

Mascot Search Results

Protein View

Match to: **gi|156937173** Score: **1010** Expect: **3.5e-096**
AMP-dependent synthetase/ligase [Ignicoccus hospitalis KIN4/I]

Nominal mass (M_r): **52696**; Calculated pI value: **5.62**
 NCBI BLAST search of [gi|156937173](#) 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|156566157](#) 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: **59%**

Matched peptides shown in **Bold Red**

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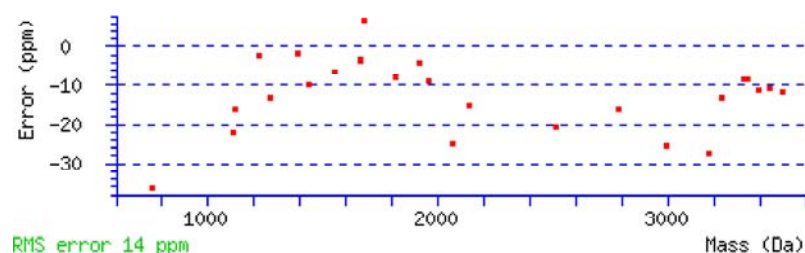
1 MYHDPGKPVH KIIERARES PDKVALVYED GTELTYKDLI SKAKAVANLL
51 YENKVRKCDT VFLIMFNRPE FVTSLLGALY AGARVVIVDA LTQKEDLAFQ
101 LNDSAPKVVL ADEEVLQRES ETLKGAVLT EKDLSSASGE HEVVVGIEDD
151 ARVFYYAGIA GRTMQVIHSH RSFTGAIMPL VQAEGINAND VSLVTVPLTH
201 VLGLDAALLS ALVSGATALL LKKFNMDKIK EMVARRSPTY LVAVPLVFQT
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351 MKCYPDPEEN SKAFVEVNGK VWMRTGDILA KDEEGFYYFR GVRKRMLKYK
401 GYPIFPKDLE LILLKHPCVA EAEEVVGEPAG EVGQIPVAKV KLKEGCKATP
451 EEIMDFVNKR VAAYKKVRKV IILE
```

Show predicted peptides also

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

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
45 - 56	1389.7825	1388.7752	1388.7776	-2	1	K.AVANLLYENKVR.K (No match)
85 - 107	2514.2925	2513.2852	2513.3377	-21	1	R.VVIVDALTQKEDLAFQLNDSAPK.V (No match)
108 - 118	1270.6833	1269.6760	1269.6929	-13	0	K.VVLADEEVLQR.E (No match)
108 - 118	1270.6834	1269.6761	1269.6929	-13	0	K.VVLADEEVLQR.E (Ions score 74)
108 - 124	1958.0269	1957.0196	1957.0368	-9	1	K.VVLADEEVLQRESETLK.G (No match)

125 - 152	2996.3359	2995.3286	2995.4047	-25	1	K.GYAVLTEKDLSSASGEHEVVVGIEDDAR.V	(No match)
133 - 152	2134.9199	2133.9126	2133.9451	-15	0	K.DLSSASGEHEVVVGIEDDAR.V	(No match)
133 - 162	3232.4761	3231.4688	3231.5109	-13	1	K.DLSSASGEHEVVVGIEDDARVFYYAGIAGR.T	(No match)
153 - 162	1116.5660	1115.5587	1115.5764	-16	0	R.VFYYAGIAGR.T	(No match)
153 - 162	1116.5660	1115.5588	1115.5764	-16	0	R.VFYYAGIAGR.T	(Ions score 72)
163 - 171	1108.5437	1107.5364	1107.5607	-22	0	R.TMQVIHSHR.S	(No match)
236 - 253	2063.1211	2062.1138	2062.1649	-25	1	R.RSPTYLVAVPLVFQTLMK.E	(No match)
237 - 260	2783.4126	2782.4053	2782.4503	-16	1	R.SPTYLVAVPLVFQTLMKDEEFVK.S	(No match)
237 - 260	2783.4126	2782.4053	2782.4503	-16	1	R.SPTYLVAVPLVFQTLMKDEEFVK.S	(Ions score 79)
261 - 267	760.4036	759.3963	759.4239	-36	0	K.SLGQSLR.W	(No match)
268 - 282	1663.7477	1662.7404	1662.7460	-3	0	R.WAMSGGAYLPPDDQR.R	(Ions score 115)
268 - 282	1663.7477	1662.7404	1662.7460	-3	0	R.WAMSGGAYLPPDDQR.R	(No match)
268 - 282	1679.7594	1678.7521	1678.7410	7	0	R.WAMSGGAYLPPDDQR.R	Oxidation (M) (No match)
268 - 283	1819.8400	1818.8327	1818.8471	-8	1	R.WAMSGGAYLPPDDQRR.W	(Ions score 52)
268 - 283	1819.8400	1818.8327	1818.8471	-8	1	R.WAMSGGAYLPPDDQRR.W	(No match)
283 - 311	3333.6902	3332.6829	3332.7115	-9	1	R.RWEELTGKPLLQVYGMTEAPQIFATTPEK.H	(Ions score 77)
283 - 311	3333.6902	3332.6829	3332.7115	-9	1	R.RWEELTGKPLLQVYGMTEAPQIFATTPEK.H	(No match)
283 - 311	3349.6863	3348.6790	3348.7064	-8	1	R.RWEELTGKPLLQVYGMTEAPQIFATTPEK.H	Oxidation (M) (No match)
284 - 311	3177.5308	3176.5235	3176.6104	-27	0	R.WEELTGKPLLQVYGMTEAPQIFATTPEK.H	(No match)
284 - 313	3442.7341	3441.7268	3441.7642	-11	1	R.WEELTGKPLLQVYGMTEAPQIFATTPEKH.K	(No match)
314 - 346	3500.8484	3499.8411	3499.8814	-12	0	K.IGSLGFPLPGVEALLVNPETLEPVEDQGELLVR.G	(Ions score 164)
314 - 346	3500.8484	3499.8411	3499.8814	-12	0	K.IGSLGFPLPGVEALLVNPETLEPVEDQGELLVR.G	(No match)
363 - 374	1435.7377	1434.7304	1434.7442	-10	1	K.AFVEVNGKVWMR.T	(No match)
375 - 390	1923.9044	1922.8971	1922.9050	-4	1	R.TGDILAKDEEGFYFR.G	(No match)
375 - 390	1923.9044	1922.8971	1922.9050	-4	1	R.TGDILAKDEEGFYFR.G	(Ions score 163)
382 - 390	1225.5134	1224.5061	1224.5087	-2	0	K.DEEGFYFR.G	(No match)
408 - 439	3394.7915	3393.7842	3393.8217	-11	1	K.DLELILLKHPCAEAEVVGEPAGEVGQIPVAK.V	Propionamide (C) (No match)
448 - 460	1549.7582	1548.7509	1548.7606	-6	1	K.ATPEEIMDFVNKR.V	(No match)



LOCUS YP_001434969 474 aa linear CON 10-JUN-2013
 DEFINITION AMP-dependent synthetase/ligase [Ignicoccus hospitalis KIN4/I].
 ACCESSION YP_001434969
 VERSION YP_001434969.1 GI:156937173
 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 474)
 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 474)
 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 474)
 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 ABU81562.
 Method: conceptual translation.
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II [Lipid metabolism / Secondary metabolites biosynthesis,
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Mascot: <http://www.matrixscience.com/>