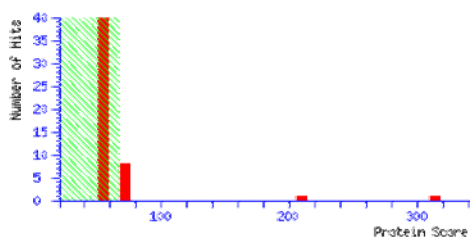


**Mascot Search Results**

User : Hasan  
 Email : hmuharem@irb.hr  
 Search title : Fe-161-G\_26102018  
 MS data file : DATA.TXT  
 Database 1 : NCBI nr 20150108 (54183042 sequences; 19531459180 residues)  
 Database 2 : SwissProtNew 1 (551705 sequences; 197114987 residues)  
 Timestamp : 31 Oct 2018 at 14:36:23 GMT  
 Protein hits : 2::HBB1\_DANRE Hemoglobin subunit beta-1 OS=Danio rerio GN=ba1 PE=1 SV=3  
               1::qi|516023988 hypothetical protein [Herbaspirillum rubrisubalbicans]  
               1::qi|448518684 hypothetical protein CORT\_0B08280 [Candida orthopsilosis Co 90-125]  
               1::qi|655034712 glutamate dehydrogenase [Omnitrophica bacterium SCGC AAA252-B19]  
               1::qi|672894577 hypothetical protein CG50\_10655 [Paenirhodobacter enshiensis]

**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 > 66 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. [2::HBB1\\_DANRE](#) Mass: 16606 Score: 313 Matches: 10(2) Sequences: 5(2) emPAI: 0.52  
 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="#">182</a>	479.6500	957.2854	957.5647	-0.2793	0	60	0.21	1	U	R.TAILGLWGK.L
<input type="checkbox"/> <a href="#">183</a>	479.6600	957.3054	957.5647	-0.2593	0	(53)	1.1	2	U	R.TAILGLWGK.L
<input type="checkbox"/> <a href="#">299</a>	668.2100	1334.4054	1334.6805	-0.2751	0	(47)	3.4	8		R.CLIVYPWTQR.Y
<input type="checkbox"/> <a href="#">301</a>	668.7000	1335.3854	1334.6805	0.7049	0	48	2.5	6		R.CLIVYPWTQR.Y
<input checked="" type="checkbox"/> <a href="#">407</a>	713.2600	1424.5054	1424.7623	-0.2569	0	(48)	2.2	1	U	K.LNIDEIGPQALSR.C
<input checked="" type="checkbox"/> <a href="#">408</a>	713.2700	1424.5254	1424.7623	-0.2369	0	65	0.098	1	U	K.LNIDEIGPQALSR.C
<input checked="" type="checkbox"/> <a href="#">453</a>	733.2300	1464.4454	1464.7139	-0.2684	0	(50)	1.5	1		R.LLADCITVCAAMK.F
<input checked="" type="checkbox"/> <a href="#">454</a>	733.2700	1464.5254	1464.7139	-0.1884	0	72	0.0095	1		R.LLADCITVCAAMK.F
<input checked="" type="checkbox"/> <a href="#">457</a>	733.7800	1465.5454	1464.7139	0.8316	0	(50)	1.4	1		R.LLADCITVCAAMK.F
<input checked="" type="checkbox"/> <a href="#">942</a>	788.9900	2363.9482	2364.3165	-0.3683	1	68	0.014	1	U	R.TAILGLWGKLNIDEIGPQALSR.C

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

[2::HBB2\\_DANRE](#) Mass: 16606 Score: 313 Matches: 10(2) Sequences: 5(2)  
 Hemoglobin subunit beta-2 OS=Danio rerio GN=ba2 PE=1 SV=3  
[1::qi|18858329](#) Mass: 16606 Score: 313 Matches: 10(2) Sequences: 5(2)  
 hemoglobin subunit beta-1 [Danio rerio]  
[1::qi|53749219](#) Mass: 16606 Score: 313 Matches: 10(2) Sequences: 5(2)  
 hemoglobin subunit beta-2 [Danio rerio]  
[1::qi|226358543](#) Mass: 16516 Score: 313 Matches: 10(2) Sequences: 5(2)  
 ba1 globin [Hypophthalmichthys nobilis]  
[1::qi|22135546](#) Mass: 16443 Score: 309 Matches: 10(2) Sequences: 5(2)  
 beta globin [Ctenopharyngodon idella]