

Mascot Search Results

Protein View

Match to: **gi|156937135** Score: **569** Expect: **2.1e-050**
phosphoenolpyruvate carboxylase [Ignicoccus hospitalis KIN4/I]

Nominal mass (M_r): **55898**; Calculated pI value: **5.78**

NCBI BLAST search of [gi|156937135](#) against nr

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

Taxonomy: [Ignicoccus hospitalis KIN4/I](#)

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

[gi|156566119](#) from [Ignicoccus hospitalis KIN4/I](#)

Variable modifications: Oxidation (M), Propionamide (C)

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

Sequence Coverage: **45%**

Matched peptides shown in **Bold Red**

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1 MKVPKLMATQ HPDSTVVLMP QDEVEEAIQD VLPLDQGGRG CDEKMVDYEG
51 KATPYNQMRD IIEEVRKYDV VPGEDFLITP RVPNPKLEDK DRHLLAITAA
101 VTANMYSQMY FNTDAIKYII LPMSTSTLEL AEVQRRLKV ERLVSEEFSL
151 RIEEWIKLIP LFETAESHMH IDEIVEGLRI AFIKEIGMFE NEFRIFMGKS
201 DSGIHSGHIA SSIGVRMGLL KLWNWQKDTM FKVYPIIGMG KPPLRGHMAE
251 WVIEDWVEAW RGYYTATVQS ALRFNTDRKD YVHTITVVTK NSGKQPPEL
301 LGYAKEMVNV AWRASEVYLS RLERLADMIS FMAKFVTRTR ARLDSYKRRA
351 KTGKEMPRAI RFCASLYSMG LGPTLIGAGV IEELASGTAE KLEHLLKFVP
401 LLPKDFAFDY AFTDLEVFKR YVDEKTFEII KKDVDVVKEY FANVEPPKSP
451 PEGYFEKLRE LRGALDEAEV SRAKAIVMEL AEMRGFLG

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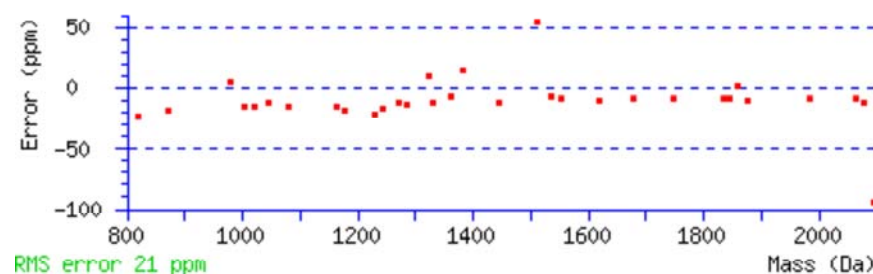
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start	End	Observed	M_r (expt)	M_r (calc)	ppm	Miss	Sequence
52	59	980.4657	979.4584	979.4545	4	0	K.ATPYNQMR.D (No match)

52 - 66	1834.8967	1833.8894	1833.9043	-8	1	K.ATPYNQMRDIIIEVR.K	(No match)
60 - 66	873.4520	872.4447	872.4603	-18	0	R.DIIIEVR.K	(No match)
60 - 66	873.4520	872.4448	872.4603	-18	0	R.DIIIEVR.K	(Ions score 27)
67 - 81	1748.9061	1747.8988	1747.9145	-9	1	R.KYDVVPGEDFLITPR.V	(No match)
67 - 81	1748.9061	1747.8989	1747.9145	-9	1	R.KYDVVPGEDFLITPR.V	(Ions score 100)
68 - 81	1620.8099	1619.8026	1619.8195	-10	0	K.YDVVPGEDFLITPR.V	(No match)
118 - 135	2064.0857	2063.0784	2063.0972	-9	0	K.YIILPMSTSTLELAEVQR.R	(Ions score 70)
118 - 135	2064.0857	2063.0784	2063.0972	-9	0	K.YIILPMSTSTLELAEVQR.R	(No match)
118 - 135	2080.0767	2079.0694	2079.0922	-11	0	K.YIILPMSTSTLELAEVQR.R	Oxidation (M) (No match)
143 - 151	1079.5564	1078.5491	1078.5659	-16	0	R.LVSEEFSLR.I	(No match)
143 - 151	1079.5564	1078.5491	1078.5659	-16	0	R.LVSEEFSLR.I	(Ions score 36)
143 - 157	1877.9823	1876.9750	1876.9934	-10	1	R.LVSEEFSLRIEELIK.L	(No match)
180 - 194	1843.9252	1842.9179	1842.9338	-9	1	R.IAFIKEIGMFENEFR.I	(No match)
180 - 194	1859.9393	1858.9320	1858.9287	2	1	R.IAFIKEIGMFENEFR.I	Oxidation (M) (No match)
185 - 194	1271.5568	1270.5495	1270.5652	-12	0	K.EIGMFENEFR.I	(Ions score 28)
185 - 194	1271.5568	1270.5495	1270.5652	-12	0	K.EIGMFENEFR.I	(No match)
185 - 194	1287.5503	1286.5430	1286.5601	-13	0	K.EIGMFENEFR.I	Oxidation (M) (No match)
200 - 216	1679.8315	1678.8242	1678.8387	-9	0	K.SDSGIHSGHIASSIGVR.M	(No match)
222 - 232	1512.8123	1511.8050	1511.7231	54	1	K.LWNWQKDTMFK.V	Oxidation (M) (No match)
228 - 245	2094.9092	2093.9019	2094.1006	-95	1	K.DTMFKVYPIIGMGKPLR.G	2 Oxidation (M) (No match)
262 - 273	1329.6637	1328.6564	1328.6725	-12	0	R.GYYTATVQSALR.F	(No match)
295 - 305	1228.6676	1227.6603	1227.6863	-21	0	K.QPPELLGYAK.E	(No match)
306 - 313	1004.4833	1003.4760	1003.4909	-15	0	K.EMVNVAVR.A	(Ions score 49)
306 - 313	1004.4833	1003.4760	1003.4909	-15	0	K.EMVNVAVR.A	(No match)
306 - 313	1020.4771	1019.4698	1019.4858	-16	0	K.EMVNVAVR.A	Oxidation (M) (No match)
352 - 358	818.4000	817.3927	817.4116	-23	1	K.TGKEMPR.A	(No match)
405 - 420	1983.9315	1982.9242	1982.9414	-9	1	K.DFAFDYAFTDLEVFKR.Y	(No match)
421 - 431	1384.7565	1383.7492	1383.7286	15	1	R.YVDEKTFEIIK.K	(No match)
449 - 459	1322.6870	1321.6797	1321.6666	10	1	K.SPPEGYFEKLR.E	(No match)
460 - 472	1444.7219	1443.7146	1443.7317	-12	1	R.ELRGALDEAEVSR.A	(No match)
463 - 472	1046.4998	1045.4925	1045.5040	-11	0	R.GALDEAEVSR.A	(No match)
463 - 474	1245.6233	1244.6160	1244.6360	-16	1	R.GALDEAEVSR.AK.A	(No match)
473 - 484	1361.7192	1360.7119	1360.7206	-6	1	R.AKAIVMELAEMR.G	(No match)
475 - 484	1162.5779	1161.5706	1161.5886	-15	0	K.AIVMELAEMR.G	(Ions score 64)
475 - 484	1162.5779	1161.5706	1161.5886	-15	0	K.AIVMELAEMR.G	(No match)
475 - 484	1178.5687	1177.5614	1177.5835	-19	0	K.AIVMELAEMR.G	Oxidation (M) (No match)
475 - 488	1536.7797	1535.7724	1535.7840	-8	1	K.AIVMELAEMRGFLG.-	(No match)
475 - 488	1552.7722	1551.7649	1551.7789	-9	1	K.AIVMELAEMRGFLG.-	Oxidation (M) (No match)



LOCUS YP_001434931 488 aa linear BCT 22-DEC-2012
 DEFINITION phosphoenolpyruvate carboxylase [Ignicoccus hospitalis KIN4/I].
 ACCESSION YP_001434931
 VERSION YP_001434931.1 GI:156937135
 DBLINK Project: 58365
 BioProject: PRJNA58365
 DBSOURCE REFSEQ: accession NC_009776.1
 KEYWORDS .
 SOURCE Ignicoccus hospitalis KIN4/I
 ORGANISM Ignicoccus hospitalis KIN4/I
 Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 Desulfurococcaceae; Ignicoccus.
 REFERENCE 1 (residues 1 to 488)
 AUTHORS Podar, M., Anderson, I., Makarova, K.S., Elkins, J.G., Ivanova, N.,
 Wall, M.A., Lykidis, A., Mavromatis, K., Sun, H., Hudson, M.E., Chen, W.,
 Deciu, C., Hutchison, D., Eads, J.R., Anderson, A., Fernandes, F.,
 Szeto, E., Lapidus, A., Kyrpides, N.C., Saier, M.H. Jr.,
 Richardson, P.M., Rachel, R., Huber, H., Eisen, J.A., Koonin, E.V.,
 Keller, M. and Stetter, K.O.
 TITLE A genomic analysis of the archaeal system Ignicoccus
 hospitalis-Nanoarchaeum equitans
 JOURNAL Genome Biol. 9 (11), R158 (2008)
 PUBMED 19000309
 REFERENCE 2 (residues 1 to 488)
 CONSRTM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (06-SEP-2007) National Center for Biotechnology
 Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 3 (residues 1 to 488)
 AUTHORS Copeland, A., Lucas, S., Lapidus, A., Barry, K., Glavina del Rio, T.,

Dalin,E., Tice,H., Pitluck,S., Martinez,M., Zharchuk,I.,
Schmutz,J., Larimer,F., Land,M., Hauser,L., Kyrpides,N.,
Anderson,I. and Richardson,P.

CONSRM US DOE Joint Genome Institute
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2007) US DOE Joint Genome Institute, 2800
Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from ABU81524.
Method: conceptual translation.

FEATURES Location/Qualifiers

source	1..488 /organism="Ignicoccus hospitalis KIN4/I" /strain="KIN4/I" /db_xref="taxon:453591"
Protein	1..488 /product="phosphoenolpyruvate carboxylase" /calculated_mol_wt=55803
Region	1..488 /region_name="PRK13655" /note="phosphoenolpyruvate carboxylase; Provisional" /db_xref="CDD:184212"
Region	3..488 /region_name="PEPCase_arch" /note="phosphoenolpyruvate carboxylase, archaeal type; TIGR02751" /db_xref="CDD:131798"
CDS	1..488 /locus_tag="Igni_0341" /coded_by="complement(NC_009776.1:298680..300146)" /note="catalyzes the formation of oxaloacetate from phosphoenolpyruvate" /transl_table=11 /db_xref="InterPro:IPR007566" /db_xref="GeneID:5562970"

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