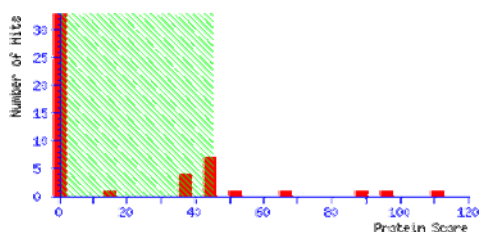


**Mascot Search Results**

User : Hasan  
 Email : hmuharem@irb.hr  
 Search title : G-162\_08122017  
 MS data file : DATA.TXT  
 Database : SwissProt 56.0 (547357 sequences; 194874700 residues)  
 Timestamp : 8 Dec 2017 at 12:04:55 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  
[HBA\\_CYPCA](#) Hemoglobin subunit alpha OS=Cyprinus carpio GN=hba PE=1 SV=3  
[CH602\\_POLNA](#) 60 kDa chaperonin 2 OS=Polaromonas naphthalenivorans (strain CJ2) GN=groL2 PE=3 SV=1  
[CJ055\\_HUMAN](#) Uncharacterized protein C10orf55 OS=Homo sapiens GN=C10orf55 PE=2 SV=1  
[RIR1\\_DICDI](#) Ribonucleoside-diphosphate reductase large subunit OS=Dictyostelium discoideum GN=rnrA PE=3 SV=1  
[EPCAM\\_BOVIN](#) Epithelial cell adhesion molecule OS=Bos taurus GN=EPCAM PE=2 SV=1  
[PPA\\_ASPFI](#) Acid phosphatase OS=Aspergillus ficuum GN=aphA PE=1 SV=1  
[ZDHC6\\_MOUSE](#) Palmitoyltransferase ZDHC6 OS=Mus musculus GN=Zdhhc6 PE=2 SV=1  
[ATKC RHOPA](#) Potassium-transporting ATPase C chain OS=Rhodospseudomonas palustris (strain ATCC BAA-98 / CGA009) GN=kdpC PE=3  
[NOP9\\_YARLI](#) Nucleolar protein 9 OS=Yarrowia lipolytica (strain CLIB 122 / E 150) GN=NOP9 PE=3 SV=1  
[MURC\\_SALAI](#) UDP-N-acetylmuramate--L-alanine ligase OS=Salinispora arenicola (strain CNS-205) GN=murC PE=3 SV=1  
[MIPA\\_ECOLI](#) MltA-interacting protein OS=Escherichia coli (strain K12) GN=mipA PE=1 SV=1  
[PYRH\\_SULNB](#) Uridylate kinase OS=Sulfurovum sp. (strain NBC37-1) GN=pyrH PE=3 SV=1  
[UL25\\_HHV11](#) Virion-packaging protein UL25 OS=Human herpesvirus 1 (strain 17) GN=UL25 PE=1 SV=1  
[PURT\\_LEPCP](#) Phosphoribosylglycinamide formyltransferase 2 OS=Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) GN

**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  [Help](#)

Significance threshold p<  Max. number of hits

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

Show pop-ups  Suppress pop-ups  Sort unassigned  Require bold red

Error tolerant

1. [HBB1\\_DANRE](#) Mass: 16606 Score: 111 Matches: 4(2) Sequences: 3(2) emPAI: 0.45  
 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
<input checked="" type="checkbox"/> <a href="#">193</a>	479.6500	957.2854	957.5647	-0.2793	0	62	0.0015	1	U	R.TAILGLWGK.L
<input type="checkbox"/> <a href="#">310</a>	668.2200	1334.4254	1334.6805	-0.2551	0	29	2.4	8		R.CLIVYPWTQR.Y
<input checked="" type="checkbox"/> <a href="#">357</a>	713.2400	1424.4654	1424.7623	-0.2969	0	95	5.7e-007	1	U	K.LNIDEIGPQALS.R.C
<input type="checkbox"/> <a href="#">359</a>	713.7700	1425.5254	1424.7623	0.7631	0	(30)	1.6	2	U	K.LNIDEIGPQALS.R.C

**Proteins matching the same set of peptides:**

[HBB2\\_DANRE](#) Mass: 16606 Score: 111 Matches: 4(2) Sequences: 3(2)  
 Hemoglobin subunit beta-2 OS=Danio rerio GN=ba2 PE=1 SV=3

2. [HBB\\_CARAU](#) Mass: 16427 Score: 96 Matches: 3(1) Sequences: 2(1) emPAI: 0.21  
 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
<input type="checkbox"/> <a href="#">310</a>	668.2200	1334.4254	1334.6805	-0.2551	0	29	2.4	8		R.CLIVYPWTQR.Y
<input checked="" type="checkbox"/> <a href="#">626</a>	890.7200	1779.4254	1779.8217	-0.3962	0	96	5.5e-008	1	U	K.FGPSGFNADVQEAQK.F
<input checked="" type="checkbox"/> <a href="#">250</a>	594.1600	1779.4582	1779.8217	-0.3635	0	(43)	0.13	1	U	K.FGPSGFNADVQEAQK.F

3. [HBB2\\_ARCGL](#) Mass: 16652 Score: 85 Matches: 2(1) 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
<input checked="" type="checkbox"/> <a href="#">243</a>	<b>574.2100</b>	<b>1146.4054</b>	<b>1146.6761</b>	<b>-0.2707</b>	<b>0</b>	<b>85</b>	<b>5.9e-006</b>	<b>1</b>	<b>U</b>	<b>K.FLSVVVSALGR.Q</b>
<a href="#">310</a>	668.2200	1334.4254	1334.6805	-0.2551	0	29	2.4	8		R.CLIVYPWTQR.Y

**Proteins matching the same set of peptides:**

[HBB2\\_BORSA](#) Mass: 16787 Score: 85 Matches: 2(1) Sequences: 2(1)

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

[HBB2\\_GADMO](#) Mass: 16796 Score: 85 Matches: 2(1) Sequences: 2(1)

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

4. [HBA\\_CYPCA](#) Mass: 15437 Score: 69 Matches: 4(2) Sequences: 2(1) emPAI: 0.49

Hemoglobin subunit alpha OS=Cyprinus carpio GN=hba 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
<input checked="" type="checkbox"/> <a href="#">242</a>	<b>573.6400</b>	<b>1145.2654</b>	<b>1145.6115</b>	<b>-0.3460</b>	<b>0</b>	<b>19</b>	<b>22</b>	<b>1</b>	<b>U</b>	<b>K.VIMGAVGDAVSK.I</b>
<input checked="" type="checkbox"/> <a href="#">684</a>	<b>934.8200</b>	<b>1867.6254</b>	<b>1868.0043</b>	<b>-0.3789</b>	<b>0</b>	<b>63</b>	<b>0.0012</b>	<b>1</b>	<b>U</b>	<b>K.IDDLVGGLAALSELHAFK.L</b>
<input checked="" type="checkbox"/> <a href="#">685</a>	<b>467.9200</b>	<b>1867.6509</b>	<b>1868.0043</b>	<b>-0.3535</b>	<b>0</b>	<b>(39)</b>	<b>0.15</b>	<b>1</b>	<b>U</b>	<b>K.IDDLVGGLAALSELHAFK.L</b>
<a href="#">686</a>	623.5700	1867.6882	1868.0043	-0.3162	0	(48)	0.019	2	U	K.IDDLVGGLAALSELHAFK.L

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