

Mascot Search Results

Protein View

Match to: **gi|156938050** Score: **877** Expect: **7e-083**
malate dehydrogenase (NAD) [*Ignicoccus hospitalis* KIN4/I]

Nominal mass (M_r): **33620**; Calculated pI value: **6.88**
 NCBI BLAST search of [gi|156938050](#) 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|156567034](#) from [Ignicoccus hospitalis KIN4/I](#)

Variable modifications: Oxidation (M), Propionamide (C)
 Semi-specific cleavage, (peptide can be non-specific at one terminus only)
 Cleavage by semiTrypsin: cuts C-term side of KR unless next residue is P
 Sequence Coverage: **79%**

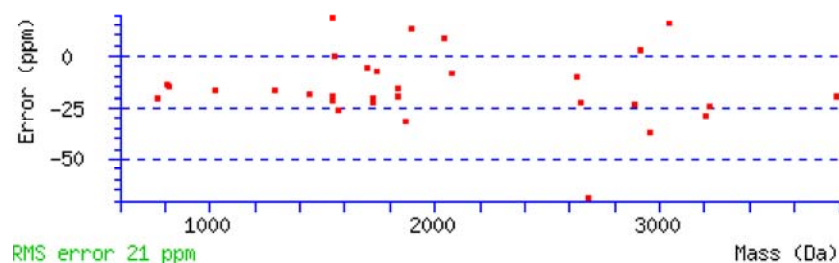
Matched peptides shown in **Bold Red**

1 MARVPYKVAV IGTGR**VGATF** AYTMAIVPGV ARMVLVD**AVP** GLSKGV**MEDI**
 51 **KHAAAVFR**S IQVEAYDDVS KVENADAIVI TAGKPRKADM SRRDLAK**VNA**
 101 **QIIRDIGDKL** RDRNPGAFYM VITNPVDVMT MILSDVIGNK GTVIGTGTSL
 151 **DTYRFR**SAVS ELLNEPIAAI DGYVVGEGHE EAFVAWSTVT VKGVPIDEYI
 201 **KEKGLD**LSRS RIEEYVKEVA ATIIAQGAT IWGPAATFQE IVVSHLANEG
 251 **RIIPVSVVQE** VPGVGRVAVS VPTKISGR**LV** PLPQLLNEEE RERLKRAAEA
 301 IKRVYEEAVS S

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

Start	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
16	32	1723.8816	1722.8743	1722.9127	-22	0	R.VGATFAYTMAIVPGVAR.M (Ions score 86)
16	32	1723.8816	1722.8743	1722.9127	-22	0	R.VGATFAYTMAIVPGVAR.M (No match)
30	44	1570.8583	1569.8510	1569.8913	-26	1	G.VARMVLVDVPGLSK.G Oxidation (M) (No match)
33	50	1872.9216	1871.9143	1871.9737	-32	1	R.MVLVDVPGLSKGV MEDI .K (No match)
45	58	1543.7728	1542.7655	1542.7977	-21	1	K.GVMEDIKHAAAVFR.R (No match)
52	58	771.4102	770.4029	770.4187	-21	0	K.HAAAVFR.R (No match)
60	86	2888.4336	2887.4263	2887.4927	-23	1	R.SIQVEAYDDVSKVENADAIVITAGKPR.K (Ions score 240)

60 - 86	2888.4336	2887.4263	2887.4927	-23	1	R.SIQVEAYDDVSKVENADAIVITAGKPR.K	(No match)
72 - 86	1553.8645	1552.8572	1552.8573	-0	0	K.VENADAIVITAGKPR.K	(No match)
98 - 104	813.4826	812.4753	812.4868	-14	0	K.VNAQIIR.D	(No match)
98 - 104	813.4826	812.4753	812.4868	-14	0	K.VNAQIIR.D	(Ions score 33)
105 - 111	816.4451	815.4378	815.4501	-15	1	R.DIGDKLR.D	(No match)
112 - 129	2038.9890	2037.9817	2037.9652	8	1	R.DRNPAGAFYMVITNPVDVM.T	(No match)
112 - 140	3210.5083	3209.5010	3209.5923	-28	1	R.DRNPAGAFYMVITNPVDVMTMILSDVIGNK.G	(No match)
112 - 140	3226.5176	3225.5103	3225.5872	-24	1	R.DRNPAGAFYMVITNPVDVMTMILSDVIGNK.G	Oxidation (M) (No match)
114 - 130	1900.9075	1899.9002	1899.8747	13	0	R.NPGAFYMVITNPVDVMT.M	2 Oxidation (M) (No match)
114 - 141	3044.5261	3043.5188	3043.4705	16	1	R.NPGAFYMVITNPVDVMTMILSDVIGNKG.T	3 Oxidation (M) (No match)
114 - 141	3044.5261	3043.5188	3043.4705	16	1	R.NPGAFYMVITNPVDVMTMILSDVIGNKG.T	3 Oxidation (M) (No match)
138 - 154	1739.8796	1738.8723	1738.8850	-7	1	I.GNKGTVIGTGTSLDTYR.F	(No match)
141 - 154	1440.7063	1439.6990	1439.7256	-18	0	K.GTVIGTGTSLDTYR.F	(No match)
141 - 154	1440.7063	1439.6990	1439.7256	-18	0	K.GTVIGTGTSLDTYR.F	(Ions score 100)
157 - 184	2915.4397	2914.4324	2914.4236	3	0	R.SAVSELLNEPIAAIDGYVVGEGEEAFV.A	(No match)
157 - 192	3787.8335	3786.8262	3786.8992	-19	0	R.SAVSELLNEPIAAIDGYVVGEGEEAFVAVSTVTK.G	(No match)
157 - 192	3787.8335	3786.8262	3786.8992	-19	0	R.SAVSELLNEPIAAIDGYVVGEGEEAFVAVSTVTK.G	(Ions score 38)
168 - 192	2635.2783	2634.2710	2634.2966	-10	0	I.AAIDGYVVGEGEEAFVAVSTVTK.G	(No match)
175 - 201	2960.3953	2959.3880	2959.4967	-37	1	V.VGEGEEAFVAVSTVTKGVPIDEYIK.E	(No match)
186 - 201	1834.9662	1833.9589	1833.9877	-16	1	A.WSTVTVKGVPIDEYIK.E	(No match)
193 - 203	1290.6721	1289.6648	1289.6867	-17	1	K.GVPIDEYIKEK.G	(No match)
210 - 217	1023.5303	1022.5230	1022.5396	-16	1	R.SRIEEYVK.E	(Ions score 34)
210 - 217	1023.5303	1022.5230	1022.5396	-16	1	R.SRIEEYVK.E	(No match)
212 - 225	1548.8805	1547.8732	1547.8446	18	1	R.IEEYVKEVAATIIA.K	(No match)
218 - 243	2684.2817	2683.2744	2683.4585	-69	1	K.EVAATIIAKQGATIWGPAATFQEIVV.S	(No match)
227 - 251	2652.2944	2651.2871	2651.3456	-22	0	K.QGATIWGPAATFQEIVVSHLANEGR.I	(No match)
227 - 251	2652.2944	2651.2872	2651.3456	-22	0	K.QGATIWGPAATFQEIVVSHLANEGR.I	(Ions score 178)
237 - 251	1699.8665	1698.8592	1698.8689	-6	0	A.TFQEIVVSHLANEGR.I	(No match)
247 - 266	2076.1382	2075.1309	2075.1487	-9	1	L.ANEGRIIPVSVVQEVPGVGR.V	(No match)
252 - 266	1548.8805	1547.8732	1547.9035	-20	0	R.IIPVSVVQEVPGVGR.V	(Ions score 89)
279 - 293	1834.9662	1833.9589	1833.9948	-20	1	R.LVPLPQLLNEEERER.L	(Ions score 82)
280 - 293	1721.8837	1720.8764	1720.9108	-20	1	L.VPLPQLLNEEERER.L	(No match)



LOCUS YP_001435846 311 aa linear CON 10-JUN-2013
DEFINITION malate dehydrogenase (NAD) [Ignicoccus hospitalis KIN4/I].
ACCESSION YP_001435846
VERSION YP_001435846.1 GI:156938050
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 311)
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 311)
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 311)
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 ABU82439.
Method: conceptual translation.
FEATURES Location/Qualifiers
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	/db_xref="CDD:247749"
Region	10..278
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	/note="L-lactate dehydrogenase; TIGR01771"
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	/db_xref="InterPro:IPR001557"
	/db_xref="InterPro:IPR001854"
	/db_xref="GeneID:5563182"
CONTIG	join(WP_012123403.1:1..311)

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