

Mascot Search Results

Protein View

Match to: **gi|156937269** Score: **629** Expect: **4.4e-058**
coenzyme F390 synthetase-like protein [Ignicoccus hospitalis KIN4/I]

Nominal mass (M_r): **56781**; Calculated pI value: **6.46**
 NCBI BLAST search of [gi|156937269](#) 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|156566253](#) 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: **48%**

Matched peptides shown in **Bold Red**

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1  MLSSRAVVFE RYSRATPLGA YLEEGRRFRE EGFIRTDYPP KRDEVLWNPK
51 IMRMPREELE KIKTQRLKAI VKWAWEHSEF YRKFWKSKGF HPDMIKTHED
101 VVKIPVLTKK DLRADLQKNP PYGTIMVPEL AKYIHFVGAT SGSTGMPTFQ
151 GWGRVELDYF EEQARYLWT FAGVKPGVVY ANYLNMSGFY SWGPPLVETA
201 MWRCGATAIA GGGETFFTWK DRHMLIMKLW KVDVFATTPW LHRWIGEQAK
251 LEGWVTPFKV LLLHGGAABE KTKEKLMEVH PNVEKVISVW GTTDGHMAIE
301 PPDAPGTLVF WEDTQIFDIV VPGSYEERPE GEPAGQGERG ELIATLLTHY
351 TMPLIRYSLG DYVKNEFICD PTPELGITHC RFAELIPGRV EWMFKVKGKL
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451 EAREIIAREL GLSPEDVEIE WIRPGESVWK GYKLQVFLDE RKK

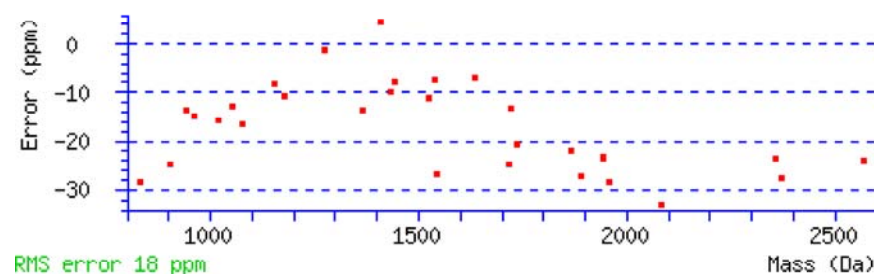
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Show predicted peptides also

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

Start - End	Observed	M_r (expt)	M_r (calc)	ppm	Miss	Sequence
15 - 26	1276.6515	1275.6442	1275.6459	-1	0	R.ATPLGAYLEEGR.R (No match)

15 - 27	1432.7399	1431.7326	1431.7470	-10	1	R.ATPLGAYLEEGRR.F	(No match)
28 - 35	1053.5342	1052.5269	1052.5403	-13	1	R.FREEGFIR.T	(Ions score 29)
28 - 35	1053.5342	1052.5269	1052.5403	-13	1	R.FREEGFIR.T	(No match)
42 - 50	1156.6016	1155.5943	1155.6036	-8	1	K.RDEVLWNP.K.I	(Ions score 44)
42 - 50	1156.6016	1155.5943	1155.6036	-8	1	K.RDEVLWNP.K.I	(No match)
73 - 82	1410.6289	1409.6216	1409.6153	5	0	K.WAWEHSEFYR.K	(No match)
73 - 82	1410.6289	1409.6216	1409.6153	5	0	K.WAWEHSEFYR.K	(Ions score 46)
73 - 83	1538.7064	1537.6991	1537.7102	-7	1	K.WAWEHSEFYR.K.F	(No match)
89 - 96	944.4532	943.4459	943.4586	-13	0	K.GFHPDMIK.T	(No match)
89 - 96	960.4467	959.4394	959.4535	-15	0	K.GFHPDMIK.T	Oxidation (M) (No match)
114 - 132	2085.0359	2084.0286	2084.0976	-33	1	R.ADLQKNPPYGTIMVPELAK.Y	(No match)
119 - 132	1545.7566	1544.7493	1544.7908	-27	0	K.NPPYGTIMVPELAK.Y	Oxidation (M) (No match)
133 - 154	2357.0576	2356.0503	2356.1059	-24	0	K.YIHFGVATSGSTGMPFQGWGR.V	(No match)
133 - 154	2357.0576	2356.0503	2356.1059	-24	0	K.YIHFGVATSGSTGMPFQGWGR.V	(Ions score 110)
133 - 154	2373.0430	2372.0357	2372.1008	-27	0	K.YIHFGVATSGSTGMPFQGWGR.V	Oxidation (M) (No match)
155 - 166	1526.6951	1525.6878	1525.7049	-11	0	R.VELDYFEEQAR.Y	(Ions score 72)
155 - 166	1526.6951	1525.6878	1525.7049	-11	0	R.VELDYFEEQAR.Y	(No match)
204 - 220	1716.7623	1715.7550	1715.7978	-25	0	R.CGATAIAGGGGETFFTWK.D	(No match)
229 - 243	1868.9762	1867.9689	1868.0097	-22	1	K.LWKVDVFATTPWLHR.W	(No match)
232 - 243	1441.7476	1440.7403	1440.7514	-8	0	K.VDVVFATTPWLHR.W	(No match)
244 - 250	831.4124	830.4051	830.4286	-28	0	R.WIGEQAK.L	(No match)
244 - 259	1888.9443	1887.9370	1887.9883	-27	1	R.WIGEQAKLEGWVTPFK.V	(No match)
251 - 259	1076.5596	1075.5523	1075.5702	-17	0	K.LEGWVTPFK.V	(No match)
260 - 271	1178.6765	1177.6692	1177.6819	-11	0	K.VLLHGGAAAEK.T	(No match)
340 - 356	1942.0378	1941.0305	1941.0757	-23	0	R.GELIATLLTHYTMLIR.Y	(No match)
340 - 356	1942.0378	1941.0306	1941.0757	-23	0	R.GELIATLLTHYTMLIR.Y	(Ions score 39)
340 - 356	1958.0225	1957.0152	1957.0706	-28	0	R.GELIATLLTHYTMLIR.Y	Oxidation (M) (No match)
382 - 389	902.4873	901.4800	901.5021	-25	0	R.FAELIPGR.V	(No match)
382 - 395	1722.8810	1721.8737	1721.8963	-13	1	R.FAELIPGRVEWMFK.V	(Ions score 41)
382 - 395	1722.8810	1721.8737	1721.8963	-13	1	R.FAELIPGRVEWMFK.V	(No match)
382 - 395	1738.8630	1737.8557	1737.8912	-20	1	R.FAELIPGRVEWMFK.V	Oxidation (M) (No match)
440 - 453	1636.8580	1635.8507	1635.8620	-7	1	R.KPIPPPPPEYDKEAR.E	(No match)
459 - 480	2568.2363	2567.2290	2567.2907	-24	0	R.ELGLSPEDVEIEWIRPGESVWK.G	(No match)
459 - 480	2568.2363	2567.2291	2567.2907	-24	0	R.ELGLSPEDVEIEWIRPGESVWK.G	(Ions score 26)
481 - 491	1367.7134	1366.7061	1366.7245	-13	1	K.GYKLQVFLDER.K	(No match)
484 - 491	1019.5359	1018.5286	1018.5447	-16	0	K.LQVFLDER.K	(No match)



LOCUS YP_001435065 493 aa linear CON 10-JUN-2013
 DEFINITION coenzyme F390 synthetase-like protein [Ignicoccus hospitalis KIN4/I].
 ACCESSION YP_001435065
 VERSION YP_001435065.1 GI:156937269
 DBLINK Project: 58365
 BioProject: PRJNA58365
 DBSOURCE REFSEQ: accession NC_009776.1
 KEYWORDS RefSeq.
 SOURCE Ignicoccus hospitalis KIN4/I
 ORGANISM Ignicoccus hospitalis KIN4/I
 Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 Desulfurococcaceae; Ignicoccus.
 REFERENCE 1 (residues 1 to 493)
 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 493)
 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 493)

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.
 CONSRTM 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 ABU81658.
 Method: conceptual translation.
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Mascot: <http://www.matrixscience.com/>