



**Table ESM.2.** The overview of isoelectric points (pI) of cytosolic biomolecules discussed within this study.

	pI value	Species	Reference
Ferritin	5.2 – 6.8	Murrel ( <i>Channa punctatus</i> )	Geetha & Deshpande, 1999 [6]
	5.9 – 7.0	Rohu ( <i>Labeo rohita</i> )	Geetha & Deshpande, 1999 [6]
	4.7 – 6.3	Mackerel ( <i>Scomberomorus cummerson</i> )	Geetha & Deshpande, 1999 [6]
	5.4 – 6.4	Salmon ( <i>Scielutheronena tetradactylum</i> )	Geetha & Deshpande, 1999 [6]
	4.1 – 5.2	Perch ( <i>Lates calcarifer</i> )	Geetha & Deshpande, 1999 [6]
Haemoglobin	5.9 – 8.1	Five tilapiine species ( <i>Oreochromis andersonii</i> , <i>O. aureus</i> , <i>O. niloticus</i> , <i>Sarotherodon galilaeus</i> and <i>S. melanotheron</i> )	Falk et al., 1998 [26]
Fumarylacetoacetase	6.2	Medaka ( <i>Oryzias latipes</i> )	Malécot et al., 2009 [35]
Malate dehydrogenase	~7.0	generally expressed teleost MDH	Merrit & Quattro, 2003 [38]

# LC-MS/MS - MASCOT search results

Select Summary Report (../data/20230810/F002143.dat)

Page 1 of 2

## *(MATRIX)* Mascot Search Results *(SCIENCE)*

```

User           : Branka
Email          :
Search title   :
MS data file   : DATA.TXT
Database       : swissprot_uniprot1_sprot_15042019 (559634 sequences; 201129965 residues)
Timestamp      : 10 Aug 2023 at 11:35:20 GMT
Enzyme         : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values    : Monoisotopic
Protein Mass   : Unrestricted
Peptide Mass Tolerance : ± 0.5 Da (# 13C = 1)
Fragment Mass Tolerance : ± 0.5 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 1001
Protein hits   : HBB\_ONCNE Hemoglobin subunit beta OS=Oncorhynchus nerka OX=8023 GN=hbb PE=2 SV=3
                  RLMH\_RHOP5 Ribosomal RNA large subunit methyltransferase H OS=Rhodopseudomonas palustris (strain BisA53) OX=316055 GN=rlmH PE=3 SV=1
                  FAAA\_BOVIN Fumarylacetoacetase OS=Bos taurus OX=9913 GN=FAH PE=2 SV=1
                  RPOB\_RICAE DNA-directed RNA polymerase subunit beta OS=Rickettsia africae (strain ESF-5) OX=347255 GN=rpoB PE=3 SV=1
                  RPOB\_RICCK DNA-directed RNA polymerase subunit beta OS=Rickettsia canadensis (strain McKiel) OX=293613 GN=rpoB PE=3 SV=1
                  CSK12\_XENLA Caskin-2 OS=Xenopus laevis OX=8355 GN=caskin2 PE=2 SV=1
    
```

### Select 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  Require bold red

Re-Search  All queries  Unassigned  Below homology threshold  Below identity threshold

1.	<a href="#">HBB_ONCNE</a>	Mass: 16214	Score: 66	Matches: 6(1)	Sequences: 3(1)	emPAI: 0.21				
Hemoglobin subunit beta OS=Oncorhynchus nerka OX=8023 GN=hbb PE=2 SV=3										
Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">313</a>	566.7500	1131.4854	1130.6812	0.8043	0	13	95	5	U	K.FLAVVVSALGR.Q
<a href="#">586</a>	717.7200	1433.4254	1432.7418	0.6836	0	17	34	1	U	R.LLADCITVCVAAK.L <a href="#">585</a>
<a href="#">697</a>	868.5200	1735.0254	1734.8577	0.1678	0	57	0.0032	1	U	K.LGPAVFNADTQEAFAQ.F <a href="#">696</a>
<a href="#">698</a>	579.7100	1736.1082	1734.8577	1.2505	0	(8)	2.2e+002	5	U	K.LGPAVFNADTQEAFAQ.F
<hr/>										
2.	<a href="#">RLMH_RHOP5</a>	Mass: 17939	Score: 45	Matches: 7(0)	Sequences: 1(0)	emPAI: 0.19				
Ribosomal RNA large subunit methyltransferase H OS=Rhodopseudomonas palustris (strain BisA53) OX=316055 GN=rlmH PE=3 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">315</a>	566.7500	1131.4854	1130.6594	0.8261	1	45	0.072	1	U	-_MRLSVIAIGR.L <a href="#">313</a> <a href="#">314</a> <a href="#">316</a> <a href="#">317</a> <a href="#">318</a> <a href="#">319</a>
<hr/>										
3.	<a href="#">FAAA_BOVIN</a>	Mass: 46525	Score: 28	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.07				

Fumarylacetoacetase OS=Bos taurus OX=9913 GN=FAH PE=2 SV=1  
**Query** **Observed** **Mr(expt)** **Mr(calc)** **Delta** **Miss** **Score** **Expect** **Rank** **Unique** **Peptide**  
683 827.6400 1653.2654 1652.9713 0.2942 0 28 2.3 1 U R.IGVAIGDQILDLSVIK.H

**Proteins matching the same set of peptides:**  
FAAA\_MOUSE **Mass:** 46488 **Score:** 28 **Matches:** 1(0) **Sequences:** 1(0)  
 Fumarylacetoacetase OS=Mus musculus OX=10090 GN=Fah PE=1 SV=2  
FAAA\_RAT **Mass:** 46231 **Score:** 28 **Matches:** 1(0) **Sequences:** 1(0)  
 Fumarylacetoacetase OS=Rattus norvegicus OX=10116 GN=Fah PE=1 SV=1

4. RPOB\_RICAF **Mass:** 154788 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0) **emPAI:** 0.02  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia africae (strain ESF-5) OX=347255 GN=rpoB PE=3 SV=1  
**Query** **Observed** **Mr(expt)** **Mr(calc)** **Delta** **Miss** **Score** **Expect** **Rank** **Unique** **Peptide**  
51 600.9300 599.9227 600.3959 -0.4732 1 9 3.3e+002 1 K.LVKNK.G  
902 637.9800 2547.8909 2547.3101 0.5807 1 26 2.4 1 K.MNSRLELNISEEVTTLTIDDIK.N

**Proteins matching the same set of peptides:**  
RPOB\_RICCN **Mass:** 154687 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0)  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia conorii (strain ATCC VR-613 / Malish 7) OX=272944 GN=rpoB PE=3 SV=1  
RPOB\_RICFE **Mass:** 154692 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0)  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia felis (strain ATCC VR-1525 / URRWXCa12) OX=315456 GN=rpoB PE=3 SV=1  
RPOB\_RICMA **Mass:** 154696 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0)  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia massiliae OX=35791 GN=rpoB PE=3 SV=1  
RPOB\_RICPU **Mass:** 154719 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0)  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia peacockii (strain Rustic) OX=562019 GN=rpoB PE=3 SV=1  
RPOB\_RICRO **Mass:** 154675 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0)  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia rickettsii (strain Iowa) OX=452659 GN=rpoB PE=3 SV=1  
RPOB\_RICRS **Mass:** 154675 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0)  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia rickettsii (strain Sheila Smith) OX=392021 GN=rpoB PE=3 SV=1  
RPOB\_RICMS **Mass:** 154710 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0)  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia massiliae (strain MtU5) OX=416276 GN=rpoB PE=3 SV=1

5. RPOB\_RICCK **Mass:** 154543 **Score:** 26 **Matches:** 2(0) **Sequences:** 2(0) **emPAI:** 0.02  
 DNA-directed RNA polymerase subunit beta OS=Rickettsia canadensis (strain McKiel) OX=293613 GN=rpoB PE=3 SV=1  
**Query** **Observed** **Mr(expt)** **Mr(calc)** **Delta** **Miss** **Score** **Expect** **Rank** **Unique** **Peptide**  
51 600.9300 599.9227 600.3595 -0.4368 0 9 3.3e+002 1 U K.LVQNK.G  
902 637.9800 2547.8909 2547.3101 0.5807 1 26 2.4 1 K.MNSRLELNISEEVTTLTIDDIK.N

6. CSKI2\_XENLA **Mass:** 131580 **Score:** 23 **Matches:** 5(0) **Sequences:** 1(0) **emPAI:** 0.02  
 Caskin-2 OS=Xenopus laevis OX=8355 GN=caskin2 PE=2 SV=1  
**Query** **Observed** **Mr(expt)** **Mr(calc)** **Delta** **Miss** **Score** **Expect** **Rank** **Unique** **Peptide**  
519 679.7800 1357.5454 1357.6482 -0.1028 0 23 9.4 1 U K.MGTALHEAALCGK.T 518 520 521 523

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

Select Summary Report (.../data/20230814/F002158.dat)

## Mascot Search Results

User : Branka  
Email :  
Search title :  
MS data file : DATA.TXT  
Database : NCBI nr 18122019 (229130272 sequences; 83483511431 residues)  
Timestamp : 15 Aug 2023 at 02:09:49 GMT  
Warning : 3 sequences ignored because length greater than maximum configured  
Enzyme : Trypsin  
Fixed modifications : [Carbamidomethyl \(C\)](#)  
Variable modifications : [Oxidation \(M\)](#)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 0.5$  Da (#  $^{13}\text{C} = 1$ )  
Fragment Mass Tolerance :  $\pm 0.5$  Da  
Max Missed Cleavages : 1  
Instrument type : ESI-TRAP  
Number of queries : 1001  
Protein hits : [AC014032.1](#) Hemoglobin subunit beta [Esox lucius]  
[XP\\_010887573.2](#) malate dehydrogenase, cytoplasmic isoform X1 [Esox lucius]

### Select 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  Require bold red

Re-Search  All queries  Unassigned  Below homology threshold  Below identity threshold

1. [AC014032.1](#) Mass: 16574 Score: 145 Matches: 4(0) Sequences: 4(0) emPAI: 0.20  
Hemoglobin subunit beta [Esox lucius]

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">592</a>	724.2000	1446.3854	1446.7574	-0.3720	0	23	2.9e+003	1		R.LLAECITVCVAAK.L
<a href="#">619</a>	739.1800	1476.3454	1475.7078	0.6376	0	24	2.7e+003	2	U	K.NTYAPLSVMHSEK.L

http://spectralab/mascot/cgi/master\_results.pl?file=.%2Fdata%2F20230814%2FF002158.dat

<a href="#">707</a>	881.4800	1760.9454	1760.8370	0.1085	0	36	1.5e+002	1	U	K.LGPSVFDADTHEAFQK.F
<a href="#">835</a>	1114.0100	2226.0054	2225.1117	0.8938	0	64	0.18	1	U	R.YFSSFGNLSPPAAIAGNPVAK.H

2. [XP\\_010887573.2](#) Mass: 38367 Score: 97 Matches: 4(0) Sequences: 2(0) emPAI: 0.18  
 malate dehydrogenase, cytoplasmic isoform X1 [Esox lucius]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">704</a>	879.4600	1756.9054	1756.8533	0.0522	0	48	9.6	1	U	K.SWTIHDGLPINDFSR.A <a href="#">703</a>
<a href="#">711</a>	885.5100	1769.0054	1768.9505	0.0549	0	49	6.7	1	U	K.VLVVGNPANTNCLIASK.S <a href="#">712</a>

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

[XP\\_010887574.1](#) Mass: 36548 Score: 97 Matches: 4(0) Sequences: 2(0)  
 malate dehydrogenase, cytoplasmic isoform X2 [Esox lucius]

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

**Mascot Search Results**

**(MATRIX) SCIENCE**

User : Hasan  
 Email : hmuharem@irb.hr  
 Search title :  
 MS data file : DATA.TXT  
 Database : swissprot\_uniprot1\_sprot\_15042019 (559634 sequences; 201129965 residues)  
 Timestamp : 23 May 2023 at 08:22:00 GMT  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance : ± 0.5 Da (# <sup>13</sup>C = 1)  
 Fragment Mass Tolerance : ± 0.5 Da  
 Max Missed Cleavages : 1  
 Instrument type : ESI-TRAP  
 Number of queries : 1001  
 Protein hits : [HBB\\_ONCNE](#) Hemoglobin subunit beta OS=Oncorhynchus nerka OX=8023 GN=hbb PE=2 SV=3  
[FAAA\\_BOVIN](#) Fumarylacetoacetase OS=Bos taurus OX=9913 GN=FAH PE=2 SV=1  
[RSE1\\_SCHPO](#) Pre-mRNA-splicing factor prp12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=prp12  
[POLG\\_HCVEV](#) Genome polyprotein OS=Hepatitis C virus genotype 5a (isolate EUH1480) OX=356419 PE=1 SV=3  
[RS3\\_METFK](#) 30S ribosomal protein S3 OS=Methylobacillus flagellatus (strain KT / ATCC 51484 / DSM 6875) OX=265072 GN

Select 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  Require bold red

Re-Search  All queries  Unassigned  Below homology threshold  Below identity threshold

1.	<a href="#">HBB_ONCNE</a>	Mass: 16214	Score: 45	Matches: 5(0)	Sequences: 2(0)	emPAI: 0.21
Hemoglobin subunit beta OS=Oncorhynchus nerka OX=8023 GN=hbb PE=2 SV=3						
Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss Score	Expect Rank Unique Peptide
<a href="#">640</a>	717.6900	1433.3654	1432.7418	0.6236	0 17	32 1 U R.LLADCIIVCVAAK.L <a href="#">639</a>
<a href="#">390</a>	579.1800	1734.5182	1734.8577	-0.3395	0 (5) 1.5e+003	8 U K.LGPAVFNADTQEAFOK.F
<a href="#">751</a>	868.4400	1734.8654	1734.8577	0.0078	0 38	0.22 1 U K.LGPAVFNADTQEAFOK.F <a href="#">752</a>
2.	<a href="#">FAAA_BOVIN</a>	Mass: 46525	Score: 43	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.07
Fumarylacetoacetase OS=Bos taurus OX=9913 GN=FAH PE=2 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss Score	Expect Rank Unique Peptide
<a href="#">725</a>	827.6000	1653.1854	1652.9713	0.2142	0 43	0.075 1 U R.IGVAIGDQIILDLSVIK.H
Proteins matching the same set of peptides:						
<a href="#">FAAA_MOUSE</a>	Mass: 46488	Score: 43	Matches: 1(0)	Sequences: 1(0)	Fumarylacetoacetase OS=Mus musculus OX=10090 GN=Fah PE=1 SV=2	
<a href="#">FAAA_RAT</a>	Mass: 46231	Score: 43	Matches: 1(0)	Sequences: 1(0)	Fumarylacetoacetase OS=Rattus norvegicus OX=10116 GN=Fah PE=1 SV=1	
3.	<a href="#">RSE1_SCHPO</a>	Mass: 135799	Score: 32	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.02
Pre-mRNA-splicing factor prp12 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) OX=284812 GN=prp12 PE=1 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss Score	Expect Rank Unique Peptide
<a href="#">617</a>	701.6900	2802.7309	2802.4957	0.2352	0 32	2.3 1 U R.EVLLWTGLLGTGVFPTPFINQEDVR.F
4.	<a href="#">POLG_HCVEV</a>	Mass: 333105	Score: 27	Matches: 2(0)	Sequences: 2(0)	emPAI: 0.01
Genome polyprotein OS=Hepatitis C virus genotype 5a (isolate EUH1480) OX=356419 PE=1 SV=3						
Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss Score	Expect Rank Unique Peptide
<a href="#">295</a>	507.7000	1520.0782	1519.7704	0.3077	0 13	2.4e+002 1 U K.AETLKPAATSMWSK.A
<a href="#">435</a>	600.2000	2396.7709	2396.1834	0.5875	1 27	8.5 1 U K.AETLKPAATSMWSKAEQFWAK.H
5.	<a href="#">RS3_METFK</a>	Mass: 26324	Score: 27	Matches: 1(0)	Sequences: 1(0)	emPAI: 0.13
30S ribosomal protein S3 OS=Methylobacillus flagellatus (strain KT / ATCC 51484 / DSM 6875) OX=265072 GN=rpsC PE=3 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss Score	Expect Rank Unique Peptide
<a href="#">835</a>	658.7000	1973.0782	1972.8989	0.1793	0 27	2.4 1 U R.WYANSNNFPAMLSDDIK.V

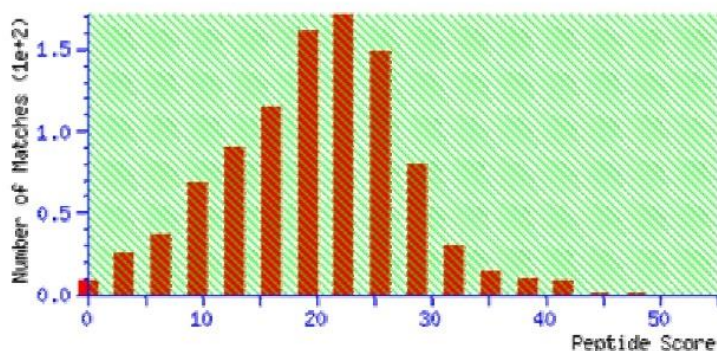
**MATRIX SCIENCE** MASCOT Search Results

**User** : Hasan  
**E-mail** : hmuharem@irb.hr  
**MS data file** : DATA.TXT  
**Database** : NCBI nr 18122019 (229,130,272 sequences; 83,483,511,431 residues)  
**Timestamp** : 23 May 2023 at 01:51:02 GMT  
**Warning** : 3 sequences ignored because length greater than maximum configured

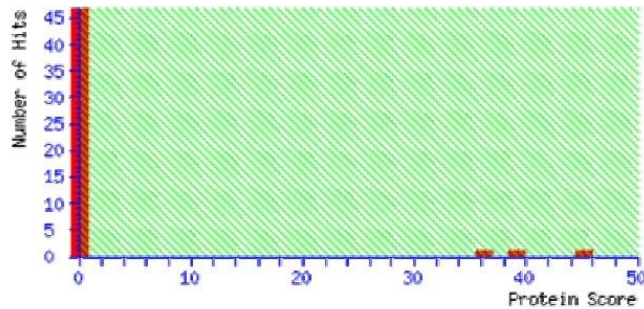
Not what you expected? Try [the select summary](#).

**▼ Search parameters**

**Type of search** : MS/MS Ion Search  
**Enzyme** : Trypsin  
**Fixed modifications** : **Carbamidomethyl (C)**  
**Variable modifications** : **Oxidation (M)**  
**Mass values** : Monoisotopic  
**Protein mass** : Unrestricted  
**Peptide mass tolerance** :  $\pm 0.5$  Da (#  $^{13}\text{C}$  = 1)  
**Fragment mass tolerance** :  $\pm 0.5$  Da  
**Max missed cleavages** : 1  
**Instrument type** : ESI-TRAP  
**Number of queries** : 1,001

**▼ Score distribution**

Peptide score distribution. Ions score is  $-10 \log(P)$ , where  $P$  is the probability that the observed match is a random event. Individual ions scores **> 72** indicate **identity** or **extensive homology** ( $p < 0.05$ ).



**[Deprecated]** Score distribution for family members in the first 50 proteins. Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein families.

▼Legend

Dupes	Expect	Rank	U	1	2	Peptide	
	0.037	▶ 2				<b>GAYLSLR</b>	significant
	9	▶ 1				<b>GFFLFVEGGR</b>	top ranking
	6.4e-005	▶ 1				<b>GSSIFGLAPGK</b>	significant and top ranking
	1.3e-006	▶ 1	■			<b>SSGTSYPDVLK</b>	peptide is found in all proteins in family member 1
	6.2e-007	▶ 1	■			<b>VCNYVSWIK</b>	peptide is found in some but not all proteins in family member 2
	6.4e-005	▶ 1	U			<b>GSSIFGLAPGK</b>	unique
▶ 2	5.7e-005	▶ 1				<b>LNTLETEEWFFK</b>	peptide has two duplicates
	0.18	▶ 1				<b>LNTLETEEWFFK</b>	duplicate peptide

Right-facing triangle (▶) in the Dupes or Rank column indicates content that can be expanded by clicking on it. Down-facing triangle (▼) indicates the content is expanded and can be collapsed. For more details about particular columns, see [results format help](#).

**Protein Family Summary**

Significance threshold p<  Max. number of families   
 Ions score or expect cut-off  Dendrograms cut at

**Protein families 1–3 (out of 3)**

per page 1

▼ 1	<b>EPB87887.1</b>	45	tRNA(Met) cytidine acetyltransferase [Mucor circinelloid.			
	<b>Score</b>	<b>Mass</b>	<b>Matches</b>	<b>Sequences</b>	<b>emPA</b>	
1.1	<b><u>EPB87887.1</u></b>	45	120650	2 (1)	1 (1)	0.0
	tRNA(Met) cytidine acetyltransferase [Mucor circinelloides f. circinelloides 1006PhL]					

▼ **2 peptide matches (1 non-duplicate, 1 duplicate)**

Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Ran
<u>365</u> ▶ <u>1</u>	<b>566.7400</b>	<b>1131.4654</b>	<b>1130.5204</b>	<b>0.9450</b>	<b>0</b>	<b>45</b>	<b>0.045</b> ▶ <u>1</u>

▼ **2**      **XP\_010898384.1**      38    hemoglobin subunit beta-like [Esox lucius]

	Score	Mass	Matches	Sequences	emPA
<b>2.1</b> <b><u>XP_010898384.1</u></b>	38	16405	3 (1)	2 (1)	0.2
hemoglobin subunit beta-like [Esox lucius]					
▶ <b>4 samesets of XP_010898384.1</b>					

▼ **3 peptide matches (2 non-duplicate, 1 duplicate)**

Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Ran
<u>751</u> ▶ <u>1</u>	<b>868.4400</b>	<b>1734.8654</b>	<b>1734.8577</b>	<b>0.0078</b>	<b>0</b>	<b>38</b>	<b>0.032</b> ▶ <u>1</u>
<u>888</u>	756.9600	2267.8582	2267.1586	0.6996	0	25	4.5 ▶ <u>7</u>

▼ **3**      **WP\_151441692.1**      37    ATP-binding cassette domain-containing protein [Halosp

	Score	Mass	Matches	Sequences	emPA
<b>3.1</b> <b><u>WP_151441692.1</u></b>	37	40419	1 (1)	1 (1)	0.0
ATP-binding cassette domain-containing protein [Halospina sp. K52047b]					

▼ **1 peptide matches (1 non-duplicate, 0 duplicate)**

Query Dupes	Observed	Mr (expt)	Mr (calc)	Delta M	Score	Expect	Ran
<u>970</u>	<b>731.6200</b>	<b>2922.4509</b>	<b>2921.3907</b>	<b>1.0601</b>	<b>1</b>	<b>37</b>	<b>0.014</b> ▶ <u>1</u>

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