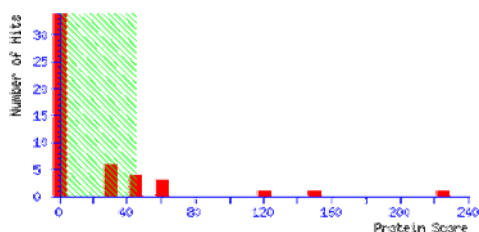


Mascot Search Results

User : Hasan
Email : hmuhammed@irb.hr
Search title : L-162_08122017
MS data file : DATA.TXT
Database : SwissProt 56.0 (547357 sequences; 194874700 residues)
Timestamp : 8 Dec 2017 at 10:16:35 GMT
Protein hits : [HBB1_DANRE](#) Hemoglobin subunit beta-1 OS=Danio rerio GN=ba1 PE=1 SV=3
[HBB_CARAU](#) Hemoglobin subunit beta OS=Carassius auratus GN=hbb PE=1 SV=1
[HBB2_ARCGL](#) Hemoglobin subunit beta-2 OS=Arctogadus glacialis GN=hbb2 PE=1 SV=2
[RNH_SYNAS](#) Ribonuclease H OS=Syntrophus aciditrophicus (strain SB) GN=rnhA PE=3 SV=1
[HXA2_BOVIN](#) Homeobox protein Hox-A2 OS=Bos taurus GN=HOXA2 PE=2 SV=1
[PGK_HELPJ](#) Phosphoglycerate kinase OS=Helicobacter pylori (strain J99 / ATCC 700824) GN=pgk PE=3 SV=1
[5HT2A_DROME](#) 5-hydroxytryptamine receptor 2A OS=Drosophila melanogaster GN=5-HT1A PE=2 SV=2
[SECA_CLOTE](#) Protein translocase subunit SecA OS=Clostridium tetani (strain Massachusetts / E88) GN=secA PE=3 SV=2
[DNAG_METBF](#) DNA primase DnaG OS=Methanosarcina barkeri (strain Fusaro / DSM 804) GN=dnaG PE=3 SV=1
[Y1127_ANASK](#) UPF0173 metal-dependent hydrolase AnaeK_1127 OS=Anaeromyxobacter sp. (strain K) GN=AnaeK_1127 PE=3 SV=1
[GCSFA_FLAPR](#) Glycine dehydrogenase (decarboxylating) A, mitochondrial OS=Flaveria pringlei GN=GDCSPA PE=2 SV=1
[B3G2P_DROME](#) Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase P OS=Drosophila melanogaster GN=GlcAT-P PE=2 SV=1
[SYR_DESVH](#) Arginine--tRNA ligase OS=Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303) GN=argS PE=3 SV=1
[TBX39_CAEEL](#) Putative T-box protein 39 OS=Caenorhabditis elegans GN=tbx-39 PE=1 SV=1
[RS11_METST](#) 30S ribosomal protein S11 OS=Methanospaera stadtmanae (strain ATCC 43021 / DSM 3091 / JCM 11832 / MCB-3) GN=r
[SDHD_BURTA](#) Probable D-serine dehydratase OS=Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 10630

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 45 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold $p < 0.05$ Max. number of hits AUTO

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off 0 Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☒

☐ Select All Select None Search Selected ☐ Error tolerant Archive Report

1. [HBB1_DANRE](#) Mass: 16606 Score: 225 Matches: 8(5) Sequences: 4(3) emPAI: 0.74
Hemoglobin subunit beta-1 OS=Danio rerio GN=ba1 PE=1 SV=3
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☒ 185	479.6700	957.3254	957.5647	-0.2393	0	65	0.00064	1	U	R.TAILGLWGK.L
☒ 291	668.2100	1334.4054	1334.6805	-0.2751	0	(34)	0.73	4		R.CLIVYPWTQR.Y
☒ 292	668.2300	1334.4454	1334.6805	-0.2351	0	44	0.065	1		R.CLIVYPWTQR.Y
☒ 358	713.2300	1424.4454	1424.7623	-0.3169	0	(69)	0.00022	1	U	K.LNIDEIGPQALSR.C
☒ 359	713.2300	1424.4454	1424.7623	-0.3169	0	95	4.9e-007	1	U	K.LNIDEIGPQALSR.C
☒ 360	713.2300	1424.4454	1424.7623	-0.3169	0	(79)	3.2e-005	1	U	K.LNIDEIGPQALSR.C
☒ 361	713.2800	1424.5454	1424.7623	-0.2169	0	(48)	0.055	1	U	K.LNIDEIGPQALSR.C
☒ 383	733.2100	1464.4054	1464.7139	-0.3084	0	90	1.4e-006	1		R.LLADCITVCAAMK.F

Proteins matching the same set of peptides:

[HBB2_DANRE](#) Mass: 16606 Score: 225 Matches: 8(5) Sequences: 4(3)
Hemoglobin subunit beta-2 OS=Danio rerio GN=ba2 PE=1 SV=3

2. [HBB_CARAU](#) Mass: 16427 Score: 156 Matches: 4(2) Sequences: 3(2) emPAI: 0.45
Hemoglobin subunit beta OS=Carassius auratus GN=hbb PE=1 SV=1
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
291	668.2100	1334.4054	1334.6805	-0.2751	0	(34)	0.73	4		R.CLIVYPWTQR.Y
292	668.2300	1334.4454	1334.6805	-0.2351	0	44	0.065	1		R.CLIVYPWTQR.Y
383	733.2100	1464.4054	1464.7139	-0.3084	0	90	1.4e-006	1		R.LLADCITVCAAMK.F

☒ [550](#) 890.7200 1779.4254 1779.8217 -0.3962 0 106 5.4e-009 1 U K.FGPSGFNADVQEAQK.F

3. [HBB2_ARCGL](#) Mass: 16652 Score: 122 Matches: 4(2) Sequences: 2(1) emPAI: 0.20

Hemoglobin subunit beta-2 OS=Arctogadus glacialis GN=hbb2 PE=1 SV=2

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☒ 226	574.2200	1146.4254	1146.6761	-0.2507	0	(81)	1.8e-005	1	U	K.FLSVVVSALGR.Q
☒ 227	574.2400	1146.4654	1146.6761	-0.2107	0	87	4e-006	1	U	K.FLSVVVSALGR.Q
291	668.2100	1334.4054	1334.6805	-0.2751	0	(34)	0.73	4		R.CLIVYPWTQR.Y
292	668.2300	1334.4454	1334.6805	-0.2351	0	44	0.065	1		R.CLIVYPWTQR.Y

Proteins matching the same set of peptides:

[HBB2_BORSA](#) Mass: 16787 Score: 122 Matches: 4(2) Sequences: 2(1)

Hemoglobin subunit beta-2 OS=Boreogadus saida GN=hbb2 PE=1 SV=3

[HBB2_GADMO](#) Mass: 16796 Score: 122 Matches: 4(2) Sequences: 2(1)

Hemoglobin subunit beta-2 OS=Gadus morhua GN=hbb2 PE=1 SV=2

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