



Mascot Search Results

Protein View

Match to: **gi|156937847** Score: **863** Expect: **8.4e-080**
3-hydroxyacyl-CoA dehydrogenase [Ignicoccus hospitalis KIN4/I]

Nominal mass (M_r): **74651**; Calculated pI value: **5.88**

NCBI BLAST search of [gi|156937847](#) 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|156566831](#) 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: **34%**

Matched peptides shown in **Bold Red**

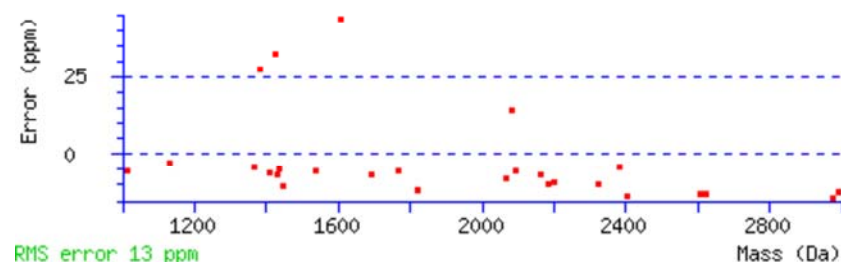
1	MGGALALYSL	LRLWTADQAL	QEV	RKVLVVG	AGVMGHGIAQ	VAAMSGLNVR
51	MIDIKQEF	LD	RAMERIKESL	EKLYAKGKLK	EPPEEVLKRI	ETMVANPDDE
101	SSYAEAAKDV	DFVIEAVPEK	LELKRAVFSV	LDKYAPPHAI	LASNTSSIPI	
151	TEIAKATK	RP	DKVVG	MHFFN	PPVILK	LVEV VRGKETSDET VKITVELAKK
201	MGK	VPIVVNK	DVPGFIVNRI	MAR	FLNEGCW	LVERGVYTKE QVDAALRYKL
251	NFPMGAFELA	DYVGLDVLVH	LMEAMK	ERGM	NLTICPLFKK	LLEEGKLGVK
301	SGEGFYKYP	APGKFKKPVVK	ASAAEGVDYI	SIVDTAVNEG	AWLVENG	VAG
351	PEEVD	TATVL	GLNLPMGILK	LGDSLGLDNV	LDSINEKKEK	YGLEDYRPVQ
401	LLENMVKEGK	CGVKCGKGFY	EYEVSEEDLG	EIKVRREGEA	LWIIILNRPKQ	
451	RNALTP	EMLL	KMAEVAQKAC	EDEGVRAIVL	YGGDVFSAGF	DLTVMKD
501	TKAPET	VARP	FKKLALALEG	CPKPVIAYIT	GYALGGGLEV	AMMADLR
551	EDSL	LQGPEI	NVGIMPGGGG	TQRLP	RLVGL	GRAMQLVLLG DPIDAVEAEK
601	WGLVNW	AVPK	RIADSEVRLL	VKKLSSKPKE	ALALAKKAVR	VAQEVPLIDG
651	LEMEAE	AFAR	ALATENAKEG	IAAFLEK	RKP	NFK

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
13 - 24	1429.7338	1428.7265	1428.7361	-7	0	R.LWTADQALQEV.R.K (No match)
26 - 50	2406.2781	2405.2708	2405.3036	-14	0	K.VLVVGAGVMGHGIAQVAAMSGLNVR.M (No match)
51 - 61	1407.7216	1406.7143	1406.7228	-6	1	R.MIDIKQEFLDR.A (No match)
51 - 61	1423.7711	1422.7638	1422.7177	32	1	R.MIDIKQEFLDR.A Oxidation (M) (No match)
159 - 176	2094.1565	2093.1492	2093.1608	-6	1	K.RPDKVVGMMHFFNPPVILK.L (No match)
204 - 219	1766.0228	1765.0155	1765.0251	-5	1	K.VPIVVKDVPGFIVNR.I (No match)
211 - 219	1016.5469	1015.5396	1015.5451	-5	0	K.DVPGFIVNR.I (Ions score 59)
211 - 219	1016.5469	1015.5396	1015.5451	-5	0	K.DVPGFIVNR.I (No match)
224 - 234	1365.6565	1364.6492	1364.6547	-4	0	R.FLNEGCWLVER.G (No match)
224 - 234	1436.6926	1435.6853	1435.6918	-5	0	R.FLNEGCWLVER.G Propionamide (C) (No match)
224 - 234	1436.6926	1435.6854	1435.6918	-4	0	R.FLNEGCWLVER.G Propionamide (C) (Ions score 30)
235 - 247	1449.7549	1448.7476	1448.7623	-10	1	R.GVYTKEQVDAALR.Y (No match)
277 - 289	1608.8933	1607.8860	1607.8163	43	1	K.ERGMNLTICPLFK.K Oxidation (M); Propionamide (C) (No match)
279 - 290	1380.7754	1379.7681	1379.7305	27	1	R.GMNLITICPLFKK.L Oxidation (M) (No match)
389 - 407	2324.1726	2323.1653	2323.1882	-10	1	K.EKYGLEDYRPVQLLENMVK.E (No match)
391 - 407	2067.0410	2066.0337	2066.0506	-8	0	K.YGLEDYRPVQLLENMVK.E (No match)
391 - 407	2067.0410	2066.0337	2066.0506	-8	0	K.YGLEDYRPVQLLENMVK.E (Ions score 50)
391 - 407	2083.0828	2082.0755	2082.0455	14	0	K.YGLEDYRPVQLLENMVK.E Oxidation (M) (No match)
391 - 410	2381.2063	2380.1990	2380.2096	-4	1	K.YGLEDYRPVQLLENMVKEGK.C (No match)
418 - 435	2162.0142	2161.0069	2161.0215	-7	1	K.GFYEYEVSEEDLGEIKVR.R (No match)
436 - 449	1694.9591	1693.9518	1693.9627	-6	1	R.REGALWIILNRPK.Q (No match)
436 - 449	1694.9591	1693.9518	1693.9627	-6	1	R.REGALWIILNRPK.Q (Ions score 58)
437 - 449	1538.8610	1537.8537	1537.8616	-5	0	R.EGEALWIILNRPK.Q (Ions score 89)
437 - 449	1538.8610	1537.8537	1537.8616	-5	0	R.EGEALWIILNRPK.Q (No match)
437 - 451	1823.0071	1821.9998	1822.0213	-12	1	R.EGEALWIILNRPKQR.N (No match)
548 - 573	2610.2861	2609.2788	2609.3119	-13	0	R.LATEDSLLGQPEINVGIMPGGGGTQR.L (No match)
548 - 573	2610.2861	2609.2789	2609.3119	-13	0	R.LATEDSLLGQPEINVGIMPGGGGTQR.L (Ions score 184)
548 - 573	2626.2810	2625.2737	2625.3068	-13	0	R.LATEDSLLGQPEINVGIMPGGGGTQR.L Oxidation (M) (No match)
548 - 576	2976.5154	2975.5081	2975.5498	-14	1	R.LATEDSLLGQPEINVGIMPGGGGTQRLPR.L (Ions score 132)
548 - 576	2976.5154	2975.5081	2975.5498	-14	1	R.LATEDSLLGQPEINVGIMPGGGGTQRLPR.L (No match)
548 - 576	2992.5146	2991.5073	2991.5448	-13	1	R.LATEDSLLGQPEINVGIMPGGGGTQRLPR.L Oxidation (M) (No match)
641 - 660	2188.0740	2187.0667	2187.0881	-10	0	R.VAQEVPLIDGLEMEAEAFAR.A (Ions score 130)
641 - 660	2188.0740	2187.0667	2187.0881	-10	0	R.VAQEVPLIDGLEMEAEAFAR.A (No match)
641 - 660	2204.0703	2203.0630	2203.0831	-9	0	R.VAQEVPLIDGLEMEAEAFAR.A Oxidation (M) (No match)
669 - 678	1133.6278	1132.6205	1132.6240	-3	1	K.EGIAAFLEKR.K (No match)



LOCUS YP_001435643 683 aa linear BCT 22-DEC-2012
 DEFINITION 3-hydroxyacyl-CoA dehydrogenase [Ignicoccus hospitalis KIN4/I].
 ACCESSION YP_001435643
 VERSION YP_001435643.1 GI:156937847
 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 683)
 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 683)
 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 683)
 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 ABU82236.
 Method: conceptual translation.
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Mascot: <http://www.matrixscience.com/>