

Mascot Search Results

Protein View

Match to: **gi|156936927** Score: **698** Expect: **5.5e-065**
alcohol dehydrogenase [Ignicoccus hospitalis KIN4/I]

Nominal mass (M_r): **45011**; Calculated pI value: **6.13**
 NCBI BLAST search of [gi|156936927](#) 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|156565911](#) 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: **78%**

Matched peptides shown in **Bold Red**

1 MYNPFGDYVW EFRSPRSK**FG PGALNELKVD LERLRVEKPF LITTK**GWVKR
 51 GIVDRL**REIL GKDPYWDGV EPEPSAESVE EAAKALAESG ADSVIAIGGG**
 101 **SALDTAKIAN LLATYGGRVR DYVAPPYGEG KPVPGPVKPM VAVPTTAGTG**
 151 **SEVTSVAVVT LKDVGVKVGI SSDFLRPSLA LLDPELTMTV PPKVTADTGM**
 201 **DALTHAVESY IAKPYWARER PEDPAKRPVY VGSFTVTDAL AERAIELIGK**
 251 YLRRAVYQGR **TDLEARSGML IASYLAGLAF GNAGVGLAHA ASYPLGGRYK**
 301 **VTHGEAVGIL LPAVLEFNAP ANYEAKRVG ELLTGEKCPE RDPAKCAEWA**
 351 ANAIRELQRD IK**FTPGLEAV GVKEEDLMEM AKETLNQKRL LATNPRPVTE**
 401 **EDVYWYKRS** MRNY

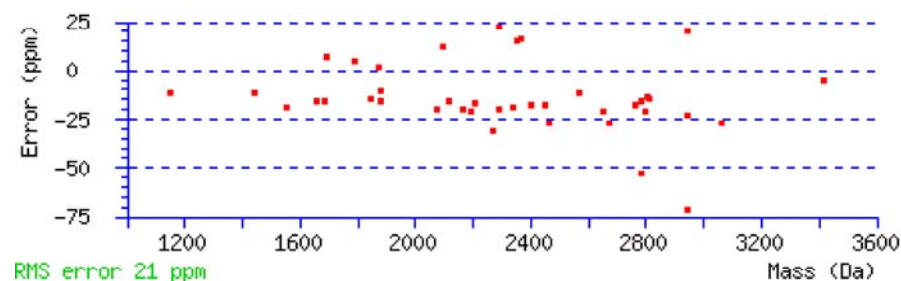
Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
19 - 33	1657.8643	1656.8570	1656.8835	-16	1	K.FGPGALNELKVDLER.L	(Ions score 132)
19 - 33	1657.8643	1656.8570	1656.8835	-16	1	K.FGPGALNELKVDLER.L	(No match)
34 - 45	1444.8713	1443.8640	1443.8813	-12	1	R.LRVEKPFLITTK.G	(No match)
34 - 45	1444.8713	1443.8641	1443.8813	-12	1	R.LRVEKPFLITTK.G	(Ions score 42)

58 - 84	2944.4697	2943.4624	2943.4025	20	1	R.EILGKDPVYWDGVEPEPSAESVEEAAK.A	(No match)
63 - 84	2404.0398	2403.0325	2403.0754	-18	0	K.DVPYWDGVEPEPSAESVEEAAK.A	(No match)
64 - 84	2289.1067	2288.0994	2288.0484	22	0	D.VPYWDGVEPEPSAESVEEAAK.A	(No match)
83 - 107	2273.1277	2272.1204	2272.1910	-31	1	A.AKALAESGADSVIAIGGGSALDTAK.I	(No match)
85 - 107	2074.0259	2073.0186	2073.0590	-19	0	K.ALAESGADSVIAIGGGSALDTAK.I	(No match)
108 - 118	1148.6287	1147.6214	1147.6349	-12	0	K.IANLLATYGGR.V	(Ions score 100)
108 - 118	1148.6287	1147.6214	1147.6349	-12	0	K.IANLLATYGGR.V	(No match)
121 - 140	2114.0295	2113.0222	2113.0554	-16	0	R.DYVAPPYGEKPGVPKPM.V	Oxidation (M) (No match)
121 - 144	2464.2266	2463.2193	2463.2872	-28	0	R.DYVAPPYGEKPGVPKPMVAVP.T	(No match)
138 - 167	2941.4177	2940.4104	2940.6206	-71	1	V.KPMVAVPTTAGTGSEVTSVAVVTLKDVGVK.V	(No match)
168 - 193	2796.4646	2795.4573	2795.5143	-20	0	K.VGISSDFLRPSLALLDPELTMTVPPK.V	(No match)
168 - 193	2812.4741	2811.4668	2811.5092	-15	0	K.VGISSDFLRPSLALLDPELTMTVPPK.V	Oxidation (M) (No match)
188 - 218	3419.6938	3418.6865	3418.7054	-6	1	T.MTVPPKVTADTGMDALTHAVESYIAKPYWAR.E	(No match)
188 - 218	3419.6939	3418.6866	3418.7054	-5	1	T.MTVPPKVTADTGMDALTHAVESYIAKPYWAR.E	(No match)
194 - 213	2093.0466	2092.0393	2092.0147	12	0	K.VTADTGMDALTHAVESYIAK.P	(No match)
194 - 215	2353.1733	2352.1660	2352.1308	15	0	K.VTADTGMDALTHAVESYIAKPY.W	(No match)
194 - 215	2369.1724	2368.1651	2368.1257	17	0	K.VTADTGMDALTHAVESYIAKPY.W	Oxidation (M) (No match)
194 - 218	2766.3052	2765.2979	2765.3483	-18	0	K.VTADTGMDALTHAVESYIAKPYWAR.E	(Ions score 162)
194 - 218	2766.3052	2765.2979	2765.3483	-18	0	K.VTADTGMDALTHAVESYIAKPYWAR.E	(No match)
194 - 218	2782.3069	2781.2996	2781.3432	-16	0	K.VTADTGMDALTHAVESYIAKPYWAR.E	Oxidation (M) (No match)
196 - 218	2566.2097	2565.2024	2565.2322	-12	0	T.ADTGMDALTHAVESYIAKPYWAR.E	(No match)
206 - 218	1553.7811	1552.7738	1552.8038	-19	0	H.AVESYIAKPYWAR.E	(No match)
219 - 234	1846.9167	1845.9094	1845.9373	-15	1	R.ERPEDPAKRPVYVGSF.T	(No match)
219 - 243	2803.3994	2802.3921	2802.4300	-14	1	R.ERPEDPAKRPVYVGSFTVTDALAER.A	(No match)
220 - 243	2674.3237	2673.3164	2673.3875	-27	1	E.RPEDPAKRPVYVGSFTVTDALAER.A	(No match)
227 - 243	1880.9579	1879.9506	1879.9792	-15	0	K.RPVYVGSFTVTDALAER.A	(Ions score 117)
261 - 278	1880.9579	1879.9506	1879.9713	-11	1	R.TDLEARSGMLIASYLAGL.A	(No match)
267 - 298	3062.5066	3061.4993	3061.5807	-27	0	R.SGMLIASYLAGLAFGNAGVGLAHAASYPLGGR.Y	(No match)
270 - 298	2787.3469	2786.3396	2786.4868	-53	0	M.LIASYLAGLAFGNAGVGLAHAASYPLGGR.Y	(No match)
299 - 325	2943.4929	2942.4856	2942.5542	-23	1	R.YKVTHGEAVGILLPAVLEFNAPANYEK.A	(No match)
301 - 325	2652.3484	2651.3411	2651.3959	-21	0	K.VTHGEAVGILLPAVLEFNAPANYEK.A	(No match)
363 - 382	2194.0305	2193.0232	2193.0697	-21	1	K.FTPGLEAVGVKEEDLMEK.E	(No match)
363 - 382	2210.0349	2209.0276	2209.0646	-17	1	K.FTPGLEAVGVKEEDLMEK.E	Oxidation (M) (No match)
367 - 382	1791.8947	1790.8874	1790.8794	4	1	G.LEAVGVKEEDLMEK.E	(No match)
375 - 388	1695.8053	1694.7980	1694.7855	7	1	E.EDLMEK.ETLNQK.R	Oxidation (M) (No match)
389 - 404	1872.9850	1871.9777	1871.9741	2	1	K.RLLATNPRPVTEEDVY.W	(No match)
390 - 407	2165.0474	2164.0401	2164.0841	-20	0	R.LLATNPRPVTEEDVYWVY.K	(Ions score 22)
390 - 407	2165.0474	2164.0401	2164.0841	-20	0	R.LLATNPRPVTEEDVYWVY.K	(No match)
390 - 408	2293.1418	2292.1345	2292.1790	-19	0	R.LLATNPRPVTEEDVYWVYK.R	(No match)
390 - 408	2293.1419	2292.1346	2292.1790	-19	0	R.LLATNPRPVTEEDVYWVYK.R	(Ions score 56)
390 - 409	2449.2444	2448.2371	2448.2801	-18	1	R.LLATNPRPVTEEDVYWVYKR.S	(Ions score 69)
390 - 409	2449.2444	2448.2371	2448.2801	-18	1	R.LLATNPRPVTEEDVYWVYKR.S	(No match)
391 - 409	2336.1599	2335.1526	2335.1961	-19	1	L.LATNPRPVTEEDVYWVYKR.S	(No match)

397 - 409 1683.8119 1682.8046 1682.8304 -15 1 R.PVTEEDVYWVYKR.S ([No match](#))



LOCUS YP_001434723 414 aa linear CON 10-JUN-2013
 DEFINITION alcohol dehydrogenase [Ignicoccus hospitalis KIN4/I].
 ACCESSION YP_001434723
 VERSION YP_001434723.1 GI:156936927
 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 414)
 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 414)
 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 414)

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 ABU81316. Method: conceptual translation.

FEATURES

Location/Qualifiers

source 1..414

/organism="Ignicoccus hospitalis KIN4/I"

/strain="KIN4/I"

/db_xref="taxon:453591"

Protein 1..414

/product="alcohol dehydrogenase"

/calculated_mol_wt=44909

Region 10..411

/region_name="EutG"

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Region 15..411

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CDS 1..414

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      /db_xref="GeneID:5562575"  
CONTIG      join(WP_011998168.1:1..414)
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Mascot: <http://www.matrixscience.com/>