39/75 (52%), Gaps = 1/75 (1%)

Query: 75 GPWKARNAYDWTVE-STVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133

G + Y+W + VS ++R G+ + L H+ +++A+G V + N P+
 Sbjct: 61 GKYLESKLYEWHGHVCALTVSDDYRRTGVATLLMRHIARALDAKGALYVDLFLRCSNRPA 120

Query: 134 VRLHEALGYTARGTL 148

+ L+ +LGY R T+
 Sbjct: 121 LSLYSSSLGYVLRRTV 135

>ref|YP_003906914.1| phosphinothricin acetyltransferase [Burkholderia sp. CCGE1003]

gb|ADN57623.1| Phosphinothricin acetyltransferase [Burkholderia sp. CCGE1003]

Length = 174

Score = 37.4 bits (85), Expect = 0.81, Method: Compositional matrix adjust.

Identities = 38/146 (26%), Positives = 63/146 (43%), Gaps = 6/146 (4%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQ-DRYPWLVAEVEG 66

+ R AT D+ A+ I N + + V EP + + + + P V E G
 Sbjct: 3 LSYRDATLDDLPAIVAIYNSTVASRQVTADLEPVSVESRVAVFWFHAHGPBKRPLWVVEDAG 62

Query: 67 ---VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV 122

V A +++ + R AY T E ++Y+ R + GLG L L + A G +
 Sbjct: 63 QPGRVTAWLSFS-DFYGRPAYQRTAELSIYLDERARGKGLKQLLAAALTAAPALGIDTA 121

Query: 123 VAVIGLPNDPSVRLHEALGYTARGTL 148

+ I N+ S+RL G+ G+L
 Sbjct: 122 LGFIFGHNEASLRLFRGFGFDTWGSL 147

>ref|ZP_06700579.1| phosphinothricin N-acetyltransferase [Enterococcus faecium U0317]

gb|EFF30027.1| phosphinothricin N-acetyltransferase [Enterococcus faecium U0317]

Length = 164

Score = 37.4 bits (85), Expect = 0.82, Method: Compositional matrix adjust.

Identities = 30/135 (22%), Positives = 58/135 (42%), Gaps = 5/135 (3%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAY 73

D+ + +I N I T EP ++ + W D + ++R W V +++ +AG
 Sbjct: 11 DLPRIVEIYNQAIPTLSTADLEPVTIESKKAQFD-AHQSKERPMW-VMKIDQNIAGWVS 68

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133

+ R AY T E ++Y+ +++ GLG + + +++A + N S
 Sbjct: 69 LSDFYGRPAYAKTAEISIIYIDSNYRKHGLGQKALSFAESQLLDCKIDTLAFAVFATNQAS 128

Query: 134 VRLHEALGYTARGTL 148

+ L G+ G L
 Sbjct: 129 INLFRKNGFEQWGH 143

>ref|ZP_06474333.1| mycothiol biosynthesis acetyltransferase [Frankia symbiont of
Datisca glomerata]
gb|EFD28976.1| mycothiol biosynthesis acetyltransferase [Frankia symbiont of
Datisca glomerata]
Length = 389

Score = 37.4 bits (85), Expect = 0.82, Method: Compositional matrix adjust.
Identities = 35/129 (27%), Positives = 59/129 (45%), Gaps = 26/129 (20%)

Query: 28 YIETSTVNFRTEPQTPQEWIDDLERLQDRYPWL-----VAEVEGVVAGIAYAGPWKARN 81
++ ++V F T P+ + ++DL RL++ PW +AE G + G
Sbjct: 251 WVVVNSVAFATHPEQGRWTVEDL-RLREAEPWFDPAAGFFLAEEAAGQLVG----- 298

Query: 82 AYDWT-VES-----TVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSV 134
+ WT VE+ V V+ GLG L L + +G +V+ + N P+V
Sbjct: 299 -FHWTKVEAGIGEVYVVGVAPTAAGRGLGRVLTIGLHHLRDRGLATVMLYVDDTNRPV 357

Query: 135 RLHEALGYT 143
RL+E LG++
Sbjct: 358 RLYETLGFS 366

>ref|ZP_05965160.1| putative phosphinothricin N-acetyltransferase [Bifidobacterium
gallicum DSM 20093]
gb|EFA23495.1| putative phosphinothricin N-acetyltransferase [Bifidobacterium
gallicum DSM 20093]
Length = 172

Score = 37.4 bits (85), Expect = 0.82, Method: Compositional matrix adjust.
Identities = 45/171 (26%), Positives = 69/171 (40%), Gaps = 15/171 (8%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTEP---QTPQEWIDDLERLQDRYPWLVAEV- 64
+ R ATA D V I N + + T + +EWI E D Y + E
Sbjct: 6 QARVATAHDAQIVAAIYNAAVVEGGASADTAASVSASRREWI---EAHTDPYAVFIIIEAV 62

Query: 65 --EGV----VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQG 118
+GV VA A + + R YD + YV+ +R G+G LL +G
Sbjct: 63 DEQGVPSIPVAFCALSNYYP-RPGYDGVTDLAYVVAPEWRRRGVGVQFALRTLLEARNRG 121

Query: 119 FKSVVAVIGLPNDPSVRLHEALGYTARGTL-RAAGYKHGGWHDVGFQWRDF 168
+ V +I N S+ L + G+T G + +AA G D+ ++ D
Sbjct: 122 MRKAVCIIFADNTASIALCTSFQFTRFGLMAQAATDALGVMRDMAYYDLDL 172

>ref|XP_002021961.1| GL14242 [Drosophila persimilis]
gb|EDW25902.1| GL14242 [Drosophila persimilis]
Length = 391

Score = 37.4 bits (85), Expect = 0.83, Method: Compositional matrix adjust.
Identities = 18/50 (36%), Positives = 31/50 (62%)

Query: 93 VSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPSVRLHEALGY 142
V +++L +GSTL T +++M A VV + N+P++RL+E LG+
Sbjct: 318 VRKEYRKLKIGSTLVTKAIEAMLADNADEVVLETEMRNEPALRLYENLGF 367

>ref|ZP_03978230.1| phosphinothricin N-acetyltransferase [Corynebacterium
lipophiloflavum DSM 44291]
gb|EEI17705.1| phosphinothricin N-acetyltransferase [Corynebacterium
lipophiloflavum DSM 44291]
Length = 178

Score = 37.4 bits (85), Expect = 0.84, Method: Compositional matrix adjust.
Identities = 36/172 (20%), Positives = 73/172 (42%), Gaps = 8/172 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
+RP D V +I +++ ++ ++ Q+ +E+ + ++ + + +E V
Sbjct: 8 LRPIRPEDYPQVREIYELGLKSGHASYESKGQSWEEFRSKM-IIETVFAVDSEDNSRVV 66

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 129
G A +R+ + VE ++Y+ Q G+ S L L+ + + ++ + I
Sbjct: 67 GWVAAKASSRSVFGVVEDSIYIHPDAQGRGVSSALLDKLIDTCTSLDMWAIHSWIFPE 126

Query: 130 NDPSVRLHEALGYTARGLRAA-----GYKHGGWHDVGFQWQDFELPAPPRP 176
N S +LH + G+T GT G G W ++ LP P +P
Sbjct: 127 NKGSSKLHMSRGFTKVGTFHNAKMTYGDMAQWRATDVYE--LLLPTPGKP 176

>ref|XP_001355453.2| GA10986 [Drosophila pseudoobscura pseudoobscura]
gb|EAL32512.2| GA10986 [Drosophila pseudoobscura pseudoobscura]
Length = 432

Score = 37.4 bits (85), Expect = 0.86, Method: Compositional matrix adjust.
Identities = 18/54 (33%), Positives = 33/54 (61%)

Query: 89 STVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGY 142
+ + V +++L +GSTL T +++M A VV + N+P++RL+E LG+
Sbjct: 355 AMLAVRKEYRKLKIGSTLVTKAIEAMLADNADEVVLETEMNEPALRLYENLGF 408

>ref|ZP_01066033.1| Histone acetyltransferase HPA2 and related acetyltransferase
[Vibrio sp. MED222]
gb|EAQ52656.1| Histone acetyltransferase HPA2 and related acetyltransferase
[Vibrio sp. MED222]
Length = 166

Score = 37.4 bits (85), Expect = 0.87, Method: Compositional matrix adjust.
Identities = 35/154 (22%), Positives = 63/154 (40%), Gaps = 7/154 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVA--EVEGV 67
IR T D + D++N I + + T E +E +R + VA E
Sbjct: 5 IREVTVEDAQGIIDVLNPIIIEARYTILDQTFTVDEEKAFIESFPERGVFSVAVNEATSQ 64

Query: 68 VAGIAYAGPWKA-RNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLP 126
+ G P+ A+D YV + G+ L+ + KS +A+G++ + A +
Sbjct: 65 LLGFQNVFATYTKAFDHVGIIGTYVDANSRGQGVAKQLFDYTFKSAKAKGYEKLFAVY 124

Query: 127 GLPNDPSVRLHEALGYTARGLRAAGYKHGGWHD 160
N+ ++ ++ G+ GT + KHG D
Sbjct: 125 RADNERALAVYFKQGFEIVGTAK----KHGKIGD 154

>ref|YP_658242.1| protein N-acetyltransferase-like protein [Haloquadratum walsbyi DSM
16790]
emb|CAJ52634.1| protein N-acetyltransferase homolog [Haloquadratum walsbyi DSM
16790]
Length = 210

Score = 37.4 bits (85), Expect = 0.88, Method: Compositional matrix adjust.
Identities = 19/57 (33%), Positives = 28/57 (49%)

Query: 91 VYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVAVIGLPNDPSVRLHEALGYTARGT 147
VYV H+ G+ + L T + A+ VA++ + N PS L E G+T R T
Sbjct: 135 VYVDQAHNRNMGVATALITAANRYASARDATQAVALVAIDNRPSQALFETCGFTVRST 191

>ref|ZP_00785850.1| acetyltransferase, GNAT family [Streptococcus agalactiae COH1]
 gb|EA075419.1| acetyltransferase, GNAT family [Streptococcus agalactiae COH1]
 Length = 163

Score = 37.4 bits (85), Expect = 0.92, Method: Compositional matrix adjust.
 Identities = 40/162 (24%), Positives = 70/162 (43%), Gaps = 7/162 (4%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWID-DLER-LQDRYPWLVAEVEGV 67
 IRP D AV + N + T P +W + DLE+ L + + VAE++
 Sbjct: 3 IRPMQNCDEAVLTLQN-----TGWTALTSPVYDHKWTESDLEKNLANGMSFFVAEIDDK 57

Query: 68 VAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIG 127
 +AG+ GP+ A + ++ +Q GLG L LL +AQG+ + +
 Sbjct: 58 IAGVLDFGPYPFPAGKHVATFGILIAEPYQGQGLGKALLKALLTEAKAQGYIKIAMHVM 117

Query: 128 LPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFWRDQDFE 169
 N ++ L++ G+T + A + + D + +D E
 Sbjct: 118 GNNRAISLYQKYGFTEEARITKAFFIENHYVDALIFAKDLE 159

>ref|ZP_05666635.1| phosphinothricin N-acetyltransferase [Enterococcus faecium
 1,141,733]
 gb|EEV49968.1| phosphinothricin N-acetyltransferase [Enterococcus faecium
 1,141,733]
 Length = 164

Score = 37.4 bits (85), Expect = 0.93, Method: Compositional matrix adjust.
 Identities = 28/135 (20%), Positives = 61/135 (45%), Gaps = 5/135 (3%)

Query: 17 DMAAVCDIVNHYIETSTVNFRTPE---QTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAY 73
 D+ + +I N I EP ++ Q W D + ++R W++ + +V ++
 Sbjct: 11 DLPRIVEIYNQAIPARLSTADLEPVTIESRQAWFD-AHQTKERPLWVIKIDQNIVGWLSL 69

Query: 74 AGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLPNDPS 133
 + + R AY T E ++Y+ +++ GLG + ++ +++A + N S
 Sbjct: 70 SDFY-GRPAYANTAEISIIYIDSTYRKHGLGQKALSFAESQLKDCKIDTLLAFVFTINQAS 128

Query: 134 VRLHEALGYTARGTL 148
 ++L + G+ G L
 Sbjct: 129 IKLFQKNGFEQWGH 143

>ref|ZP_05749879.1| probable phosphinothricin acetyltransferase protein
 [Corynebacterium efficiens YS-314]
 gb|EEW49985.1| probable phosphinothricin acetyltransferase protein
 [Corynebacterium efficiens YS-314]
 Length = 177

Score = 37.4 bits (85), Expect = 0.94, Method: Compositional matrix adjust.
 Identities = 40/175 (22%), Positives = 70/175 (40%), Gaps = 10/175 (5%)

Query: 10 IRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVVA 69
 IRP D V I +ET ++ + T +++ ++ ++ + + V
 Sbjct: 8 IRPIREVDFFQVRAIYEMGLETHASERYKRGPTWKQFTR-MKIMETVFVAAEKKDPDFVL 66

Query: 70 GIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGLP 129
 G A P R + VE ++Y+ + Q G+G L L++ + S+ + I
 Sbjct: 67 GWVAAAPASTRAVFGVVEDSIYIHPQGGRGVGGALLDKLIEVCQDLHKWSIHSWIFPE 126

Query: 130 NDPSVRLHEALGYTARGTLRAA-----GYKHGGWHDVGFWRDQDFELPAPPRPVRP 179
 N S +LH + G+ T G G W D W++ LP P +RP
 Sbjct: 127 NVGSAKLHASRGFEKVATFHHLAKMPYGEWAGEWRDQVWEK--LLPKP--DIRP 177

>ref|YP_003176066.1| GCN5-related N-acetyltransferase [Halomicrobium mukohataei DSM
12286]
gb|ACV46359.1| GCN5-related N-acetyltransferase [Halomicrobium mukohataei DSM
12286]
Length = 174

Score = 37.4 bits (85), Expect = 0.95, Method: Compositional matrix adjust.
Identities = 37/152 (24%), Positives = 68/152 (44%), Gaps = 17/152 (11%)

Query: 4 ERRPVEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTP-----QEWDLLERLQDRY 57
E R +++R A A D A+ ++ + R + P + W++++ DRY
Sbjct: 24 EGRSIQLRRADATDRTALIEMYKQFDPAD----RAQGIPPARETAIERWLENILDT-DRY 78

Query: 58 PWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQ 117
+VA EG + G A P D E ++V +Q G+G+ L LL +++
Sbjct: 79 N-VVASHEGDLVGHATLVPDD-----DDGYELAIFVLSAYQGAGIGTELVELLGHGQSE 132

Query: 118 GFKSVVAVIGLPNDPSVRLHEALGYTARGTLR 149
G + V + NDP++ L+ +G+ + R
Sbjct: 133 GIEQVWLTVERWNDPAIALYRKVGFTSNSER 164

>ref|XP_001374166.1| PREDICTED: similar to putative N-acetyltransferase Camello 4
[Monodelphis domestica]
Length = 223

Score = 37.4 bits (85), Expect = 0.95, Method: Compositional matrix adjust.
Identities = 27/83 (32%), Positives = 39/83 (46%), Gaps = 1/83 (1%)

Query: 61 VAEVEGVVAGIAYAGP-WKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGF 119
VAE G V G+ A P KA A + V H+ G+ TL ++ + QG+
Sbjct: 111 VAEAGGQVVLVCACPAQKASGAQKHLELLHLSVRQDHRGQGIAKTLTQTVIHFAQDQGY 170

Query: 120 KSVVAVIGLPNDPSVRLHEALGY 142
+V V N P+ RL+E LG+
Sbjct: 171 SGIVLVTASLNFPARRLYERLGF 193

>ref|YP_002633376.1| putative N-acetyltransferase [Staphylococcus carnosus subsp.
carnosus TM300]
emb|CAL27191.1| putative N-acetyltransferase [Staphylococcus carnosus subsp.
carnosus TM300]
Length = 163

Score = 37.4 bits (85), Expect = 0.98, Method: Compositional matrix adjust.
Identities = 32/160 (20%), Positives = 60/160 (37%), Gaps = 1/160 (0%)

Query: 8 VEIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWDLLERLQDRYP-WLVAEVEG 66
V+++ A AD+ + N I V + + +E P + + + +G
Sbjct: 2 VKLKIAEKADLPVFTKVYNQAIRMRNVTADVDEVSDEEMAPIFNSHDTSRPLYTIWDDQG 61

Query: 67 VVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVI 126
G A + R AYD T E ++Y+ + + G G+ + L + + + +
Sbjct: 62 QAIGYASLNHFYGRPAYDETAELSIYLDEQTRGQGYGTVKMQLLEQEAASLNHYLTGYV 121

Query: 127 GLPNDPSVRLHEALGYTARGTLRAAGYKHGGWHDVGFQWR 166
N P +L E GY G L + D+ W +
Sbjct: 122 FAQNVPCNKLFEKQGYALWGNLPQIAHIDKNRLDLCIWGK 161

>ref|ZP_07721400.1| acetyltransferase, GNAT family [Algoriphagus sp. PR1]

gb|EAZ79908.1| acetyltransferase, GNAT family [Algoriphagus sp. PR1]
Length = 167

Score = 37.4 bits (85), Expect = 0.98, Method: Compositional matrix adjust.
Identities = 30/118 (25%), Positives = 50/118 (42%), Gaps = 3/118 (2%)

Query: 39 EPQTPQEWIDDLERLQDRYPWLVAEVEGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQ 98
EP TP+E ++ +++ + GVV P + D ++ V HQ
Sbjct: 33 EPDTPKEKLEGYWFASYMDSFVLVDEYGVVLATYIIKPNQIGLG-DHIANASYMVHPDHQ 91

Query: 99 RLGLGSTLYTHLLKSMEAQGFKSV-VAVIGLPNDPSVRLHEALGYTARGTLRAAGYKH 155
G G+ L H + +GFK + ++ N P+V L E G+ GT G++H
Sbjct: 92 GKGFAMLCESISFATEKGFKGIQFNIVSTNKPAVHLWEKFGFNIIGT-TPGGFRH 148

>gb|EFR90833.1| gnat family acetyltransferase [Listeria innocua FSL S4-378]
Length = 123

Score = 37.4 bits (85), Expect = 0.98, Method: Compositional matrix adjust.
Identities = 29/123 (23%), Positives = 57/123 (46%), Gaps = 4/123 (3%)

Query: 9 EIRPATAADMAAVCDIVNHYIETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEVEGVV 68
+I P + V + I+T F+ + + W D + L+ LV EG V
Sbjct: 5 KILPMLKEHYSVARVHQEGIDTGNATFQEKLSFEAW--DEKYLKTCR--LVVLTEGQV 60

Query: 69 AGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAVIGL 128
G A P+ + +AY E ++Y++ + G+G L ++++ E GF ++ ++I
Sbjct: 61 IGWAALLPFSSMHAYRGVAELSIYIAKSARGKGIGKALMQAIIQTSEQNGFWTLQSLIFP 120

Query: 129 PND 131
N+
Sbjct: 121 ENE 123

>dbj|BAJ27343.1| putative acetyltransferase [Kitasatospora setae KM-6054]
Length = 163

Score = 37.4 bits (85), Expect = 0.98, Method: Compositional matrix adjust.
Identities = 43/152 (28%), Positives = 62/152 (40%), Gaps = 8/152 (5%)

Query: 8 VEIRPATAADMAAVCDIVNHYI---ETSTVNFRTPEQTPQEWIDDLERLQDRYPWLVAEV 64
+EIR AT D +AV I ET T T ++W L +R V E
Sbjct: 1 MEIREATPQDWSAVWPFRRVIAAGETFTYPTDLTSDTARDWW--LLDAPNRTVVAVDEA 58

Query: 65 EGVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSV-V 123
G V G A + N ++ V H G G L L+ QGF+++
Sbjct: 59 AGTVLGTAKMNNNQWNGGGH-VASASFLVDPDHAGRTGRALCVEALRWAREQGFRAMQF 117

Query: 124 AVIGLPNDPSVRLHEALGYTARGTLRAAGYKH 155
+ N P+V L+ +LG+T GT+ G+ H
Sbjct: 118 NAVVASNAPAVGLYRSLGFTVVGTV-PEGFHH 148

>ref|YP_001084545.1| putative antibiotic resistance [Acinetobacter baumannii ATCC 17978]

gb|ABO11943.1| putative antibiotic resistance [Acinetobacter baumannii ATCC 17978]
Length = 90

Score = 37.4 bits (85), Expect = 0.99, Method: Compositional matrix adjust.
Identities = 18/61 (29%), Positives = 32/61 (52%)

Query: 66 GVVAGIAYAGPWKARNAYDWTVESTVYVSHRHQRLGLGSTLYTHLLKSMEAQGFKSVVAV 125
G + G A G ++A AY +TVE ++Y+ H H+ GL L L++ + ++ V

Sbjct: 23 GKLLGFASWGTFRAFPAYKYTVEHSIYIHHEHRGCGLSKVLQMQUALIQRAQQAQLHVLMMV 82

Query: 126 I 126

+

Sbjct: 83 L 83

Database: /usr/local/blast/db/blastlibs/nr

Posted date: Apr 13, 2011 11:46 AM

Number of letters in database: 4,621,495,809

Number of sequences in database: 13,473,798

Lambda	K	H
0.319	0.135	0.432

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 13473798

Number of Hits to DB: 1,835,885,264

Number of extensions: 75419055

Number of successful extensions: 205931

Number of sequences better than 1.0: 1721

Number of HSP's gapped: 206322

Number of HSP's successfully gapped: 1721

Length of query: 183

Length of database: 4,621,495,809

Length adjustment: 130

Effective length of query: 53

Effective length of database: 2,869,902,069

Effective search space: 152104809657

Effective search space used: 152104809657

Neighboring words threshold: 11

Window for multiple hits: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.8 bits)

S2: 85 (37.4 bits)