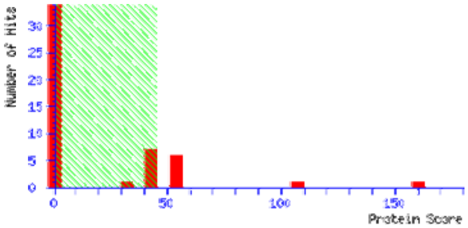
Mascot Search Results

User : Hasan
Email : hmuharem@irb.hr
Search title : L-165_08122017
MS data file : DATA.TXT
Database : SwissProt 56.0 (547357 sequences; 194874700 residues)
Timestamp : 8 Dec 2017 at 11:08:08 GMT
Protein hits :

HBB1_DANRE	Hemoglobin subunit beta-1 OS=Danio rerio GN=ba1 PE=1 SV=3
HBB2_ARCGL	Hemoglobin subunit beta-2 OS=Arctogadus glacialis GN=hbb2 PE=1 SV=2
HXA2_BOVIN	Homeobox protein Hox-A2 OS=Bos taurus GN=HOXA2 PE=2 SV=1
FHUD_BACSU	Iron(3+)-hydroxamate-binding protein FhuD OS=Bacillus subtilis (strain 168) GN=fhuD PE=1 SV=1
RS20_BIFAA	30S ribosomal protein S20 OS=Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a)
HBA_CYPCA	Hemoglobin subunit alpha OS=Cyprinus carpio GN=hba PE=1 SV=3
ACKA_CAMJ8	Acetate kinase OS=Campylobacter jejuni subsp. jejuni serotype O:6 (strain 81116 / NCTC 11828) GN=ackA PE=3 SV=
MKS3_MOUSE	Meckelin OS=Mus musculus GN=Tmem67 PE=1 SV=2
SOCS1_HUMAN	Suppressor of cytokine signaling 1 OS=Homo sapiens GN=SOCS1 PE=1 SV=1
NM111_ASPCL	Pro-apoptotic serine protease nma111 OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3
TADA3_MOUSE	Transcriptional adapter 3 OS=Mus musculus GN=Tada3 PE=1 SV=1
CH60_COXB1	60 kDa chaperonin OS=Coxiella burnetii (strain CbuK_Q154) GN=groL PE=3 SV=1
PYRD_RHOFT	Dihydroorotate dehydrogenase (quinone) OS=Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) GN
SYA_VIBPA	Alanine--tRNA ligase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=alaS PE=3 SV=1
UBP36_DROVI	Ubiquitin carboxyl-terminal hydrolase 36 OS=Drosophila virilis GN=Usp36 PE=3 SV=1
CSLF4_ORYSJ	Mixed-linked glucan synthase 4 OS=Oryza sativa subsp. japonica GN=CSLF4 PE=3 SV=1

Mascot Score Histogram

Ions score is -10*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

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 ☑

☐ **Error tolerant**

1. HBB1_DANRE **Mass:** 16606 **Score:** 160 **Matches:** 5(3) **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
☑	209	**479.6700**	**957.3254**	**957.5647**	**-0.2393**	**0**	**45**	**0.069**	**1**	**U**	**R.TAILGLWGK.L**
	210	**479.7000**	**957.3854**	**957.5647**	**-0.1793**	**0**	**(29)**	**2.8**	**6**	**U**	**R.TAILGLWGK.L**
☑	361	**668.2100**	**1334.4054**	**1334.6805**	**-0.2751**	**0**	**53**	**0.0082**	**1**		**R.CLIVYPWTQR.Y**
☑	427	**713.2300**	**1424.4454**	**1424.7623**	**-0.3169**	**0**	**100**	**1.5e-007**	**1**	**U**	**K.LNIDEIGPQALSR.C**
☑	453	**733.2000**	**1464.3854**	**1464.7139**	**-0.3284**	**0**	**95**	**4.3e-007**	**1**		**R.LLADCITVCAAMK.F**

Proteins matching the same set of peptides:
HBB2_DANRE **Mass:** 16606 **Score:** 160 **Matches:** 5(3) **Sequences:** 4(3)
Hemoglobin subunit beta-2 OS=Danio rerio GN=ba2 PE=1 SV=3

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2. HBB2_ARCGL **Mass:** 16652 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2) **emPAI:** 0.45
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
☑	269	**574.2300**	**1146.4454**	**1146.6761**	**-0.2307**	**0**	**98**	**3.5e-007**	**1**	**U**	**K.FLSVVVSALGR.Q**
	361	668.2100	1334.4054	1334.6805	-0.2751	0	53	0.0082	1		R.CLIVYPWTQR.Y

Proteins matching the same set of peptides:
HBB2_BORSA **Mass:** 16787 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)

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Hemoglobin subunit beta-2 OS=Boreogadus saida GN=hbb2 PE=1 SV=3
HBB2_GADMO    Mass: 16796    Score: 106    Matches: 2(2) Sequences: 2(2)
Hemoglobin subunit beta-2 OS=Gadus morhua GN=hbb2 PE=1 SV=2
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