



Mascot Search Results

Protein View

Match to: [gi|126642864](#) Score: 788

outer membrane protein A [Acinetobacter baumannii ATCC 17978]

Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS8c.TMP

Nominal mass (Mr): 37342; Calculated pI value: 5.13

NCBI BLAST search of [gi|126642864](#) against nrUnformatted [sequence string](#) for pasting into other applicationsTaxonomy: [Acinetobacter baumannii ATCC 17978](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

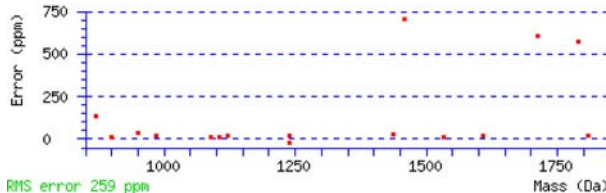
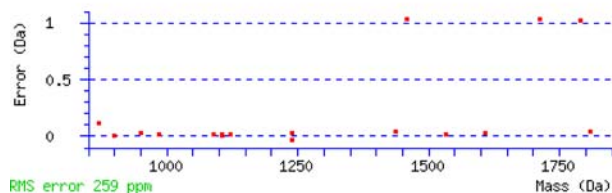
Sequence Coverage: 46%

Matched peptides shown in **Bold Red**

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101 ITKNYDSKIK PYVLLGAGHY KYDFDGVNRG TRGTSEEGTL GNAGVGAFWR
151 LNDALSLRTE ARATYNADDE FWNNTALAGL NVVLGGHLKP AAPVVEVAVP
201 EPTPVTPQPQ ELTEDLNMEL RVFFDTTKSN IKDQYKPEIA KVAEKLSEYP
251 NATARIEGHT DNTGPRKLNE RLSLARANSV KSALVNEYNV DASRLSTQGF
301 AWDQPIADNK TKEGRAMNR VFATITGSRT VVVQPGQEAA APAAAAQ
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[Show predicted peptides also](#)Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
74 - 86	620.2643	1238.5141	1238.5415	-0.0274	0	K.GDVDGASAGAEYK.Q (Ions score 46)
74 - 86	620.2907	1238.5669	1238.5415	0.0254	0	K.GDVDGASAGAEYK.Q (Ions score 80)
89 - 103	857.4617	1712.9089	1711.8781	1.0308	0	K.QINGNFYVTSDLITK.N (Ions score 57)
109 - 121	487.2980	1458.8722	1457.8394	1.0328	0	K.IKPYVLLGAGHYK.Y (Ions score 33)
122 - 129	493.2306	984.4467	984.4301	0.0166	0	K.YDFDGVNR.G (Ions score 44)
122 - 129	493.2331	984.4517	984.4301	0.0216	0	K.YDFDGVNR.G (Ions score 31)
133 - 150	904.9529	1807.8912	1807.8489	0.0422	0	R.GTSEEGTLGNAGVGAFWR.L (Ions score 84)
151 - 158	451.2638	900.5131	900.5029	0.0102	0	R.LNDALSLR.T (Ions score 42)
222 - 228	435.7812	869.5478	869.4283	0.1194	0	R.VFFDTNK.S (Ions score 28)
229 - 241	511.9551	1532.8434	1532.8198	0.0236	1	K.SNIKDQYKPEIAK.V (Ions score 48)
233 - 241	546.2962	1090.5778	1090.5658	0.0119	0	K.DQYKPEIAK.V (Ions score 39)
246 - 255	561.2933	1120.5721	1120.5513	0.0208	0	K.LSEYPNATAR.I (Ions score 40)
282 - 294	719.3707	1436.7268	1436.6895	0.0372	0	K.SALVNEYNVDASR.L (Ions score 74)
295 - 310	896.4505	1790.8864	1789.8635	1.0229	0	R.LSTQGFQWDQPIADNK.T (Ions score 84)
320 - 329	554.3227	1106.6309	1106.6196	0.0113	1	R.RVFATITGSR.T (Ions score 60)
320 - 329	554.3258	1106.6371	1106.6196	0.0174	1	R.RVFATITGSR.T (Ions score 63)
321 - 329	476.2820	950.5495	950.5185	0.0310	0	R.VFATITGSR.T (Ions score 40)
330 - 346	804.4364	1606.8582	1606.8315	0.0267	0	R.TVVVQPGQEAAAPAAQ.- (Ions score 33)



LOCUS YP_001085848 346 aa linear BCT 29-MAY-2010
DEFINITION outer membrane protein A [Acinetobacter baumannii ATCC 17978].
ACCESSION YP_001085848
VERSION YP_001085848.1 GI:126642864
DBLINK Project: [58731](#)
DBSOURCE REFSEQ: accession [NC_009085.1](#)
KEYWORDS .
SOURCE Acinetobacter baumannii ATCC 17978
ORGANISM [Acinetobacter baumannii ATCC 17978](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
complex.
REFERENCE 1 (residues 1 to 346)

12/22/2010

Mascot Search Results: Protein View

AUTHORS Smith,M.G., Gianoulis,T.A., Pukatzki,S., Mekalanos,J.J.,
Ornston,L.N., Gerstein,M. and Snyder,M.

TITLE New insights into *Acinetobacter baumannii* pathogenesis revealed by
high-density pyrosequencing and transposon mutagenesis

JOURNAL Genes Dev. 21 (5), 601-614 (2007)

PUBMED [17344419](#)

REFERENCE 2 (residues 1 to 346)

CONSRTM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (05-MAR-2007) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (residues 1 to 346)

AUTHORS Smith,M.G., Gianoulis,T.A., Pukatzki,S., Mekalanos,J.,
Ornston,L.N., Gerstein,M. and Snyder,M.

TITLE Direct Submission

JOURNAL Submitted (27-NOV-2006) Department of Molecular, Cellular, and
Developmental Biology, Yale University, 266 Whitney Ave, New Haven,
CT 06520, USA

COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final
NCBI review. The reference sequence was derived from [AB013246](#).
Source DNA and bacteria available from Michael Snyder
(michael.snyder@yale.edu).
Method: conceptual translation.

FEATURES Location/Qualifiers

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/strain="ATCC 17978"
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/db_xref="taxon:[400667](#)"

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/calculated_mol_wt=37234

[Region](#) <109..186
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/note="OprF membrane domain; pfam05736"
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[Region](#) 219..321
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[Site](#) order(226..227,260..261,264,268..269,272,315,319)
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[CDS](#) 1..346
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Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Protein View

Match to: [gi|260557248](#) Score: 172

outer membrane transporter [*Acinetobacter baumannii* ATCC 19606]

Found in search of C:\DOCUME~1\DRAF40~1\JIT\LOCALS~1\Temp\mas2F.tmp

Nominal mass (M_r): 50406; Calculated pI value: 4.96

NCBI BLAST search of [gi|260557248](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii ATCC 19606](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|260409354](#) from [Acinetobacter baumannii ATCC 19606](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 12%

Matched peptides shown in **Bold Red**

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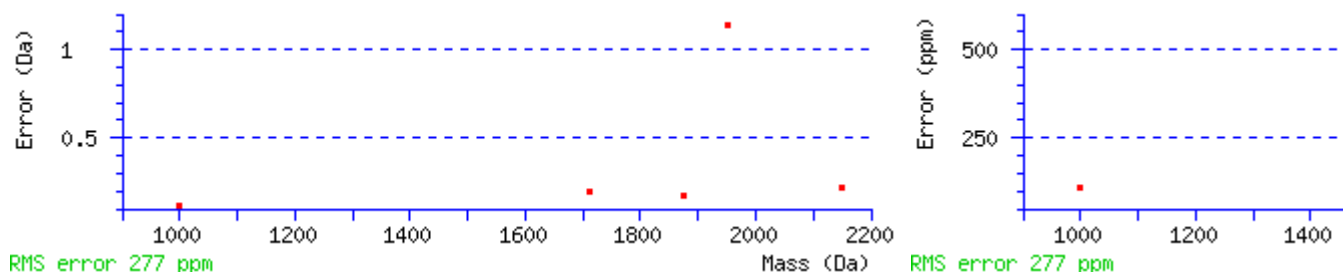
1 MKLKLHSLTAM ILATLPATGV FAAALDRSQ SMSAFFQPGN YFEAGISILD
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151 AIAKGQVLAS PQFQQLAGAL AVANNYLGTG GTKVEVDTQN LSFVFGYQPT
201 KNFNFYAGPV LQTVKGNVSL RGQAYSLYNG YDASIKETTG AGWLAGAAYQ
251 IPEIALRASV TYRSEIDHKV NIDENLSILN FPGLTSVLG LDVPASKLQA
301 INSSGKTTIT TPQSVNLDFQ TGIMADTVAF ANVRWVNWKD FSIQPYKFGK
351 VSEAVGGLVG RPNGFNLVEY SDDQWSVNAG VGRKLNDKWA GNVSVGWDSG
401 AGNPVTTLGP TEGYWNVGLG VQYSPTPQTF IAGGVKYFWL GDAKAQTGAQ
451 AGSDEYVADF SDNNAIAYGL KLGKFK
    
```

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
66 - 82	938.0212	1874.0279	1873.8556	0.1723	0	R. NIGDMADDYFFPSAALK.L (Ions score 19)
134 - 154	717.4836	2149.4289	2149.2106	0.2182	1	K. AKEALVAQGLPVNDQTLAIK.G (Ions score
136 - 154	976.6164	1951.2182	1950.0786	1.1396	0	K. EALVAQGLPVNDQTLAIK.G (Ions score 42
335 - 347	571.0259	1710.0559	1709.8566	0.1993	1	R. WVNWKDFSIPYK.F (Ions score 20)
437 - 444	500.3061	998.5977	998.4862	0.1115	0	K. YFWLGDAK.A (Ions score 44)



LOCUS ZP_05829464 476 aa linear BCT 09-JUN-2010
 DEFINITION outer membrane transporter [*Acinetobacter baumannii* ATCC 19606].
 ACCESSION ZP_05829464
 VERSION ZP_05829464.1 GI:260557248
 DBLINK Project: [40853](#)
 DBSOURCE REFSEQ: accession [NZ_GG704577.1](#)
 KEYWORDS .
 SOURCE *Acinetobacter baumannii* ATCC 19606
 ORGANISM [Acinetobacter baumannii ATCC 19606](#)

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii complex.

REFERENCE 1 (residues 1 to 476)

AUTHORS Ward,D., Feldgarden,M., Earl,A., Young,S.K., Zeng,Q., Koehrsen,M., Alvarado,L., Berlin,A., Bochicchio,J., Borenstein,D., Chapman,S., Chen,Z., Engels,R., Freedman,E., Gellesch,M., Goldberg,J., Griggs,A., Gujja,S., Heilman,E., Heiman,D., Hepburn,T., Howarth,C., Jen,D., Larson,L., Lewis,B., Mehta,T., Park,D., Pearson,M., Roberts,A., Saif,S., Shea,T., Shenoy,N., Sisk,P., Stolte,C., Sykes,S., Thomson,T., Walk,T., White,J., Yandava,C., Peleg,A., Haas,B., Nusbaum,C. and Birren,B.

CONSRTM The Broad Institute Genome Sequencing Platform

TITLE The Genome Sequence of Acinetobacter baumannii strain ATCC 19606

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 476)

AUTHORS Ward,D., Feldgarden,M., Earl,A., Young,S.K., Zeng,Q., Koehrsen,M., Alvarado,L., Berlin,A., Bochicchio,J., Borenstein,D., Chapman,S., Chen,Z., Engels,R., Freedman,E., Gellesch,M., Goldberg,J., Griggs,A., Gujja,S., Heilman,E., Heiman,D., Hepburn,T., Howarth,C., Jen,D., Larson,L., Lewis,B., Mehta,T., Park,D., Pearson,M., Roberts,A., Saif,S., Shea,T., Shenoy,N., Sisk,P., Stolte,C., Sykes,S., Thomson,T., Walk,T., White,J., Yandava,C., Peleg,A., Haas,B., Nusbaum,C. and Birren,B.

CONSRTM The Broad Institute Genome Sequencing Platform

TITLE Direct Submission

JOURNAL Submitted (19-AUG-2009) Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA

COMMENT PREDICTED [REFSEQ](#): This record has not been reviewed and the function is unknown. The reference sequence was derived from [EEX02656](#).

Method: conceptual translation.

FEATURES

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[CDS](#)

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Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Protein View

Match to: **gi|184159810** Score: **540**
34 kDa outer membrane protein [Acinetobacter baumannii ACICU]
Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS8e.TMP
Nominal mass (M_r): **32095**; Calculated pI value: **4.77**
NCBI BLAST search of **gi|184159810** against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii ACICU](#)
Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|260557941](#) from [Acinetobacter baumannii ATCC 19606](#)
[gi|294841479](#) from [Acinetobacter baumannii 6014059](#)
[gi|82654966](#) from [Acinetobacter baumannii](#)
[gi|183211404](#) from [Acinetobacter baumannii ACICU](#)
[gi|260408732](#) from [Acinetobacter baumannii ATCC 19606](#)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **38%**

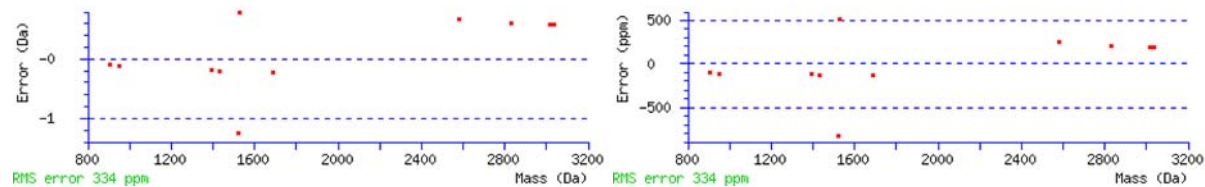
Matched peptides shown in **Bold Red**

1 MKKLGLATAV LLAMTGAHAY QFEVQQQSEY VDTTANDK**NF TGDVAGTFYL**
51 **KNVDTAKGPL** AEAFLNQAS SVSLGYSYQQ YDQNNVNYHI GTYGVK**GEAY**
101 **VPTPYLPVYA SATYNHTDVD** GKNNFSKDDN GDRYALEVGA MLLPNFLMTV
151 GYTSVANQFA LDNFGIIGNG IYSAVNQTAA IQNDQDAVTA RAK**YVGPIDG**
201 **TNMAIGFEAA GAFGQENQYG** LKTDLYLTPK LSVGATFVGN DGEADIKGND
251 **LGEFRQAWG** NVNYFITPAL AVGASYMKAD VK**KSSYDTQT** IGLNAKFRF

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
39 - 51	716.7591	1431.5037	1431.7034	-0.1997	0	K.NFTGDVAGTFYLK.N (Ions score 46)
97 - 122	943.6529	2827.9367	2827.3341	0.6026	0	K.GEAYVPTPYLPVYASATYNHTDVDGK.N (Ions score 46)
194 - 222	1007.0133	3018.0181	3017.4229	0.5952	0	K.YVGPIDGTNMAIGFEAAGAFGQENQYGLK.T (Ions score 46)
194 - 222	1012.3435	3034.0087	3033.4178	0.5909	0	K.YVGPIDGTNMAIGFEAAGAFGQENQYGLK.T Oxidation
223 - 230	475.7037	949.3928	949.5120	-0.1192	0	K.TDLYLTPK.L (Ions score 59)
231 - 247	846.8092	1691.6039	1691.8366	-0.2327	0	K.LSVGATFVGNDGEADIK.G (Ions score 75)
231 - 255	861.3105	2580.9097	2580.2456	0.6641	1	K.LSVGATFVGNDGEADIKGNDLGEFR.Q (Ions score 14)
248 - 255	454.1715	906.3285	906.4195	-0.0911	0	K.GNDLGEFR.Q (Ions score 52)
283 - 296	762.7648	1523.5150	1524.7784	-1.2634	1	K.KSSYDTQTIGLNAK.F (Ions score 27)
283 - 296	763.7951	1525.5757	1524.7784	0.7973	1	K.KSSYDTQTIGLNAK.F (Ions score 44)
284 - 296	699.2605	1396.5064	1396.6834	-0.1770	0	K.SSYDTQTIGLNAK.F (Ions score 72)



LOCUS YP_001848149 299 aa linear BCT 30-MAY-2010
DEFINITION 34 kDa outer membrane protein [Acinetobacter baumannii ACICU].
ACCESSION YP_001848149
VERSION YP_001848149.1 GI:184159810
DBLINK Project: [58765](#)
DBSOURCE REFSEQ: accession [NC_010611.1](#)
KEYWORDS .
SOURCE Acinetobacter baumannii ACICU
ORGANISM [Acinetobacter baumannii ACICU](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
complex.
REFERENCE 1 (residues 1 to 299)
AUTHORS Iacono,M., Villa,L., Fortini,D., Bordoni,R., Imperi,F.,
Bonnal,R.J., Sicheritz-Ponten,T., De Bellis,G., Visca,P.,
Cassone,A. and Carattoli,A.
TITLE Whole-genome pyrosequencing of an epidemic multidrug-resistant
Acinetobacter baumannii strain belonging to the European clone II
group
JOURNAL Antimicrob. Agents Chemother. 52 (7), 2616-2625 (2008)

PUBMED [18411315](#)
REFERENCE 2 (residues 1 to 299)
CONSRM NCBI Genome Project
TITLE Direct Submission
JOURNAL Submitted (21-APR-2008) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
REFERENCE 3 (residues 1 to 299)
AUTHORS Carattoli,A., Villa,L., Fortini,D. and Cassone,A.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2007) Department of Infectious, Parasitic and Immune-Mediated Diseases, Istituto Superiore di Sanita', Viale regina Elena 299, Roma 00161, Italy
REFERENCE 4 (residues 1 to 299)
AUTHORS Iacono,M., Bordonni,R., Bonnal,R.J. and De Bellis,G.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2007) Institute for Biomedical Technologies, National Research Council, via Fratelli Cervi 93, Segrate, Milano 20090, Italy
COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final NCBI review. The reference sequence was derived from [ACC58802](#).
Method: conceptual translation.
FEATURES Location/Qualifiers
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Mascot: <http://www.matrixscience.com/>

MATRIX SCIENCE Mascot Search Results

Protein View

Match to: gi|72535025 Score: 920
putative outer membrane protein [Acinetobacter baumannii]
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Nominal mass (M_r): 24757; Calculated pI value: 4.50
NCBI BLAST search of gi|72535025 against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii](#)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 55%

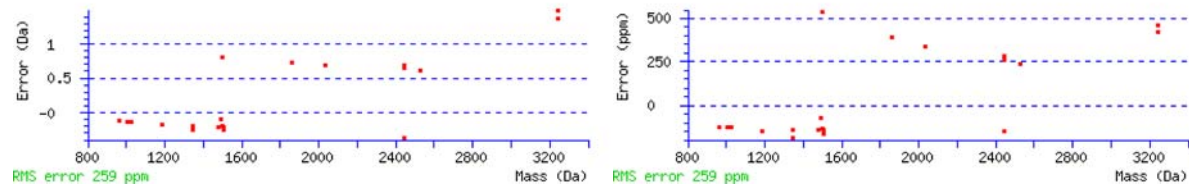
Matched peptides shown in **Bold Red**

1 **DEAVVHDSYA FDKNQLIPVG** ARAEVGTTGY GGALLWQANP YVGLALGYNG
51 GDISWTDVVS VNGTKYDLDM DNNNVYLNAE IRPWGASTNP WAQGLYIAAG
101 AAYLDNDYDL **AKRIGNGDTL SIDGKNYQQA VPGQEGGVRG** KMSYKNDIAP
151 **YLGFGFAPKI** SKNWGVFGEV GAYYTGPNKV ELTQYNLAPV TGNPTSAQDA
201 **VDKEANEIRN DNKYEWMPVG** KVGNVFFW

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 13	499.1929	1494.5569	1494.6627	-0.1058	0	-.DEAVVHDSYAFDK.N (Ions score 20)
1 - 13	748.7413	1495.4681	1494.6627	0.8054	0	-.DEAVVHDSYAFDK.N (Ions score 72)
1 - 22	815.2878	2442.8415	2443.2132	-0.3717	1	-.DEAVVHDSYAFDKNQLIPVGAR.A (Ions score 84)
1 - 22	815.6248	2443.8526	2443.2132	0.6395	1	-.DEAVVHDSYAFDKNQLIPVGAR.A (Ions score 57)
1 - 22	815.6406	2443.9001	2443.2132	0.6869	1	-.DEAVVHDSYAFDKNQLIPVGAR.A (Ions score 42)
14 - 22	484.2263	966.4380	966.5611	-0.1231	0	K.NQLIPVGAR.A (Ions score 38)
113 - 125	673.2320	1344.4495	1344.6997	-0.2502	1	K.RIGNGDTLSIDGK.N (Ions score 24)
113 - 125	673.2620	1344.5094	1344.6997	-0.1903	1	K.RIGNGDTLSIDGK.N (Ions score 52)
114 - 125	595.2197	1188.4248	1188.5986	-0.1738	0	R.IGNGDTLSIDGK.N (Ions score 89)
126 - 139	751.7696	1501.5247	1501.7274	-0.2026	0	K.NYQAVPGQEGGV.R (Ions score 77)
142 - 159	1018.3497	2034.6849	2033.9921	0.6929	1	K.MSYKNDIAPYLGFGFAPK.I Oxidation (M) (Ions score 105)
146 - 159	755.2659	1508.5172	1508.7664	-0.2492	0	K.NDIAPYLGFGFAPK.I (Ions score 72)
146 - 159	755.2841	1508.5536	1508.7664	-0.2127	0	K.NDIAPYLGFGFAPK.I (Ions score 26)
146 - 159	755.2860	1508.5575	1508.7664	-0.2089	0	K.NDIAPYLGFGFAPK.I (Ions score 61)
163 - 179	930.3054	1858.5962	1857.8686	0.7276	0	K.NWGVFGEVGAYYTGPNK.V (Ions score 105)
180 - 203	1266.4392	2530.8638	2530.2551	0.6087	0	K.VELTQYNLAPVTGNPTSAQDAVDK.E (Ions score 63)
180 - 209	812.0000	3243.9709	3242.6055	1.3654	1	K.VELTQYNLAPVTGNPTSAQDAVDKEANEIR.N (Ions score 68)
180 - 209	1082.3725	3244.0957	3242.6055	1.4902	1	K.VELTQYNLAPVTGNPTSAQDAVDKEANEIR.N (Ions score 68)
210 - 221	740.7412	1479.4678	1479.6816	-0.2138	1	R.NDNKYEWMPVGK.V (Ions score 68)
214 - 221	505.1811	1008.3476	1008.4739	-0.1263	0	K.YEWMPVGK.V (Ions score 40)
214 - 221	513.1758	1024.3370	1024.4688	-0.1318	0	K.YEWMPVGK.V Oxidation (M) (Ions score 45)



LOCUS CAI79414 228 aa linear BCT 13-AUG-2005
DEFINITION putative outer membrane protein [Acinetobacter baumannii].
ACCESSION CAI79414
VERSION CAI79414.1 GI:72535025
DBSOURCE embl accession [AJ938079.1](#)
KEYWORDS .
SOURCE Acinetobacter baumannii
ORGANISM [Acinetobacter baumannii](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
complex.
REFERENCE 1
AUTHORS Siroy,A., Molle,V., Lemaitre-Guillier,C., Glinel,K., Vallenet,D.,
Pestel-Caron,M., Jouenne,T., Cozzzone,A.J. and De,E.
TITLE Characterization at functional and structural level of

12/22/2010

Mascot Search Results: Protein View

Acinetobacter baumannii outer membrane proteins involved in
imipenem resistance

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 228)

AUTHORS Molle,V.

TITLE Direct Submission

JOURNAL Submitted (13-APR-2005) Molle V., Phosphorylation des proteines,
Ibcp, 7 passage du Vercors, LYON, 69367, FRANCE

FEATURES Location/Qualifiers

source 1..228
/organism="Acinetobacter baumannii"
/strain="ATCC 19606"
/db_xref="taxon:[470](#)"
/country="France"

[Protein](#) 1..228
/product="putative outer membrane protein"

[mat_peptide](#) 1..228
/product="putative outer membrane protein"

[CDS](#) 1..228
/gene="carO"
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/experiment="experimental evidence, no additional details
recorded"
/transl_table=[11](#)
/db_xref="UniProtKB/TrEMBL:[Q4A209](#)"

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Protein View

Match to: [gi|56131242](#) Score: 390
carbapenem-associated resistance protein precursor [*Acinetobacter baumannii*]
 Found in search of C:\DOCUME~1\DRAF40~1.JIT\LOCALS~1\Temp\mas38.tmp

Nominal mass (M_r): **26403**; Calculated pI value: **4.79**
 NCBI BLAST search of [gi|56131242](#) against nr
 Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii](#)
 Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|224015984](#) from [Acinetobacter baumannii](#)
[gi|224015988](#) from [Acinetobacter baumannii](#)

Fixed modifications: Carbamidomethyl (C)
 Variable modifications: Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Sequence Coverage: **27%**

Matched peptides shown in **Bold Red**

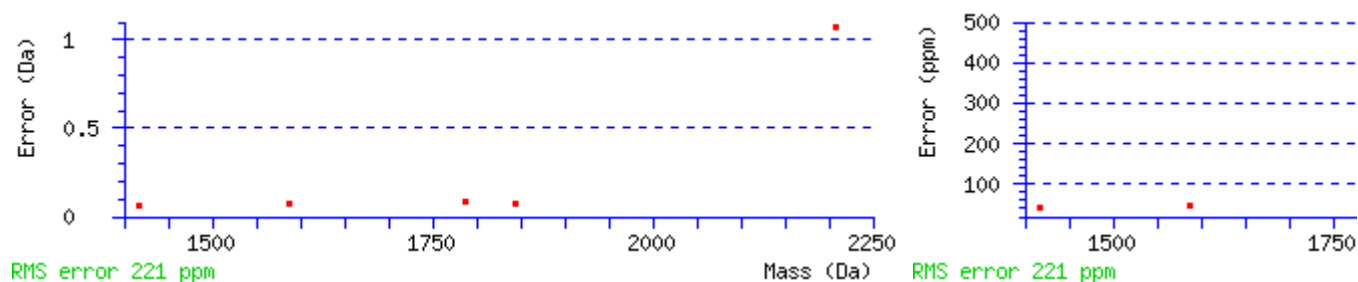
1 MKVLRVLVTT TALLAAGAAM ADEAVVHDSY AFDKNQLIPV GARAEVGTTG
 51 YGGALLWQAN PYVGLALGYN GGDISWSDDL SINGTKYDMD MDNKLAYLNA
 101 EIRPWGASTN PWAQGLYVAA GAAYVDNQYD LTKNVGTNAS VEIDGNR**FNG**
 151 **GANGVSIAGN LKYDNDIAPY IGFGFAPKFS KNWGVFGEVG AYYSGNPKVS**
 201 **LASNNDALIG SDGR**TLGKTL DDQERKIAND DKYKWLPGVK VGVNFYW

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
148 - 162	709.9039	1417.7932	1417.7314	0.0618	0	R.FNGGANGVSIAGNLK.Y (Ions score 68)
163 - 178	894.4774	1786.9403	1786.8566	0.0837	0	K.YDNDIAPYIGFGFAPK.F (Ions score 39)
179 - 198	736.7151	2207.1235	2206.0484	1.0752	1	K.FSKNMGVFGEVGAYYSGNPK.V (Ions score 4)
182 - 198	922.9680	1843.9214	1843.8530	0.0685	0	K.NWGVFGEVGAYYSGNPK.V (Ions score 99)
199 - 214	794.9364	1587.8582	1587.7852	0.0730	0	K.VSLASNNDALIGSDGR.T (Ions score 143)



LOCUS AAV80243 247 aa linear BCT 28-MAR-2005
 DEFINITION carbapenem-associated resistance protein precursor [*Acinetobacter baumannii*].
 ACCESSION AAV80243
 VERSION AAV80243.1 GI:56131242
 DBSOURCE accession [AY684798.1](#)
 KEYWORDS .
 SOURCE *Acinetobacter baumannii*
 ORGANISM [Acinetobacter baumannii](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; *Acinetobacter*; *Acinetobacter calcoaceticus/baumannii* complex.
 REFERENCE 1 (residues 1 to 247)

AUTHORS Mussi,M.A., Limansky,A.S. and Viale,A.M.
 TITLE Acquisition of resistance to carbapenems in multidrug-resistant clinical strains of *Acinetobacter baumannii*: natural insertional inactivation of a gene encoding a member of a novel family of beta-barrel outer membrane proteins
 JOURNAL Antimicrob. Agents Chemother. 49 (4), 1432-1440 (2005)
 PUBMED [15793123](#)
 REFERENCE 2 (residues 1 to 247)
 AUTHORS Mussi,M.A., Limansky,A.S. and Viale,A.M.
 TITLE Direct Submission
 JOURNAL Submitted (13-JUL-2004) Microbiology, IBR, Suipacha 531, Rosario, Santa Fe 2000, Argentina
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..247
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 /isolate="Ab244"
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 /name="outer membrane protein"
 [sig_peptide](#) 1..21
 [mat_peptide](#) 22..247
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 [CDS](#) 1..247
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 /note="associated with carbapenem resistance; heat-modifiable protein"
 /transl_table=[11](#)

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Protein View

Match to: [gi|72535025](#) Score: 693

putative outer membrane protein [Acinetobacter baumannii]

Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS91.TMP

Nominal mass (M_r): 24757; Calculated pI value: 4.50

NCBI BLAST search of [gi|72535025](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 50%

Matched peptides shown in **Bold Red**

1 **DEAVVHDSYA FDKNQLIPVG** ARAEVGTTGY GGALLWQANP YVGLALGYNG
51 GDISWTDVVS VNGTKYDLDM DNNNVYLNAE IRPWGASTNP WAQGLYIAAG
101 AAYLDNDYDL **AKRIGNGDTL SIDGKNYQQA VPGQEGGVGR** KMSYKNDIAP
151 **YLGFGFAPKI** SKNWGVFGEV GAYYTGPNKV ELTQYNLAPV TGNPTSAQDA
201 **VDK**EANEIRN **DNKYEWMPVG** KVGNVFFW

Show predicted peptides also

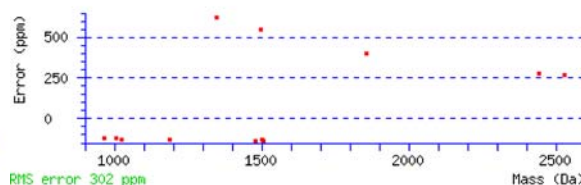
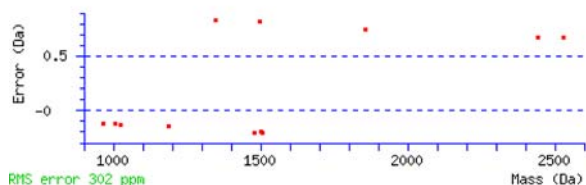
Sort Peptides By

☒ Residue Number

☐ Increasing Mass

☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 13	748.7463	1495.4781	1494.6627	0.8154	0	-.DEAVVHDSYA FDK .N (Ions score 76)
1 - 22	815.6334	2443.8784	2443.2132	0.6653	1	-.DEAVVHDSYA FDKNQLIPVGAR .A (Ions score 70)
14 - 22	484.2301	966.4457	966.5611	-0.1153	0	K.NQLIPVGAR .A (Ions score 38)
113 - 125	673.7740	1345.5334	1344.6997	0.8337	1	K.RIGNGDTLSIDGK .N (Ions score 49)
114 - 125	595.2316	1188.4486	1188.5986	-0.1500	0	R.IGNGDTLSIDGK .N (Ions score 84)
126 - 139	751.7761	1501.5376	1501.7274	-0.1898	0	K.NYQQAVPGQEGGV R.G (Ions score 83)
146 - 159	755.2853	1508.5561	1508.7664	-0.2103	0	K.NDIAPYLGFGFAPK .I (Ions score 72)
163 - 179	930.3123	1858.6101	1857.8686	0.7415	0	K.NWGVFGEV GAYYTGPNK.V (Ions score 47)
180 - 203	844.6479	2530.9218	2530.2551	0.6667	0	K.VELTQYNLAPVTGNPTSAQDA VDK.E (Ions score 83)
210 - 221	740.7438	1479.4730	1479.6816	-0.2086	1	R.NDNKYEWMPVGK .V (Ions score 58)
214 - 221	505.1834	1008.3523	1008.4739	-0.1216	0	K.YEWMPVGK .V (Ions score 39)
214 - 221	513.1772	1024.3398	1024.4688	-0.1290	0	K.YEWMPVGK .V Oxidation (M) (Ions score 38)



LOCUS CAI79414 228 aa linear BCT 13-AUG-2005
DEFINITION putative outer membrane protein [Acinetobacter baumannii].
ACCESSION CAI79414
VERSION CAI79414.1 GI:72535025
DBSOURCE embl accession [AJ938079.1](#)
KEYWORDS .
SOURCE Acinetobacter baumannii
ORGANISM [Acinetobacter baumannii](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
complex.
REFERENCE 1
AUTHORS Siroy,A., Molle,V., Lemaitre-Guillier,C., Glinel,K., Vallenet,D.,
Pestel-Caron,M., Jouenne,T., Cozzzone,A.J. and De,E.
TITLE Characterization at functional and structural level of
Acinetobacter baumannii outer membrane proteins involved in
imipenem resistance
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 228)
AUTHORS Molle,V.
TITLE Direct Submission
JOURNAL Submitted (13-APR-2005) Molle V., Phosphorylation des proteines,
Ibcp, 7 passage du Vercors, LYON, 69367, FRANCE
FEATURES Location/Qualifiers
source 1..228

[Protein](#)[mat_peptide](#)[CDS](#)

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/db_xref="taxon:470"  
/country="France"  
1..228  
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/experiment="experimental evidence, no additional details  
recorded"  
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/db_xref="UniProtKB/TrEMBL:Q4A209"
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Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Protein View

Match to: [gi|301512444](#) Score: 194
hypothetical protein AbauAB05_12702 [Acinetobacter baumannii AB058]
Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS92.TMP

Nominal mass (M_r): 26403; Calculated pI value: 4.68
NCBI BLAST search of [gi|301512444](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii AB058](#)
Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|109255198](#) from [Acinetobacter baumannii](#)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 25%

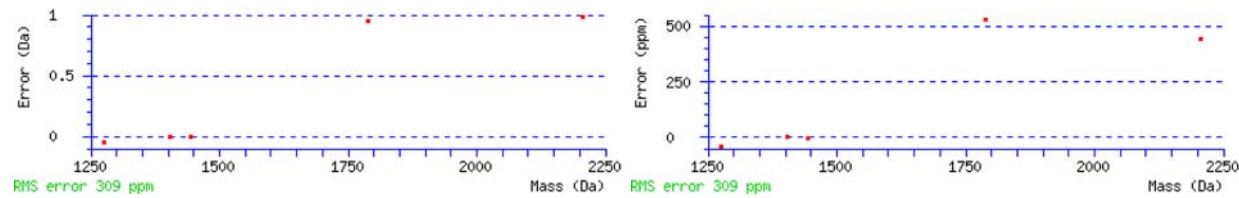
Matched peptides shown in **Bold Red**

1 MKVLRVLVTT TALLAAGAAM ADEAVVHDSY AFDKNQLIPV GARAEVGTG
51 YGGALLWQAN PYVGLALGYN GGDISWSDDL SINGTKYDMD MDNKLAYLNA
101 EIRPWGASTN PWAQGLYVAA GAAYVDNQYD LTK**NVGTNAS VEIDG**NR**F**NG
151 GANGVSIAGN LK**YDNDIAPY IGFGFAPKFS KNWGVFGEVG AYYSGNPKVS**
201 LASNNDALIG SDGR**TLGQTL DDQER**KIAND DKYKWLPGVK VGVNFYV

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
134 - 147	723.3520	1444.6894	1444.6906	-0.0012	0	K.NVGTNASVEIDG NR.F (Ions score 16)
163 - 178	894.9085	1787.8025	1786.8566	0.9458	0	K.YDNDIAPYIGFG FAPK.F (Ions score 20)
179 - 198	736.6833	2207.0280	2206.0484	0.9797	1	K.FSKNWGVFGEVGAYYSG NP K.V (Ions score 69)
215 - 225	638.2875	1274.5604	1274.6103	-0.0499	0	R.TLGQTLDD QER.K (Ions score 56)
215 - 226	702.3606	1402.7067	1402.7052	0.0015	1	R.TLGQTLDD QERK.I (Ions score 34)



LOCUS ZP_07237681 247 aa linear BCT 10-DEC-2010
DEFINITION hypothetical protein AbauAB05_12702 [Acinetobacter baumannii AB058].
ACCESSION ZP_07237681
VERSION ZP_07237681.1 GI:301512444
DBLINK Project: [50773](#)
DBSOURCE REFSEQ: accession [NZ_ADHA01000326.1](#)
KEYWORDS .
SOURCE Acinetobacter baumannii AB058
ORGANISM [Acinetobacter baumannii AB058](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii complex.
REFERENCE 1 (residues 1 to 247)
AUTHORS Adams,M.D., Chan,E.R., Molyneaux,N.D. and Bonomo,R.A.
TITLE Genomewide analysis of divergence of antibiotic resistance determinants in closely related isolates of Acinetobacter baumannii
JOURNAL Antimicrob. Agents Chemother. 54 (9), 3569-3577 (2010)
PUBMED [20530228](#)
REFERENCE 2 (residues 1 to 247)
AUTHORS Adams,M.D., Chan,E.R., Molyneaux,N. and Bonomo,R.A.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-2010) Dept. of Genetics, Case Western Reserve University, 10900 Euclid Ave, Cleveland, OH 44106-4955, USA
COMMENT WGS [REFSEQ](#): This record is provided to represent a collection of whole genome shotgun sequences. The reference sequence was derived from [ADHA01000326](#).
Annotation was added by the NCBI Prokaryotic Genomes Automatic

Annotation Pipeline Group. Information about the Pipeline can be found here:
<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>. Please be aware that the annotation is done automatically with little or no manual curation.

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##Genome-Assembly-Data-START##  
Assembly Method      :: Velvet v. 0.7.55  
Genome Coverage      :: 40x  
Sequencing Technology :: Solexa  
##Genome-Assembly-Data-END##  
Method: conceptual translation.
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              /coded_by="complement(NZ_ADHA01000326.1:1731..2474)"  
              /transl_table=11
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Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Protein View

Match to: [gi|301513596](#) Score: **342**

peroxiredoxin [Acinetobacter baumannii AB058]

Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS93.TMP

Nominal mass (M_r): **20905**; Calculated pI value: **4.91**

NCBI BLAST search of [gi|301513596](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii AB058](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **45%**

Matched peptides shown in **Bold Red**

```

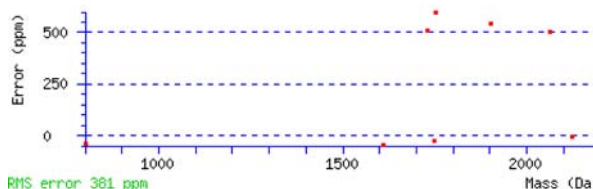
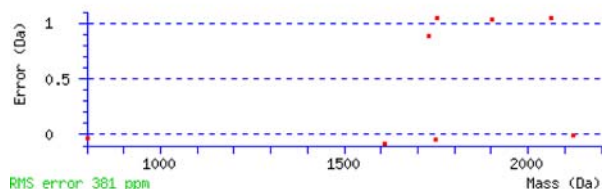
1 MSLINTEVKP FQATAYHNGQ FIEVNETNLK GKWSVVFYFP ADFTFVCPTE
51 LEDLADNYAE FQKLGVEIYG VSTDTHFTHK AWHDTSDAIK KIQYPLIGDP
101 TWTLSKNFDV LIESEGLADR GTFVIDPEGK IQIVEIDAGG IGRDASELLR
151 KVKAAQYVHS HPGEVCPAKW KEGEATLAPS IDLVGKI

```

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
64 - 80	635.6664	1903.9775	1902.9476	1.0299	0	K.LGVEIYG VSTDTHFTHK.A (Ions score 60)
92 - 106	866.9101	1731.8056	1730.9243	0.8812	0	K.IQYPLIGDPTWTL SK.N (Ions score 64)
131 - 150	709.0554	2124.1444	2124.1539	-0.0095	1	K.IQIVEIDAGGIGRDASELLR .K (Ions score 78)
144 - 150	402.1997	802.3849	802.4185	-0.0335	0	R.DASELLR .K (Ions score 36)
154 - 169	584.2672	1749.7798	1749.8257	-0.0459	0	K.AAQYVHSHHPGEVCPAK .W (Ions score 32)
154 - 169	584.6306	1750.8699	1749.8257	1.0442	0	K.AAQYVHSHHPGEVCPAK .W (Ions score 30)
154 - 171	517.2676	2065.0411	2064.0000	1.0411	1	K.AAQYVHSHHPGEVCPAKWK .E (Ions score 22)
172 - 187	806.9045	1611.7944	1611.8719	-0.0776	1	K.EGEATLAPSIDLVGKI .- (Ions score 50)



LOCUS ZP_07238833 187 aa linear BCT 10-DEC-2010

DEFINITION peroxiredoxin [Acinetobacter baumannii AB058].

ACCESSION ZP_07238833

VERSION ZP_07238833.1 GI:301513596

DBLINK Project: [50773](#)

DBSOURCE REFSEQ: accession [NZ_ADHA01000745.1](#)

KEYWORDS .

SOURCE Acinetobacter baumannii AB058

ORGANISM [Acinetobacter baumannii AB058](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
complex.

REFERENCE 1 (residues 1 to 187)

AUTHORS Adams,M.D., Chan,E.R., Molyneaux,N.D. and Bonomo,R.A.

TITLE Genomewide analysis of divergence of antibiotic resistance
determinants in closely related isolates of Acinetobacter baumannii

JOURNAL Antimicrob. Agents Chemother. 54 (9), 3569-3577 (2010)

PUBMED [20530228](#)

REFERENCE 2 (residues 1 to 187)

AUTHORS Adams,M.D., Chan,E.R., Molyneaux,N. and Bonomo,R.A.

TITLE Direct Submission

JOURNAL Submitted (20-JAN-2010) Dept. of Genetics, Case Western Reserve
University, 10900 Euclid Ave, Cleveland, OH 44106-4955, USA

COMMENT WGS [REFSEQ](#): This record is provided to represent a collection of
whole genome shotgun sequences. The reference sequence was derived
from [ADHA01000745](#).
Annotation was added by the NCBI Prokaryotic Genomes Automatic
Annotation Pipeline Group. Information about the Pipeline can be

found here:

<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>. Please be aware that the annotation is done automatically with little or no manual curation.

##Genome-Assembly-Data-START##

Assembly Method :: Velvet v. 0.7.55

Genome Coverage :: 40x

Sequencing Technology :: Solexa

##Genome-Assembly-Data-END##

Method: conceptual translation.

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Protein	1..187 /product="peroxiredoxin" /calculated_mol_wt=20672
Region	1..187 /region_name="AhpC" /note="peroxiredoxin; TIGR03137" /db_xref="CDD:163149"
Region	4..173 /region_name="PRX_Typ2cys" /note="Peroxiredoxin (PRX) family, Typical 2-Cys PRX subfamily; PRXs are thiol-specific antioxidant (TSA) proteins, which confer a protective role in cells through its peroxidase activity by reducing hydrogen peroxide, peroxyxynitrite, and organic...; cd03015" /db_xref="CDD:48564"
Site	order(4,45..46,49,109,119,132..134,136..138,142..143,150,166..169) /site_type="other" /note="dimer interface" /db_xref="CDD:48564"
Site	order(43,77..78,100,102,114) /site_type="other" /note="decamer (pentamer of dimers) interface" /db_xref="CDD:48564"
Site	order(44,47,120) /site_type="other" /note="catalytic triad" /db_xref="CDD:48564"
Site	order(47,166) /site_type="other" /note="peroxidatic and resolving cysteines" /db_xref="CDD:48564"
CDS	1..187 /locus_tag="AbauAB05_010100018494" /coded_by="complement(NZ_ADHA01000745.1:1533..2096)" /note="COG0450 Peroxiredoxin" /transl_table=11 /db_xref="CDD:163149"

Mascot: <http://www.matrixscience.com/>

MASCOT SCIENCE Mascot Search Results

Protein View

Match to: gi|169794796 Score: 340
putative antioxidant protein [Acinetobacter baumannii AYE]
Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS90.TMP

Nominal mass (M_r): 24194; Calculated pI value: 5.18
NCBI BLAST search of gi|169794796 against nr
Unformatted sequence string for pasting into other applications

Taxonomy: Acinetobacter baumannii AYE
Links to retrieve other entries containing this sequence from NCBI Entrez:
gi|213157877 from Acinetobacter baumannii AB0057
gi|215482340 from Acinetobacter baumannii AB307-0294
gi|294836868 from Acinetobacter baumannii 6013113
gi|294857075 from Acinetobacter baumannii 6013150
gi|301346258 from Acinetobacter baumannii AB056
gi|301512779 from Acinetobacter baumannii AB058
gi|301597751 from Acinetobacter baumannii AB059
gi|169147723 from Acinetobacter baumannii AYE
gi|213057037 from Acinetobacter baumannii AB0057
gi|213987433 from Acinetobacter baumannii AB307-0294

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 32%

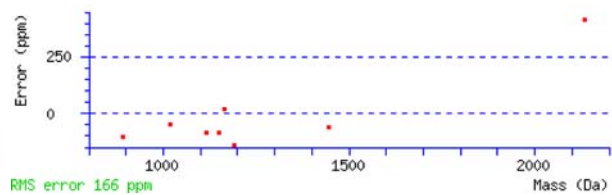
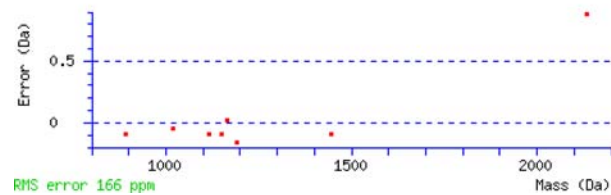
Matched peptides shown in Bold Red

1 MTLRLGDTAP DFQQESSEGT INFYDFLGDS WGLFSPAD YTPVCTTELG
51 YTAALKDEFE KRNVKAIALS VDDVESHKGW INDINETQNT TVNFPPIADK
101 DRK**VSELYGF** **IHPNASETLT** **VRSLVIIDPH** **KKVRLIITYP** **ASTGRNFNEV**
151 **LRVVDSLQLT** **DK**HKVATPAN WQQGEDVVIV PSLKDDEEEK QRFPK**GYTAV**
201 **KPYLR**LTPQP EQD

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start	End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
104	122	711.9986	2132.9739	2132.0902	0.8837	0	K.VSELYGFIHPNASETLTVR.S (Ions score 49)
123	131	511.2801	1020.5457	1020.5968	-0.0511	0	R.SLVIIDPHK.K (Ions score 39)
123	132	575.3059	1148.5973	1148.6917	-0.0945	1	R.SLVIIDPHKK.V (Ions score 51)
133	145	723.8803	1445.7461	1445.8354	-0.0893	1	K.VRLIITYPASTGR.N (Ions score 37)
135	145	596.2579	1190.5012	1190.6659	-0.1647	0	R.LIITYPASTGR.N (Ions score 46)
146	152	446.1921	890.3696	890.4610	-0.0914	0	R.NFNEVLR.V (Ions score 36)
153	162	559.2610	1116.5074	1116.6027	-0.0953	0	R.VVDSLQLTDK.H (Ions score 37)
196	205	584.3410	1166.6674	1166.6448	0.0226	0	K.GYTAVKPYLR.L (Ions score 44)



LOCUS YP_001712589 213 aa linear BCT 04-MAY-2010
DEFINITION putative antioxidant protein [Acinetobacter baumannii AYE].
ACCESSION YP_001712589
VERSION YP_001712589.1 GI:169794796
DBLINK Project: [28921](#)
DBSOURCE REFSEQ: accession [NC_010410.1](#)
KEYWORDS .
SOURCE Acinetobacter baumannii AYE
ORGANISM [Acinetobacter baumannii AYE](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
complex.
REFERENCE 1 (residues 1 to 213)
AUTHORS Vallenet,D., Nordmann,P., Barbe,V., Poirel,L., Mangenot,S.,
Bataille,E., Dossat,C., Gas,S., Kreimeyer,A., Lenoble,P., Oztas,S.,
Poulain,J., Segurens,B., Robert,C., Abergel,C., Claverie,J.M.,

Raoult,D., Medigue,C., Weissenbach,J. and Cruveiller,S.
 TITLE Comparative analysis of Acinetobacters: three genomes for three lifestyles
 JOURNAL PLoS ONE 3 (3), E1805 (2008)
 PUBMED [18350144](#)
 REMARK Publication Status: Online-Only
 REFERENCE 2 (residues 1 to 213)
 CONSRTM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-2008) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 3 (residues 1 to 213)
 AUTHORS Genoscope -,C.E.A.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-2008) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final NCBI review. The reference sequence was derived from [CAM85586](#). Annotation data relative to BLAST similarities, COG assignments, enzymatic function prediction (PRIAM software), TMHMM and SignalP predictions, and syntenly results (Syntonzizer software) are available in BaumannoScope database via the MaGe annotation system <http://www.genoscope.cns.fr/agc/mage/baumannoscope>. Method: conceptual translation.
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 [Protein](#) 1..213
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 /function="5.6 : protection"
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 /note="Peroxiredoxin [Posttranslational modification, protein turnover, chaperones]; COG0450"
 /db_xref="CDD:[30799](#)"
 [Region](#) 5..208
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 /note="Peroxiredoxin (PRX) family, 1-cys PRX subfamily; composed of PRXs containing only one conserved cysteine, which serves as the peroxidatic cysteine. They are homodimeric thiol-specific antioxidant (TSA) proteins that confer a protective role in cells by...; cd03016"
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 /inference="ab initio prediction:AMIGene:2.0"
 /note="Evidence 3 : Function proposed based on presence of conserved amino acid motif, structural feature or limited homology; Product type ph : phenotype"
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 /db_xref="GeneID:[6000685](#)"

MATRIX SCIENCE Mascot Search Results

Protein View

Match to: **gi|169632628** Score: **607**
succinyl-CoA synthetase subunit alpha [Acinetobacter baumannii SDF]
Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS94.TMP

Nominal mass (M_r): **30845**; Calculated pI value: **5.60**
NCBI BLAST search of **gi|169632628** against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii SDF](#)
Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|169794950](#) from [Acinetobacter baumannii AYE](#)
[gi|184159271](#) from [Acinetobacter baumannii ACICU](#)
[gi|213157645](#) from [Acinetobacter baumannii AB0057](#)
[gi|215482498](#) from [Acinetobacter baumannii AB307-0294](#)
[gi|239502281](#) from [Acinetobacter baumannii AB900](#)
[gi|260557317](#) from [Acinetobacter baumannii ATCC 19606](#)
[gi|294838319](#) from [Acinetobacter baumannii 6013113](#)
[gi|294843055](#) from [Acinetobacter baumannii 6014059](#)
[gi|294857478](#) from [Acinetobacter baumannii 6013150](#)
[gi|301346631](#) from [Acinetobacter baumannii AB056](#)
[gi|301510303](#) from [Acinetobacter baumannii AB058](#)
[gi|301596859](#) from [Acinetobacter baumannii AB059](#)
[gi|169147877](#) from [Acinetobacter baumannii AYE](#)
[gi|169151420](#) from [Acinetobacter baumannii](#)
[gi|183210865](#) from [Acinetobacter baumannii ACICU](#)
[gi|193078185](#) from [Acinetobacter baumannii ATCC 17978](#)
[gi|213056805](#) from [Acinetobacter baumannii AB0057](#)
[gi|213988850](#) from [Acinetobacter baumannii AB307-0294](#)
[gi|260409423](#) from [Acinetobacter baumannii ATCC 19606](#)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **40%**

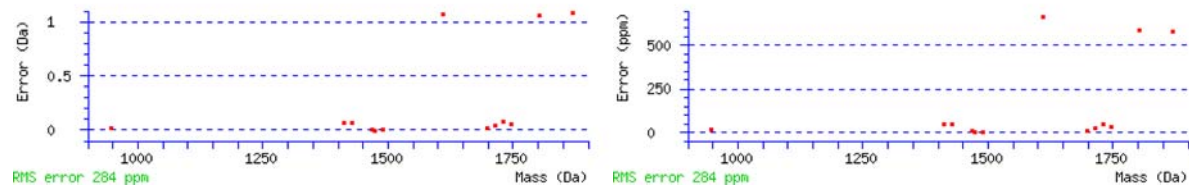
Matched peptides shown in **Bold Red**

1 MSVLINKDTK **VLVQGF**TKGN **GFHSAQALD** YGTVVGGVT PGKGGTTHLD
51 LPVFNTMKEA VRETNADASV IYVPAPFVLD SIVEAVDSGV GLIVVITEGV
101 PTIDMLKAKR YLETNGNGTR **LVGPNC**PGVI **TPGECK**IGIM **PGHIHQ**PGR I
151 GIISRS**SGTLT** **YEAVAQ**TTKL GLGQSTCIGI GGDPIPGMNQ IEALQLFQDD
201 PDTDALIMIG EIGGTAEAAA AEFIK**SNVTK** **PVVG**YIAGVT **APK**GKRMGHA
251 **GAIISGGQGT** **AEEK**FAAFEK AGMAYTRSPA **ELGSTMLQVL** **KEK**GLA

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
11 - 19	474.7864	947.5583	947.5440	0.0143	0	K.VLVQGF TK.N (Ions score 55)
20 - 34	537.6141	1609.8205	1608.7532	1.0672	0	K.NGTFHSAQALDY GTK.V (Ions score 35)
121 - 136	849.4284	1696.8423	1696.8277	0.0146	0	R.LVGPNC PGVITPGECK.I (Ions score 88)
137 - 149	471.6124	1411.8152	1411.7507	0.0646	0	K.IGIMP PGHIHQ PGR.I (Ions score 38)
137 - 149	476.9457	1427.8153	1427.7456	0.0697	0	K.IGIMP PGHIHQ PGR.I Oxidation (M) (Ions score 55)
156 - 169	735.3819	1468.7492	1468.7409	0.0082	0	R.SGTLTYEAVA QTTK.L (Ions score 57)
226 - 243	601.3644	1801.0714	1800.0145	1.0569	0	K.SNVTK PVVG YIAGVT APK.G (Ions score 62)
246 - 264	624.3417	1870.0034	1868.9163	1.0871	1	K.RMGHAGAIISGGQGT AEEK.F (Ions score 59)
247 - 264	571.9587	1712.8543	1712.8152	0.0391	0	R.MGHAGAIISGGQGT AEEK.F (Ions score 55)
247 - 264	577.3049	1728.8928	1728.8101	0.0827	0	R.MGHAGAIISGGQGT AEEK.F Oxidation (M) (Ions score 55)
278 - 291	737.4021	1472.7896	1472.7908	-0.0012	0	R.SP AELGSTMLQVLK.E (Ions score 82)
278 - 291	745.4031	1488.7916	1488.7858	0.0059	0	R.SP AELGSTMLQVLK.E Oxidation (M) (Ions score 82)
278 - 293	577.6772	1730.0097	1729.9284	0.0814	1	R.SP AELGSTMLQVLKEK.G (Ions score 62)
278 - 293	583.0003	1745.9790	1745.9233	0.0556	1	R.SP AELGSTMLQVLKEK.G Oxidation (M) (Ions score 62)



LOCUS YP_001706364 296 aa linear BCT 15-APR-2010
DEFINITION succinyl-CoA synthetase subunit alpha [Acinetobacter baumannii SDF].
ACCESSION YP_001706364

VERSION YP_001706364.1 GI:169632628
 DBLINK Project: [13001](#)
 DBSOURCE REFSEQ: accession [NC_010400.1](#)
 KEYWORDS .
 SOURCE Acinetobacter baumannii SDF
 ORGANISM [Acinetobacter baumannii SDF](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii complex.
 REFERENCE 1 (residues 1 to 296)
 AUTHORS Vallenet,D., Nordmann,P., Barbe,V., Poirel,L., Mangenot,S., Bataille,E., Dossat,C., Gas,S., Kreimayer,A., Lenoble,P., Oztas,S., Poulain,J., Segurens,B., Robert,C., Abergel,C., Claverie,J.M., Raoult,D., Medigue,C., Weissenbach,J. and Cruveiller,S.
 TITLE Comparative analysis of Acinetobacters: three genomes for three lifestyles
 JOURNAL PLoS ONE 3 (3), E1805 (2008)
 PUBMED [18350144](#)
 REMARK Publication Status: Online-Only
 REFERENCE 2 (residues 1 to 296)
 CONSRM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-2008) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 3 (residues 1 to 296)
 AUTHORS Genoscope -,C.E.A.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-2008) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT VALIDATED [REFSEQ](#): This record has undergone validation or preliminary review. The reference sequence was derived from [CAP00151](#).
 Annotation data relative to BLAST similarities, COG assignments, enzymatic function prediction (PRIAM software), TMHMM and SignalP predictions, and synten results (Syntozier software) are available in BaumannScope database via the MaGe annotation system <http://www.genoscope.cns.fr/agc/mage/baumannscope>.
 Method: conceptual translation.
 FEATURES
 source Location/Qualifiers
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 [Protein](#) 1..296
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 /EC_number="[6.2.1.5](#)"
 /function="1.3.4 : tricarboxylic acid cycle"
 /calculated_mol_wt=30562
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 [CDS](#) 1..296
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 /transl_table=[11](#)
 /db_xref="GeneID:[5987402](#)"

MATRIX SCIENCE Mascot Search Results

Protein View

Match to: [gi|169796408](#) Score: 225
enoyl-CoA hydratase, phenylacetic acid degradation [*Acinetobacter baumannii* AYE]
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Nominal mass (M_r): 29297; Calculated pI value: 5.75
NCBI BLAST search of [gi|169796408](#) against nr
Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii AYE](#)
Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|169149335](#) from [Acinetobacter baumannii AYE](#)

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: 26%

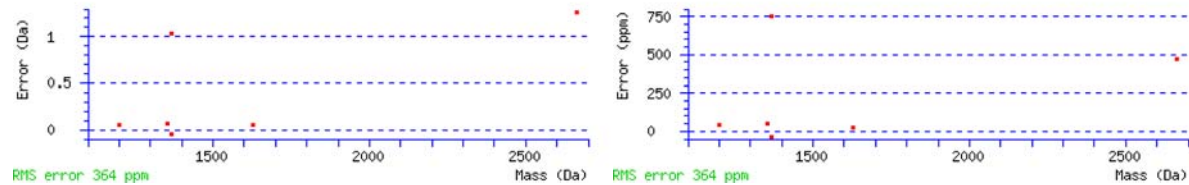
Matched peptides shown in **Bold Red**

1 **MDYQNIIEA EKNGVG**YLT**F NRPK**ALNSFN VDMHREVAEV LNLWTKNPDV
51 RCVVISGEGR GFCAGQDLGD RVVDPNAEAP DLGYSIETYY NPLIKTIVNM
101 PKPVICAVNG VAAGAGANIA LACDLVIAAK **SANFVQAFCR LGLVPDSAGT**
151 **WFLPRA**VGHA RAMGLALLGD KLPAAETAKEW GMIWDVVEDA ELKTKVTELA
201 ERLAQPTFG LSLIKK**AIHQ SSNNTFDEQM LLERDLQR**IA GRSEDYREGV
251 QAFMNKREPN FKGR

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 12	677.3564	1352.6983	1352.6282	0.0701	0	M.MDYQNIIEAEEK.N (Ions score 34)
2 - 12	685.2965	1368.5784	1368.6231	-0.0447	0	M.MDYQNIIEAEEK.N Oxidation (M) (Ions score 4)
13 - 24	683.8810	1365.7474	1364.7201	1.0273	0	K.NGVGYLTFFNRPK.A (Ions score 23)
131 - 140	600.3079	1198.6012	1198.5553	0.0458	0	K.SANFVQAFCR.L (Ions score 47)
141 - 155	814.9667	1627.9189	1627.8722	0.0466	0	R.LGLVPDSAGTWFLPR.A (Ions score 68)
217 - 238	666.3880	2661.5228	2660.2612	1.2615	1	K.AIHQSSNNTFDEQMLLERDLQR.I Oxidation (M) (Ions score 34)



LOCUS YP_001714201 264 aa linear BCT 04-MAY-2010
DEFINITION enoyl-CoA hydratase, phenylacetic acid degradation [*Acinetobacter baumannii* AYE].
ACCESSION YP_001714201
VERSION YP_001714201.1 GI:169796408
DBLINK Project: [28921](#)
DBSOURCE REFSEQ: accession [NC_010410.1](#)
KEYWORDS .
SOURCE *Acinetobacter baumannii* AYE
ORGANISM [Acinetobacter baumannii AYE](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; *Acinetobacter*; *Acinetobacter calcoaceticus/baumannii* complex.
REFERENCE 1 (residues 1 to 264)
AUTHORS Vallenet,D., Nordmann,P., Barbe,V., Poiriel,L., Mangenot,S., Bataille,E., Dossat,C., Gas,S., Kreimeyer,A., Lenoble,P., Oztas,S., Poulain,J., Segurens,B., Robert,C., Abergel,C., Claverie,J.M., Raoult,D., Medigue,C., Weissenbach,J. and Cruveiller,S.
TITLE Comparative analysis of *Acinetobacter*s: three genomes for three lifestyles
JOURNAL PLoS ONE 3 (3), E1805 (2008)
PUBMED [18350144](#)
REMARK Publication Status: Online-Only
REFERENCE 2 (residues 1 to 264)
CONSRTM NCBI Genome Project
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2008) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
REFERENCE 3 (residues 1 to 264)

AUTHORS Genoscope -,C.E.A.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-2008) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final
 NCBI review. The reference sequence was derived from [CAM87219](#).
 Annotation data relative to BLAST similarities, COG assignments,
 enzymatic function prediction (PRIAM software), TMHMM and SignalP
 predictions, and synteny results (Syntonyzer software) are
 available in BaumannoScope database via the MaGe annotation system
<http://www.genoscope.cns.fr/agc/mage/baumannoscope>.
 Method: conceptual translation.

FEATURES

Location/Qualifiers

source 1..264
 /organism="Acinetobacter baumannii AYE"
 /strain="AYE"
 /db_xref="taxon:[509173](#)"

[Protein](#) 1..264
 /product="enoyl-CoA hydratase, phenylacetic acid
 degradation"
 /EC_number="[4.2.1.17](#)"
 /function="1.1.5.1 : Phenylacetic acid degradation"
 /calculated_mol_wt=28899

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 /db_xref="CDD:[168327](#)"

[Region](#) 7..203
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 enzymes including enoyl-CoA hydratase, naphthoate synthase,
 methylmalonyl-CoA decarboxylase, 3-hydroxybutyryl-CoA
 dehydratase, and dienoyl-CoA isomerase...; cd06558"
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[Site](#) order(26,28,60,64..68,111,113..115,137..138,141)
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[Site](#) order(95,103,124..127,139..142,148,150..152,154..155,
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[CDS](#) 1..264
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 /inference="ab initio prediction:AMIGene:2.0"
 /note="Evidence 2b : Function of strongly homologous gene;
 PubMedId : 9748275; Product type e : enzyme"
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 /db_xref="GeneID:[6003595](#)"

Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Protein View

Match to: [gi|193735465](#) Score: 203

OprD [[Acinetobacter genomosp. 3](#)]

Found in search of C:\DOCUME~1\DRAF40~1\JIT\LOCALS~1\Temp\mas3E.tmp

Nominal mass (M_r): 48078; Calculated pI value: 6.40

NCBI BLAST search of [gi|193735465](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter genomosp. 3](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 11%

Matched peptides shown in **Bold Red**

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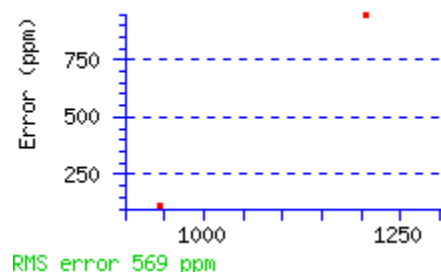
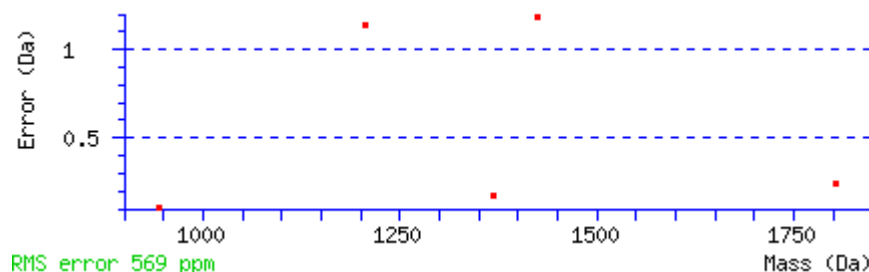
1  MLKAQKLTLA VLIFAAIISS AQASEQSEAK GFVEDANGSI LFRTGYLTRD
51  KKQGAKDTSS VAQSAIVNLE SGFTPGIVGF GVGVVGDGSF KIGENKNAGN
101 QMIPKNNDGS AYDHWGRGGG SVKARFSNTT VR.YGTQVLDL PVLASNTGRM
151 VPEYFTGTLL TSHEIKNLEL VAGKFTKDQM SDQINTDADA SGRGLDRAIV
201 WGGKYKFNDN LNASYGLDS KNALERHYAN VNFKQPLTNG SSLTYDFSGY
251 HTKFDANAHT YSATGTVAPN YGATGVAGEE KTNNIWAFTS TYNTGPHSVM
301 LAYQQNTGNV GYDYGQNADG FQSIYLPNSY MSDFIGNHEK SAQIQYNVDF
351 GKLGVLPLGN WTTAFVYGWD IKVRNVTDDA QEREFFNQVK YTVQSGFAKD
401 ASLRIRNSYY RASDAYQSNQ YIGDTNEWRI FLDIPVKLF
    
```

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
31 - 43	713.4513	1424.8880	1423.7096	1.1784	0	K.GFVEDANGSILFR.T (Ions score 21)
133 - 149	902.6019	1803.1892	1802.9527	0.2365	0	R.YGTQVLDLPLASNTGR.M (Ions score 64)
341 - 352	685.4294	1368.8442	1368.6674	0.1768	0	K.SAQIQYNVDFGK.L (Ions score 62)
430 - 437	472.8481	943.6817	943.5742	0.1075	0	R.IFLDIPVK.L (Ions score 33)
430 - 439	603.4396	1204.8647	1203.7267	1.1380	1	R.IFLDIPVKLF.- (Ions score 23)



LOCUS ACF20231 439 aa linear BCT 01-APR-2010
 DEFINITION OprD [[Acinetobacter genomosp. 3](#)].
 ACCESSION ACF20231
 VERSION ACF20231.1 GI:193735465
 DBSOURCE accession [EU808007.1](#)
 KEYWORDS .
 SOURCE [Acinetobacter genomosp. 3](#)
 ORGANISM [Acinetobacter genomosp. 3](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
 complex.
 REFERENCE 1 (residues 1 to 439)

AUTHORS Lin,Y.C., Sheng,W.H., Chen,Y.C., Chang,S.C., Hsia,K.C. and Li,S.Y.
 TITLE Differences in carbapenem resistance genes among
 Acinetobacterbaumannii, Acinetobacter genospecies 3 and
 Acinetobacter genospecies 13TU in Taiwan
 JOURNAL Int. J. Antimicrob. Agents 35 (5), 439-443 (2010)
 PUBMED [20106635](#)
 REFERENCE 2 (residues 1 to 439)
 AUTHORS Lin,Y.-C., Sheng,W.-H., Chen,Y.-C., Chang,S.-C., Hsia,K.-C.,
 Wu,R.-J. and Li,S.-Y.
 TITLE Loss of OprD porin is associated with a higher level of imipenem
 resistance in MBL-positive Acinetobacter spp. in Taiwan
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 439)
 AUTHORS Lin,Y.-C., Sheng,W.-H., Chen,Y.-C., Chang,S.-C., Hsia,K.-C.,
 Wu,R.-J. and Li,S.-Y.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-2008) Research and Diagnostic Center, Centers for
 Disease Control, No. 161, Kun-Yang St., Taipei 115, Taiwan
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
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 [Protein](#) 1..439
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 [Region](#) 30..438
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 [CDS](#) 1..439
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 /coded_by="EU808007.1:1..1320"
 /transl_table=[11](#)

Mascot: <http://www.matrixscience.com/>



Mascot Search Results

Protein View

Match to: [gi|126642784](#) Score: 110

putative protein (DcaP-like) [Acinetobacter baumannii ATCC 17978]

Found in search of C:\Temp\mas87.tmp

Nominal mass (M_r): **44818**; Calculated pI value: **5.79**

NCBI BLAST search of [gi|126642784](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii ATCC 17978](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **13%**

Matched peptides shown in **Bold Red**

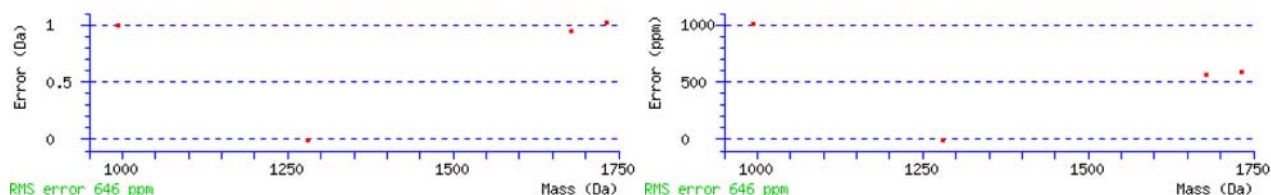
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1 MMSGANAATS DKEEIRKLKQ EVEALKALVQ EQRQVQQQQQ QVQQQQQVQL
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101 DVSKSDGKTH DKLRAKTAT RLGLDFNTPV GDDKVGGKIE VDFAGSTTDS
151 NGSRLIRHAY LTYNNWLFQ TTSNFLSNHA PEMIDFSTNI GGGTKRVPQV
201 RYNYKLGPTT QLFVSAEKGD STSVTGDSE KYSLPALTAK ITQGYAEGRG
251 SASARVLVEN YKSQALDDDK TGWGVAVGTD FKVSDPLKLF ADASYVVGDN
301 SYLYGNSPNY AVDGNSEIQN EFVAVQVGGT YKILPNLRST LAYGAQFSDD
351 GTDYARLNAS ANEKVQQAWI NFIYTPVKPI DLGVEYVNGK RDTFDGKSYK
401 DNRVGLMAKY SF
  
```

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
55 - 71	839.9416	1677.8686	1676.9250	0.9436	0	K.AQPQPVAAPVSPLAGFK.S (Ions score 29)
74 - 85	641.3304	1280.6463	1280.6513	-0.0050	0	K.AGADVNLVYGFVR.G (Ions score 26)
122 - 138	578.3080	1731.9020	1730.8839	1.0181	1	R.LGLDFNTPVGGDKVGGK.I (Ions score 23)
241 - 249	498.2515	994.4884	993.4879	1.0004	0	K.ITQGYAEGR.G (Ions score 33)



LOCUS YP_001085768 412 aa linear BCT 29-MAY-2010

DEFINITION putative protein (DcaP-like) [Acinetobacter baumannii ATCC 17978].

ACCESSION YP_001085768

VERSION YP_001085768.1 GI:126642784

DBLINK Project: [58731](#)

DBSOURCE REFSEQ: accession [NC_009085.1](#)

KEYWORDS .

SOURCE Acinetobacter baumannii ATCC 17978

ORGANISM [Acinetobacter baumannii ATCC 17978](#)
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
complex.

REFERENCE 1 (residues 1 to 412)

AUTHORS Smith,M.G., Gianoulis,T.A., Pukatzki,S., Mekalanos,J.J.,
Ornston,L.N., Gerstein,M. and Snyder,M.

TITLE New insights into Acinetobacter baumannii pathogenesis revealed by
high-density pyrosequencing and transposon mutagenesis

JOURNAL Genes Dev. 21 (5), 601-614 (2007)

PUBMED [17344419](#)

REFERENCE 2 (residues 1 to 412)

CONSRTM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (05-MAR-2007) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (residues 1 to 412)

12/22/2010

Mascot Search Results: Protein View

AUTHORS Smith,M.G., Gianoulis,T.A., Pukatzki,S., Mekalanos,J.,
Ornston,L.N., Gerstein,M. and Snyder,M.

TITLE Direct Submission

JOURNAL Submitted (27-NOV-2006) Department of Molecular, Cellular, and
Developmental Biology, Yale University, 266 Whitney Ave, New Haven,
CT 06520, USA

COMMENT PROVISIONAL [REFSEQ](#): This record has not yet been subject to final
NCBI review. The reference sequence was derived from [ABO13166](#).
Source DNA and bacteria available from Michael Snyder
(michael.snyder@yale.edu).
Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..412
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/strain="ATCC 17978"
/db_xref="ATCC:[17978](#)"
/db_xref="taxon:[400667](#)"

[Protein](#) 1..412
/product="putative protein (DcaP-like)"
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[Region](#) 95..355
/region_name="Porin_2"
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[CDS](#) 1..412
/locus_tag="A1S_2753"
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Mascot: <http://www.matrixscience.com/>

Mascot Search Results

Protein View

Match to: [gi|169632653](#) Score: 747

chaperonin GroEL [Acinetobacter baumannii SDF]

Found in search of c:\docume~1\draf40~1.jit\locals~1\TEMP\MAS9b.TMP

Nominal mass (M_r): 57000; Calculated pI value: 4.92

NCBI BLAST search of [gi|169632653](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Acinetobacter baumannii SDF](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|226704072](#) from [Acinetobacter baumannii SDF](#)

[gi|169151445](#) from [Acinetobacter baumannii](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 41%

Matched peptides shown in **Bold Red**

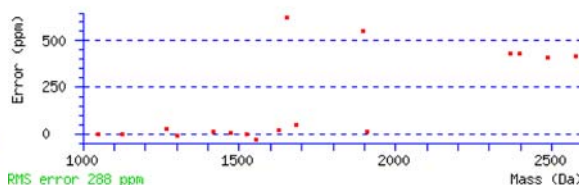
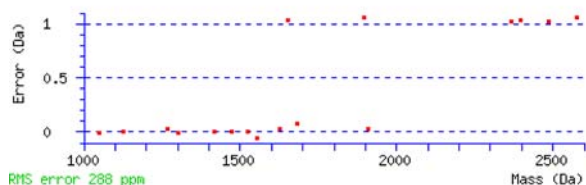
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101 NEGIKSVTAG  MNPMDLKRGI DIAVKTVVEN  IRSIAKPADD  FKAIEQVGS
151 SANSDDTVGK  LIAQAMEKVG  KEGVITVEEG  SGFEDALDVV  EGMQFDRGYI
201 SPYFANKQDT  LTAELNPFI  LLVDKKISNI  RELISVLEAV  AKTGKPLLI
251 AEDVEGEALA  TLVVNNMRGI  IKVCAVKAPG  FGDRRKAMLQ  DIAILTGTAT
301 ISEEVGMSLE  QATLQDLGTA  HKITVSKENT  VIVDGAGDAA  AIAERVQQIR
351 AQIEESTSEY  DREKLQERVA  KLAGGVAVIK  IGAATEVEMK  EKKDRVDDAL
401 HATRAAVEEG  VVAGGGVALV  RAVNALEGLK  GANEDQTAGI  NILRRRAIEAP
451 LRQIVANAGD  EPSVVINAVK  NGEGNFGYNA  ATGEYGDMLE  MGILDPAKVT
501 RSALHHAASV  AGLMLTTECM  ITDIPEDKPA  APDMGGMGGM  M
  
```

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
16 - 28	650.8622	1299.7098	1299.7220	-0.0123	0	K.MIAGVNVLADAVK.V (Ions score 22)
16 - 34	633.0555	1896.1447	1895.0914	1.0533	1	K.MIAGVNVLADAVKVTLGPK.G (Ions score 53)
16 - 34	638.0453	1911.1139	1911.0863	0.0276	1	K.MIAGVNVLADAVKVTLGPK.G Oxidation (M) (Ions score 33)
37 - 51	552.3167	1653.9282	1652.8998	1.0283	1	R.NVIDRSFGAPHITK.D (Ions score 33)
81 - 105	830.1102	2487.3089	2486.2864	1.0225	0	K.TNDIAGDGTATVLAQAILNEGK.S (Ions score 53)
106 - 118	710.3634	1418.7122	1418.7010	0.0112	1	K.SVTAGMNPMDLKR.G (Ions score 47)
119 - 132	763.9487	1525.8828	1525.8828	0.0000	1	R.GIDIAVKTIVENIR.S (Ions score 67)
328 - 350	799.7658	2396.2755	2395.2455	1.0300	1	K.ENTVIVDAGDAAIAIAERVQQIR.A (Ions score 48)
351 - 364	562.2881	1683.8424	1683.7587	0.0837	1	R.AQIEESTSEYDREK.L (Ions score 25)
369 - 380	563.3711	1124.7276	1124.7281	-0.0006	1	R.VAKLAGGVAVIK.I (Ions score 21)
381 - 390	524.7687	1047.5229	1047.5270	-0.0042	0	K.IGAATEVEMK.E (Ions score 27)
394 - 404	423.5606	1267.6599	1267.6269	0.0330	1	K.DRVDDALHATR.A (Ions score 34)
405 - 421	777.4097	1552.8048	1552.8573	-0.0525	0	R.AAVEEGVVAGGGVALVR.A (Ions score 67)
422 - 444	790.1009	2367.2809	2366.2553	1.0255	1	R.AVNALEGLKGANEDQTAGINILR.R (Ions score 97)
431 - 444	736.3819	1470.7493	1470.7426	0.0067	0	K.GANEDQTAGINILR.R (Ions score 30)
431 - 445	543.2994	1626.8762	1626.8438	0.0325	1	K.GANEDQTAGINILRR.A (Ions score 38)
446 - 470	859.1669	2574.4788	2573.4177	1.0611	1	R.AIEAPLRQIVANAGDEPSVVINAVK.N (Ions score 81)



LOCUS YP_001706389 541 aa linear BCT 15-APR-2010
 DEFINITION chaperonin GroEL [Acinetobacter baumannii SDF].
 ACCESSION YP_001706389
 VERSION YP_001706389.1 GI:169632653
 DBLINK Project: [13001](#)
 DBSOURCE REFSEQ: accession [NC_010400.1](#)
 KEYWORDS .
 SOURCE Acinetobacter baumannii SDF
 ORGANISM [Acinetobacter baumannii SDF](#)
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Moraxellaceae; Acinetobacter; Acinetobacter calcoaceticus/baumannii
 complex.

REFERENCE 1 (residues 1 to 541)
AUTHORS Vallenet,D., Nordmann,P., Barbe,V., Poirel,L., Mangenot,S., Bataille,E., Dossat,C., Gas,S., Kreimeyer,A., Lenoble,P., Oztas,S., Poulain,J., Segurens,B., Robert,C., Abergel,C., Claverie,J.M., Raoult,D., Medigue,C., Weissenbach,J. and Cruveillier,S.
TITLE Comparative analysis of Acinetobacters: three genomes for three lifestyles
JOURNAL PLoS ONE 3 (3), E1805 (2008)
PUBMED [18350144](#)
REMARK Publication Status: Online-Only

REFERENCE 2 (residues 1 to 541)
CONSRTM NCBI Genome Project
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2008) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (residues 1 to 541)
AUTHORS Genoscope -,C.E.A.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2008) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [CAP00185](#). Annotation data relative to BLAST similarities, COG assignments, enzymatic function prediction (PRIAM software), TMHMM and SignalP predictions, and synteny results (Syntonyzer software) are available in BaumannScope database via the MaGe annotation system <http://www.genoscope.cns.fr/agc/mage/baumannscope>. Method: conceptual translation.

FEATURES Location/Qualifiers
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/strain="SDF"
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[Protein](#) 1..541
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/function="5.1 : cell division"
/calculated_mol_wt=56790

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/note="chaperonin GroEL; Reviewed; PRK12849"
/db_xref="CDD:[171768](#)"

[Region](#) 4..523
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[Site](#) order(109,434,452,461,463..464,467)
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/note="stacking interactions"
/db_xref="CDD:[48161](#)"

[Site](#) order(141,186,193,375,409..410)
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[CDS](#) 1..541
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/inference="ab initio prediction:AMIGene:2.0"
/note="60 kDa chaperone family; promotes refolding of misfolded polypeptides especially under stressful conditions; forms two stacked rings of heptamers to form a barrel-shaped 14mer; ends can be capped by GroES; misfolded proteins enter the barrel where they are refolded when GroES binds; many bacteria have multiple copies of the groEL gene which are active under different environmental conditions; the B.japonicum protein in this

12/22/2010

Mascot Search Results: Protein View

cluster is expressed constitutively; in Rhodobacter,
Corynebacterium and Rhizobium this protein is essential
for growth"
/transl_table=[11](#)
/db_xref="GeneID:[5986839](#)"

Mascot: <http://www.matrixscience.com/>