Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus. (16281 sequences)**

Timestamp : **22 Nov 2010 at 05:06:54 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

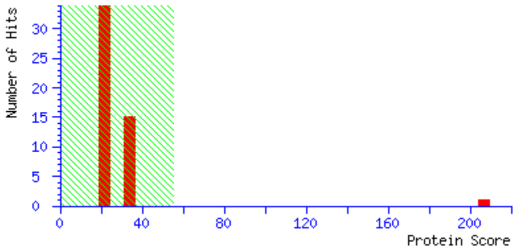
Top Score : **207 for PDIA1_MOUSE, Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**PDIA1_MOUSE**	57507	207	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1
2.	**KLC1_MOUSE**	61868	37	Kinesin light chain 1 OS=Mus musculus GN=Klc1 PE=1 SV=3
3.	**K1143_MOUSE**	17525	33	Uncharacterized protein KIAA1143 homolog OS=Mus musculus PE=1 SV=1
4.	**CCD46_MOUSE**	113119	33	Coiled-coil domain-containing protein 46 OS=Mus musculus GN=Ccdc46 PE=2 SV=2
5.	**CCPG1_MOUSE**	86757	31	Cell cycle progression protein 1 OS=Mus musculus GN=Ccpg1 PE=1 SV=2
6.	**PTC1_MOUSE**	160711	30	Protein patched homolog 1 OS=Mus musculus GN=Ptch1 PE=2 SV=1
7.	**AMOL2_MOUSE**	85454	29	Angiomotin-like protein 2 OS=Mus musculus GN=Amotl2 PE=2 SV=1
8.	**MP2K4_MOUSE**	44542	29	Dual specificity mitogen-activated protein kinase kinase 4 OS=Mus musculus GN=Map2k4 PE=1 SV=2
9.	**UBIQ_MOUSE**	8560	29	Ubiquitin OS=Mus musculus GN=Rps27a PE=1 SV=1
10.	**RHG20_MOUSE**	132887	29	Rho GTPase-activating protein 20 OS=Mus musculus GN=Arhgap20 PE=2 SV=1

Results List

1. PDIA1_MOUSE **Mass:** 57507 **Score:** 207 **Expect:** 3.2e-017 **Matches:** 9

Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
910.4295	909.4223	909.4345	-13.41	447	-	454	0	7	K.FFPASADR.T
962.4472	961.4399	961.4440	-4.20	341	-	347	0	7	K.ITEFCHR.F
988.4860	987.4788	987.4807	-2.01	311	-	318	1	---	K.KEECPAVR.L
1002.5491	1001.5418	1001.5505	-8.71	72	-	80	1	---	K.LKAEGSEIR.L
1655.7423	1654.7350	1654.7587	-14.32	211	-	224	1	---	K.FDEGRNNFEGEITK.E
1780.8137	1779.8064	1779.8275	-11.87	84	-	99	0	42	K.VDATEESDLAQQYGVR.G
1794.8568	1793.8495	1793.9200	-39.28	373	-	388	1	---	K.VLVGANFEEVAFDEKK.N
1833.8947	1832.8875	1832.9057	-9.96	288	-	302	0	36	K.ILFIFIDSDHTDNQR.I
2353.0895	2352.0822	2352.1056	-9.95	329	-	347	1	---	K.YKPESDELTAEKITEFCHR.F

No match to: 1081.5038, 1732.8452, 1912.8891, 1987.0118, 1998.9932

2. KLC1_MOUSE **Mass:** 61868 **Score:** 37 **Expect:** 3.3 **Matches:** 3

Kinesin light chain 1 OS=Mus musculus GN=Klc1 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
910.4295	909.4223	909.4668	-48.99	495	-	502	0	---	K.QGLDNVHK.Q
1002.5491	1001.5418	1001.4964	45.3	313	-	320	1	---	K.EAEPLCKR.A
1780.8137	1779.8064	1779.8461	-22.31	476	-	491	1	19	R.QGKFEAAETLEEAAMR.S

No match to: 962.4472, 988.4860, 1081.5038, 1655.7423, 1732.8452, 1794.8568, 1833.8947, 1912.8891, 1987.0118, 1998.9932, 2353.0895

3. K1143_MOUSE **Mass:** 17525 **Score:** 33 **Expect:** 7.8 **Matches:** 3

Uncharacterized protein KIAA1143 homolog OS=Mus musculus PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
910.4295	909.4223	909.4226	-0.34	109	-	117	0	---	K.CSGLTASSK.K
988.4860	987.4788	987.5237	-45.47	29	-	37	1	---	K.EGPTVETKK.I
1833.8947	1832.8875	1832.9533	-35.93	5	-	20	0	---	R.NQVSYVRPAEPAFLSR.F

No match to: 962.4472, 1002.5491, 1081.5038, 1655.7423, 1732.8452, 1780.8137, 1794.8568, 1912.8891, 1987.0118, 1998.9932, 2353.0895

4. CCD46_MOUSE **Mass:** 113119 **Score:** 33 **Expect:** 8.5 **Matches:** 5

Coiled-coil domain-containing protein 46 OS=Mus musculus GN=Ccdc46 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
988.4860	987.4788	987.4872	-8.59	290	-	297	0	---	K.NNELEELK.I
1655.7423	1654.7350	1654.7872	-31.56	608	-	621	1	---	R.QVEVNSEKVYGEMK.E + Oxidation (M)
1732.8452	1731.8380	1731.8210	9.81	416	-	430	0	---	R.VQQLMGEAENSNLQR.Q + Oxidation (M)
1794.8568	1793.8495	1793.9271	-43.28	940	-	954	1	---	R.ASILQEELTTYQSRR.-
2353.0895	2352.0822	2352.1276	-19.30	391	-	410	1	---	R.LSKMEADYVVQMQSTNHMIK.E

No match to: 910.4295, 962.4472, 1002.5491, 1081.5038, 1780.8137, 1833.8947, 1912.8891, 1987.0118, 1998.9932

5. CCPG1_MOUSE **Mass:** 86757 **Score:** 31 **Expect:** 12 **Matches:** 4

Cell cycle progression protein 1 OS=Mus musculus GN=Ccpg1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
1732.8452	1731.8380	1731.8389	-0.57	482	-	496	1	---	K.ETFLGTVKETFDAMK.N + Oxidation (M)

1780.8137	1779.8064	1779.8097	-1.88	279 -	292	1	0	K.ENLERCWTVTESEK.I
1912.8891	1911.8818	1911.9519	-36.68	674 -	689	0	---	K.ELDQFISPFFPNGVFR.H
1987.0118	1986.0045	1985.9404	32.3	284 -	299	1	---	R.CWTVTESEKITFETQK.K

No match to: 910.4295, 962.4472, 988.4860, 1002.5491, 1081.5038, 1655.7423, 1794.8568, 1833.8947, 1998.9932, 2353.0895

6. PTC1_MOUSE **Mass:** 160711 **Score:** 30 **Expect:** 15 **Matches:** 5

Protein patched homolog 1 OS=Mus musculus GN=Ptch1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
962.4472	961.4399	961.4691	-30.34	185 -	191	0	---	K.LEHLCYK.S
1081.5038	1080.4965	1080.5175	-19.37	174 -	181	0	---	R.VHVYMYNR.Q
1780.8137	1779.8064	1779.8719	-36.83	242 -	255	0	---	R.WTNFDPLEFLEELK.K
1912.8891	1911.8818	1911.9036	-11.41	256 -	270	1	---	K.KINYQVDSWEEMLNK.A + Oxidation (M)
1998.9932	1997.9859	1997.9516	17.1	854 -	871	1	---	R.IMPNNYKNGSDDGVLAYK.L

No match to: 910.4295, 988.4860, 1002.5491, 1655.7423, 1732.8452, 1794.8568, 1833.8947, 1987.0118, 2353.0895

7. AMOL2_MOUSE **Mass:** 85454 **Score:** 29 **Expect:** 20 **Matches:** 4

Angiomotin-like protein 2 OS=Mus musculus GN=Amotl2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
910.4295	909.4223	909.3797	46.9	376 -	382	1	---	K.MDGEMRR.L + Oxidation (M)
1002.5491	1001.5418	1001.5505	-8.71	545 -	552	1	---	R.LSEQLREK.E
1780.8137	1779.8064	1779.8508	-24.96	575 -	591	1	---	R.AMRQFAMDAAATAAAQR.D
1833.8947	1832.8875	1832.9744	-47.45	15 -	29	1	---	R.LIQEQLRYGNLTETR.T

No match to: 962.4472, 988.4860, 1081.5038, 1655.7423, 1732.8452, 1794.8568, 1912.8891, 1987.0118, 1998.9932, 2353.0895

8. MP2K4_MOUSE **Mass:** 44542 **Score:** 29 **Expect:** 20 **Matches:** 3

Dual specificity mitogen-activated protein kinase kinase 4 OS=Mus musculus GN=Map2k4 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1780.8137	1779.8064	1779.8059	0.26	382 -	397	0	1	K.ILDQMPATPSSPMYVD.- + Oxidation (M)
1833.8947	1832.8875	1832.9494	-33.82	358 -	371	1	---	K.ELLKHPFILMYEER.T + Oxidation (M)
2353.0895	2352.0822	2352.1935	-47.31	53 -	73	1	---	K.STARFTLNPNTTGVQNPHIER.L

No match to: 910.4295, 962.4472, 988.4860, 1002.5491, 1081.5038, 1655.7423, 1732.8452, 1794.8568, 1912.8891, 1987.0118, 1998.9932

9. UBIQ_MOUSE **Mass:** 8560 **Score:** 29 **Expect:** 20 **Matches:** 2

Ubiquitin OS=Mus musculus GN=Rps27a PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1081.5038	1080.4965	1080.5451	-44.96	55 -	63	0	---	R.TLSDYNIQK.E
1987.0118	1986.0045	1986.0521	-23.95	12 -	29	1	---	K.TITLEVEPSDTIENVKAK.I

No match to: 910.4295, 962.4472, 988.4860, 1002.5491, 1655.7423, 1732.8452, 1780.8137, 1794.8568, 1833.8947, 1912.8891, 1998.9932, 2353.0895

10. RHG20_MOUSE **Mass:** 132887 **Score:** 29 **Expect:** 20 **Matches:** 5

Rho GTPase-activating protein 20 OS=Mus musculus GN=Arhgap20 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide

910.4295	909.4223	909.4443	-24.26	738 - 744	1	---	R.KDEDYLK.Q
1081.5038	1080.4965	1080.4804	14.9	400 - 408	1	---	R.QSANMKSCR.E
1655.7423	1654.7350	1654.7733	-23.15	2 - 17	0	---	M.EAMSPQQDALGAQPGR.S
1732.8452	1731.8380	1731.9156	-44.81	780 - 795	1	---	K.KSLSGHEGTQVTLFTK.S
1987.0118	1986.0045	1985.9946	5.01	703 - 719	1	---	R.SSEPSIDYLDTKLSYLR.E

No match to: 962.4472, 988.4860, 1002.5491, 1780.8137, 1794.8568, 1833.8947, 1912.8891, 1998.9932, 2353.0895

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (910.4295,1+) : <no title>

Query2 (962.4472,1+) : <no title>

Query3 (988.4860,1+) : <no title>

Query4 (1002.5491,1+) : <no title>

Query5 (1081.5038,1+) : <no title>

Query6 (1655.7423,1+) : <no title>

Query7 (1732.8452,1+) : <no title>

Query8 (1780.8137,1+) : <no title>

Query9 (1794.8568,1+) : <no title>

Query10 (1833.8947,1+) : <no title>

Query11 (1912.8891,1+) : <no title>

Query12 (1987.0118,1+) : <no title>

Query13 (1998.9932,1+) : <no title>

Query14 (2353.0895,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus. (16281 sequences)**

Timestamp : **22 Nov 2013 at 05:06:36 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

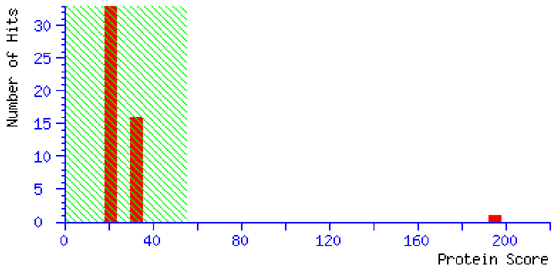
Top Score : **195 for ALBU_MOUSE, Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**ALBU_MOUSE**	70700	195	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3
2.	**ZN672_MOUSE**	54002	34	Zinc finger protein 672 OS=Mus musculus GN=Znf672 PE=2 SV=1
3.	**TTLL3_MOUSE**	105388	32	Tubulin monoglycylase TTLL3 OS=Mus musculus GN=Ttll3 PE=1 SV=1
4.	**MAP9_MOUSE**	73580	31	Microtubule-associated protein 9 OS=Mus musculus GN=Map9 PE=2 SV=2
5.	**TBCD4_MOUSE**	148954	31	TBC1 domain family member 4 OS=Mus musculus GN=Tbc1d4 PE=1 SV=2
6.	**TRI27_MOUSE**	59786	30	Zinc finger protein RFP OS=Mus musculus GN=Trim27 PE=1 SV=2
7.	**CALCA_MOUSE**	14227	30	Calcitonin gene-related peptide 1 OS=Mus musculus GN=Calca PE=2 SV=1
8.	**KGP1_MOUSE**	76929	30	cGMP-dependent protein kinase 1 OS=Mus musculus GN=Prkg1 PE=1 SV=1
9.	**CQ067_MOUSE**	10728	29	Uncharacterized protein C17orf67 homolog OS=Mus musculus GN=Gm525 PE=2 SV=1
10.	**CIDEC_MOUSE**	27502	29	Cell death activator CIDE-3 OS=Mus musculus GN=Cidec PE=2 SV=1

Results List

1. ALBU_MOUSE **Mass:** 70700 **Score:** 195 **Expect:** 5.1e-016 **Matches:** 7

Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1067.5103	1066.5030	1066.4536	46.4	500 -	508	0	---	K.CCSGSLVER.R
1439.7960	1438.7887	1438.7780	7.45	439 -	452	0	42	K.APQVSTPTLVEAAR.N
1455.8118	1454.8045	1454.7994	3.52	361 -	372	1	21	R.RHPDYSVSLLLR.L
1479.8037	1478.7964	1478.7881	5.58	422 -	434	0	23	K.LGEYGFQNAILVR.Y
1609.8013	1608.7941	1608.7824	7.25	348 -	360	0	31	K.DVFLGTFLYEYSR.R
1882.9407	1881.9334	1881.9295	2.08	509 -	524	0	---	R.RPCFSALTVDETYVPK.E
1981.9331	1980.9258	1980.9211	2.37	585 -	602	1	---	K.AADKDTCFSTEGPNLVTR.C

No match to: 856.5451, 879.4699, 1032.5657, 1523.7787, 1703.8452, 2603.1735

2. ZN672_MOUSE **Mass:** 54002 **Score:** 34 **Expect:** 6.8 **Matches:** 3

Zinc finger protein 672 OS=Mus musculus GN=Znf672 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1439.7960	1438.7887	1438.7178	49.3	175 -	187	1	0	R.AFHSSAGLRNHSR.I
1455.8118	1454.8045	1454.8623	-39.70	108 -	119	1	6	R.RFPHVPALLLHR.A
1882.9407	1881.9334	1881.9203	6.99	122 -	136	1	---	R.QHPPEKPHRCPLCAR.S

No match to: 856.5451, 879.4699, 1032.5657, 1067.5103, 1479.8037, 1523.7787, 1609.8013, 1703.8452, 1981.9331, 2603.1735

3. TTLL3_MOUSE **Mass:** 105388 **Score:** 32 **Expect:** 9.6 **Matches:** 3

Tubulin monoglycylase TTLL3 OS=Mus musculus GN=Ttll3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1439.7960	1438.7887	1438.7245	44.6	332 -	343	0	8	K.AFIEDFWLTAAR.N
1455.8118	1454.8045	1454.7882	11.2	711 -	723	0	5	K.QPAVEVPQYVGIR.L
1981.9331	1980.9258	1980.9392	-6.78	492 -	507	1	---	R.LDEMLKLVDCNPMLMK.D + 2 Oxidation (M)

No match to: 856.5451, 879.4699, 1032.5657, 1067.5103, 1479.8037, 1523.7787, 1609.8013, 1703.8452, 1882.9407, 2603.1735

4. MAP9_MOUSE **Mass:** 73580 **Score:** 31 **Expect:** 13 **Matches:** 5

Microtubule-associated protein 9 OS=Mus musculus GN=Map9 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1032.5657	1031.5584	1031.5135	43.6	544 -	552	1	---	K.EEEAVAEKK.K
1439.7960	1438.7887	1438.7503	26.7	436 -	446	1	---	K.NVYLHEMHRIK.R
1455.8118	1454.8045	1454.7452	40.7	436 -	446	1	---	K.NVYLHEMHRIK.R + Oxidation (M)
1523.7787	1522.7715	1522.7667	3.12	597 -	608	1	---	K.QAISEYEKWLEK.K
1703.8452	1702.8379	1702.7646	43.1	304 -	318	1	---	K.DGQVAADDLEEEREK.G

No match to: 856.5451, 879.4699, 1067.5103, 1479.8037, 1609.8013, 1882.9407, 1981.9331, 2603.1735

5. TBCD4_MOUSE **Mass:** 148954 **Score:** 31 **Expect:** 14 **Matches:** 5

TBC1 domain family member 4 OS=Mus musculus GN=Tbc1d4 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1032.5657	1031.5584	1031.5182	39.0	527 -	534	1	---	R.QLCEAKQR.T
1439.7960	1438.7887	1438.7378	35.4	1168 -	1179	0	---	K.IITQVFEMDISK.Q + Oxidation (M)
1523.7787	1522.7715	1522.7932	-14.30	934 -	945	0	---	R.GEIWQFLALQYR.L

1703.8452	1702.8379	1702.8786	-23.90	50 -	63	0	---	R.TTLPMLPWLMAEIR.R + 2 Oxidation (M)
1981.9331	1980.9258	1981.0098	-42.38	129 -	144	0	---	R.FIHNSHDLTYFAYLIK.A

No match to: 856.5451, 879.4699, 1067.5103, 1455.8118, 1479.8037, 1609.8013, 1882.9407, 2603.1735

6. TRI27_MOUSE **Mass:** 59786 **Score:** 30 **Expect:** 15 **Matches:** 3

Zinc finger protein RFP OS=Mus musculus GN=Trim27 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.5451	855.5378	855.4967	48.1	277 -	283	0	---	K.IHIFAQK.C
1523.7787	1522.7715	1522.7119	39.1	298 -	309	1	---	K.MQSDMEKIQELR.E + Oxidation (M)
1609.8013	1608.7941	1608.7389	34.3	383 -	395	1	5	K.WTIGVCEDSVCRK.G

No match to: 879.4699, 1032.5657, 1067.5103, 1439.7960, 1455.8118, 1479.8037, 1703.8452, 1882.9407, 1981.9331, 2603.1735

7. CALCA_MOUSE **Mass:** 14227 **Score:** 30 **Expect:** 16 **Matches:** 2

Calcitonin gene-related peptide 1 OS=Mus musculus GN=Calca PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1523.7787	1522.7715	1522.7887	-11.34	48 -	60	0	---	R.LLAALVQDYMQMK.A
1609.8013	1608.7941	1608.7533	25.4	107 -	121	0	5	K.DNFVPTNVGSEAFGR.R

No match to: 856.5451, 879.4699, 1032.5657, 1067.5103, 1439.7960, 1455.8118, 1479.8037, 1703.8452, 1882.9407, 1981.9331, 2603.1735

8. KGP1_MOUSE **Mass:** 76929 **Score:** 30 **Expect:** 17 **Matches:** 3

cGMP-dependent protein kinase 1 OS=Mus musculus GN=Prkg1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1067.5103	1066.5030	1066.4818	19.8	2 -	10	0	---	M.SELEEDFAK.I
1439.7960	1438.7887	1438.7569	22.1	251 -	263	1	9	R.QGARGDTFFIISK.G
2603.1735	2602.1662	2602.2746	-41.64	433 -	453	1	---	K.YLYMLMEACLGGELWTILRDR.G

No match to: 856.5451, 879.4699, 1032.5657, 1455.8118, 1479.8037, 1523.7787, 1609.8013, 1703.8452, 1882.9407, 1981.9331

9. CQ067_MOUSE **Mass:** 10728 **Score:** 29 **Expect:** 20 **Matches:** 2

Uncharacterized protein C17orf67 homolog OS=Mus musculus GN=Gm525 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.5451	855.5378	855.5290	10.3	28 -	34	1	---	K.QAKQLLR.S
2603.1735	2602.1662	2602.1594	2.62	65 -	84	0	---	R.AEEQFLEHWLNPHCKPHCDR.N

No match to: 879.4699, 1032.5657, 1067.5103, 1439.7960, 1455.8118, 1479.8037, 1523.7787, 1609.8013, 1703.8452, 1882.9407, 1981.9331

10. CIDEC_MOUSE **Mass:** 27502 **Score:** 29 **Expect:** 21 **Matches:** 3

Cell death activator CIDE-3 OS=Mus musculus GN=Cidec PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.5451	855.5378	855.5542	-19.15	184 -	190	1	---	R.IVKEIVR.W
1439.7960	1438.7887	1438.7820	4.65	139 -	150	1	---	K.IDVARVTFDLYK.L
1703.8452	1702.8379	1702.8422	-2.52	1 -	14	1	---	-.MDYAMKSLSLLYPR.S + Oxidation (M)

No match to: 879.4699, 1032.5657, 1067.5103, 1455.8118, 1479.8037, 1523.7787, 1609.8013, 1882.9407, 1981.9331, 2603.1735

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (856.5451,1+) : <no title>

Query2 (879.4699,1+) : <no title>

Query3 (1032.5657,1+) : <no title>

Query4 (1067.5103,1+) : <no title>

Query5 (1439.7960,1+) : <no title>

Query6 (1455.8118,1+) : <no title>

Query7 (1479.8037,1+) : <no title>

Query8 (1523.7787,1+) : <no title>

Query9 (1609.8013,1+) : <no title>

Query10 (1703.8452,1+) : <no title>

Query11 (1882.9407,1+) : <no title>

Query12 (1981.9331,1+) : <no title>

Query13 (2603.1735,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:47:14 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

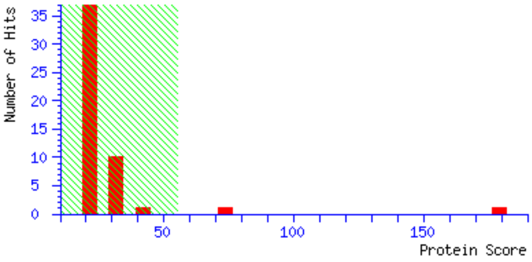
Top Score : **179 for HS90B_MOUSE, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary ReportIndex

	Accession	Mass	Score	Description
1.	**HS90B_MOUSE**	83615	179	Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2
2.	**HS90A_MOUSE**	85134	79	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4
3.	**FGF22_MOUSE**	18972	42	Fibroblast growth factor 22 OS=Mus musculus GN=Fgf22 PE=2 SV=1
4.	**TPD53_MOUSE**	22558	35	Tumor protein D53 OS=Mus musculus GN=Tpd52l1 PE=2 SV=1
5.	**EHD1_MOUSE**	60622	33	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1
6.	**EHD3_MOUSE**	60840	33	EH domain-containing protein 3 OS=Mus musculus GN=Ehd3 PE=1 SV=2
7.	**CNTRB_MOUSE**	99515	32	Centrobin OS=Mus musculus GN=Cntrob PE=2 SV=2
8.	**NAL10_MOUSE**	77288	29	NACHT, LRR and PYD domains-containing protein 10 OS=Mus musculus GN=Nlrp10 PE=1 SV=1
9.	**LMLN_MOUSE**	78350	29	Leishmanolysin-like peptidase OS=Mus musculus GN=Lmln PE=2 SV=1
10.	**1433B_MOUSE**	28183	28	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3

Results List

1. HS90B_MOUSE **Mass:** 83615 **Score:** 179 **Expect:** 2e-014 **Matches:** 12

Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide

901.4876	900.4803	900.5181	-42.00	285	291	0	---	K.TKPIWTR.N
951.4228	950.4155	950.4570	-43.60	169	177	0	---	R.ADHGEPIGR.G
1194.5982	1193.5909	1193.6404	-41.47	73	82	0	39	K.IDILPNPQER.T
1208.6127	1207.6055	1207.6237	-15.11	339	348	1	---	R.APFDLFENKK.K
1236.5903	1235.5830	1235.6299	-37.88	338	347	1	11	R.RAPFDLFENK.K
1311.5509	1310.5437	1310.5626	-14.45	187	196	0	---	K.EDQTEYLEER.R
1348.6237	1347.6165	1347.6572	-30.18	320	330	0	40	K.HFSVEGQLEFR.A
1376.6449	1375.6377	1375.5934	32.2	613	624	1	---	R.DNSTMGYMMAKK.H
1544.7883	1543.7811	1543.8205	-25.57	42	55	1	---	R.ELISNASDALDKIR.Y
1564.8235	1563.8162	1563.8620	-29.28	70	82	1	---	K.ELKIDILPNPQER.T
2015.0267	2014.0194	2014.0371	-8.78	181	196	1	---	K.VILHLKEDQTEYLEER.R
2255.9581	2254.9508	2254.9516	-0.32	149	168	0	---	K.HNDDEQYAWESSAGGSFTVR.A

No match to: 829.4898, 856.4776, 933.4688, 993.4153, 1325.5927, 1360.6220, 1364.6877, 1406.6520, 1526.7419, 1549.6964, 1557.7993, 1561.7675, 1587.7966, 1673.8614, 1869.7689, 2171.0948, 2267.9857

2. HS90A_MOUSE **Mass:** 85134 **Score:** 79 **Expect:** 0.00021 **Matches:** 8

Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
901.4876	900.4803	900.5181	-42.00	294	300	0	---	K.TKPIWTR.N
1208.6127	1207.6055	1207.6237	-15.12	491	500	0	---	K.HIYFITGETK.D
1236.5903	1235.5830	1235.6299	-37.88	348	357	1	---	R.APFDLFENRK.K
1311.5509	1310.5437	1310.5626	-14.45	192	201	0	---	K.EDQTEYLEER.R
1348.6237	1347.6165	1347.6572	-30.18	329	339	0	40	K.HFSVEGQLEFR.A
1544.7883	1543.7811	1543.7253	36.1	548	560	1	---	K.EGLELPEDEEEKK.K
2015.0267	2014.0194	2014.0371	-8.78	186	201	1	---	K.VILHLKEDQTEYLEER.R
2255.9581	2254.9508	2254.9516	-0.32	154	173	0	---	K.HNDDEQYAWESSAGGSFTVR.T

No match to: 829.4898, 856.4776, 933.4688, 951.4228, 993.4153, 1194.5982, 1325.5927, 1360.6220, 1364.6877, 1376.6449, 1406.6520, 1526.7419, 1549.6964, 1557.7993, 1561.7675, 1564.8235, 1587.7966, 1673.8614, 1869.7689, 2171.0948, 2267.9857

3. FGF22_MOUSE **Mass:** 18972 **Score:** 42 **Expect:** 1.1 **Matches:** 4

Fibroblast growth factor 22 OS=Mus musculus GN=Fgf22 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1549.6964	1548.6892	1548.7507	-39.74	79	91	1	---	K.AVYSGFYVAMNRR.G + Oxidation (M)
1564.8235	1563.8162	1563.8409	-15.81	149	162	0	---	R.HQLSTHFLPVLVSS.-
1673.8614	1672.8541	1672.8719	-10.65	127	141	0	---	R.GRPMFLALDSQGIPR.Q + Oxidation (M)
2015.0267	2014.0194	2014.0531	-16.71	127	144	1	---	R.GRPMFLALDSQGIPRQGR.R + Oxidation (M)

No match to: 829.4898, 856.4776, 901.4876, 933.4688, 951.4228, 993.4153, 1194.5982, 1208.6127, 1236.5903, 1311.5509, 1325.5927, 1348.6237, 1360.6220, 1364.6877, 1376.6449, 1406.6520, 1526.7419, 1544.7883, 1557.7993, 1561.7675, 1587.7966, 1869.7689, 2171.0948, 2255.9581, 2267.9857

4. TPD53_MOUSE **Mass:** 22558 **Score:** 35 **Expect:** 5.5 **Matches:** 4

Tumor protein D53 OS=Mus musculus GN=Tpd52l1 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**

1194.5982	1193.5909	1193.5784	10.5	71	80	0	---	K.LGMNLMNELK.Q + 2 Oxidation (M)
1208.6127	1207.6055	1207.5945	9.04	99	109	0	---	K.THETLSHAGQK.A
1364.6877	1363.6804	1363.7096	-21.37	110	123	0	---	K.ATAAFNNVGTAISK.K
1564.8235	1563.8162	1563.7650	32.8	130	142	1	---	R.YSIRHSISMPAMR.N + Oxidation (M)

No match to: 829.4898, 856.4776, 901.4876, 933.4688, 951.4228, 993.4153, 1236.5903, 1311.5509, 1325.5927, 1348.6237, 1360.6220, 1376.6449, 1406.6520, 1526.7419, 1544.7883, 1549.6964, 1557.7993, 1561.7675, 1587.7966, 1673.8614, 1869.7689, 2015.0267, 2171.0948, 2255.9581, 2267.9857

5. EHD1_MOUSE **Mass:** 60622 **Score:** 33 **Expect:** 7.6 **Matches:** 4

EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1236.5903	1235.5830	1235.6411	-46.97	125	135	0	---	K.LNAFGNAFLNR.F
1348.6237	1347.6165	1347.6452	-21.35	221	231	0	12	K.ADQIETQQLMR.V + Oxidation (M)
1364.6877	1363.6804	1363.7360	-40.78	124	135	1	---	R.KLNAFGNAFLNR.F
1673.8614	1672.8541	1672.7885	39.2	168	181	0	---	R.GYDFAAVLEWFAER.V

No match to: 829.4898, 856.4776, 901.4876, 933.4688, 951.4228, 993.4153, 1194.5982, 1208.6127, 1311.5509, 1325.5927, 1360.6220, 1376.6449, 1406.6520, 1526.7419, 1544.7883, 1549.6964, 1557.7993, 1561.7675, 1564.8235, 1587.7966, 1869.7689, 2015.0267, 2171.0948, 2255.9581, 2267.9857

6. EHD3_MOUSE **Mass:** 60840 **Score:** 33 **Expect:** 8.1 **Matches:** 4

EH domain-containing protein 3 OS=Mus musculus GN=Ehd3 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1236.5903	1235.5830	1235.6411	-46.97	125	135	0	---	K.LNAFGNAFLNR.F
1348.6237	1347.6165	1347.6452	-21.35	221	231	0	12	K.ADQIETQQLMR.V + Oxidation (M)
1364.6877	1363.6804	1363.7360	-40.78	124	135	1	---	R.KLNAFGNAFLNR.F
1673.8614	1672.8541	1672.7885	39.2	168	181	0	---	R.GYDFAAVLEWFAER.V

No match to: 829.4898, 856.4776, 901.4876, 933.4688, 951.4228, 993.4153, 1194.5982, 1208.6127, 1311.5509, 1325.5927, 1360.6220, 1376.6449, 1406.6520, 1526.7419, 1544.7883, 1549.6964, 1557.7993, 1561.7675, 1564.8235, 1587.7966, 1869.7689, 2015.0267, 2171.0948, 2255.9581, 2267.9857

7. CNTRB_MOUSE **Mass:** 99515 **Score:** 32 **Expect:** 11 **Matches:** 6

Centrobin OS=Mus musculus GN=Cntrob PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
829.4898	828.4825	828.4817	0.92	864	870	1	---	K.TEKPARK.K
1544.7883	1543.7811	1543.7590	14.3	529	541	1	---	R.DLKSGNQQLEEQR.A
1557.7993	1556.7920	1556.8158	-15.28	302	314	1	---	K.EALEEERQALTLR.L
1561.7675	1560.7602	1560.8181	-37.12	224	236	1	---	K.DLMIEQLDKTLAR.V + Oxidation (M)
1564.8235	1563.8162	1563.7688	30.3	194	205	1	---	K.HCERHIQSLQTR.V
1673.8614	1672.8541	1672.8454	5.20	440	453	0	---	R.IQMESELAVQLEQR.V

No match to: 856.4776, 901.4876, 933.4688, 951.4228, 993.4153, 1194.5982, 1208.6127, 1236.5903, 1311.5509, 1325.5927, 1348.6237, 1360.6220, 1364.6877, 1376.6449, 1406.6520, 1526.7419, 1549.6964, 1587.7966, 1869.7689, 2015.0267, 2171.0948, 2255.9581, 2267.9857

8. NAL10_MOUSE **Mass:** 77288 **Score:** 29 **Expect:** 19 **Matches:** 6

NACHT, LRR and PYD domains-containing protein 10 OS=Mus musculus GN=Nlrp10 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
951.4228	950.4155	950.4379	-23.50	663 -	670	1	---	K.KDGEMIDK.M + Oxidation (M)
993.4153	992.4080	992.3692	39.2	638 -	645	0	---	K.GHMEMNDK.E + 2 Oxidation (M)
1194.5982	1193.5909	1193.5533	31.6	397 -	407	0	---	K.SLCSLAAEGMR.H
1208.6127	1207.6055	1207.6231	-14.58	120 -	131	0	---	K.LLLMATSSSGGR.R + Oxidation (M)
1364.6877	1363.6804	1363.7242	-32.08	120 -	132	1	---	K.LLLMATSSSGGRR.S + Oxidation (M)
1587.7966	1586.7893	1586.8021	-8.03	253 -	265	1	---	K.SSRAECVLHILMR.R + Oxidation (M)

No match to: 829.4898, 856.4776, 901.4876, 933.4688, 1236.5903, 1311.5509, 1325.5927, 1348.6237, 1360.6220, 1376.6449, 1406.6520, 1526.7419, 1544.7883, 1549.6964, 1557.7993, 1561.7675, 1564.8235, 1673.8614, 1869.7689, 2015.0267, 2171.0948, 2255.9581, 2267.9857

9. LMLN_MOUSE **Mass:** 78350 **Score:** 29 **Expect:** 21 **Matches:** 5

Leishmanolysin-like peptidase OS=Mus musculus GN=Lmln PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1236.5903	1235.5830	1235.6007	-14.30	2 -	17	0	---	M.AAAGSGGAGGPGPGPR.G
1325.5927	1324.5854	1324.5540	23.7	150 -	160	0	---	R.YCTGECAVHTK.C
1376.6449	1375.6377	1375.6455	-5.73	426 -	435	1	---	K.SCKFWIDQHR.Q
1557.7993	1556.7920	1556.7841	5.04	459 -	471	1	---	R.QDQRAVAVCNLQR.F
1564.8235	1563.8162	1563.7616	34.9	412 -	424	1	---	K.LDWGRGLGCEFVR.K

No match to: 829.4898, 856.4776, 901.4876, 933.4688, 951.4228, 993.4153, 1194.5982, 1208.6127, 1311.5509, 1348.6237, 1360.6220, 1364.6877, 1406.6520, 1526.7419, 1544.7883, 1549.6964, 1561.7675, 1587.7966, 1673.8614, 1869.7689, 2015.0267, 2171.0948, 2255.9581, 2267.9857

10. 1433B_MOUSE **Mass:** 28183 **Score:** 28 **Expect:** 28 **Matches:** 3

14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1194.5982	1193.5909	1193.5962	-4.41	2 -	11	1	---	M.TMDKSELVQK.A + Oxidation (M)
1236.5903	1235.5830	1235.6445	-49.70	160 -	169	1	10	K.KEMQPTHPIR.L
1325.5927	1324.5854	1324.6367	-38.70	1 -	11	1	---	-.MTMDKSELVQK.A + Oxidation (M)

No match to: 829.4898, 856.4776, 901.4876, 933.4688, 951.4228, 993.4153, 1208.6127, 1311.5509, 1348.6237, 1360.6220, 1364.6877, 1376.6449, 1406.6520, 1526.7419, 1544.7883, 1549.6964, 1557.7993, 1561.7675, 1564.8235, 1587.7966, 1673.8614, 1869.7689, 2015.0267, 2171.0948, 2255.9581, 2267.9857

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1

Instrument type : **MALDI-TOF-TOF**

Query1 (829.4898,1+) : **<no title>**

Query2 (856.4776,1+) : **<no title>**

Query3 (901.4876,1+) : **<no title>**

Query4 (933.4688,1+) : **<no title>**

Query5 (951.4228,1+) : **<no title>**

Query6 (993.4153,1+) : **<no title>**

Query7 (1194.5982,1+) : **<no title>**

Query8 (1208.6127,1+) : **<no title>**

Query9 (1236.5903,1+) : **<no title>**

Query10 (1311.5509,1+) : **<no title>**

Query11 (1325.5927,1+) : **<no title>**

Query12 (1348.6237,1+) : **<no title>**

Query13 (1360.6220,1+) : **<no title>**

Query14 (1364.6877,1+) : **<no title>**

Query15 (1376.6449,1+) : **<no title>**

Query16 (1406.6520,1+) : **<no title>**

Query17 (1526.7419,1+) : **<no title>**

Query18 (1544.7883,1+) : **<no title>**

Query19 (1549.6964,1+) : **<no title>**

Query20 (1557.7993,1+) : **<no title>**

Query21 (1561.7675,1+) : **<no title>**

Query22 (1564.8235,1+) : **<no title>**

Query23 (1587.7966,1+) : **<no title>**

Query24 (1673.8614,1+) : **<no title>**

Query25 (1869.7689,1+) : **<no title>**

Query26 (2015.0267,1+) : **<no title>**

Query27 (2171.0948,1+) : **<no title>**

Query28 (2255.9581,1+) : **<no title>**

Query29 (2267.9857,1+) : **<no title>**

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus. (16281 sequences)**

Timestamp : **22 Nov 2013 at 05:06:17 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

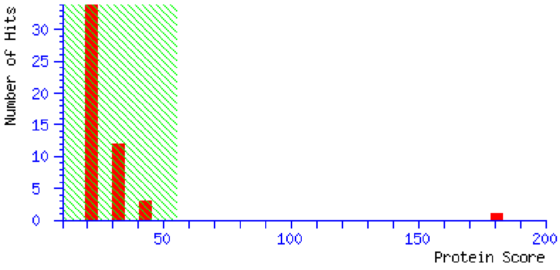
Top Score : **181 for DESM_MOUSE, Desmin OS=Mus musculus GN=Des PE=1 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary ReportIndex

	Accession	Mass	Score	Description
1.	DESM_MOUSE	53522	181	Desmin OS=Mus musculus GN=Des PE=1 SV=3
2.	NT5C_MOUSE	23290	43	5'(3')-deoxyribonucleotidase, cytosolic type OS=Mus musculus GN=Nt5c PE=1 SV=1
3.	COG5_MOUSE	92113	39	Conserved oligomeric Golgi complex subunit 5 OS=Mus musculus GN=Cog5 PE=2 SV=2
4.	ATPB_MOUSE	56265	39	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2
5.	AP1G1_MOUSE	92147	34	AP-1 complex subunit gamma-1 OS=Mus musculus GN=Ap1g1 PE=1 SV=3
6.	NEIL1_MOUSE	44015	34	Endonuclease VIII-like 1 OS=Mus musculus GN=Neil1 PE=2 SV=3
7.	SNIP_MOUSE	135403	34	p130Cas-associated protein OS=Mus musculus GN=P140 PE=1 SV=2
8.	NDUV1_MOUSE	51486	30	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Mus musculus GN=Ndufv1 PE=1 SV=1
9.	CQ049_MOUSE	18042	30	MLL1/MLL complex subunit C17orf49 homolog OS=Mus musculus PE=1 SV=1
10.	USH1C_MOUSE	102620	29	Harmonin OS=Mus musculus GN=Ush1c PE=1 SV=1

Results List

1. DESM_MOUSE **Mass:** 53522 **Score:** 181 **Expect:** 1.3e-014 **Matches:** 14

Desmin OS=Mus musculus GN=Des PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
999.5116	998.5044	998.4967	7.66	375 -	382	1	---	R.HLKDEMAR.H
1039.5560	1038.5487	1038.5458	2.86	240 -	247	1	---	K.KVHEEEIR.E
1060.5584	1059.5512	1059.5560	-4.56	406 -	414	1	---	R.KLLEGEESR.I
1086.5800	1085.5727	1085.5829	-9.42	164 -	172	0	---	R.QVEVLTNQR.A
1268.5814	1267.5742	1267.5754	-0.99	150 -	159	0	---	R.VAELYEEEMR.E
1281.6396	1280.6323	1280.6434	-8.68	395 -	405	0	---	K.MALDVEIATYR.K
1555.7232	1554.7160	1554.7063	6.25	355 -	368	0	---	R.FASEANGYQDNIAR.L
1561.8577	1560.8504	1560.8511	-0.43	227 -	239	1	---	R.RIESLNEEIAFLK.K
1587.7867	1586.7795	1586.7900	-6.63	105 -	117	1	---	R.TNEKVELQELNDR.F
1633.8962	1632.8890	1632.8988	-6.00	415 -	428	0	---	R.INLPIQTFSALNFR.E
1673.8520	1672.8448	1672.8532	-5.06	127 -	141	0	29	R.FLEQQNAALAAEVNR.L
1699.8530	1698.8458	1698.8537	-4.65	175 -	188	1	---	R.VDVERDNLIDDLQR.L
1729.8773	1728.8700	1728.8754	-3.13	299 -	314	1	---	K.VSDLTQAANKNNDALR.Q
2755.3299	2754.3226	2754.3501	-9.96	79 -	104	0	---	R.APSYGAGELLDFSLADAVNQEFLATR.T

No match to: 956.5613, 1011.5072, 1104.0397, 1406.6731, 1435.7531, 1601.8007, 1650.9003, 1689.9384, 1822.9070, 1988.0221, 2453.2004

2. NT5C_MOUSE **Mass:** 23290 **Score:** 43 **Expect:** 0.78 **Matches:** 4

5'(3')-deoxyribonucleotidase, cytosolic type OS=Mus musculus GN=Nt5c PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
956.5613	955.5540	955.5749	-21.87	1 -	8	1	---	-.MAVKRPVR.V
1561.8577	1560.8504	1560.8069	27.9	135 -	148	1	---	R.DKTVVMGDLLIDDK.D
1633.8962	1632.8890	1632.8372	31.7	32 -	44	1	---	R.FPEEPHVPLEQRR.G
2453.2004	2452.1931	2452.2421	-19.96	9 -	30	1	---	R.VLVDMDGVLADFESGLLQGFRR.R + Oxidation (M)

No match to: 999.5116, 1011.5072, 1039.5560, 1060.5584, 1086.5800, 1104.0397, 1268.5814, 1281.6396, 1406.6731, 1435.7531, 1555.7232, 1587.7867, 1601.8007, 1650.9003, 1673.8520, 1689.9384, 1699.8530, 1729.8773, 1822.9070, 1988.0221, 2755.3299

3. COG5_MOUSE **Mass:** 92113 **Score:** 39 **Expect:** 1.9 **Matches:** 6

Conserved oligomeric Golgi complex subunit 5 OS=Mus musculus GN=Cog5 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
999.5116	998.5044	998.5509	-46.59	107 -	116	0	---	R.IGALQGAVDR.M
1086.5800	1085.5727	1085.5829	-9.39	206 -	214	1	---	R.LEVENQAKR.L
1435.7531	1434.7458	1434.7579	-8.41	793 -	805	1	---	R.GALEAYVQSVRSR.D
1699.8530	1698.8458	1698.8651	-11.37	329 -	342	0	---	R.DPVSHICFIEEIIK.D
1988.0221	1987.0148	1987.0374	-11.40	46 -	63	0	---	K.TYTSQSIHQAVIAEQLAK.L
2453.2004	2452.1931	2452.2898	-39.42	809 -	829	1	---	K.EFAPVYPIMVQLLQKAMYALQ.-

No match to: 956.5613, 1011.5072, 1039.5560, 1060.5584, 1104.0397, 1268.5814, 1281.6396, 1406.6731, 1555.7232, 1561.8577, 1587.7867, 1601.8007, 1633.8962, 1650.9003, 1673.8520, 1689.9384, 1729.8773, 1822.9070, 2755.3299

4. ATPB_MOUSE **Mass:** 56265 **Score:** 39 **Expect:** 2 **Matches:** 5

ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1406.6731	1405.6658	1405.6739	-5.73	226 -	239	0	---	K.AHGGYSVFAGVGER.T

1435.7531	1434.7458	1434.7467	-0.59	311 -	324	0	---	R.FTQAGSEVSALLGR.I
1601.8007	1600.7934	1600.8031	-6.07	265 -	279	0	---	K.VALVYGQMNEPPGAR.A
1650.9003	1649.8930	1649.9101	-10.32	95 -	109	0	---	R.LVLEVAQHLGESTVR.T
1988.0221	1987.0148	1987.0262	-5.74	388 -	406	0	---	R.AIAELGIYPAVDPLDSTSR.I

No match to: 956.5613, 999.5116, 1011.5072, 1039.5560, 1060.5584, 1086.5800, 1104.0397, 1268.5814, 1281.6396, 1555.7232, 1561.8577, 1587.7867, 1633.8962, 1673.8520, 1689.9384, 1699.8530, 1729.8773, 1822.9070, 2453.2004, 2755.3299

5. AP1G1_MOUSE **Mass:** 92147 **Score:** 34 **Expect:** 6.3 **Matches:** 6

AP-1 complex subunit gamma-1 OS=Mus musculus GN=Ap1g1 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1268.5814	1267.5742	1267.6269	-41.63	335 -	345	0	---	K.TVQTDHNAVQR.H
1406.6731	1405.6658	1405.6772	-8.10	573 -	583	1	---	K.YDHMRSALLER.M + Oxidation (M)
1435.7531	1434.7458	1434.7210	17.3	578 -	589	1	---	R.SALLERMPVMEK.V + 2 Oxidation (M)
1561.8577	1560.8504	1560.7869	40.7	335 -	347	1	---	K.TVQTDHNAVQRHR.S
1633.8962	1632.8890	1632.8619	16.6	167 -	180	1	---	R.KVPELMEMFLPATK.N
2453.2004	2452.1931	2452.1741	7.74	53 -	72	0	---	K.LLYMHMLGYPAHFGQLECLK.L + 2 Oxidation (M)

No match to: 956.5613, 999.5116, 1011.5072, 1039.5560, 1060.5584, 1086.5800, 1104.0397, 1281.6396, 1555.7232, 1587.7867, 1601.8007, 1650.9003, 1673.8520, 1689.9384, 1699.8530, 1729.8773, 1822.9070, 1988.0221, 2755.3299

6. NEIL1_MOUSE **Mass:** 44015 **Score:** 34 **Expect:** 6.6 **Matches:** 4

Endonuclease VIII-like 1 OS=Mus musculus GN=Neil1 PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1633.8962	1632.8890	1632.8637	15.5	96 -	109	1	---	R.HAHLRFYTAPPAPR.L
1673.8520	1672.8448	1672.8016	25.8	374 -	389	1	---	K.TIPDTRPREAGESSAS.-
1822.9070	1821.8997	1821.9084	-4.76	79 -	95	0	---	R.FGMSGSFQLVPAEALPR.H + Oxidation (M)
1988.0221	1987.0148	1986.9799	17.6	35 -	52	0	---	R.NPEVPFESSAYHISALAR.G

No match to: 956.5613, 999.5116, 1011.5072, 1039.5560, 1060.5584, 1086.5800, 1104.0397, 1268.5814, 1281.6396, 1406.6731, 1435.7531, 1555.7232, 1561.8577, 1587.7867, 1601.8007, 1650.9003, 1689.9384, 1699.8530, 1729.8773, 2453.2004, 2755.3299

7. SNIP_MOUSE **Mass:** 135403 **Score:** 34 **Expect:** 6.9 **Matches:** 7

p130Cas-associated protein OS=Mus musculus GN=P140 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
956.5613	955.5540	955.5702	-16.94	293 -	301	0	---	K.SPNTAILIK.D
999.5116	998.5044	998.4603	44.1	1194 -	1200	1	---	K.QRTEYMR.I + Oxidation (M)
1011.5072	1010.4999	1010.4967	3.13	347 -	354	1	---	R.REMVYASR.E
1060.5584	1059.5512	1059.5309	19.2	723 -	732	0	---	R.GLQNSASDLR.G
1281.6396	1280.6323	1280.5745	45.1	34 -	45	1	---	R.DPGGRGEPDPER.S
1822.9070	1821.8997	1821.9082	-4.65	186 -	203	1	---	R.SSRHTQGAQPGLADQAAK.L
1988.0221	1987.0148	1986.9581	28.5	813 -	829	1	---	R.DVAHNHRLMPGPELEEK.A + Oxidation (M)

No match to: 1039.5560, 1086.5800, 1104.0397, 1268.5814, 1406.6731, 1435.7531, 1555.7232, 1561.8577, 1587.7867, 1601.8007, 1633.8962, 1650.9003, 1673.8520, 1689.9384, 1699.8530, 1729.8773, 2453.2004, 2755.3299

8. NDUV1_MOUSE **Mass:** 51486 **Score:** 30 **Expect:** 15 **Matches:** 3

NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Mus musculus GN=Ndufv1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1435.7531	1434.7458	1434.6748	49.5	387 -	398	1	---	R.EGVDWMNKVMAR.F
1561.8577	1560.8504	1560.7865	41.0	138 -	152	1	---	K.LVEGCLVGGRAMGAR.A + Oxidation (M)
1673.8520	1672.8448	1672.8468	-1.19	133 -	147	1	11	R.HDPHKLVEGCLVGGR.A

No match to: 956.5613, 999.5116, 1011.5072, 1039.5560, 1060.5584, 1086.5800, 1104.0397, 1268.5814, 1281.6396, 1406.6731, 1555.7232, 1587.7867, 1601.8007, 1633.8962, 1650.9003, 1689.9384, 1699.8530, 1729.8773, 1822.9070, 1988.0221, 2453.2004, 2755.3299

9. CQ049_MOUSE **Mass:** 18042 **Score:** 30 **Expect:** 16 **Matches:** 3

MLL1/MLL complex subunit C17orf49 homolog OS=Mus musculus PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1601.8007	1600.7934	1600.7984	-3.13	84 -	98	0	---	K.VYEDSGIPLPAESPK.K
1673.8520	1672.8448	1672.8355	5.53	56 -	69	1	---	K.RFGDDLNHISCVIK.E
1729.8773	1728.8700	1728.8934	-13.51	84 -	99	1	---	K.VYEDSGIPLPAESPKK.G

No match to: 956.5613, 999.5116, 1011.5072, 1039.5560, 1060.5584, 1086.5800, 1104.0397, 1268.5814, 1281.6396, 1406.6731, 1435.7531, 1555.7232, 1561.8577, 1587.7867, 1633.8962, 1650.9003, 1689.9384, 1699.8530, 1822.9070, 1988.0221, 2453.2004, 2755.3299

10. USH1C_MOUSE **Mass:** 102620 **Score:** 29 **Expect:** 20 **Matches:** 5

Harmonin OS=Mus musculus GN=Ush1c PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1406.6731	1405.6658	1405.7201	-38.64	779 -	792	0	---	K.VVVSAVYEGGAAER.H
1561.8577	1560.8504	1560.8736	-14.85	90 -	103	1	---	R.LDRLHPEGLGLSVR.G
1587.7867	1586.7795	1586.7834	-2.52	330 -	341	1	---	K.ILQEQQEMERQR.R
1699.8530	1698.8458	1698.8537	-4.67	120 -	136	0	---	K.GGQADSVGLQVGDEIVR.I
2755.3299	2754.3226	2754.4197	-35.23	32 -	55	1	---	R.MYHQTMDVAVLVGDLKLVINEPNR.L

No match to: 956.5613, 999.5116, 1011.5072, 1039.5560, 1060.5584, 1086.5800, 1104.0397, 1268.5814, 1281.6396, 1435.7531, 1555.7232, 1601.8007, 1633.8962, 1650.9003, 1673.8520, 1689.9384, 1729.8773, 1822.9070, 1988.0221, 2453.2004

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (956.5613,1+) : <no title>

Query2 (999.5116,1+) : <no title>

Query3 (1011.5072,1+) : <no title>

Query4 (1039.5560,1+) : <no title>

Query5 (1060.5584,1+) : <no title>

Query6 (1086.5800,1+) : <no title>

Query7 (1104.0397,1+) : <no title>

Query8 (1268.5814,1+) : <no title>

Query9 (1281.6396,1+) : <no title>

Query10 (1406.6731,1+) : <no title>

Query11 (1435.7531,1+) : <no title>

Query12 (1555.7232,1+) : <no title>

Query13 (1561.8577,1+) : <no title>

Query14 (1587.7867,1+) : <no title>

Query15 (1601.8007,1+) : <no title>

Query16 (1633.8962,1+) : <no title>

Query17 (1650.9003,1+) : <no title>

Query18 (1673.8520,1+) : <no title>

Query19 (1689.9384,1+) : <no title>

Query20 (1699.8530,1+) : <no title>

Query21 (1729.8773,1+) : <no title>

Query22 (1822.9070,1+) : <no title>

Query23 (1988.0221,1+) : <no title>

Query24 (2453.2004,1+) : <no title>

Query25 (2755.3299,1+) : <no title>

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:46:36 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

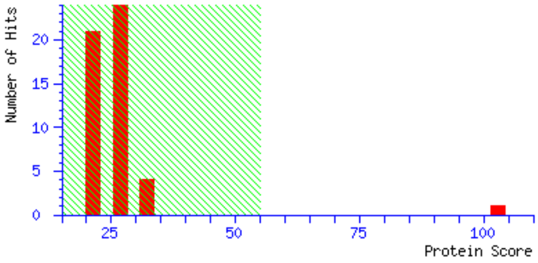
Top Score : **103 for ATPB_MOUSE, ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary ReportIndex

	Accession	Mass	Score	Description
1.	**ATPB_MOUSE**	56265	103	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2
2.	**CRYM_MOUSE**	33673	34	Mu-crystallin homolog OS=Mus musculus GN=Crym PE=1 SV=1
3.	**DYH12_MOUSE**	358738	30	Dynein heavy chain 12, axonemal OS=Mus musculus GN=Dnah12 PE=2 SV=2
4.	**IRK11_MOUSE**	43933	30	ATP-sensitive inward rectifier potassium channel 11 OS=Mus musculus GN=Kcnj11 PE=2 SV=1
5.	**AN33B_MOUSE**	53797	30	Ankyrin repeat domain-containing protein 33B OS=Mus musculus GN=Ankrd33b PE=2 SV=1
6.	**RRBP1_MOUSE**	173232	29	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2
7.	**AT2B2_MOUSE**	133701	29	Plasma membrane calcium-transporting ATPase 2 OS=Mus musculus GN=Atp2b2 PE=1 SV=2
8.	**TBX1_MOUSE**	51807	28	T-box transcription factor TBX1 OS=Mus musculus GN=Tbx1 PE=2 SV=2
9.	**CLPB_MOUSE**	76355	28	Caseinolytic peptidase B protein homolog OS=Mus musculus GN=Clpb PE=1 SV=1
10.	**CATM_MOUSE**	37898	27	Cathepsin M OS=Mus musculus GN=Ctsm PE=2 SV=1

Results List

1. ATPB_MOUSE **Mass:** 56265 **Score:** 103 **Expect:** 8.1e-007 **Matches:** 8

ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide

1038.5673	1037.5601	1037.5869	-25.90	134 -	143	0	---	K.IPVGPETLGR.I
1262.6369	1261.6296	1261.6336	-3.17	110 -	121	0	---	R.TIAMDGTEGLVR.G
1406.6653	1405.6580	1405.6739	-11.27	226 -	239	0	23	K.AHGGYSVFAGVGER.T
1435.7244	1434.7172	1434.7467	-20.58	311 -	324	0	---	R.FTQAGSEVSALLGR.I
1601.7755	1600.7682	1600.8031	-21.82	265 -	279	0	---	K.VALVYGQMNEPPGAR.A
1617.7612	1616.7539	1616.7981	-27.29	265 -	279	0	---	K.VALVYGQMNEPPGAR.A + Oxidation (M)
1650.8884	1649.8811	1649.9101	-17.53	95 -	109	0	18	R.LVLEVAQHLGESTVR.T
1919.0559	1918.0486	1918.0888	-20.92	125 -	143	1	---	K.VLDSGAPIKIPVGPETLGR.I

No match to: 856.5261, 936.5114, 997.5256, 1012.4944, 1112.5431, 1141.5575, 1148.5789, 1169.6429, 1170.6307, 1231.5890, 1244.5933, 1249.5964, 1376.7110, 1562.8891, 1718.8403, 1782.9277, 2176.9539, 2421.1422

2. CRYM_MOUSE **Mass:** 33673 **Score:** 34 **Expect:** 6.6 **Matches:** 4

Mu-crystallin homolog OS=Mus musculus GN=Crym PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1112.5431	1111.5359	1111.5444	-7.73	37 -	47	0	---	K.GPDGGVMQPVR.T
1141.5575	1140.5502	1140.5451	4.44	304 -	313	0	---	K.LVYDSWSSGK.-
1562.8891	1561.8818	1561.8464	22.7	242 -	255	1	---	R.QAVLYVDSREAALK.E
1650.8884	1649.8811	1649.8009	48.6	171 -	185	1	---	R.ENAEKFASTVQGDVR.V

No match to: 856.5261, 936.5114, 997.5256, 1012.4944, 1038.5673, 1148.5789, 1169.6429, 1170.6307, 1231.5890, 1244.5933, 1249.5964, 1262.6369, 1376.7110, 1406.6653, 1435.7244, 1601.7755, 1617.7612, 1718.8403, 1782.9277, 1919.0559, 2176.9539, 2421.1422

3. DYH12_MOUSE **Mass:** 358738 **Score:** 30 **Expect:** 14 **Matches:** 8

Dynein heavy chain 12, axonemal OS=Mus musculus GN=Dnah12 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1012.4944	1011.4871	1011.4881	-1.03	942 -	949	1	---	K.DIMKFCAK.D
1141.5575	1140.5502	1140.5961	-40.23	1900 -	1908	1	---	K.LMNHLEKEK.Y
1244.5933	1243.5861	1243.6408	-44.01	2 -	13	1	---	M.SDPNKTAIAAEK.E
1262.6369	1261.6296	1261.6302	-0.48	1600 -	1610	1	---	R.EFALAESPDRK.W
1435.7244	1434.7172	1434.7394	-15.53	668 -	678	1	---	K.WELTKYPELEK.L
1601.7755	1600.7682	1600.7766	-5.25	752 -	764	1	---	K.RSLMEEKPEEEPK.E
1617.7612	1616.7539	1616.7715	-10.87	752 -	764	1	---	K.RSLMEEKPEEEPK.E + Oxidation (M)
1650.8884	1649.8811	1649.9188	-22.82	2111 -	2123	1	15	K.HTMIRLFVHEVLR.V

No match to: 856.5261, 936.5114, 997.5256, 1038.5673, 1112.5431, 1148.5789, 1169.6429, 1170.6307, 1231.5890, 1249.5964, 1376.7110, 1406.6653, 1562.8891, 1718.8403, 1782.9277, 1919.0559, 2176.9539, 2421.1422

4. IRK11_MOUSE **Mass:** 43933 **Score:** 30 **Expect:** 17 **Matches:** 4

ATP-sensitive inward rectifier potassium channel 11 OS=Mus musculus GN=Kcnj11 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
997.5256	996.5183	996.4876	30.8	17 -	25	0	---	R.LAEDPAEPR.Y
1231.5890	1230.5817	1230.6245	-34.75	315 -	325	0	---	R.FVPIVAEEDGR.Y
1376.7110	1375.7037	1375.7347	-22.56	378 -	390	1	---	K.AKPKFSISPDSLS.-
1601.7755	1600.7682	1600.8429	-46.66	208 -	221	0	---	K.SMIISATIHMQVVR.K + Oxidation (M)

No match to: 856.5261, 936.5114, 1012.4944, 1038.5673, 1112.5431, 1141.5575, 1148.5789, 1169.6429, 1170.6307, 1244.5933, 1249.5964,

1262.6369, 1406.6653, 1435.7244, 1562.8891, 1617.7612, 1650.8884, 1718.8403, 1782.9277, 1919.0559, 2176.9539, 2421.1422

5. AN33B_MOUSE **Mass:** 53797 **Score:** 30 **Expect:** 18 **Matches:** 5

Ankyrin repeat domain-containing protein 33B OS=Mus musculus GN=Ankrd33b PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1141.5575	1140.5502	1140.6001	-43.79	183	192	0	---	R.NIFGFTALMK.A
1249.5964	1248.5892	1248.5955	-5.05	204	215	0	2	R.ALMMAGADVQAR.D + Oxidation (M)
1435.7244	1434.7172	1434.6892	19.5	220	232	0	---	R.GLSPQEWAAYTGR.A
1601.7755	1600.7682	1600.7814	-8.21	204	218	1	---	R.ALMMAGADVQARDPR.R
1617.7612	1616.7539	1616.7763	-13.81	204	218	1	---	R.ALMMAGADVQARDPR.R + Oxidation (M)

No match to: 856.5261, 936.5114, 997.5256, 1012.4944, 1038.5673, 1112.5431, 1148.5789, 1169.6429, 1170.6307, 1231.5890, 1244.5933, 1262.6369, 1376.7110, 1406.6653, 1562.8891, 1650.8884, 1718.8403, 1782.9277, 1919.0559, 2176.9539, 2421.1422

6. RRBP1_MOUSE **Mass:** 173232 **Score:** 29 **Expect:** 20 **Matches:** 7

Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
997.5256	996.5183	996.5101	8.27	1097	1105	0	---	R.AQTSHANLR.A
1148.5789	1147.5716	1147.5833	-10.18	189	200	1	---	K.ASSPATSSQGKK.G
1249.5964	1248.5892	1248.6197	-24.48	1244	1254	1	---	R.SLTQAKEESEK.Q
1376.7110	1375.7037	1375.6765	19.7	1516	1526	1	---	R.TACRIQEELEK.L
1601.7755	1600.7682	1600.8308	-39.09	1427	1440	0	---	R.QLLLESQSQLDEAK.S
1782.9277	1781.9204	1781.9523	-17.91	1118	1133	1	---	R.VAELHSKLQSSEVEVK.S
2176.9539	2175.9466	2176.0153	-31.56	1407	1426	1	---	K.HMAAASAECQNYAKEVAGLR.Q

No match to: 856.5261, 936.5114, 1012.4944, 1038.5673, 1112.5431, 1141.5575, 1169.6429, 1170.6307, 1231.5890, 1244.5933, 1262.6369, 1406.6653, 1435.7244, 1562.8891, 1617.7612, 1650.8884, 1718.8403, 1919.0559, 2421.1422

7. AT2B2_MOUSE **Mass:** 133701 **Score:** 29 **Expect:** 22 **Matches:** 6

Plasma membrane calcium-transporting ATPase 2 OS=Mus musculus GN=Atp2b2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1170.6307	1169.6234	1169.5928	26.2	478	488	0	---	K.EIPDPSSINAK.T
1231.5890	1230.5817	1230.5840	-1.88	723	732	1	---	R.NEKGEIEQER.I
1376.7110	1375.7037	1375.7460	-30.73	186	196	1	---	R.IEQEQKFTVVR.A
1406.6653	1405.6580	1405.6006	40.9	570	580	1	---	K.MPDESFRMYSK.G + Oxidation (M)
1650.8884	1649.8811	1649.8447	22.1	785	801	1	---	K.KADVGFAMGIAGTDVAK.E
1718.8403	1717.8330	1717.7764	33.0	255	270	0	---	K.DPMLLSGTHVMEGSGR.M + 2 Oxidation (M)

No match to: 856.5261, 936.5114, 997.5256, 1012.4944, 1038.5673, 1112.5431, 1141.5575, 1148.5789, 1169.6429, 1244.5933, 1249.5964, 1262.6369, 1435.7244, 1562.8891, 1601.7755, 1617.7612, 1782.9277, 1919.0559, 2176.9539, 2421.1422

8. TBX1_MOUSE **Mass:** 51807 **Score:** 28 **Expect:** 28 **Matches:** 4

T-box transcription factor TBX1 OS=Mus musculus GN=Tbx1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
997.5256	996.5183	996.5103	8.06	128	135	0	---	R.MFPTFQVK.L
1169.6429	1168.6356	1168.6063	25.1	127	135	1	---	R.RMFPTFQVK.L + Oxidation (M)

1718.8403	1717.8330	1717.8246	4.87	41 -	57	0	---	R.YDPCAAVPGAPGPPPPR.A
1782.9277	1781.9204	1781.8849	19.9	387 -	402	0	---	R.LEAPGASEPLHHHPYK.Y

No match to: 856.5261, 936.5114, 1012.4944, 1038.5673, 1112.5431, 1141.5575, 1148.5789, 1170.6307, 1231.5890, 1244.5933, 1249.5964, 1262.6369, 1376.7110, 1406.6653, 1435.7244, 1562.8891, 1601.7755, 1617.7612, 1650.8884, 1919.0559, 2176.9539, 2421.1422

9. CLPB_MOUSE **Mass:** 76355 **Score:** 28 **Expect:** 29 **Matches:** 5

Caseinolytic peptidase B protein homolog OS=Mus musculus GN=Clpb PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
936.5114	935.5041	935.4932	11.6	1 -	8	0	---	-.MMLSAVLR.R + Oxidation (M)
997.5256	996.5183	996.5352	-16.96	591 -	598	1	---	R.SIKHEVER.R
1249.5964	1248.5892	1248.5880	0.89	481 -	490	1	2	R.QEALEMSRNR.I + Oxidation (M)
1435.7244	1434.7172	1434.6660	35.6	491 -	503	0	---	R.IAENLGDVQMSDK.I + Oxidation (M)
1718.8403	1717.8330	1717.8093	13.8	379 -	392	1	---	R.LDMSEFQERHEVAK.F

No match to: 856.5261, 1012.4944, 1038.5673, 1112.5431, 1141.5575, 1148.5789, 1169.6429, 1170.6307, 1231.5890, 1244.5933, 1262.6369, 1376.7110, 1406.6653, 1562.8891, 1601.7755, 1617.7612, 1650.8884, 1782.9277, 1919.0559, 2176.9539, 2421.1422

10. CATM_MOUSE **Mass:** 37898 **Score:** 27 **Expect:** 30 **Matches:** 5

Cathepsin M OS=Mus musculus GN=Ctsm PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1012.4944	1011.4871	1011.5178	-30.34	253 -	260	0	---	R.HASFLFYK.R
1038.5673	1037.5601	1037.5254	33.4	61 -	70	0	---	K.LHNGENGLGK.H
1148.5789	1147.5716	1147.5444	23.7	49 -	57	1	---	K.RAVWEDNMK.K
1601.7755	1600.7682	1600.7126	34.7	300 -	313	1	---	K.NSMGTQWGNKGYMK.I
1617.7612	1616.7539	1616.7075	28.7	300 -	313	1	---	K.NSMGTQWGNKGYMK.I + Oxidation (M)

No match to: 856.5261, 936.5114, 997.5256, 1112.5431, 1141.5575, 1169.6429, 1170.6307, 1231.5890, 1244.5933, 1249.5964, 1262.6369, 1376.7110, 1406.6653, 1435.7244, 1562.8891, 1650.8884, 1718.8403, 1782.9277, 1919.0559, 2176.9539, 2421.1422

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (856.5261,1+) : <no title>

Query2 (936.5114,1+) : <no title>

Query3 (997.5256,1+) : <no title>

Query4 (1012.4944,1+) : <no title>

Query5 (1038.5673,1+) : <no title>

Query6 (1112.5431,1+) : <no title>

Query7 (1141.5575,1+) : <no title>

Query8 (1148.5789,1+) : <no title>

Query9 (1169.6429,1+) : <no title>

Query10 (1170.6307,1+) : <no title>

Query11 (1231.5890,1+) : <no title>

Query12 (1244.5933,1+) : <no title>

Query13 (1249.5964,1+) : <no title>

Query14 (1262.6369,1+) : <no title>

Query15 (1376.7110,1+) : <no title>

Query16 (1406.6653,1+) : <no title>

Query17 (1435.7244,1+) : <no title>

Query18 (1562.8891,1+) : <no title>

Query19 (1601.7755,1+) : <no title>

Query20 (1617.7612,1+) : <no title>

Query21 (1650.8884,1+) : <no title>

Query22 (1718.8403,1+) : <no title>

Query23 (1782.9277,1+) : <no title>

Query24 (1919.0559,1+) : <no title>

Query25 (2176.9539,1+) : <no title>

Query26 (2421.1422,1+) : <no title>

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:46:17 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

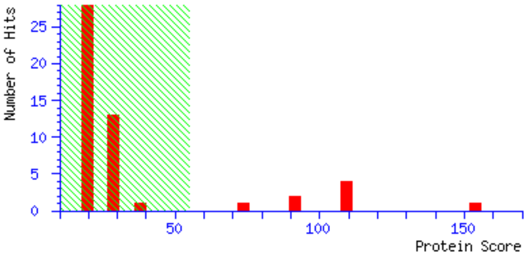
Top Score : **154 for COPE_MOUSE, Coatomer subunit epsilon OS=Mus musculus GN=Cope PE=2 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**COPE_MOUSE**	34773	154	Coatomer subunit epsilon OS=Mus musculus GN=Cope PE=2 SV=3
2.	**ACTH_MOUSE**	42249	108	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1
3.	**ACTA_MOUSE**	42381	108	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1
4.	**ACTC_MOUSE**	42334	108	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1
5.	**ACTS_MOUSE**	42366	107	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1
6.	**ACTB_MOUSE**	42052	96	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1
7.	**ACTG_MOUSE**	42108	96	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1
8.	**ACTBL_MOUSE**	42319	73	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1
9.	**CCD73_MOUSE**	121056	40	Coiled-coil domain-containing protein 73 OS=Mus musculus GN=Ccdc73 PE=1 SV=2
10.	**NHRF2_MOUSE**	37722	32	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Mus musculus GN=Slc9a3r2 PE=1 SV=2

Results List

1. COPE_MOUSE **Mass:** 34773 **Score:** 154 **Expect:** 6.5e-012 **Matches:** 7

Coatomer subunit epsilon OS=Mus musculus GN=Cope PE=2 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
812.4127	811.4054	811.4228	-21.48	53 -	58	0	---	R.DVFLYR.A
1059.5264	1058.5191	1058.5608	-39.34	98 -	106	0	---	R.DSIVLELDR.E
1458.6116	1457.6044	1457.6609	-38.77	86 -	97	0	24	R.MFAEYLASENQR.D
1474.5907	1473.5834	1473.6558	-49.10	86 -	97	0	---	R.MFAEYLASENQR.D + Oxidation (M)
2061.8752	2060.8679	2060.9374	-33.71	24 -	40	0	32	K.NAFYIGSYQQCINEAQR.V
2171.1007	2170.0934	2170.1634	-32.22	66 -	85	0	37	K.YGVVLDEIKPSSAPELQAVR.M
2299.1626	2298.1553	2298.2583	-44.82	65 -	85	1	---	R.KYGVVLDEIKPSSAPELQAVR.M

No match to: 937.5480, 945.5285, 976.4209, 1130.5238, 1132.4911, 1194.5902, 1198.6609, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1790.8248, 1804.8276, 1976.9548, 2137.9493, 2148.9656, 2154.9821

2. ACTH_MOUSE **Mass:** 42249 **Score:** 108 **Expect:** 2.6e-007 **Matches:** 5

Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
976.4209	975.4136	975.4410	-28.06	20 -	29	0	---	K.AGFAGDDAPR.A
1130.5238	1129.5165	1129.5404	-21.13	198 -	207	0	---	R.GYSFVTTAER.E
1198.6609	1197.6536	1197.6982	-37.25	30 -	40	0	---	R.AVFPSIVGRPR.H
1790.8248	1789.8175	1789.8846	-37.51	240 -	255	0	67	K.SYELPDGQVITIGNER.F
1976.9548	1975.9475	1975.8986	24.8	70 -	85	0	---	K.YPIEHGIITNWDDMEK.I + Oxidation (M)

No match to: 812.4127, 937.5480, 945.5285, 1059.5264, 1132.4911, 1194.5902, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1458.6116, 1474.5907, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1804.8276, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

3. ACTA_MOUSE **Mass:** 42381 **Score:** 108 **Expect:** 2.6e-007 **Matches:** 5

Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
976.4209	975.4136	975.4410	-28.06	21 -	30	0	---	K.AGFAGDDAPR.A
1130.5238	1129.5165	1129.5404	-21.13	199 -	208	0	---	R.GYSFVTTAER.E
1198.6609	1197.6536	1197.6982	-37.25	31 -	41	0	---	R.AVFPSIVGRPR.H
1790.8248	1789.8175	1789.8846	-37.51	241 -	256	0	67	K.SYELPDGQVITIGNER.F
1976.9548	1975.9475	1975.8986	24.8	71 -	86	0	---	K.YPIEHGIITNWDDMEK.I + Oxidation (M)

No match to: 812.4127, 937.5480, 945.5285, 1059.5264, 1132.4911, 1194.5902, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1458.6116, 1474.5907, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1804.8276, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

4. ACTC_MOUSE **Mass:** 42334 **Score:** 108 **Expect:** 2.6e-007 **Matches:** 5

Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
976.4209	975.4136	975.4410	-28.06	21 -	30	0	---	K.AGFAGDDAPR.A
1130.5238	1129.5165	1129.5404	-21.13	199 -	208	0	---	R.GYSFVTTAER.E
1198.6609	1197.6536	1197.6982	-37.25	31 -	41	0	---	R.AVFPSIVGRPR.H
1790.8248	1789.8175	1789.8846	-37.51	241 -	256	0	67	K.SYELPDGQVITIGNER.F
1976.9548	1975.9475	1975.8986	24.8	71 -	86	0	---	K.YPIEHGIITNWDDMEK.I + Oxidation (M)

No match to: 812.4127, 937.5480, 945.5285, 1059.5264, 1132.4911, 1194.5902, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1458.6116,

1474.5907, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1804.8276, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

5. ACTS_MOUSE **Mass:** 42366 **Score:** 107 **Expect:** 3.2e-007 **Matches:** 5

Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
976.4209	975.4136	975.4410	-28.06	21 -	30	0	---	K.AGFAGDDAPR.A
1130.5238	1129.5165	1129.5404	-21.13	199 -	208	0	---	R.GYSFVTTAER.E
1198.6609	1197.6536	1197.6982	-37.25	31 -	41	0	---	R.AVFPSIVGRPR.H
1790.8248	1789.8175	1789.8846	-37.51	241 -	256	0	67	K.SYELPDGQVITIGNER.F
1976.9548	1975.9475	1975.8986	24.8	71 -	86	0	---	K.YPIEHGIITNWDDMEK.I + Oxidation (M)

No match to: 812.4127, 937.5480, 945.5285, 1059.5264, 1132.4911, 1194.5902, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1458.6116, 1474.5907, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1804.8276, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

6. ACTB_MOUSE **Mass:** 42052 **Score:** 96 **Expect:** 4.3e-006 **Matches:** 4

Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
976.4209	975.4136	975.4410	-28.06	19 -	28	0	---	K.AGFAGDDAPR.A
1132.4911	1131.4839	1131.5197	-31.62	197 -	206	0	---	R.GYSFTTTAER.E
1198.6609	1197.6536	1197.6982	-37.25	29 -	39	0	---	R.AVFPSIVGRPR.H
1790.8248	1789.8175	1789.8846	-37.51	239 -	254	0	67	K.SYELPDGQVITIGNER.F

No match to: 812.4127, 937.5480, 945.5285, 1059.5264, 1130.5238, 1194.5902, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1458.6116, 1474.5907, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1804.8276, 1976.9548, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

7. ACTG_MOUSE **Mass:** 42108 **Score:** 96 **Expect:** 4.3e-006 **Matches:** 4

Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
976.4209	975.4136	975.4410	-28.06	19 -	28	0	---	K.AGFAGDDAPR.A
1132.4911	1131.4839	1131.5197	-31.62	197 -	206	0	---	R.GYSFTTTAER.E
1198.6609	1197.6536	1197.6982	-37.25	29 -	39	0	---	R.AVFPSIVGRPR.H
1790.8248	1789.8175	1789.8846	-37.51	239 -	254	0	67	K.SYELPDGQVITIGNER.F

No match to: 812.4127, 937.5480, 945.5285, 1059.5264, 1130.5238, 1194.5902, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1458.6116, 1474.5907, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1804.8276, 1976.9548, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

8. ACTBL_MOUSE **Mass:** 42319 **Score:** 73 **Expect:** 0.00089 **Matches:** 1

Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1790.8248	1789.8175	1789.8846	-37.51	240 -	255	0	67	R.SYELPDGQVITIGNER.F

No match to: 812.4127, 937.5480, 945.5285, 976.4209, 1059.5264, 1130.5238, 1132.4911, 1194.5902, 1198.6609, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1458.6116, 1474.5907, 1533.6625, 1547.6838, 1556.6491, 1752.7941, 1804.8276, 1976.9548, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

9. CCD73_MOUSE **Mass:** 121056 **Score:** 40 **Expect:** 1.8 **Matches:** 8

Coiled-coil domain-containing protein 73 OS=Mus musculus GN=Ccdc73 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
945.5285	944.5213	944.5178	3.64	117 -	124	1	---	K.EKEIEGLK.E
1059.5264	1058.5191	1058.5720	-49.96	936 -	944	1	---	K.NVVLDDTRK.N
1198.6609	1197.6536	1197.6353	15.3	207 -	216	1	---	K.QESEIHSLKK.E
1347.6438	1346.6365	1346.6426	-4.54	944 -	955	1	---	R.KNIESDPTSNSR.A
1379.6173	1378.6100	1378.5605	35.9	575 -	587	0	---	K.ASSNGMSNEMAHK.R + Oxidation (M)
1533.6625	1532.6553	1532.6929	-24.57	432 -	443	1	---	K.NTKSFCLDTEYR.E
1752.7941	1751.7868	1751.7567	17.2	664 -	677	1	---	K.QMVREESQCSTEPR.S + Oxidation (M)
1976.9548	1975.9475	1976.0401	-46.85	927 -	943	1	---	R.VITPVTFCKNVVLDDTR.K

No match to: 812.4127, 937.5480, 976.4209, 1130.5238, 1132.4911, 1194.5902, 1395.7317, 1419.8006, 1458.6116, 1474.5907, 1547.6838, 1556.6491, 1790.8248, 1804.8276, 2061.8752, 2137.9493, 2148.9656, 2154.9821, 2171.1007, 2299.1626

10. NHRF2_MOUSE **Mass:** 37722 **Score:** 32 **Expect:** 9.8 **Matches:** 4

Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Mus musculus GN=Slc9a3r2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1059.5264	1058.5191	1058.5356	-15.55	216 -	224	1	---	R.IKAQEDEAR.L
1458.6116	1457.6044	1457.6688	-44.19	17 -	29	0	---	R.GEQGYGFHLHGEK.G
1547.6838	1546.6765	1546.6980	-13.91	99 -	110	1	---	R.RQLTCTEEMAHR.G + Oxidation (M)
2154.9821	2153.9748	2154.0593	-39.22	293 -	312	1	---	R.DPFQESGLHLSPTAAEAKEK.A

No match to: 812.4127, 937.5480, 945.5285, 976.4209, 1130.5238, 1132.4911, 1194.5902, 1198.6609, 1347.6438, 1379.6173, 1395.7317, 1419.8006, 1474.5907, 1533.6625, 1556.6491, 1752.7941, 1790.8248, 1804.8276, 1976.9548, 2061.8752, 2137.9493, 2148.9656, 2171.1007, 2299.1626

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (812.4127,1+) : <no title>
Query2 (937.5480,1+) : <no title>
Query3 (945.5285,1+) : <no title>
Query4 (976.4209,1+) : <no title>
Query5 (1059.5264,1+) : <no title>
Query6 (1130.5238,1+) : <no title>
Query7 (1132.4911,1+) : <no title>

Query8 (1194.5902,1+)   : <no title>

Query9 (1198.6609,1+)   : <no title>

Query10 (1347.6438,1+) : <no title>

Query11 (1379.6173,1+) : <no title>

Query12 (1395.7317,1+) : <no title>

Query13 (1419.8006,1+) : <no title>

Query14 (1458.6116,1+) : <no title>

Query15 (1474.5907,1+) : <no title>

Query16 (1533.6625,1+) : <no title>

Query17 (1547.6838,1+) : <no title>

Query18 (1556.6491,1+) : <no title>

Query19 (1752.7941,1+) : <no title>

Query20 (1790.8248,1+) : <no title>

Query21 (1804.8276,1+) : <no title>

Query22 (1976.9548,1+) : <no title>

Query23 (2061.8752,1+) : <no title>

Query24 (2137.9493,1+) : <no title>

Query25 (2148.9656,1+) : <no title>

Query26 (2154.9821,1+) : <no title>

Query27 (2171.1007,1+) : <no title>

Query28 (2299.1626,1+) : <no title>

MATRIX SCIENCE Mascot Search Results

User :

Email :

Search title : Auto submitted by BioTools

Database : SwissProt 57.15 (515203 sequences; 181334896 residues)

Taxonomy : Mus musculus (house mouse) (16230 sequences)

Timestamp : 5 Nov 2013 at 04:45:50 GMT

Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.

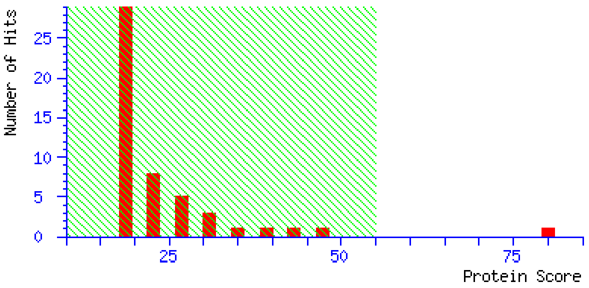
Top Score : 80 for TRY2_MOUSE, Anionic trypsin-2 OS=Mus musculus GN=Prss2 PE=2 SV=1

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**TRY2_MOUSE**	26871	80	Anionic trypsin-2 OS=Mus musculus GN=Prss2 PE=2 SV=1
2.	**Z518A_MOUSE**	167667	48	Zinc finger protein 518A OS=Mus musculus GN=Znf518a PE=1 SV=1
3.	**FOXQ1_MOUSE**	41716	44	Forkhead box protein Q1 OS=Mus musculus GN=Foxq1 PE=2 SV=2
4.	**EI2BD_MOUSE**	58130	41	Translation initiation factor eIF-2B subunit delta OS=Mus musculus GN=Eif2b4 PE=2 SV=1
5.	**NPS3A_MOUSE**	28405	34	Protein NipSnap homolog 3A OS=Mus musculus GN=Nipsnap3a PE=1 SV=1
6.	**K1C18_MOUSE**	47509	31	Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5
7.	**FUMH_MOUSE**	54564	30	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=2
8.	**KANK3_MOUSE**	84648	29	KN motif and ankyrin repeat domain-containing protein 3 OS=Mus musculus GN=Kank3 PE=2 SV=1
9.	**NINJ2_MOUSE**	15984	28	Ninjurin-2 OS=Mus musculus GN=Ninj2 PE=2 SV=1
10.	**TSAP1_MOUSE**	32744	27	tRNA selenocysteine 1-associated protein 1 OS=Mus musculus GN=Trnau1ap PE=1 SV=2

Results List

1. TRY2_MOUSE **Mass:** 26871 **Score:** 80 **Expect:** 0.00016 **Matches:** 2

Anionic trypsin-2 OS=Mus musculus GN=Prss2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.5978	-10.96	113 -	122	0	57	K.LASPVTLNAR.V
2213.0290	2212.0217	2212.0760	-24.54	73 -	92	0	---	R.LGEHNINVLEGNEQFVDSAK.I

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1520.7523, 1856.8076, 2121.9352, 2235.0383, 2250.0416

2. Z518A_MOUSE **Mass:** 167667 **Score:** 48 **Expect:** 0.24 **Matches:** 3

Zinc finger protein 518A OS=Mus musculus GN=Znf518a PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.6230	-35.14	960 -	969	0	31	R.SVPATLLVNK.K
1520.7523	1519.7451	1519.7842	-25.75	24 -	37	1	---	R.NEIADTIRSVSTSK.I
2235.0383	2234.0310	2233.9885	19.0	1434 -	1451	1	---	K.TTSEDVLKSQFNCWFCGR.V

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1856.8076, 2121.9352, 2213.0290, 2250.0416

3. FOXQ1_MOUSE **Mass:** 41716 **Score:** 44 **Expect:** 0.72 **Matches:** 2

Forkhead box protein Q1 OS=Mus musculus GN=Foxq1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.5727	13.2	244 -	253	1	26	R.SSPIARSPAR.Q
1520.7523	1519.7451	1519.7361	5.90	149 -	160	1	---	K.FPFFRGSYTGWR.N

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1856.8076, 2121.9352, 2213.0290, 2235.0383, 2250.0416

4. EI2BD_MOUSE **Mass:** 58130 **Score:** 41 **Expect:** 1.3 **Matches:** 1

Translation initiation factor eIF-2B subunit delta OS=Mus musculus GN=Eif2b4 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.6342	-45.92	313 -	322	0	35	K.IVLAAQAISR.F

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1520.7523, 1856.8076, 2121.9352, 2213.0290, 2235.0383, 2250.0416

5. NPS3A_MOUSE **Mass:** 28405 **Score:** 34 **Expect:** 6.9 **Matches:** 2

Protein NipSnap homolog 3A OS=Mus musculus GN=Nipsnap3a PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.6091	-21.76	6 -	15	1	12	R.SGLRTALAPR.V
2213.0290	2212.0217	2212.0953	-33.26	31 -	48	1	---	R.QSNGTFYEFRTYFLKPSK.T

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1520.7523, 1856.8076, 2121.9352, 2235.0383, 2250.0416

6. K1C18_MOUSE **Mass:** 47509 **Score:** 31 **Expect:** 14 **Matches:** 2

Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.5978	-10.96	143 -	151	0	12	R.IVLQIDNAR.L
2250.0416	2249.0343	2249.0746	-17.91	161 -	179	1	---	K.YETELAMRQSVESDIHGLR.K + Oxidation (M)

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1520.7523, 1856.8076, 2121.9352, 2213.0290, 2235.0383

7. FUMH_MOUSE **Mass:** 54564 **Score:** 30 **Expect:** 14 **Matches:** 3

Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1069.5950	1068.5877	1068.5927	-4.69	211 -	220	1	---	K.LHDALSAKSK.E
2121.9352	2120.9279	2120.9837	-26.30	41 -	58	1	---	R.MASQNSFRVEFDTFGELK.V + Oxidation (M)
2235.0383	2234.0310	2234.1252	-42.18	99 -	119	1	---	R.AAAEVNQEYGLDPKIASAIMK.A + Oxidation (M)

No match to: 1011.6013, 1041.5937, 1250.7584, 1266.7452, 1520.7523, 1856.8076, 2213.0290, 2250.0416

8. KANK3_MOUSE **Mass:** 84648 **Score:** 29 **Expect:** 19 **Matches:** 2

KN motif and ankyrin repeat domain-containing protein 3 OS=Mus musculus GN=Kank3 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.6091	-21.76	149 -	158	1	15	R.ALSPARAVTR.S
2213.0290	2212.0217	2211.9815	18.2	509 -	528	1	---	K.DAGDCELETHPELTAGREGR.C

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1520.7523, 1856.8076, 2121.9352, 2235.0383, 2250.0416

9. NINJ2_MOUSE **Mass:** 15984 **Score:** 28 **Expect:** 25 **Matches:** 2

Ninjurin-2 OS=Mus musculus GN=Ninj2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1520.7523	1519.7451	1519.7491	-2.68	2 -	13	1	---	M.ESDRETIHLQHR.H
2213.0290	2212.0217	2212.1054	-37.82	33 -	52	1	---	K.SVAESMLDVALFMSNAMRLK.S

No match to: 1011.6013, 1041.5937, 1069.5950, 1250.7584, 1266.7452, 1856.8076, 2121.9352, 2235.0383, 2250.0416

10. TSAP1_MOUSE **Mass:** 32744 **Score:** 27 **Expect:** 31 **Matches:** 1

tRNA selenocysteine 1-associated protein 1 OS=Mus musculus GN=Trnau1ap PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5937	1040.5864	1040.6342	-45.92	170 -	179	1	19	R.LSVAIPKASR.V

No match to: 1011.6013, 1069.5950, 1250.7584, 1266.7452, 1520.7523, 1856.8076, 2121.9352, 2213.0290, 2235.0383, 2250.0416

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (1011.6013,1+) : <no title>

Query2 (1041.5937,1+) : <no title>

Query3 (1069.5950,1+) : <no title>

Query4 (1250.7584,1+) : <no title>

Query5 (1266.7452,1+) : <no title>

Query6 (1520.7523,1+) : <no title>

Query7 (1856.8076,1+) : <no title>

Query8 (2121.9352,1+) : <no title>

Query9 (2213.0290,1+) : <no title>

Query10 (2235.0383,1+) : <no title>

Query11 (2250.0416,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:45:41 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

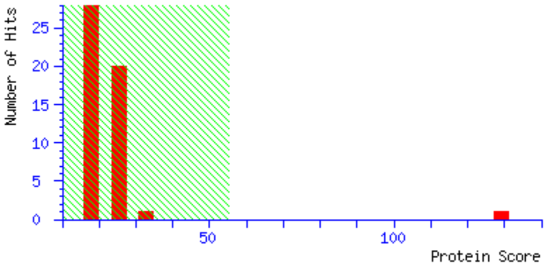
Top Score : **129 for OAT_MOUSE, Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**OAT_MOUSE**	48723	129	Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1
2.	**DDX3Y_MOUSE**	73838	31	ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2
3.	**CDK3_MOUSE**	34038	28	Cell division protein kinase 3 OS=Mus musculus GN=Cdk3 PE=1 SV=2
4.	**SGPP2_MOUSE**	40507	28	Sphingosine-1-phosphate phosphatase 2 OS=Mus musculus GN=Sgpp2 PE=2 SV=1
5.	**IFI4_MOUSE**	72347	28	Interferon-activable protein 204 OS=Mus musculus GN=Ifi204 PE=1 SV=2
6.	**LSM11_MOUSE**	40054	27	U7 snRNA-associated Sm-like protein LSm11 OS=Mus musculus GN=Lsm11 PE=1 SV=1
7.	**SEP11_MOUSE**	50005	26	Septin-11 OS=Mus musculus GN=Sept11 PE=1 SV=4
8.	**CF226_MOUSE**	12063	26	Uncharacterized protein C6orf226 homolog OS=Mus musculus PE=2 SV=1
9.	**ARI3C_MOUSE**	43834	26	AT-rich interactive domain-containing protein 3C OS=Mus musculus GN=Arid3c PE=2 SV=2
10.	**NKPD1_MOUSE**	67758	25	NTPase KAP family P-loop domain-containing protein 1 OS=Mus musculus GN=Nkpd1 PE=2 SV=2

Results List

1. OAT_MOUSE **Mass:** 48723 **Score:** 129 **Expect:** 2e-009 **Matches:** 5

Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1072.6388	1071.6316	1071.5924	36.5	363 -	372	0	---	K.LPSDVVTSVR.G
1492.9196	1491.9124	1491.8660	31.1	414 -	426	1	48	R.LAPPLVIKEDEIR.E
1619.9221	1618.9148	1618.8791	22.1	399 -	413	0	---	R.DNGLLAKPTHGDIIR.L
1811.0434	1810.0361	1809.9737	34.5	256 -	271	0	33	R.HQVLFIADEIQTGLAR.T
1889.1275	1888.1202	1888.0643	29.6	397 -	413	1	---	R.LRDNGLLAKPTHGDIIR.L

No match to: 1313.6580, 1535.8966, 1550.8923, 1602.9078, 1684.9577, 1823.0406, 1831.0568, 2085.1858, 2140.1497, 2177.1696, 2399.2348, 2405.4313, 2414.2248, 2431.2467

2. DDX3Y_MOUSE **Mass:** 73838 **Score:** 31 **Expect:** 13 **Matches:** 4

ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1313.6580	1312.6507	1312.6809	-23.03	362 -	372	1	---	R.RIVEQDTMPPK.G
2177.1696	2176.1624	2176.1012	28.1	2 -	22	0	---	M.SQVAAESTAGLDQQFVGLDLK.S
2399.2348	2398.2275	2398.2355	-3.33	387 -	406	1	---	K.EIQMLARDFLDEYIFLAVGR.V
2431.2467	2430.2394	2430.2438	-1.80	294 -	314	1	---	R.VRPCVVYGGADTVQQIRDLER.G

No match to: 1072.6388, 1492.9196, 1535.8966, 1550.8923, 1602.9078, 1619.9221, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2085.1858, 2140.1497, 2405.4313, 2414.2248

3. CDK3_MOUSE **Mass:** 34038 **Score:** 28 **Expect:** 25 **Matches:** 3

Cell division protein kinase 3 OS=Mus musculus GN=Cdk3 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1072.6388	1071.6316	1071.6539	-20.86	51 -	59	1	---	R.EISLLKELK.H
1602.9078	1601.9005	1601.9042	-2.29	143 -	157	1	---	K.LADFGLARAFGVPLR.T
2140.1497	2139.1424	2139.1787	-16.95	37 -	56	1	---	R.LDLEAEGVPSTAVREISLLK.E

No match to: 1313.6580, 1492.9196, 1535.8966, 1550.8923, 1619.9221, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2085.1858, 2177.1696, 2399.2348, 2405.4313, 2414.2248, 2431.2467

4. SGPP2_MOUSE **Mass:** 40507 **Score:** 28 **Expect:** 28 **Matches:** 3

Sphingosine-1-phosphate phosphatase 2 OS=Mus musculus GN=Sgpp2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1823.0406	1822.0333	1822.0505	-9.44	300 -	314	1	---	K.LSLQVLFSWFKVVTR.N
1831.0568	1830.0495	1830.0841	-18.91	76 -	91	0	---	R.LVVIWVLVMYIGQVAK.D
2414.2248	2413.2176	2413.1379	33.0	28 -	46	1	---	R.EASGEEHVVKNYFYYYLFR.F

No match to: 1072.6388, 1313.6580, 1492.9196, 1535.8966, 1550.8923, 1602.9078, 1619.9221, 1684.9577, 1811.0434, 1889.1275, 2085.1858, 2140.1497, 2177.1696, 2399.2348, 2405.4313, 2431.2467

5. IFI4_MOUSE **Mass:** 72347 **Score:** 28 **Expect:** 29 **Matches:** 4

Interferon-activable protein 204 OS=Mus musculus GN=Ifi204 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1313.6580	1312.6507	1312.6663	-11.91	560 -	571	0	---	R.GTFVSGEYLVNK.K
1535.8966	1534.8893	1534.8290	39.3	590 -	602	1	---	K.MEVVVYGRLTNVR.C

1602.9078	1601.9005	1601.8453	34.5	301	313	1	---	K.KNFIIISNYFESK.G
2177.1696	2176.1624	2176.0616	46.3	523	542	0	---	R.ASCVSDVNVNPTMVISNTLR.Q

No match to: 1072.6388, 1492.9196, 1550.8923, 1619.9221, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2085.1858, 2140.1497, 2399.2348, 2405.4313, 2414.2248, 2431.2467

6. LSM11_MOUSE **Mass:** 40054 **Score:** 27 **Expect:** 31 **Matches:** 3

U7 snRNA-associated Sm-like protein LSm11 OS=Mus musculus GN=Lsm11 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1313.6580	1312.6507	1312.6486	1.59	182	193	0	---	R.GVCTGFLVAFDK.F
2177.1696	2176.1624	2176.1542	3.77	334	350	1	---	K.VDYQQVFTRHINQIFIR.G
2399.2348	2398.2275	2398.1991	11.8	194	213	1	---	K.FWNMALTDVDETYRKPVLGK.A + Oxidation (M)

No match to: 1072.6388, 1492.9196, 1535.8966, 1550.8923, 1602.9078, 1619.9221, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2085.1858, 2140.1497, 2405.4313, 2414.2248, 2431.2467

7. SEP11_MOUSE **Mass:** 50005 **Score:** 26 **Expect:** 38 **Matches:** 3

Septin-11 OS=Mus musculus GN=Sept11 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1619.9221	1618.9148	1618.8567	35.9	96	110	0	---	K.LTIVDTVGFGDQINK.D
2085.1858	2084.1785	2084.0974	38.9	400	419	1	---	K.AAAQLLQSQAQQSGAQQTKK.D
2140.1497	2139.1424	2139.0960	21.7	15	34	0	---	R.NLSLSGHVGFDSLPDQLVNK.S

No match to: 1072.6388, 1313.6580, 1492.9196, 1535.8966, 1550.8923, 1602.9078, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2177.1696, 2399.2348, 2405.4313, 2414.2248, 2431.2467

8. CF226_MOUSE **Mass:** 12063 **Score:** 26 **Expect:** 45 **Matches:** 2

Uncharacterized protein C6orf226 homolog OS=Mus musculus PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1313.6580	1312.6507	1312.6735	-17.39	90	100	1	---	R.TQPPTIEERSR.G
2399.2348	2398.2275	2398.1699	24.0	68	89	0	---	R.RPKPWEDAGSAASPCTIALDTR.T

No match to: 1072.6388, 1492.9196, 1535.8966, 1550.8923, 1602.9078, 1619.9221, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2085.1858, 2140.1497, 2177.1696, 2405.4313, 2414.2248, 2431.2467

9. ARI3C_MOUSE **Mass:** 43834 **Score:** 26 **Expect:** 46 **Matches:** 3

AT-rich interactive domain-containing protein 3C OS=Mus musculus GN=Arid3c PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1313.6580	1312.6507	1312.6922	-31.59	319	330	1	---	K.RAVLMGPVDSPR.L + Oxidation (M)
1602.9078	1601.9005	1601.8447	34.9	295	309	1	---	R.LALPMGLASEATREK.L + Oxidation (M)
2177.1696	2176.1624	2176.1827	-9.33	320	340	1	---	R.AVLMGPVDSPRLGAPPSFLPR.G

No match to: 1072.6388, 1492.9196, 1535.8966, 1550.8923, 1619.9221, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2085.1858, 2140.1497, 2399.2348, 2405.4313, 2414.2248, 2431.2467

10. NKPD1_MOUSE **Mass:** 67758 **Score:** 25 **Expect:** 47 **Matches:** 3

NTPase KAP family P-loop domain-containing protein 1 OS=Mus musculus GN=Nkpd1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide

2140.1497	2139.1424	2139.1246	8.34	156 - 178	0	---	K.ALGGAATTLSGSGLLMAVYSVGK.H + Oxidation (M)
2399.2348	2398.2275	2398.2605	-13.74	540 - 563	1	---	R.AVSALKPPSPPKSPSQDGPQASPR.A
2414.2248	2413.2176	2413.2590	-17.16	427 - 447	1	---	R.VGPTPRHAVAWVVLANQWPCR.L

No match to: 1072.6388, 1313.6580, 1492.9196, 1535.8966, 1550.8923, 1602.9078, 1619.9221, 1684.9577, 1811.0434, 1823.0406, 1831.0568, 1889.1275, 2085.1858, 2177.1696, 2405.4313, 2431.2467

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (1072.6388,1+) : <no title>
Query2 (1313.6580,1+) : <no title>
Query3 (1492.9196,1+) : <no title>
Query4 (1535.8966,1+) : <no title>
Query5 (1550.8923,1+) : <no title>
Query6 (1602.9078,1+) : <no title>
Query7 (1619.9221,1+) : <no title>
Query8 (1684.9577,1+) : <no title>
Query9 (1811.0434,1+) : <no title>
Query10 (1823.0406,1+) : <no title>
Query11 (1831.0568,1+) : <no title>
Query12 (1889.1275,1+) : <no title>
Query13 (2085.1858,1+) : <no title>
Query14 (2140.1497,1+) : <no title>
Query15 (2177.1696,1+) : <no title>
Query16 (2399.2348,1+) : <no title>
Query17 (2405.4313,1+) : <no title>
Query18 (2414.2248,1+) : <no title>
Query19 (2431.2467,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : Auto submitted by BioTools

Database : SwissProt 57.15 (515203 sequences; 181334896 residues)

Taxonomy : Mus musculus (house mouse) (16230 sequences)

Timestamp : 5 Nov 2013 at 04:45:32 GMT

Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.

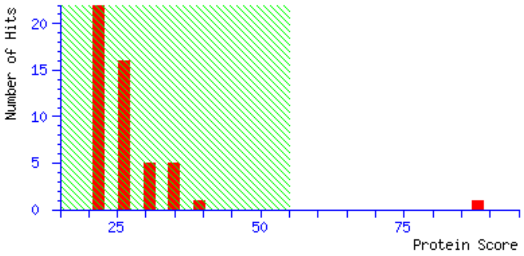
Top Score : 88 for ALBU_MOUSE, Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**ALBU_MOUSE**	70700	88	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3
2.	**EEA1_MOUSE**	161958	38	Early endosome antigen 1 OS=Mus musculus GN=Eea1 PE=2 SV=2
3.	**FTSJ2_MOUSE**	96641	34	S-adenosyl-L-methionine-dependent methyltransferase FTSJD2 OS=Mus musculus GN=Ftsjd2 PE=1 SV=1
4.	**YPEL4_MOUSE**	14762	34	Protein yippee-like 4 OS=Mus musculus GN=Ypel4 PE=2 SV=1
5.	**ACTB_MOUSE**	42052	34	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1
6.	**ACTG_MOUSE**	42108	34	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1
7.	**HCN4_MOUSE**	128075	33	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4 OS=Mus musculus GN=Hcn4 PE=1 SV=2
8.	**GPX1_MOUSE**	22544	32	Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2
9.	**AP2A1_MOUSE**	108679	32	AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 PE=1 SV=1
10.	**NB5R4_MOUSE**	61113	31	Cytochrome b5 reductase 4 OS=Mus musculus GN=Cyb5r4 PE=2 SV=2

Results List

1. ALBU_MOUSE **Mass:** 70700 **Score:** 88 **Expect:** 2.6e-005 **Matches:** 8

Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
956.5409	955.5336	955.5273	6.63	98 -	105	0	25	K.LCAIPNLR.E
1149.6040	1148.5967	1148.6077	-9.60	66 -	75	0	---	K.LVQEVTDFAK.T
1177.6202	1176.6129	1176.5999	11.0	25 -	34	1	---	R.EAHKSEIAHR.Y
1250.5847	1249.5774	1249.5727	3.76	35 -	44	0	---	R.YNDLGEQHFK.G
1714.7979	1713.7906	1713.7893	0.76	118 -	130	1	---	K.QEPERNECFLQHK.D
1901.9028	1900.8956	1900.8890	3.45	153 -	168	0	---	K.ENPTTFMGHYLHEVAR.R
1917.8885	1916.8812	1916.8839	-1.40	153 -	168	0	---	K.ENPTTFMGHYLHEVAR.R + Oxidation (M)
2538.1183	2537.1110	2537.1203	-3.64	131 -	152	0	---	K.DDNPSLPPFERPEAEAMCTSFK.E

No match to: 890.5589, 1016.5220, 1039.5307, 1132.5409, 1171.6085, 1272.5814, 1288.5841, 1481.5916, 1711.9100, 1790.8935, 1862.9356, 1883.9080, 2432.2121

2. EEA1_MOUSE **Mass:** 161958 **Score:** 38 **Expect:** 2.5 **Matches:** 8

Early endosome antigen 1 OS=Mus musculus GN=Eea1 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
956.5409	955.5336	955.5087	26.1	1149 -	1156	1	---	K.SHKQESIK.E
1016.5220	1015.5148	1015.5549	-39.56	465 -	472	1	---	R.LEEQLKEK.V
1039.5307	1038.5235	1038.5346	-10.68	725 -	733	0	---	K.VEDLEGHIK.K
1171.6085	1170.6012	1170.5993	1.62	819 -	828	1	---	K.LSQDSKTQHK.E
1177.6202	1176.6129	1176.6060	5.87	1124 -	1133	1	---	K.SKLAEMEEIK.C
1883.9080	1882.9007	1882.9860	-45.32	1068 -	1084	1	---	R.NQIGNQNKSIQELQAAK.A
1901.9028	1900.8956	1900.9214	-13.57	701 -	715	1	---	K.QEHCIQLESHLKDHK.E
1917.8885	1916.8812	1916.9340	-27.54	663 -	679	0	---	R.ADLQNHLDTAQHALQDK.Q

No match to: 890.5589, 1132.5409, 1149.6040, 1250.5847, 1272.5814, 1288.5841, 1481.5916, 1711.9100, 1714.7979, 1790.8935, 1862.9356, 2432.2121, 2538.1183

3. FTSJ2_MOUSE **Mass:** 96641 **Score:** 34 **Expect:** 5.8 **Matches:** 6

S-adenosyl-L-methionine-dependent methyltransferase FTSJD2 OS=Mus musculus GN=Ftsjd2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
890.5589	889.5516	889.5306	23.6	718 -	724	1	---	R.LEMKLIK.G + Oxidation (M)
1250.5847	1249.5774	1249.5397	30.2	83 -	92	0	---	R.YSMYNSVSQR.L + Oxidation (M)
1711.9100	1710.9027	1710.8610	24.4	498 -	512	1	---	R.SNESYCSLQIKALAK.I
1714.7979	1713.7906	1713.7702	11.9	201 -	214	1	---	K.CKSVFDILDGEEMR.R + Oxidation (M)
1883.9080	1882.9007	1882.8632	19.9	752 -	767	1	---	R.TVNEPWTMGFSKSNNR.K + Oxidation (M)
2538.1183	2537.1110	2537.1851	-29.22	180 -	200	1	---	R.KMVIEDETEFCGEELLHSMLK.C

No match to: 956.5409, 1016.5220, 1039.5307, 1132.5409, 1149.6040, 1171.6085, 1177.6202, 1272.5814, 1288.5841, 1481.5916, 1790.8935, 1862.9356, 1901.9028, 1917.8885, 2432.2121

4. YPEL4_MOUSE **Mass:** 14762 **Score:** 34 **Expect:** 6.5 **Matches:** 3

Protein yippee-like 4 OS=Mus musculus GN=Ypel4 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**

1039.5307	1038.5235	1038.5611	-36.18	17 -	24	1	---	K.TFRSYLPR.C
1250.5847	1249.5774	1249.6199	-33.96	113 -	122	0	---	K.YIIEMSHMVK.D
1714.7979	1713.7906	1713.7525	22.2	1 -	16	0	---	-.MPSCDPGPAPACLPTK.T + Oxidation (M)

No match to: 890.5589, 956.5409, 1016.5220, 1132.5409, 1149.6040, 1171.6085, 1177.6202, 1272.5814, 1288.5841, 1481.5916, 1711.9100, 1790.8935, 1862.9356, 1883.9080, 1901.9028, 1917.8885, 2432.2121, 2538.1183

5. ACTB_MOUSE **Mass:** 42052 **Score:** 34 **Expect:** 7.1 **Matches:** 4

Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1132.5409	1131.5337	1131.5197	12.4	197 -	206	0	---	R.GYSFTTTAER.E
1171.6085	1170.6012	1170.5638	31.9	40 -	50	0	---	R.HQGVMVGMGQK.D
1177.6202	1176.6129	1176.6060	5.85	316 -	326	0	---	K.EITALAPSTMK.I + Oxidation (M)
1790.8935	1789.8862	1789.8846	0.90	239 -	254	0	---	K.SYELPDGQVITIGNER.F

No match to: 890.5589, 956.5409, 1016.5220, 1039.5307, 1149.6040, 1250.5847, 1272.5814, 1288.5841, 1481.5916, 1711.9100, 1714.7979, 1862.9356, 1883.9080, 1901.9028, 1917.8885, 2432.2121, 2538.1183

6. ACTG_MOUSE **Mass:** 42108 **Score:** 34 **Expect:** 7.1 **Matches:** 4

Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1132.5409	1131.5337	1131.5197	12.4	197 -	206	0	---	R.GYSFTTTAER.E
1171.6085	1170.6012	1170.5638	31.9	40 -	50	0	---	R.HQGVMVGMGQK.D
1177.6202	1176.6129	1176.6060	5.85	316 -	326	0	---	K.EITALAPSTMK.I + Oxidation (M)
1790.8935	1789.8862	1789.8846	0.90	239 -	254	0	---	K.SYELPDGQVITIGNER.F

No match to: 890.5589, 956.5409, 1016.5220, 1039.5307, 1149.6040, 1250.5847, 1272.5814, 1288.5841, 1481.5916, 1711.9100, 1714.7979, 1862.9356, 1883.9080, 1901.9028, 1917.8885, 2432.2121, 2538.1183

7. HCN4_MOUSE **Mass:** 128075 **Score:** 33 **Expect:** 8.5 **Matches:** 6

Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4 OS=Mus musculus GN=Hcn4 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1016.5220	1015.5148	1015.5046	9.96	239 -	246	1	---	K.AVEREQER.V
1039.5307	1038.5235	1038.4917	30.6	208 -	216	0	---	R.LGQSGFMQR.Q + Oxidation (M)
1132.5409	1131.5337	1131.5097	21.2	551 -	558	0	---	R.IHDYYEHR.Y
1272.5814	1271.5741	1271.6106	-28.66	69 -	82	0	---	R.GAALGATESEGPGR.S
1714.7979	1713.7906	1713.8396	-28.60	652 -	666	0	---	R.LADGSYFGEICLLTR.G
1862.9356	1861.9283	1861.8959	17.4	1089 -	1106	0	---	R.ASPHSSGESVAAFSLYPR.A

No match to: 890.5589, 956.5409, 1149.6040, 1171.6085, 1177.6202, 1250.5847, 1288.5841, 1481.5916, 1711.9100, 1790.8935, 1883.9080, 1901.9028, 1917.8885, 2432.2121, 2538.1183

8. GPX1_MOUSE **Mass:** 22544 **Score:** 32 **Expect:** 9.8 **Matches:** 3

Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1272.5814	1271.5741	1271.5340	31.6	53 -	62	0	---	R.DYTEMNDLQK.R + Oxidation (M)
1883.9080	1882.9007	1882.8982	1.31	129 -	146	0	---	R.NALPTPSDDPTALMTDPK.Y

1917.8885	1916.8812	1916.9567	-39.36	113	128	1	---	K.CEVNGEKAHPLFTFLR.N

No match to: 890.5589, 956.5409, 1016.5220, 1039.5307, 1132.5409, 1149.6040, 1171.6085, 1177.6202, 1250.5847, 1288.5841, 1481.5916, 1711.9100, 1714.7979, 1790.8935, 1862.9356, 1901.9028, 2432.2121, 2538.1183

9. AP2A1_MOUSE **Mass:** 108679 **Score:** 32 **Expect:** 10 **Matches:** 5

AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1250.5847	1249.5774	1249.6224	-35.99	154	165	0	---	R.ILVAGDSMDSVK.Q + Oxidation (M)
1272.5814	1271.5741	1271.6218	-37.49	621	633	1	---	K.GPGAASALDDSRR.D
1714.7979	1713.7906	1713.7814	5.36	389	403	1	---	R.AADLLYAMCDRSNAK.Q + Oxidation (M)
1862.9356	1861.9283	1861.8458	44.3	864	878	0	---	K.FFQPTEMAAQDFFQR.W
2538.1183	2537.1110	2537.2142	-40.65	142	165	1	---	R.EMGEAFAADIPRILVAGDSMDSVK.Q + Oxidation (M)

No match to: 890.5589, 956.5409, 1016.5220, 1039.5307, 1132.5409, 1149.6040, 1171.6085, 1177.6202, 1288.5841, 1481.5916, 1711.9100, 1790.8935, 1883.9080, 1901.9028, 1917.8885, 2432.2121

10. NB5R4_MOUSE **Mass:** 61113 **Score:** 31 **Expect:** 12 **Matches:** 4

Cytochrome b5 reductase 4 OS=Mus musculus GN=Cyb5r4 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
956.5409	955.5336	955.5525	-19.70	129	137	0	---	R.MAVKPAVPK.D + Oxidation (M)
1883.9080	1882.9007	1882.9070	-3.32	114	128	1	---	R.WVNYESMLKECLVGR.M
1901.9028	1900.8956	1900.9742	-41.36	204	220	0	---	K.NISLDSVIVDLQDDSLR.A
2432.2121	2431.2048	2431.3191	-47.01	362	381	1	---	K.YIYFLIKIYPAGLFTPELDR.L

No match to: 890.5589, 1016.5220, 1039.5307, 1132.5409, 1149.6040, 1171.6085, 1177.6202, 1250.5847, 1272.5814, 1288.5841, 1481.5916, 1711.9100, 1714.7979, 1790.8935, 1862.9356, 1917.8885, 2538.1183

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (890.5589,1+) : <no title>
Query2 (956.5409,1+) : <no title>
Query3 (1016.5220,1+) : <no title>
Query4 (1039.5307,1+) : <no title>
Query5 (1132.5409,1+) : <no title>
Query6 (1149.6040,1+) : <no title>
Query7 (1171.6085,1+) : <no title>

Query8 (1177.6202,1+) : <no title>

Query9 (1250.5847,1+) : <no title>

Query10 (1272.5814,1+) : <no title>

Query11 (1288.5841,1+) : <no title>

Query12 (1481.5916,1+) : <no title>

Query13 (1711.9100,1+) : <no title>

Query14 (1714.7979,1+) : <no title>

Query15 (1790.8935,1+) : <no title>

Query16 (1862.9356,1+) : <no title>

Query17 (1883.9080,1+) : <no title>

Query18 (1901.9028,1+) : <no title>

Query19 (1917.8885,1+) : <no title>

Query20 (2432.2121,1+) : <no title>

Query21 (2538.1183,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:45:23 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

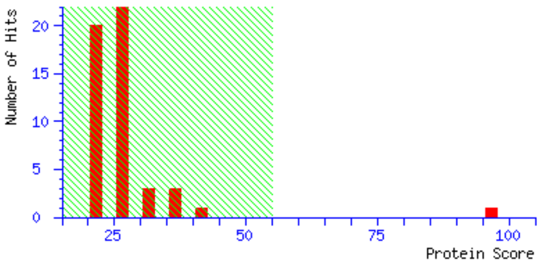
Top Score : **97 for IPYR_MOUSE, Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**IPYR_MOUSE**	33102	97	Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1
2.	**CF012_MOUSE**	25530	43	Uncharacterized protein C6orf12 homolog OS=Mus musculus GN=Tctex4 PE=2 SV=2
3.	**ENOA_MOUSE**	47453	37	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3
4.	**SMG9_MOUSE**	57812	35	Protein SMG9 OS=Mus musculus GN=Smg9 PE=2 SV=1
5.	**JARD2_MOUSE**	139013	35	Protein Jumonji OS=Mus musculus GN=Jarid2 PE=1 SV=1
6.	**KIF5A_MOUSE**	117745	32	Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3
7.	**GABT_MOUSE**	57100	30	4-aminobutyrate aminotransferase, mitochondrial OS=Mus musculus GN=Abat PE=1 SV=1
8.	**CF057_MOUSE**	11938	30	UPF0369 protein C6orf57 homolog OS=Mus musculus PE=2 SV=2
9.	**YK014_MOUSE**	14828	28	CD225 family protein FLJ76511 homolog OS=Mus musculus PE=2 SV=2
10.	**NDUC2_MOUSE**	14211	28	NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Mus musculus GN=Ndufc2 PE=1 SV=1

Results List

1. IPYR_MOUSE **Mass:** 33102 **Score:** 97 **Expect:** 3.5e-006 **Matches:** 2

Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
2230.1284	2229.1211	2229.0742	21.0	193 -	211	1	---	R.YKVPDGKPENEFAFNAEFK.N
2432.2518	2431.2445	2431.1867	23.8	156 -	177	1	71	K.VIAINVDDPDAANYKDISDVER.L

No match to: 1136.6212, 1251.6695, 1726.9363, 1805.0037, 1960.9755, 2252.1376, 2268.1269

2. CF012_MOUSE **Mass:** 25530 **Score:** 43 **Expect:** 0.76 **Matches:** 3

Uncharacterized protein C6orf12 homolog OS=Mus musculus GN=Tctex4 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1251.6695	1250.6622	1250.6983	-28.84	133 -	143	1	---	K.SPSQIPLPEKR.D
1805.0037	1803.9964	1803.9155	44.8	17 -	33	0	---	K.VQEEPPSPSPPPPPPPR.R
1960.9755	1959.9682	1960.0166	-24.70	17 -	34	1	---	K.VQEEPPSPSPPPPPPPRR.E

No match to: 1136.6212, 1726.9363, 2230.1284, 2252.1376, 2268.1269, 2432.2518

3. ENOA_MOUSE **Mass:** 47453 **Score:** 37 **Expect:** 3.4 **Matches:** 3

Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1805.0037	1803.9964	1803.9366	33.1	33 -	50	0	---	R.AAVPSGASTGIYEALELR.D
1960.9755	1959.9682	1959.9174	25.9	203 -	221	0	---	K.DATNVGDEGGFAPNILENK.E
2432.2518	2431.2445	2431.1698	30.7	163 -	183	1	---	K.LAMQEFMILPVGASSFREAMR.I + 3 Oxidation (M)

No match to: 1136.6212, 1251.6695, 1726.9363, 2230.1284, 2252.1376, 2268.1269

4. SMG9_MOUSE **Mass:** 57812 **Score:** 35 **Expect:** 5.3 **Matches:** 4

Protein SMG9 OS=Mus musculus GN=Smg9 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1960.9755	1959.9682	1959.9593	4.54	386 -	401	0	---	R.QMHLMIDQLMAHSHLR.Y
2230.1284	2229.1211	2229.1445	-10.50	384 -	401	1	---	K.LRQMHLMIDQLMAHSHLR.Y
2252.1376	2251.1303	2251.1176	5.65	386 -	403	1	---	R.QMHLMIDQLMAHSHLRYK.G
2268.1269	2267.1197	2267.1125	3.15	386 -	403	1	---	R.QMHLMIDQLMAHSHLRYK.G + Oxidation (M)

No match to: 1136.6212, 1251.6695, 1726.9363, 1805.0037, 2432.2518

5. JARD2_MOUSE **Mass:** 139013 **Score:** 35 **Expect:** 5.6 **Matches:** 5

Protein Jumonji OS=Mus musculus GN=Jarid2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1251.6695	1250.6622	1250.6289	26.7	312 -	324	1	---	R.MSSLGAGTNSAKK.I
1805.0037	1803.9964	1803.9223	41.1	659 -	674	1	---	R.LINEMGGMQQVTDLKK.W
2252.1376	2251.1303	2251.0878	18.9	587 -	604	1	---	R.VIPPPDWRPECKLNDEMR.F
2268.1269	2267.1197	2267.0827	16.3	587 -	604	1	---	R.VIPPPDWRPECKLNDEMR.F + Oxidation (M)
2432.2518	2431.2445	2431.2933	-20.06	1049 -	1069	1	---	R.HIAKPFSMEKLLYQIAQAEAK.K + Oxidation (M)

No match to: 1136.6212, 1726.9363, 1960.9755, 2230.1284

6. KIF5A_MOUSE **Mass:** 117745 **Score:** 32 **Expect:** 11 **Matches:** 4

Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1251.6695	1250.6622	1250.7095	-37.82	790 -	799	1	---	R.ELQTLHNLRK.L
1726.9363	1725.9290	1725.8971	18.5	640 -	653	1	---	K.IRSLTEYMQTVELK.K + Oxidation (M)
1805.0037	1803.9964	1803.9730	13.0	828 -	842	1	---	K.QKISFLENNLEQLTK.V
2432.2518	2431.2445	2431.1835	25.1	619 -	639	1	---	K.MEVTGRELSSCQLLISQHEAK.I + Oxidation (M)

No match to: 1136.6212, 1960.9755, 2230.1284, 2252.1376, 2268.1269

7. GABT_MOUSE **Mass:** 57100 **Score:** 30 **Expect:** 14 **Matches:** 3

4-aminobutyrate aminotransferase, mitochondrial OS=Mus musculus GN=Abat PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1136.6212	1135.6139	1135.6536	-34.88	1 -	9	1	---	-.MAFLLITRR.L + Oxidation (M)
1251.6695	1250.6622	1250.6044	46.2	368 -	377	0	---	K.EEFRPSAPYR.I
2432.2518	2431.2445	2431.3587	-46.97	414 -	434	1	---	K.TLLTGLLDLQAQYPQFISRVR.G

No match to: 1726.9363, 1805.0037, 1960.9755, 2230.1284, 2252.1376, 2268.1269

8. CF057_MOUSE **Mass:** 11938 **Score:** 30 **Expect:** 15 **Matches:** 2

UPF0369 protein C6orf57 homolog OS=Mus musculus PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1726.9363	1725.9290	1725.8938	20.4	65 -	79	1	---	R.EPLQKFPDDVNPVTK.E
1805.0037	1803.9964	1803.9189	43.0	30 -	45	1	---	K.MSYQEGKPEPAKQALK.K

No match to: 1136.6212, 1251.6695, 1960.9755, 2230.1284, 2252.1376, 2268.1269, 2432.2518

9. YK014_MOUSE **Mass:** 14828 **Score:** 28 **Expect:** 23 **Matches:** 2

CD225 family protein FLJ76511 homolog OS=Mus musculus PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1136.6212	1135.6139	1135.5583	49.0	2 -	11	0	---	M.APTLFPMESK.S + Oxidation (M)
1251.6695	1250.6622	1250.6039	46.6	1 -	11	0	---	-.MAPTLFPMESK.S

No match to: 1726.9363, 1805.0037, 1960.9755, 2230.1284, 2252.1376, 2268.1269, 2432.2518

10. NDUC2_MOUSE **Mass:** 14211 **Score:** 28 **Expect:** 26 **Matches:** 3

NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Mus musculus GN=Ndufc2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1251.6695	1250.6622	1250.6190	34.6	2 -	12	0	---	M.MNGRPGHEPLK.F + Oxidation (M)
2252.1376	2251.1303	2251.0509	35.3	31 -	49	0	---	R.LVYMGLLGYCTGLMDNMLR.M + 2 Oxidation (M)
2268.1269	2267.1197	2267.0459	32.6	31 -	49	0	---	R.LVYMGLLGYCTGLMDNMLR.M + 3 Oxidation (M)

No match to: 1136.6212, 1726.9363, 1805.0037, 1960.9755, 2230.1284, 2432.2518

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (1136.6212,1+) : <no title>

Query2 (1251.6695,1+) : <no title>

Query3 (1726.9363,1+) : <no title>

Query4 (1805.0037,1+) : <no title>

Query5 (1960.9755,1+) : <no title>

Query6 (2230.1284,1+) : <no title>

Query7 (2252.1376,1+) : <no title>

Query8 (2268.1269,1+) : <no title>

Query9 (2432.2518,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:45:14 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

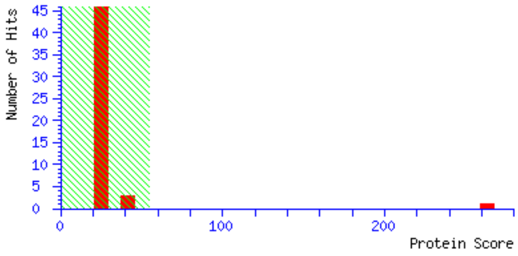
Top Score : **263 for K1C19_MOUSE, Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**K1C19_MOUSE**	44515	263	Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1
2.	**CDT1_MOUSE**	62098	40	DNA replication factor Cdt1 OS=Mus musculus GN=Cdt1 PE=1 SV=1
3.	**JPH1_MOUSE**	72374	35	Junctophilin-1 OS=Mus musculus GN=Jph1 PE=1 SV=1
4.	**AAKG2_MOUSE**	63129	34	5'-AMP-activated protein kinase subunit gamma-2 OS=Mus musculus GN=Prkag2 PE=1 SV=1
5.	**K1C18_MOUSE**	47509	33	Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5
6.	**SCG1_MOUSE**	78036	32	Secretogranin-1 OS=Mus musculus GN=Chgb PE=1 SV=2
7.	**HYLS1_MOUSE**	35461	32	Hydrolethalus syndrome protein 1 homolog OS=Mus musculus GN=Hyls1 PE=2 SV=2
8.	**SYRM_MOUSE**	65865	32	Probable arginyl-tRNA synthetase, mitochondrial OS=Mus musculus GN=Rars2 PE=2 SV=1
9.	**HXB2_MOUSE**	38528	32	Homeobox protein Hox-B2 OS=Mus musculus GN=Hoxb2 PE=2 SV=1
10.	**HXA2_MOUSE**	41167	31	Homeobox protein Hox-A2 OS=Mus musculus GN=Hoxa2 PE=2 SV=1

Results List

1. K1C19_MOUSE **Mass:** 44515 **Score:** 263 **Expect:** 8.1e-023 **Matches:** 18

Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
986.4348	985.4275	985.4294	-1.91	129 -	135	0	---	R.DYNHYFK.T
989.5228	988.5155	988.5189	-3.42	136 -	143	1	---	K.TIEDLRDK.I
995.4967	994.4894	994.4944	-5.03	33 -	43	0	---	R.APSIHGGSGGR.G
1002.4741	1001.4669	1001.4930	-26.14	172 -	179	0	---	K.FETEHALR.L
1008.5157	1007.5085	1007.5188	-10.31	115 -	121	1	---	K.IRDWYQK.Q
1029.5837	1028.5765	1028.5866	-9.86	192 -	200	0	---	R.VLDELTLAR.T
1041.6120	1040.6047	1040.5978	6.61	154 -	162	0	24	K.IVLQIDNAR.L
1064.5983	1063.5910	1063.6026	-10.87	94 -	102	1	---	R.LASYLDKVR.A
1104.5414	1103.5342	1103.5393	-4.68	85 -	93	0	---	K.ITMQNLNDR.L
1120.5442	1119.5370	1119.5342	2.44	85 -	93	0	---	K.ITMQNLNDR.L + Oxidation (M)
1186.6330	1185.6257	1185.6353	-8.12	180 -	190	0	---	R.LSVEADINGLR.R
1211.5967	1210.5894	1210.5942	-3.93	220 -	229	0	---	K.NHEEEITALR.S
1231.6372	1230.6299	1230.6357	-4.67	170 -	179	1	---	R.TKFETEHALR.L
1303.6208	1302.6136	1302.6205	-5.29	52 -	64	0	34	R.FVTSSSGSYGGVR.G
1342.7366	1341.7293	1341.7364	-5.32	180 -	191	1	43	R.LSVEADINGLRR.V
1586.7055	1585.6982	1585.7155	-10.93	8 -	24	0	---	R.QTSAMSSFGGTGGGSVR.I
1602.7088	1601.7016	1601.7104	-5.53	8 -	24	0	---	R.QTSAMSSFGGTGGGSVR.I + Oxidation (M)
1895.9084	1894.9011	1894.9272	-13.77	65 -	84	0	---	R.GGSFSGTLAVSDGLLSGNEK.I

No match to: 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1040.5397, 1056.5252, 1068.5327, 1200.6600, 1223.6135, 1225.5963, 1245.6477, 1265.6787, 1328.1044, 1506.7227, 1547.8170, 1569.6870, 1726.8702, 1782.8947, 1917.9002, 1932.8979, 2002.0042, 2297.1880

2. CDT1_MOUSE **Mass:** 62098 **Score:** 40 **Expect:** 1.8 **Matches:** 5

DNA replication factor Cdt1 OS=Mus musculus GN=Cdt1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1064.5983	1063.5910	1063.5406	47.4	381 -	389	1	---	R.SLMTPKMEK.A
1186.6330	1185.6257	1185.5700	47.0	170 -	179	0	---	K.VPTEQPCVEK.A
1200.6600	1199.6527	1199.6009	43.2	203 -	211	0	---	K.YQVLVEMFR.S + Oxidation (M)
1245.6477	1244.6404	1244.6910	-40.69	387 -	397	1	---	K.MEKALSNLALR.S
1342.7366	1341.7293	1341.7616	-24.08	535 -	547	1	23	K.LDKAVDLAGLTAR.L

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1029.5837, 1040.5397, 1041.6120, 1056.5252, 1068.5327, 1104.5414, 1120.5442, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1265.6787, 1303.6208, 1328.1044, 1506.7227, 1547.8170, 1569.6870, 1586.7055, 1602.7088, 1726.8702, 1782.8947, 1895.9084, 1917.9002, 1932.8979, 2002.0042, 2297.1880

3. JPH1_MOUSE **Mass:** 72374 **Score:** 35 **Expect:** 4.9 **Matches:** 4

Junctophilin-1 OS=Mus musculus GN=Jph1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1200.6600	1199.6527	1199.6986	-38.25	157 -	167	1	---	R.SPLRTSLASLR.S
1303.6208	1302.6136	1302.6317	-13.89	556 -	566	0	---	K.LNTPQHPPEDR.E
1342.7366	1341.7293	1341.7000	21.8	386 -	399	1	16	R.AKADAADQAALAAR.Q
2297.1880	2296.1807	2296.0679	49.1	168 -	191	0	---	R.SEQSNGSVLHEAAAAAADSPAGTR.G

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1029.5837, 1040.5397,

1041.6120, 1056.5252, 1064.5983, 1068.5327, 1104.5414, 1120.5442, 1186.6330, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1245.6477, 1265.6787, 1328.1044, 1506.7227, 1547.8170, 1569.6870, 1586.7055, 1602.7088, 1726.8702, 1782.8947, 1895.9084, 1917.9002, 1932.8979, 2002.0042

4. AAKG2_MOUSE **Mass:** 63129 **Score:** 34 **Expect:** 5.8 **Matches:** 6

5'-AMP-activated protein kinase subunit gamma-2 OS=Mus musculus GN=Prkag2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1029.5837	1028.5765	1028.5654	10.7	300 -	308	1	---	R.AAPLWESKK.Q
1056.5252	1055.5180	1055.5288	-10.24	499 -	507	0	---	R.SQYFEGVVK.C
1245.6477	1244.6404	1244.6190	17.2	172 -	181	0	---	K.QHPFPLESYK.Q
1586.7055	1585.6982	1585.7332	-22.10	133 -	148	0	---	K.ESSPNSNPSTSPGGIR.F
1602.7088	1601.7016	1601.7759	-46.42	330 -	342	0	---	K.SPMVQIYELEEHK.I
1782.8947	1781.8874	1781.8697	9.97	63 -	79	1	---	K.VDSPFSSGSPSRGLFSR.G

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1040.5397, 1041.6120, 1064.5983, 1068.5327, 1104.5414, 1120.5442, 1186.6330, 1200.6600, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1265.6787, 1303.6208, 1328.1044, 1342.7366, 1506.7227, 1547.8170, 1569.6870, 1726.8702, 1895.9084, 1917.9002, 1932.8979, 2002.0042, 2297.1880

5. K1C18_MOUSE **Mass:** 47509 **Score:** 33 **Expect:** 8.5 **Matches:** 2

Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1041.6120	1040.6047	1040.5978	6.61	143 -	151	0	24	R.IVLQIDNAR.L
1506.7227	1505.7154	1505.7647	-32.74	295 -	307	0	---	R.TLQTLEIDLDSMK.N

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1029.5837, 1040.5397, 1056.5252, 1064.5983, 1068.5327, 1104.5414, 1120.5442, 1186.6330, 1200.6600, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1245.6477, 1265.6787, 1303.6208, 1328.1044, 1342.7366, 1547.8170, 1569.6870, 1586.7055, 1602.7088, 1726.8702, 1782.8947, 1895.9084, 1917.9002, 1932.8979, 2002.0042, 2297.1880

6. SCG1_MOUSE **Mass:** 78036 **Score:** 32 **Expect:** 9.1 **Matches:** 7

Secretogranin-1 OS=Mus musculus GN=Chgb PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
986.4348	985.4275	985.4366	-9.25	122 -	130	0	---	K.WTEGGGHSR.E
1002.4741	1001.4669	1001.4753	-8.40	170 -	177	0	---	K.IYPMGEHR.E
1016.5231	1015.5158	1015.5298	-13.76	448 -	456	1	---	R.ESPIDTAKR.Y
1245.6477	1244.6404	1244.6877	-38.01	588 -	598	1	---	R.SFARAPQLDLK.R
1782.8947	1781.8874	1781.8624	14.0	499 -	512	1	---	R.FPDRQYEPYPITEK.R
1917.9002	1916.8929	1916.8024	47.2	341 -	356	1	---	R.ASEEEPEYGEESRSYR.G
1932.8979	1931.8906	1931.8530	19.4	210 -	226	1	---	K.DESVARADAHSMELEEK.T + Oxidation (M)

No match to: 989.5228, 995.4967, 1008.5157, 1012.5478, 1022.5053, 1024.4837, 1029.5837, 1040.5397, 1041.6120, 1056.5252, 1064.5983, 1068.5327, 1104.5414, 1120.5442, 1186.6330, 1200.6600, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1265.6787, 1303.6208, 1328.1044, 1342.7366, 1506.7227, 1547.8170, 1569.6870, 1586.7055, 1602.7088, 1726.8702, 1895.9084, 2002.0042, 2297.1880

7. HYLS1_MOUSE **Mass:** 35461 **Score:** 32 **Expect:** 9.8 **Matches:** 6

Hydrolethalus syndrome protein 1 homolog OS=Mus musculus GN=Hyls1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1068.5327	1067.5254	1067.5433	-16.80	34	43	0	---	R.MLAAATAFTR.I + Oxidation (M)
1104.5414	1103.5342	1103.5103	21.6	289	298	0	---	R.CDLANGVMPK.K
1120.5442	1119.5370	1119.5053	28.3	289	298	0	---	R.CDLANGVMPK.K + Oxidation (M)
1569.6870	1568.6797	1568.7464	-42.52	91	104	1	---	R.VTSSTVSETSQKCR.K
1602.7088	1601.7016	1601.7807	-49.38	285	298	1	---	R.WGVRCDLANGVMPK.K
2002.0042	2000.9969	2001.0353	-19.19	6	24	1	---	R.QAYSVPEAMKQLIGPGGQK.W

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1029.5837, 1040.5397, 1041.6120, 1056.5252, 1064.5983, 1186.6330, 1200.6600, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1245.6477, 1265.6787, 1303.6208, 1328.1044, 1342.7366, 1506.7227, 1547.8170, 1586.7055, 1726.8702, 1782.8947, 1895.9084, 1917.9002, 1932.8979, 2297.1880

8. SYRM_MOUSE **Mass:** 65865 **Score:** 32 **Expect:** 11 **Matches:** 6

Probable arginyl-tRNA synthetase, mitochondrial OS=Mus musculus GN=Rars2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1056.5252	1055.5180	1055.5301	-11.50	222	229	0	---	K.LAHEFFHR.L
1120.5442	1119.5370	1119.5408	-3.39	212	221	1	---	K.EATDDKNVTK.L
1245.6477	1244.6404	1244.6976	-45.97	276	286	1	---	K.SQDVLKLLDSK.G
1303.6208	1302.6136	1302.6276	-10.81	57	67	1	---	K.SQVDTQDQARR.L
1917.9002	1916.8929	1916.9704	-40.42	316	333	1	---	R.SDGTSLYATRDLAAAIHR.M
2002.0042	2000.9969	2000.9268	35.0	258	273	1	---	K.RLGIYFDEYSGESFYR.E

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1029.5837, 1040.5397, 1041.6120, 1064.5983, 1068.5327, 1104.5414, 1186.6330, 1200.6600, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1265.6787, 1328.1044, 1342.7366, 1506.7227, 1547.8170, 1569.6870, 1586.7055, 1602.7088, 1726.8702, 1782.8947, 1895.9084, 1932.8979, 2297.1880

9. HXB2_MOUSE **Mass:** 38528 **Score:** 32 **Expect:** 11 **Matches:** 1

Homeobox protein Hox-B2 OS=Mus musculus GN=Hoxb2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1342.7366	1341.7293	1341.7504	-15.69	172	183	0	27	R.VEIAALLDLTER.Q

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1029.5837, 1040.5397, 1041.6120, 1056.5252, 1064.5983, 1068.5327, 1104.5414, 1120.5442, 1186.6330, 1200.6600, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1245.6477, 1265.6787, 1303.6208, 1328.1044, 1506.7227, 1547.8170, 1569.6870, 1586.7055, 1602.7088, 1726.8702, 1782.8947, 1895.9084, 1917.9002, 1932.8979, 2002.0042, 2297.1880

10. HXA2_MOUSE **Mass:** 41167 **Score:** 31 **Expect:** 12 **Matches:** 1

Homeobox protein Hox-A2 OS=Mus musculus GN=Hoxa2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1342.7366	1341.7293	1341.7504	-15.69	170	181	0	27	R.VEIAALLDLTER.Q

No match to: 986.4348, 989.5228, 995.4967, 1002.4741, 1008.5157, 1012.5478, 1016.5231, 1022.5053, 1024.4837, 1029.5837, 1040.5397, 1041.6120, 1056.5252, 1064.5983, 1068.5327, 1104.5414, 1120.5442, 1186.6330, 1200.6600, 1211.5967, 1223.6135, 1225.5963, 1231.6372, 1245.6477, 1265.6787, 1303.6208, 1328.1044, 1506.7227, 1547.8170, 1569.6870, 1586.7055, 1602.7088, 1726.8702, 1782.8947, 1895.9084, 1917.9002, 1932.8979, 2002.0042, 2297.1880

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (986.4348,1+) : <no title>

Query2 (989.5228,1+) : <no title>

Query3 (995.4967,1+) : <no title>

Query4 (1002.4741,1+) : <no title>

Query5 (1008.5157,1+) : <no title>

Query6 (1012.5478,1+) : <no title>

Query7 (1016.5231,1+) : <no title>

Query8 (1022.5053,1+) : <no title>

Query9 (1024.4837,1+) : <no title>

Query10 (1029.5837,1+) : <no title>

Query11 (1040.5397,1+) : <no title>

Query12 (1041.6120,1+) : <no title>

Query13 (1056.5252,1+) : <no title>

Query14 (1064.5983,1+) : <no title>

Query15 (1068.5327,1+) : <no title>

Query16 (1104.5414,1+) : <no title>

Query17 (1120.5442,1+) : <no title>

Query18 (1186.6330,1+) : <no title>

Query19 (1200.6600,1+) : <no title>

Query20 (1211.5967,1+) : <no title>

Query21 (1223.6135,1+) : <no title>

Query22 (1225.5963,1+) : <no title>

Query23 (1231.6372,1+) : <no title>

Query24 (1245.6477,1+) : <no title>

Query25 (1265.6787,1+) : <no title>

Query26 (1303.6208,1+) : <no title>

Query27 (1328.1044,1+) : <no title>

Query28 (1342.7366,1+) : <no title>

Query29 (1506.7227,1+) : <no title>

Query30 (1547.8170,1+) : <no title>

Query31 (1569.6870,1+) : <no title>

Query32 (1586.7055,1+) : <no title>

Query33 (1602.7088,1+) : <no title>

Query34 (1726.8702,1+) : <no title>

Query35 (1782.8947,1+) : <no title>

Query36 (1895.9084,1+) : <no title>

Query37 (1917.9002,1+) : <no title>

Query38 (1932.8979,1+) : <no title>

Query39 (2002.0042,1+) : <no title>

Query40 (2297.1880,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:45:01 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

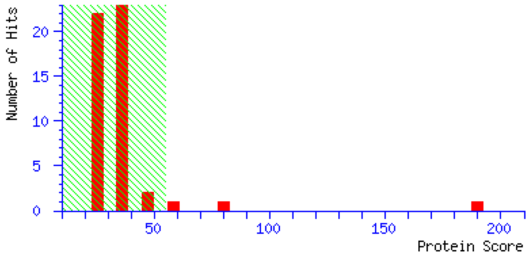
Top Score : **190 for ANXA2_MOUSE, Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	**Mass**	**Score**	**Description**
1.	**ANXA2_MOUSE**	38937	190	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2
2.	**CATB_MOUSE**	38168	82	Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2
3.	**PRDX6_MOUSE**	24969	60	Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3
4.	**APOA1_MOUSE**	30569	48	Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=1
5.	**XPO7_MOUSE**	125156	43	Exportin-7 OS=Mus musculus GN=Xpo7 PE=2 SV=3
6.	**CKP2L_MOUSE**	83689	40	Cytoskeleton-associated protein 2-like OS=Mus musculus GN=Ckap2l PE=2 SV=1
7.	**CP059_MOUSE**	48559	37	Uncharacterized protein C16orf59 homolog OS=Mus musculus PE=2 SV=1
8.	**CN138_MOUSE**	25804	37	Uncharacterized protein C14orf138 homolog OS=Mus musculus GN=Gm71 PE=2 SV=2
9.	**ECHB_MOUSE**	51639	36	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1
10.	**JAZF1_MOUSE**	27479	35	Juxtaposed with another zinc finger protein 1 OS=Mus musculus GN=Jazf1 PE=2 SV=2

Results List

1. ANXA2_MOUSE **Mass:** 38937 **Score:** 190 **Expect:** 1.6e-015 **Matches:** 10

Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1050.5622	1049.5549	1049.5505	4.20	197 -	205	1	---	R.ELYDAGVKR.K
1111.5756	1110.5684	1110.5458	20.3	69 -	77	0	53	R.QDIAFAYQR.R
1244.6387	1243.6315	1243.6156	12.7	136 -	145	0	---	R.TNQELQEINR.V
1542.8636	1541.8564	1541.8413	9.75	50 -	63	0	35	K.GVDEVTIVNILTNR.S
1772.0178	1771.0105	1770.9840	15.0	48 -	63	1	---	K.TKGVDEVTIVNILTNR.S
1777.8777	1776.8704	1776.8564	7.92	120 -	135	0	25	K.GLGTDEDSLIEIICSR.T
1811.9030	1810.8957	1810.8585	20.6	153 -	168	1	---	K.TDLEKDIISDTSGDFR.K
1908.9004	1907.8932	1907.8748	9.60	180 -	196	0	---	R.AEDGSVIDYELIDQDAR.E
2065.0159	2064.0086	2063.9760	15.8	179 -	196	1	---	R.RAEDGSVIDYELIDQDAR.E
2938.3639	2937.3566	2937.3781	-7.31	11 -	37	0	---	K.LSLEGDHSTPPSAYGSVKPYTNFDAER.D

No match to: 827.4452, 956.5438, 1039.5825, 1040.5975, 1047.5639, 1061.5757, 1083.5465, 1094.5524, 1130.6013, 1149.6219, 1171.6306, 1191.6909, 1237.6354, 1250.6190, 1258.7248, 1270.6925, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1381.6473, 1395.6805, 1479.7749, 1582.9183, 1714.8114, 1783.9305, 1790.8872, 1832.9854, 1837.9039, 1851.9086, 1862.9488, 1901.9240, 1917.9142, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2013.9730, 2142.1035, 2170.0910

2. CATB_MOUSE **Mass:** 38168 **Score:** 82 **Expect:** 9.3e-005 **Matches:** 3

Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1381.6473	1380.6400	1380.6027	27.0	269 -	281	0	---	K.HEAGDMMGGHAIR.I
1837.9039	1836.8966	1836.8788	9.70	315 -	331	0	67	R.GENHCGIESEIVAGIPR.T
1992.0198	1991.0125	1990.9677	22.5	246 -	263	0	---	K.NGPVEGAFTVFSDFLTYK.S

No match to: 827.4452, 956.5438, 1039.5825, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1083.5465, 1094.5524, 1111.5756, 1130.6013, 1149.6219, 1171.6306, 1191.6909, 1237.6354, 1244.6387, 1250.6190, 1258.7248, 1270.6925, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1395.6805, 1479.7749, 1542.8636, 1582.9183, 1714.8114, 1772.0178, 1777.8777, 1783.9305, 1790.8872, 1811.9030, 1832.9854, 1851.9086, 1862.9488, 1901.9240, 1908.9004, 1917.9142, 1922.9210, 1932.9820, 1939.9763, 2013.9730, 2065.0159, 2142.1035, 2170.0910, 2938.3639

3. PRDX6_MOUSE **Mass:** 24969 **Score:** 60 **Expect:** 0.017 **Matches:** 7

Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1149.6219	1148.6146	1148.6594	-39.00	133 -	142	1	---	R.VVFIFGPDKK.L
1191.6909	1190.6836	1190.6659	14.9	145 -	155	0	---	K.LSILYPATTGR.N
1270.6925	1269.6852	1269.7081	-18.06	98 -	108	1	---	K.LPFPIIDDKGR.D
1395.6805	1394.6732	1394.6500	16.6	42 -	53	0	---	R.DFTPVCTTELGR.A
1542.8636	1541.8564	1541.8375	12.3	109 -	122	0	---	R.DLAILLGMLDPVEK.D + Oxidation (M)
1832.9854	1831.9781	1831.9237	29.7	183 -	199	1	---	K.KGESVMVVPTLSEEEAK.Q
2142.1035	2141.0962	2141.0753	9.77	2 -	22	0	---	M.PGGLLLGDEAPNFEANTTIGR.I

No match to: 827.4452, 956.5438, 1039.5825, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1083.5465, 1094.5524, 1111.5756, 1130.6013, 1171.6306, 1237.6354, 1244.6387, 1250.6190, 1258.7248, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1381.6473, 1479.7749, 1582.9183, 1714.8114, 1772.0178, 1777.8777, 1783.9305, 1790.8872, 1811.9030, 1837.9039, 1851.9086, 1862.9488, 1901.9240, 1908.9004, 1917.9142, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2013.9730, 2065.0159, 2170.0910, 2938.3639

4. APOA1_MOUSE **Mass:** 30569 **Score:** 48 **Expect:** 0.28 **Matches:** 9

Apolipoprotein A-I OS=Mus musculus GN=Apoa1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
827.4452	826.4379	826.4297	9.94	177 -	183	0	---	R.THVDSLR.T
1040.5975	1039.5903	1039.5774	12.4	228 -	236	0	---	K.ARPALEDLR.H
1047.5639	1046.5566	1046.5396	16.2	164 -	172	0	---	R.LSPVAEEFR.D
1130.6013	1129.5941	1129.5662	24.6	175 -	183	1	---	R.MRTHVDSLR.T + Oxidation (M)
1237.6354	1236.6281	1236.6139	11.5	131 -	139	1	---	K.WKEDVELYR.Q
1297.6702	1296.6629	1296.6245	29.7	184 -	194	0	---	R.TQLAPHSEQMR.E
1318.6896	1317.6824	1317.6677	11.1	164 -	174	1	---	R.LSPVAEEFRDR.M
1331.6596	1330.6523	1330.6625	-7.65	237 -	247	0	---	R.HSLMPMLETLK.T + 2 Oxidation (M)
1340.7277	1339.7204	1339.7095	8.10	142 -	154	0	---	K.VAPLGAELQESAR.Q

No match to: 956.5438, 1039.5825, 1050.5622, 1061.5757, 1083.5465, 1094.5524, 1111.5756, 1149.6219, 1171.6306, 1191.6909, 1244.6387, 1250.6190, 1258.7248, 1270.6925, 1272.5969, 1288.6172, 1312.6763, 1314.6471, 1329.6845, 1345.6813, 1354.7322, 1381.6473, 1395.6805, 1479.7749, 1542.8636, 1582.9183, 1714.8114, 1772.0178, 1777.8777, 1783.9305, 1790.8872, 1811.9030, 1832.9854, 1837.9039, 1851.9086, 1862.9488, 1901.9240, 1908.9004, 1917.9142, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2013.9730, 2065.0159, 2142.1035, 2170.0910, 2938.3639

5. XPO7_MOUSE **Mass:** 125156 **Score:** 43 **Expect:** 0.79 **Matches:** 11

Exportin-7 OS=Mus musculus GN=Xpo7 PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1083.5465	1082.5393	1082.5509	-10.74	1058 -	1066	0	---	R.FTQNLSAFR.R
1149.6219	1148.6146	1148.5938	18.1	293 -	302	1	---	R.SLFNNAERAK.F
1171.6306	1170.6233	1170.5777	39.0	831 -	840	0	---	K.GISICFSMLK.A + Oxidation (M)
1191.6909	1190.6836	1190.6659	14.9	559 -	568	1	---	R.KIYIGDQVQK.S
1270.6925	1269.6852	1269.7194	-26.92	303 -	313	1	---	K.FLSHLVDGVKR.I
1345.6813	1344.6740	1344.6609	9.81	664 -	674	1	---	R.CRTTFYTALGR.L
1354.7322	1353.7249	1353.6789	33.9	1056 -	1066	1	---	R.DRFTQNLSAFR.R
1395.6805	1394.6732	1394.7017	-20.42	115 -	125	1	---	R.ITKLGWFDCQK.D
1862.9488	1861.9415	1861.8768	34.8	396 -	411	0	---	K.ATEPHMLETYTPEVTK.A + Oxidation (M)
2013.9730	2012.9657	2013.0030	-18.53	757 -	773	0	---	R.AIELWYHDPACTTPVLK.L
2142.1035	2141.0962	2141.1150	-8.79	54 -	73	1	---	R.GSSSYSQLLAATCLTKLVSR.T

No match to: 827.4452, 956.5438, 1039.5825, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1094.5524, 1111.5756, 1130.6013, 1237.6354, 1244.6387, 1250.6190, 1258.7248, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1381.6473, 1479.7749, 1542.8636, 1582.9183, 1714.8114, 1772.0178, 1777.8777, 1783.9305, 1790.8872, 1811.9030, 1832.9854, 1837.9039, 1851.9086, 1901.9240, 1908.9004, 1917.9142, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2065.0159, 2170.0910, 2938.3639

6. CKP2L_MOUSE **Mass:** 83689 **Score:** 40 **Expect:** 1.7 **Matches:** 9

Cytoskeleton-associated protein 2-like OS=Mus musculus GN=Ckap2l PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1130.6013	1129.5941	1129.5437	44.5	138 -	146	0	---	R.QCPDIQELK.T

1149.6219	1148.6146	1148.6223	-6.73	286 -	295	1	---	K.TQTSKKPMTK.N
1191.6909	1190.6836	1190.6407	36.0	305 -	314	1	---	R.VRYGKPNETK.I
1244.6387	1243.6315	1243.6924	-49.01	31 -	41	1	---	K.DPNAKPYLKAK.N
1288.6172	1287.6099	1287.6320	-17.13	447 -	459	0	---	K.GAPSATQTHPHGK.K
1312.6763	1311.6690	1311.6419	20.7	2 -	15	0	---	M.VGPGPTASAAAEER.W
1395.6805	1394.6732	1394.7015	-20.27	147 -	159	1	---	K.TKQQQQAHGGNAK.C
1901.9240	1900.9167	1900.9101	3.46	1 -	18	1	---	-.MVGPGPTASAAAEERWQK.L + Oxidation (M)
2170.0910	2169.0838	2169.1793	-44.06	77 -	96	0	---	K.FQTKPASITASQKPESKPPK.L

No match to: 827.4452, 956.5438, 1039.5825, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1083.5465, 1094.5524, 1111.5756, 1171.6306, 1237.6354, 1250.6190, 1258.7248, 1270.6925, 1272.5969, 1297.6702, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1381.6473, 1479.7749, 1542.8636, 1582.9183, 1714.8114, 1772.0178, 1777.8777, 1783.9305, 1790.8872, 1811.9030, 1832.9854, 1837.9039, 1851.9086, 1862.9488, 1908.9004, 1917.9142, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2013.9730, 2065.0159, 2142.1035, 2938.3639

7. CP059_MOUSE **Mass:** 48559 **Score:** 37 **Expect:** 3 **Matches:** 7

Uncharacterized protein C16orf59 homolog OS=Mus musculus PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1111.5756	1110.5684	1110.6186	-45.19	46 -	54	0	---	R.LLQVWEPAR.T
1250.6190	1249.6117	1249.5898	17.5	232 -	243	1	---	R.TNDSTDATRAAK.T
1381.6473	1380.6400	1380.6786	-27.94	147 -	158	1	---	R.ATAPPKDYPEHR.L
1783.9305	1782.9232	1782.9199	1.86	2 -	17	1	---	M.LGVKGNYLLPADCAHR.L
1832.9854	1831.9781	1831.9111	36.6	216 -	231	1	---	K.AVSRNSCLWAQLNSAR.T
1901.9240	1900.9167	1900.9425	-13.57	18 -	34	1	---	R.LVAELQGALDSCADRQR.Q
2142.1035	2141.0962	2141.0211	35.1	183 -	201	0	---	R.DQQMTPSSAHHTTELFALK.E

No match to: 827.4452, 956.5438, 1039.5825, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1083.5465, 1094.5524, 1130.6013, 1149.6219, 1171.6306, 1191.6909, 1237.6354, 1244.6387, 1258.7248, 1270.6925, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1395.6805, 1479.7749, 1542.8636, 1582.9183, 1714.8114, 1772.0178, 1777.8777, 1790.8872, 1811.9030, 1837.9039, 1851.9086, 1862.9488, 1908.9004, 1917.9142, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2013.9730, 2065.0159, 2170.0910, 2938.3639

8. CN138_MOUSE **Mass:** 25804 **Score:** 37 **Expect:** 3.2 **Matches:** 5

Uncharacterized protein C14orf138 homolog OS=Mus musculus GN=Gm71 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1039.5825	1038.5752	1038.5822	-6.74	113 -	122	0	---	K.HLVTGSVQAK.V
1244.6387	1243.6315	1243.6561	-19.78	211 -	220	0	---	R.SEDIHIVYIR.K
1777.8777	1776.8704	1776.8431	15.4	52 -	68	0	10	K.YLETPGFSGDGAHALSR.R
1901.9240	1900.9167	1900.9499	-17.46	106 -	122	1	---	K.MNIDMNKHLVTGSVQAK.V + Oxidation (M)
1917.9142	1916.9070	1916.9448	-19.74	106 -	122	1	---	K.MNIDMNKHLVTGSVQAK.V + 2 Oxidation (M)

No match to: 827.4452, 956.5438, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1083.5465, 1094.5524, 1111.5756, 1130.6013, 1149.6219, 1171.6306, 1191.6909, 1237.6354, 1250.6190, 1258.7248, 1270.6925, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1381.6473, 1395.6805, 1479.7749, 1542.8636, 1582.9183, 1714.8114, 1772.0178, 1783.9305, 1790.8872, 1811.9030, 1832.9854, 1837.9039, 1851.9086, 1862.9488, 1908.9004, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2013.9730, 2065.0159, 2142.1035, 2170.0910, 2938.3639

9. ECHB_MOUSE **Mass:** 51639 **Score:** 36 **Expect:** 4 **Matches:** 8

Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1039.5825	1038.5752	1038.5710	4.07	2 -	10	0	---	M.TTILTSTFR.N
1083.5465	1082.5393	1082.5179	19.8	74 -	82	0	---	K.DLMPHDLAR.A + Oxidation (M)
1130.6013	1129.5941	1129.6390	-39.75	438 -	447	1	---	R.LVMAAANRLR.K + Oxidation (M)
1714.8114	1713.8041	1713.8726	-39.97	336 -	349	1	---	K.AYLRDFIYVSQDPK.D
1777.8777	1776.8704	1776.8464	13.5	240 -	254	1	---	R.MEQDEYALRSHSLAK.K
1837.9039	1836.8966	1836.9873	-49.37	97 -	112	0	---	K.DVVDYIIFGTVIQEVK.T
1901.9240	1900.9167	1900.9928	-40.04	1 -	17	1	---	-.MTTILTSTFRNLSTTSK.W
1917.9142	1916.9070	1916.9877	-42.13	1 -	17	1	---	-.MTTILTSTFRNLSTTSK.W + Oxidation (M)

No match to: 827.4452, 956.5438, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1094.5524, 1111.5756, 1149.6219, 1171.6306, 1191.6909, 1237.6354, 1244.6387, 1250.6190, 1258.7248, 1270.6925, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1381.6473, 1395.6805, 1479.7749, 1542.8636, 1582.9183, 1772.0178, 1783.9305, 1790.8872, 1811.9030, 1832.9854, 1851.9086, 1862.9488, 1908.9004, 1922.9210, 1932.9820, 1939.9763, 1992.0198, 2013.9730, 2065.0159, 2142.1035, 2170.0910, 2938.3639

10. JAZF1_MOUSE **Mass:** 27479 **Score:** 35 **Expect:** 4.7 **Matches:** 5

Juxtaposed with another zinc finger protein 1 OS=Mus musculus GN=Jazf1 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
827.4452	826.4379	826.4297	9.94	95 -	102	0	---	R.GNVSTPPR.H
1149.6219	1148.6146	1148.6401	-22.19	84 -	94	0	---	K.LSLTLSSSVSR.G
1901.9240	1900.9167	1900.9366	-10.48	224 -	239	0	---	R.HHTINFHPPVSAEMIR.K + Oxidation (M)
1922.9210	1921.9137	1921.9897	-39.55	48 -	63	0	---	K.QELQQPTYVALSYINR.F
2013.9730	2012.9657	2013.0367	-35.26	224 -	240	1	---	R.HHTINFHPPVSAEMIRK.M

No match to: 956.5438, 1039.5825, 1040.5975, 1047.5639, 1050.5622, 1061.5757, 1083.5465, 1094.5524, 1111.5756, 1130.6013, 1171.6306, 1191.6909, 1237.6354, 1244.6387, 1250.6190, 1258.7248, 1270.6925, 1272.5969, 1288.6172, 1297.6702, 1312.6763, 1314.6471, 1318.6896, 1329.6845, 1331.6596, 1340.7277, 1345.6813, 1354.7322, 1381.6473, 1395.6805, 1479.7749, 1542.8636, 1582.9183, 1714.8114, 1772.0178, 1777.8777, 1783.9305, 1790.8872, 1811.9030, 1832.9854, 1837.9039, 1851.9086, 1862.9488, 1908.9004, 1917.9142, 1932.9820, 1939.9763, 1992.0198, 2065.0159, 2142.1035, 2170.0910, 2938.3639

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (827.4452,1+) : <no title>

Query2 (956.5438,1+) : <no title>

Query3 (1039.5825,1+) : <no title>

Query4 (1040.5975,1+) : <no title>

Query5 (1047.5639,1+) : <no title>

Query6 (1050.5622,1+) : <no title>

Query7 (1061.5757,1+) : <no title>

Query8 (1083.5465,1+) : <no title>

Query9 (1094.5524,1+) : <no title>

Query10 (1111.5756,1+) : <no title>

Query11 (1130.6013,1+) : <no title>

Query12 (1149.6219,1+) : <no title>

Query13 (1171.6306,1+) : <no title>

Query14 (1191.6909,1+) : <no title>

Query15 (1237.6354,1+) : <no title>

Query16 (1244.6387,1+) : <no title>

Query17 (1250.6190,1+) : <no title>

Query18 (1258.7248,1+) : <no title>

Query19 (1270.6925,1+) : <no title>

Query20 (1272.5969,1+) : <no title>

Query21 (1288.6172,1+) : <no title>

Query22 (1297.6702,1+) : <no title>

Query23 (1312.6763,1+) : <no title>

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Query25 (1318.6896,1+) : <no title>

Query26 (1329.6845,1+) : <no title>

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Query28 (1340.7277,1+) : <no title>

Query29 (1345.6813,1+) : <no title>

Query30 (1354.7322,1+) : <no title>

Query31 (1381.6473,1+) : <no title>

Query32 (1395.6805,1+) : <no title>

Query33 (1479.7749,1+) : <no title>

Query34 (1542.8636,1+) : <no title>

Query35 (1582.9183,1+) : <no title>

Query36 (1714.8114,1+) : <no title>

Query37 (1772.0178,1+) : <no title>

Query38 (1777.8777,1+) : <no title>

Query39 (1783.9305,1+) : <no title>

Query40 (1790.8872,1+) : <no title>

Query41 (1811.9030,1+) : <no title>

Query42 (1832.9854,1+) : <no title>

Query43 (1837.9039,1+) : <no title>

Query44 (1851.9086,1+) : <no title>

Query45 (1862.9488,1+) : <no title>

Query46 (1901.9240,1+) : <no title>

Query47 (1908.9004,1+) : <no title>

Query48 (1917.9142,1+) : <no title>

Query49 (1922.9210,1+) : <no title>

Query50 (1932.9820,1+) : <no title>

Query51 (1939.9763,1+) : <no title>

Query52 (1992.0198,1+) : <no title>

Query53 (2013.9730,1+) : <no title>

Query54 (2065.0159,1+) : <no title>

Query55 (2142.1035,1+) : <no title>

Query56 (2170.0910,1+) : <no title>

Query57 (2938.3639,1+) : <no title>

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:44:30 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

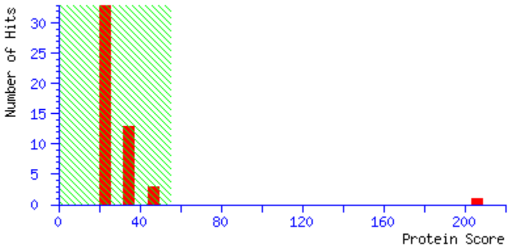
Top Score : **206 for K1C19_MOUSE, Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**K1C19_MOUSE**	44515	206	Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1
2.	**CI116_MOUSE**	18881	53	UPF0691 protein C9orf116 homolog OS=Mus musculus PE=2 SV=1
3.	**PSB1_MOUSE**	26583	44	Proteasome subunit beta type-1 OS=Mus musculus GN=Psmb1 PE=1 SV=1
4.	**K1C14_MOUSE**	53176	43	Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2
5.	**PDK1_MOUSE**	49237	38	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial OS=Mus musculus GN=Pdk1 PE=2 SV=1
6.	**SH21A_MOUSE**	14066	38	SH2 domain-containing protein 1A OS=Mus musculus GN=Sh2d1a PE=2 SV=1
7.	**TSC1_MOUSE**	129692	34	Hamartin OS=Mus musculus GN=Tsc1 PE=1 SV=1
8.	**K1C17_MOUSE**	48417	34	Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE=1 SV=3
9.	**SPEF2_MOUSE**	199477	33	Sperm flagellar protein 2 OS=Mus musculus GN=Spef2 PE=2 SV=2
10.	**IFIT2_MOUSE**	55784	31	Interferon-induced protein with tetratricopeptide repeats 2 OS=Mus musculus GN=Ifit2 PE=2 SV=1

Results List

1. K1C19_MOUSE **Mass:** 44515 **Score:** 206 **Expect:** 4.1e-017 **Matches:** 8

Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
989.5469	988.5396	988.5302	9.58	297 -	304	1	---	K.TEVTDLRR.T
1009.5146	1008.5073	1008.4876	19.5	269 -	277	0	38	K.DAEATYLAR.I
1122.5945	1121.5872	1121.5717	13.9	376 -	384	0	---	R.LEQEIATYR.S
1137.5498	1136.5425	1136.5826	-35.22	268 -	277	1	---	R.KDAEATYLAR.I
1331.6744	1330.6671	1330.6728	-4.28	321 -	333	0	41	K.AALEGTLAETEAR.Y
1365.7361	1364.7288	1364.7048	17.6	374 -	384	1	34	K.SRLEQEIATYR.S
1910.8976	1909.8903	1909.9534	-33.02	385 -	401	0	---	R.SLLEGQEAHYNNLPTPK.A
2166.0590	2165.0517	2165.1328	-37.45	278 -	296	0	---	R.IEELNTQVAVHSEQIQISK.T

No match to: 1136.5756, 1345.6617, 1351.1476, 1419.7396, 1932.9002, 2167.6396, 2188.0876, 2204.0709, 2216.1287

2. CI116_MOUSE **Mass:** 18881 **Score:** 53 **Expect:** 0.087 **Matches:** 4

UPF0691 protein C9orf116 homolog OS=Mus musculus PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1009.5146	1008.5073	1008.5062	1.03	98 -	106	0	---	R.APTVHEMPK.V
1331.6744	1330.6671	1330.6670	0.11	107 -	117	1	---	K.VFYPSSNKFSR.Q
1932.9002	1931.8929	1931.8948	-0.97	152 -	167	0	---	R.LNFHPSYNVNRPSICD.-
2188.0876	2187.0803	2187.0531	12.4	118 -	136	0	---	R.QHAAFGMFQSHNINVTLEK.S + Oxidation (M)

No match to: 989.5469, 1122.5945, 1136.5756, 1137.5498, 1345.6617, 1351.1476, 1365.7361, 1419.7396, 1910.8976, 2166.0590, 2167.6396, 2204.0709, 2216.1287

3. PSB1_MOUSE **Mass:** 26583 **Score:** 44 **Expect:** 0.62 **Matches:** 1

Proteasome subunit beta type-1 OS=Mus musculus GN=Psmb1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1009.5146	1008.5073	1008.4876	19.5	213 -	221	0	37	R.DVYTGDALR.I

No match to: 989.5469, 1122.5945, 1136.5756, 1137.5498, 1331.6744, 1345.6617, 1351.1476, 1365.7361, 1419.7396, 1910.8976, 1932.9002, 2166.0590, 2167.6396, 2188.0876, 2204.0709, 2216.1287

4. K1C14_MOUSE **Mass:** 53176 **Score:** 43 **Expect:** 0.74 **Matches:** 5

Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
989.5469	988.5396	988.5301	9.61	335 -	342	1	---	K.SEISELRR.T
1009.5146	1008.5073	1008.4876	19.5	210 -	217	0	6	K.FETEQSLR.M
1122.5945	1121.5872	1121.5717	13.9	414 -	422	0	---	R.LEQEIATYR.R
1345.6617	1344.6544	1344.6772	-16.95	141 -	152	0	---	R.ALEEANTELEVK.I
1910.8976	1909.8903	1909.9567	-34.80	123 -	138	1	---	K.VTMQNLNDRLATYLDK.V + Oxidation (M)

No match to: 1136.5756, 1137.5498, 1331.6744, 1351.1476, 1365.7361, 1419.7396, 1932.9002, 2166.0590, 2167.6396, 2188.0876, 2204.0709, 2216.1287

5. PDK1_MOUSE **Mass:** 49237 **Score:** 38 **Expect:** 2.6 **Matches:** 5

[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial OS=Mus musculus GN=Pdk1 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1009.5146	1008.5073	1008.4950	12.2	52 -	60	0	---	R.FSPSPLSMK.Q + Oxidation (M)
1345.6617	1344.6544	1344.6714	-12.60	362 -	372	0	---	R.LYAQYFQGDLK.L
1910.8976	1909.8903	1909.8377	27.5	411 -	426	1	---	K.ANHEADDWCVPSREPK.D
2188.0876	2187.0803	2187.0895	-4.18	329 -	346	1	---	R.LFNYMYSTAPRPRVETSR.A
2204.0709	2203.0636	2203.0844	-9.45	329 -	346	1	---	R.LFNYMYSTAPRPRVETSR.A + Oxidation (M)

No match to: 989.5469, 1122.5945, 1136.5756, 1137.5498, 1331.6744, 1351.1476, 1365.7361, 1419.7396, 1932.9002, 2166.0590, 2167.6396, 2216.1287

6. SH21A_MOUSE **Mass:** 14066 **Score:** 38 **Expect:** 2.6 **Matches:** 3

SH2 domain-containing protein 1A OS=Mus musculus GN=Sh2d1a PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
989.5469	988.5396	988.4978	42.3	2 -	10	0	---	M.DAVTVYHGK.I
1136.5756	1135.5683	1135.5332	30.9	1 -	10	0	---	-.MDAVTVYHGK.I + Oxidation (M)
1345.6617	1344.6544	1344.7150	-45.03	2 -	13	1	---	M.DAVTVYHGKISR.E

No match to: 1009.5146, 1122.5945, 1137.5498, 1331.6744, 1351.1476, 1365.7361, 1419.7396, 1910.8976, 1932.9002, 2166.0590, 2167.6396, 2188.0876, 2204.0709, 2216.1287

7. TSC1_MOUSE **Mass:** 129692 **Score:** 34 **Expect:** 6.8 **Matches:** 6

Hamartin OS=Mus musculus GN=Tsc1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1331.6744	1330.6671	1330.7278	-45.62	802 -	812	1	---	R.NMIAELRVELK.K + Oxidation (M)
1419.7396	1418.7323	1418.6797	37.1	1017 -	1030	1	---	R.TSRPGGTRASCGGR.V
1932.9002	1931.8929	1931.9622	-35.87	568 -	584	1	---	R.DRQTSLETSILTPSPCK.I
2188.0876	2187.0803	2187.1569	-35.00	2 -	22	0	---	M.AQLANIGELLSMLDSSTLGVR.D
2204.0709	2203.0636	2203.1518	-40.05	2 -	22	0	---	M.AQLANIGELLSMLDSSTLGVR.D + Oxidation (M)
2216.1287	2215.1214	2215.2100	-39.97	848 -	866	0	---	R.QLLVLGEVNELYLEQLQSK.H

No match to: 989.5469, 1009.5146, 1122.5945, 1136.5756, 1137.5498, 1345.6617, 1351.1476, 1365.7361, 1910.8976, 2166.0590, 2167.6396

8. K1C17_MOUSE **Mass:** 48417 **Score:** 34 **Expect:** 6.9 **Matches:** 4

Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
989.5469	988.5396	988.5301	9.61	298 -	305	1	---	K.SEISELRR.T
1122.5945	1121.5872	1121.5717	13.9	377 -	385	0	---	R.LEQEIATYR.R
1345.6617	1344.6544	1344.6772	-16.95	104 -	115	0	---	R.ALEEANTELEVK.I
2166.0590	2165.0517	2165.0925	-18.85	202 -	219	1	---	R.ADLEMQIENLKEELAYLK.K + Oxidation (M)

No match to: 1009.5146, 1136.5756, 1137.5498, 1331.6744, 1351.1476, 1365.7361, 1419.7396, 1910.8976, 1932.9002, 2167.6396, 2188.0876, 2204.0709, 2216.1287

9. SPEF2_MOUSE **Mass:** 199477 **Score:** 33 **Expect:** 8.1 **Matches:** 6

Sperm flagellar protein 2 OS=Mus musculus GN=Spef2 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
989.5469	988.5396	988.5124	27.6	145 -	152	1	---	R.RQNEIMAK.I

1136.5756	1135.5683	1135.6125	-38.86	669 -	678	0	---	K.LLEEALTGYK.R
1365.7361	1364.7288	1364.6877	30.1	1519 -	1528	0	4	R.QEHLIEFFFR.L
1419.7396	1418.7323	1418.7518	-13.68	337 -	348	1	---	K.QAKIDFAEQTLR.E
2204.0709	2203.0636	2203.0513	5.55	256 -	273	1	---	R.RLLMDQLMAHEAQEEAYR.E
2216.1287	2215.1214	2215.0909	13.8	1658 -	1676	1	---	K.SENIYAENFIKTFQDLGAR.N

No match to: 1009.5146, 1122.5945, 1137.5498, 1331.6744, 1345.6617, 1351.1476, 1910.8976, 1932.9002, 2166.0590, 2167.6396, 2188.0876

10. IFIT2_MOUSE **Mass:** 55784 **Score:** 31 **Expect:** 12 **Matches:** 4

Interferon-induced protein with tetratricopeptide repeats 2 OS=Mus musculus GN=Ifit2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1122.5945	1121.5872	1121.5903	-2.74	159 -	167	1	---	K.VCFQKALEK.D
1137.5498	1136.5425	1136.5873	-39.38	290 -	298	1	---	R.SKVHHMLNR.R + Oxidation (M)
2166.0590	2165.0517	2165.0424	4.29	329 -	346	0	---	K.EMLEYSCSFLADLYIIAK.K
2216.1287	2215.1214	2215.1783	-25.67	219 -	238	1	---	K.LDAVHVHKNQAMALVEEALK.K

No match to: 989.5469, 1009.5146, 1136.5756, 1331.6744, 1345.6617, 1351.1476, 1365.7361, 1419.7396, 1910.8976, 1932.9002, 2167.6396, 2188.0876, 2204.0709

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (989.5469,1+) : <no title>
Query2 (1009.5146,1+) : <no title>
Query3 (1122.5945,1+) : <no title>
Query4 (1136.5756,1+) : <no title>
Query5 (1137.5498,1+) : <no title>
Query6 (1331.6744,1+) : <no title>
Query7 (1345.6617,1+) : <no title>
Query8 (1351.1476,1+) : <no title>
Query9 (1365.7361,1+) : <no title>
Query10 (1419.7396,1+) : <no title>
Query11 (1910.8976,1+) : <no title>
Query12 (1932.9002,1+) : <no title>
Query13 (2166.0590,1+) : <no title>
Query14 (2167.6396,1+) : <no title>
Query15 (2188.0876,1+) : <no title>

Query16 (2204.0709,1+) : <no title>

Query17 (2216.1287,1+) : <no title>

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus. (16281 sequences)**

Timestamp : **22 Nov 2013 at 05:05:43 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

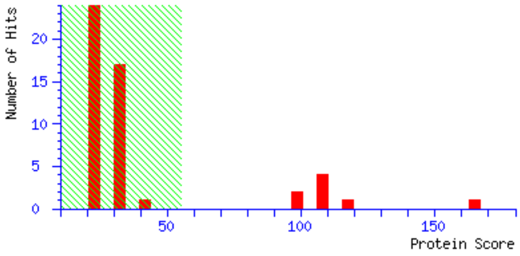
Top Score : **165 for EZRI_MOUSE, Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**EZRI_MOUSE**	69478	165	Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3
2.	**ACTS_MOUSE**	42366	120	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1
3.	**ACTB_MOUSE**	42052	109	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1
4.	**ACTG_MOUSE**	42108	109	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1
5.	**ACTA_MOUSE**	42381	109	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1
6.	**ACTC_MOUSE**	42334	109	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1
7.	**ACTBL_MOUSE**	42319	101	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1
8.	**ACTH_MOUSE**	42249	101	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1
9.	**YB019_MOUSE**	193930	43	Uncharacterized protein FLJ44048 homolog OS=Mus musculus PE=1 SV=2
10.	**WDR67_MOUSE**	116563	36	WD repeat-containing protein 67 OS=Mus musculus GN=Wdr67 PE=2 SV=1

Results List

1. EZRI_MOUSE **Mass:** 69478 **Score:** 165 **Expect:** 5.1e-013 **Matches:** 8

Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
816.4523	815.4451	815.4389	7.58	231 -	237	1	---	K.DDKLTPK.I
1089.5406	1088.5334	1088.5462	-11.76	518 -	526	1	20	R.ITEAEKNER.V
1138.5084	1137.5011	1137.5124	-9.97	578 -	586	1	---	K.QRIDEFEAM.-
1154.4972	1153.4899	1153.5074	-15.14	578 -	586	1	---	K.QRIDEFEAM.- + Oxidation (M)
1303.6651	1302.6579	1302.6667	-6.75	361 -	371	1	---	R.AEKELSEQIEK.A
1472.7903	1471.7830	1471.7994	-11.16	530 -	542	0	63	R.QLLTLSNELSQAR.D
1493.6772	1492.6700	1492.6841	-9.46	548 -	559	0	61	R.THNDIIHNENMR.Q
1509.6830	1508.6758	1508.6790	-2.15	548 -	559	0	---	R.THNDIIHNENMR.Q + Oxidation (M)

No match to: 856.5109, 863.4077, 901.4877, 905.4367, 919.4593, 923.5634, 1000.4515, 1245.6469, 1425.6241, 1454.8196, 1455.7877, 1487.6950, 1500.7159, 1507.6865, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1790.8737, 1804.8876, 1891.8577, 1981.9633, 2047.9647, 2246.0753

2. ACTS_MOUSE **Mass:** 42366 **Score:** 120 **Expect:** 1.6e-008 **Matches:** 5

Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
919.4593	918.4520	918.4593	-7.93	287 -	293	1	---	K.CDIDIRK.D
923.5634	922.5562	922.5600	-4.12	331 -	338	1	---	K.IIAPPERK.Y
1500.7159	1499.7086	1499.7005	5.43	362 -	374	0	---	K.QEYDEAGPSIVHR.K
1790.8737	1789.8665	1789.8846	-10.15	241 -	256	0	84	K.SYELPDGQVITIGNER.F
2246.0753	2245.0680	2245.0143	23.9	294 -	314	0	---	K.DLYANNVMSGGTTMYPGIADR.M

No match to: 816.4523, 856.5109, 863.4077, 901.4877, 905.4367, 1000.4515, 1089.5406, 1138.5084, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1455.7877, 1472.7903, 1487.6950, 1493.6772, 1507.6865, 1509.6830, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1891.8577, 1981.9633, 2047.9647

3. ACTB_MOUSE **Mass:** 42052 **Score:** 109 **Expect:** 2e-007 **Matches:** 4

Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
905.4367	904.4294	904.4436	-15.75	285 -	291	1	---	K.CDVDIRK.D
923.5634	922.5562	922.5600	-4.12	329 -	336	1	---	K.IIAPPERK.Y
1516.6822	1515.6749	1515.6954	-13.48	360 -	372	0	---	K.QEYDESGPSIVHR.K
1790.8737	1789.8665	1789.8846	-10.15	239 -	254	0	84	K.SYELPDGQVITIGNER.F

No match to: 816.4523, 856.5109, 863.4077, 901.4877, 919.4593, 1000.4515, 1089.5406, 1138.5084, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1455.7877, 1472.7903, 1487.6950, 1493.6772, 1500.7159, 1507.6865, 1509.6830, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1891.8577, 1981.9633, 2047.9647, 2246.0753

4. ACTG_MOUSE **Mass:** 42108 **Score:** 109 **Expect:** 2e-007 **Matches:** 4

Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
905.4367	904.4294	904.4436	-15.75	285 -	291	1	---	K.CDVDIRK.D
923.5634	922.5562	922.5600	-4.12	329 -	336	1	---	K.IIAPPERK.Y
1516.6822	1515.6749	1515.6954	-13.48	360 -	372	0	---	K.QEYDESGPSIVHR.K

1790.8737	1789.8665	1789.8846	-10.15	239 -	254	0	84	K.SYELPDGQVITIGNER.F

No match to: 816.4523, 856.5109, 863.4077, 901.4877, 919.4593, 1000.4515, 1089.5406, 1138.5084, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1455.7877, 1472.7903, 1487.6950, 1493.6772, 1500.7159, 1507.6865, 1509.6830, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1891.8577, 1981.9633, 2047.9647, 2246.0753

5. ACTA_MOUSE **Mass:** 42381 **Score:** 109 **Expect:** 2e-007 **Matches:** 4

Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
919.4593	918.4520	918.4593	-7.93	287 -	293	1	---	K.CDIDIRK.D
923.5634	922.5562	922.5600	-4.12	331 -	338	1	---	K.IIAPPERK.Y
1500.7159	1499.7086	1499.7005	5.43	362 -	374	0	---	K.QEYDEAGPSIVHR.K
1790.8737	1789.8665	1789.8846	-10.15	241 -	256	0	84	K.SYELPDGQVITIGNER.F

No match to: 816.4523, 856.5109, 863.4077, 901.4877, 905.4367, 1000.4515, 1089.5406, 1138.5084, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1455.7877, 1472.7903, 1487.6950, 1493.6772, 1507.6865, 1509.6830, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1891.8577, 1981.9633, 2047.9647, 2246.0753

6. ACTC_MOUSE **Mass:** 42334 **Score:** 109 **Expect:** 2e-007 **Matches:** 4

Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
919.4593	918.4520	918.4593	-7.93	287 -	293	1	---	K.CDIDIRK.D
923.5634	922.5562	922.5600	-4.12	331 -	338	1	---	K.IIAPPERK.Y
1500.7159	1499.7086	1499.7005	5.43	362 -	374	0	---	K.QEYDEAGPSIVHR.K
1790.8737	1789.8665	1789.8846	-10.15	241 -	256	0	84	K.SYELPDGQVITIGNER.F

No match to: 816.4523, 856.5109, 863.4077, 901.4877, 905.4367, 1000.4515, 1089.5406, 1138.5084, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1455.7877, 1472.7903, 1487.6950, 1493.6772, 1507.6865, 1509.6830, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1891.8577, 1981.9633, 2047.9647, 2246.0753

7. ACTBL_MOUSE **Mass:** 42319 **Score:** 101 **Expect:** 1.3e-006 **Matches:** 3

Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
905.4367	904.4294	904.4436	-15.75	286 -	292	1	---	K.CDVDIRK.D
923.5634	922.5562	922.5600	-4.12	330 -	337	1	---	K.IIAPPERK.Y
1790.8737	1789.8665	1789.8846	-10.15	240 -	255	0	84	R.SYELPDGQVITIGNER.F

No match to: 816.4523, 856.5109, 863.4077, 901.4877, 919.4593, 1000.4515, 1089.5406, 1138.5084, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1455.7877, 1472.7903, 1487.6950, 1493.6772, 1500.7159, 1507.6865, 1509.6830, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1891.8577, 1981.9633, 2047.9647, 2246.0753

8. ACTH_MOUSE **Mass:** 42249 **Score:** 101 **Expect:** 1.3e-006 **Matches:** 3

Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
919.4593	918.4520	918.4593	-7.93	286 -	292	1	---	K.CDIDIRK.D
923.5634	922.5562	922.5600	-4.12	330 -	337	1	---	K.IIAPPERK.Y
1790.8737	1789.8665	1789.8846	-10.15	240 -	255	0	84	K.SYELPDGQVITIGNER.F

No match to: 816.4523, 856.5109, 863.4077, 901.4877, 905.4367, 1000.4515, 1089.5406, 1138.5084, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1455.7877, 1472.7903, 1487.6950, 1493.6772, 1500.7159, 1507.6865, 1509.6830, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1891.8577, 1981.9633, 2047.9647, 2246.0753

9. YB019_MOUSE **Mass:** 193930 **Score:** 43 **Expect:** 0.82 **Matches:** 11

Uncharacterized protein FLJ44048 homolog OS=Mus musculus PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
901.4877	900.4804	900.5029	-24.90	205 -	212	0	---	K.QNQLALSK.I
1000.4515	999.4443	999.4444	-0.11	1701 -	1708	0	---	K.EHVSEMPR.S + Oxidation (M)
1138.5084	1137.5011	1137.5527	-45.34	1740 -	1749	1	---	K.SSSPPHQDKR.-
1454.8196	1453.8123	1453.8042	5.62	19 -	33	1	---	K.LPHFGGASVVAKSGK.E
1493.6772	1492.6700	1492.6828	-8.59	1421 -	1435	0	---	R.GIGPSSTDVSEMGTR.Q
1507.6865	1506.6792	1506.6620	11.4	1342 -	1355	1	---	K.HAALMSSDSDKDSK.K + Oxidation (M)
1509.6830	1508.6758	1508.6777	-1.29	1421 -	1435	0	---	R.GIGPSSTDVSEMGTR.Q + Oxidation (M)
1790.8737	1789.8665	1789.8768	-5.76	219 -	234	0	---	K.DDTQDPILNSIATIMK.S + Oxidation (M)
1891.8577	1890.8504	1890.9105	-31.78	389 -	406	1	---	R.GAQVQESSTSPPTTMKSR.G
2047.9647	2046.9574	2046.9463	5.45	368 -	386	1	---	K.ESRGAQVQQSAMSPPPSMK.D + 2 Oxidation (M)
2246.0753	2245.0680	2245.1121	-19.63	279 -	299	1	---	K.SQGSQVQQLATSPPTSMKSQR.I

No match to: 816.4523, 856.5109, 863.4077, 905.4367, 919.4593, 923.5634, 1089.5406, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1455.7877, 1472.7903, 1487.6950, 1500.7159, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1702.8261, 1804.8876, 1981.9633

10. WDR67_MOUSE **Mass:** 116563 **Score:** 36 **Expect:** 4.4 **Matches:** 8

WD repeat-containing protein 67 OS=Mus musculus GN=Wdr67 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
816.4523	815.4451	815.4575	-15.25	251 -	257	0	---	R.IIQMPAK.V + Oxidation (M)
919.4593	918.4520	918.4447	8.00	881 -	887	1	---	R.WKEAEEK.E
1138.5084	1137.5011	1137.5454	-38.98	721 -	729	1	---	R.AKDEAWYQK.Q
1455.7877	1454.7804	1454.7657	10.2	97 -	109	0	---	K.SEFLVALADYSIK.C
1472.7903	1471.7830	1471.7882	-3.54	390 -	402	1	---	R.VLKQDLTGDLENK.E
1702.8261	1701.8188	1701.8785	-35.06	352 -	367	0	---	K.VIEDLPSNTVSSSNLK.M
1891.8577	1890.8504	1890.8741	-12.53	707 -	722	1	---	R.QTVENMQAEVDEQRAK.D + Oxidation (M)
2246.0753	2245.0680	2245.0710	-1.31	393 -	412	1	---	K.QDLTGDLENKENELSEGLNK.K

No match to: 856.5109, 863.4077, 901.4877, 905.4367, 923.5634, 1000.4515, 1089.5406, 1154.4972, 1245.6469, 1303.6651, 1425.6241, 1454.8196, 1487.6950, 1493.6772, 1500.7159, 1507.6865, 1509.6830, 1516.6822, 1524.6759, 1531.6647, 1537.6935, 1681.9647, 1790.8737, 1804.8876, 1981.9633, 2047.9647

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (816.4523,1+) : <no title>

Query2 (856.5109,1+) : <no title>

Query3 (863.4077,1+) : <no title>

Query4 (901.4877,1+) : <no title>

Query5 (905.4367,1+) : <no title>

Query6 (919.4593,1+) : <no title>

Query7 (923.5634,1+) : <no title>

Query8 (1000.4515,1+) : <no title>

Query9 (1089.5406,1+) : <no title>

Query10 (1138.5084,1+) : <no title>

Query11 (1154.4972,1+) : <no title>

Query12 (1245.6469,1+) : <no title>

Query13 (1303.6651,1+) : <no title>

Query14 (1425.6241,1+) : <no title>

Query15 (1454.8196,1+) : <no title>

Query16 (1455.7877,1+) : <no title>

Query17 (1472.7903,1+) : <no title>

Query18 (1487.6950,1+) : <no title>

Query19 (1493.6772,1+) : <no title>

Query20 (1500.7159,1+) : <no title>

Query21 (1507.6865,1+) : <no title>

Query22 (1509.6830,1+) : <no title>

Query23 (1516.6822,1+) : <no title>

Query24 (1524.6759,1+) : <no title>

Query25 (1531.6647,1+) : <no title>

Query26 (1537.6935,1+) : <no title>

Query27 (1681.9647,1+) : <no title>

Query28 (1702.8261,1+) : <no title>

Query29 (1790.8737,1+) : <no title>

Query30 (1804.8876,1+) : <no title>

Query31 (1891.8577,1+) : <no title>

Query32 (1981.9633,1+) : <no title>

Query33 (2047.9647,1+) : <no title>

Query34 (2246.0753,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:50:02 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

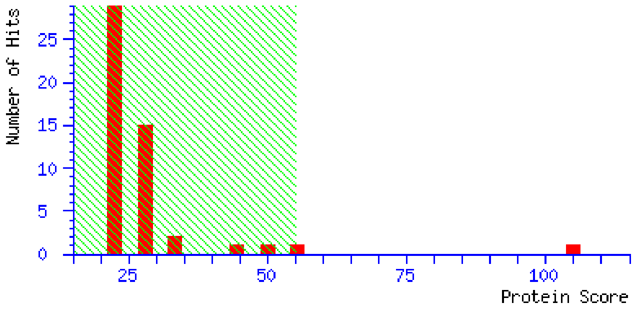
Top Score : **105 for HNRPK_MOUSE, Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	HNRPK_MOUSE	51230	105	Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1
2.	VATA_MOUSE	68625	58	V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2
3.	NR2E3_MOUSE	43947	48	Photoreceptor-specific nuclear receptor OS=Mus musculus GN=Nr2e3 PE=1 SV=1
4.	ACBD7_MOUSE	10092	47	Acyl-CoA-binding domain-containing protein 7 OS=Mus musculus GN=Acbd7 PE=2 SV=1
5.	ANR46_MOUSE	25435	36	Ankyrin repeat domain-containing protein 46 OS=Mus musculus GN=Ankrd46 PE=2 SV=1
6.	NXT1_MOUSE	16065	31	NTF2-related export protein 1 OS=Mus musculus GN=Nxt1 PE=1 SV=2
7.	ACTN1_MOUSE	103631	30	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=2 SV=1
8.	ALBU_MOUSE	70700	30	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3
9.	MK15_MOUSE	61040	30	Mitogen-activated protein kinase 15 OS=Mus musculus GN=Mapk15 PE=1 SV=1
10.	EDF1_MOUSE	16359	29	Endothelial differentiation-related factor 1 OS=Mus musculus GN=Edf1 PE=1 SV=1

Results List

1. HNRPK_MOUSE **Mass:** 51230 **Score:** 105 **Expect:** 5.1e-007 **Matches:** 6

Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1053.6335	1052.6262	1052.6342	-7.65	192 -	201	0	---	R.VVLIGGKPDR.V
1098.4611	1097.4538	1097.4448	8.21	140 -	148	0	26	K.GSDFDCELR.L
1194.6953	1193.6880	1193.6921	-3.38	306 -	316	0	27	R.NLPLPPPPPPR.G
1549.6584	1548.6511	1548.6450	3.97	180 -	191	0	11	K.LFQECCPHSTDR.V
1735.8306	1734.8233	1734.7995	13.7	22 -	35	1	---	K.RPAEDMEEEQAFKR.S
1780.8137	1779.8065	1779.7911	8.62	70 -	86	0	---	R.TDYNASVSVPDSSGPER.I

No match to: 856.4939, 885.4522, 938.5014, 1206.6763, 1284.7246, 1296.6643, 1308.7093, 1316.7441, 1439.7765, 1479.7824, 1531.7724, 1542.7956, 1563.7825, 1589.7406, 1602.7672, 1609.7890, 1694.8383, 1710.8990, 1731.8218, 1749.8450, 1770.8924, 1790.9055, 1882.9347, 2087.0152, 2143.0538, 2247.1067

2. VATA_MOUSE **Mass:** 68625 **Score:** 58 **Expect:** 0.029 **Matches:** 8

V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.4939	855.4866	855.4524	40.0	581 -	587	1	---	K.LSSMKFK.D + Oxidation (M)
885.4522	884.4449	884.4392	6.50	382 -	388	0	---	R.LASFYER.A
1308.7093	1307.7021	1307.7197	-13.52	45 -	56	0	---	R.VGHSELVGEIIR.L
1316.7441	1315.7368	1315.7361	0.57	221 -	232	0	---	K.LPANHPLLTGQR.V
1531.7724	1530.7651	1530.7824	-11.29	309 -	323	0	---	R.TALVANTSNMPVAAR.E + Oxidation (M)
1731.8218	1730.8145	1730.7934	12.2	266 -	280	0	---	K.YSNSDVIIYVGCGER.G
1749.8450	1748.8377	1748.8621	-13.96	324 -	338	0	---	R.EASIYTGITLSEYFR.D
2143.0538	2142.0465	2142.0422	2.01	460 -	476	1	---	R.ALDEYYDKHFTEFVPLR.T

No match to: 938.5014, 1053.6335, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1296.6643, 1439.7765, 1479.7824, 1542.7956, 1549.6584, 1563.7825, 1589.7406, 1602.7672, 1609.7890, 1694.8383, 1710.8990, 1735.8306, 1770.8924, 1780.8137, 1790.9055, 1882.9347, 2087.0152, 2247.1067

3. NR2E3_MOUSE **Mass:** 43947 **Score:** 48 **Expect:** 0.23 **Matches:** 6

Photoreceptor-specific nuclear receptor OS=Mus musculus GN=Nr2e3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1206.6763	1205.6690	1205.6994	-25.23	214 -	223	1	---	R.LLFMAVKWAK.N
1296.6643	1295.6570	1295.6986	-32.12	287 -	296	1	---	R.FLQETISRFR.A
1609.7890	1608.7817	1608.8029	-13.14	2 -	18	0	---	M.SSTVAASTMPVSVAASK.K + Oxidation (M)
1749.8450	1748.8377	1748.7570	46.1	101 -	115	0	---	K.CLQAGMNQDAVQNER.Q + Oxidation (M)
1780.8137	1779.8065	1779.7498	31.9	51 -	65	0	---	K.HYGIYACNGCSGFFK.R
1882.9347	1881.9274	1881.8900	19.9	72 -	87	1	---	R.LIYRCQVGAGMCPVDK.A + Oxidation (M)

No match to: 856.4939, 885.4522, 938.5014, 1053.6335, 1098.4611, 1194.6953, 1284.7246, 1308.7093, 1316.7441, 1439.7765, 1479.7824, 1531.7724, 1542.7956, 1549.6584, 1563.7825, 1589.7406, 1602.7672, 1694.8383, 1710.8990, 1731.8218, 1735.8306, 1770.8924, 1790.9055, 2087.0152, 2143.0538, 2247.1067

4. ACBD7_MOUSE **Mass:** 10092 **Score:** 47 **Expect:** 0.36 **Matches:** 4

Acyl-CoA-binding domain-containing protein 7 OS=Mus musculus GN=Acbd7 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
885.4522	884.4449	884.4643	-21.93	28 -	34	0	---	K.ELYGLYK.Q
1563.7825	1562.7752	1562.7325	27.3	2 -	15	0	---	M.SLQADFDQAAQDVR.K
1694.8383	1693.8310	1693.7730	34.3	1 -	15	0	---	-.MSLQADFDQAAQDVR.K
2143.0538	2142.0465	2142.1177	-33.23	35 -	54	1	---	K.QSVIGDINIACPAMLDLKGK.A

No match to: 856.4939, 938.5014, 1053.6335, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1296.6643, 1308.7093, 1316.7441, 1439.7765, 1479.7824, 1531.7724, 1542.7956, 1549.6584, 1589.7406, 1602.7672, 1609.7890, 1710.8990, 1731.8218, 1735.8306, 1749.8450, 1770.8924, 1780.8137, 1790.9055, 1882.9347, 2087.0152, 2247.1067

5. ANR46_MOUSE **Mass:** 25435 **Score:** 36 **Expect:** 4.2 **Matches:** 4

Ankyrin repeat domain-containing protein 46 OS=Mus musculus GN=Ankrd46 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1296.6643	1295.6570	1295.6656	-6.65	56 -	66	0	---	R.GNVDICQLLHK.F
1316.7441	1315.7368	1315.6871	37.8	127 -	137	0	---	R.LLESLEEQEVK.G
1749.8450	1748.8377	1748.9243	-49.55	101 -	116	0	---	K.IDICNHQGATPLVLAK.R
1790.9055	1789.8982	1789.9210	-12.71	127 -	141	1	---	R.LLESLEEQEVKGFNR.G

No match to: 856.4939, 885.4522, 938.5014, 1053.6335, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1308.7093, 1439.7765, 1479.7824, 1531.7724, 1542.7956, 1549.6584, 1563.7825, 1589.7406, 1602.7672, 1609.7890, 1694.8383, 1710.8990, 1731.8218, 1735.8306, 1770.8924, 1780.8137, 1882.9347, 2087.0152, 2143.0538, 2247.1067

6. NXT1_MOUSE **Mass:** 16065 **Score:** 31 **Expect:** 13 **Matches:** 3

NTF2-related export protein 1 OS=Mus musculus GN=Nxt1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1602.7672	1601.7599	1601.6933	41.6	128 -	140	1	---	K.IASDCFRFQDWAS.-
1780.8137	1779.8065	1779.8025	2.21	16 -	30	0	---	R.AAEEFVNVYYTTMDK.R
1790.9055	1789.8982	1789.8127	47.8	1 -	15	1	---	-.MASVDFKTYVDQACR.A

No match to: 856.4939, 885.4522, 938.5014, 1053.6335, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1296.6643, 1308.7093, 1316.7441, 1439.7765, 1479.7824, 1531.7724, 1542.7956, 1549.6584, 1563.7825, 1589.7406, 1609.7890, 1694.8383, 1710.8990, 1731.8218, 1735.8306, 1749.8450, 1770.8924, 1882.9347, 2087.0152, 2143.0538, 2247.1067

7. ACTN1_MOUSE **Mass:** 103631 **Score:** 30 **Expect:** 16 **Matches:** 6

Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1308.7093	1307.7021	1307.6469	42.1	841 -	850	1	---	K.NYITEDELRR.E
1479.7824	1478.7751	1478.7989	-16.08	122 -	133	0	---	K.MTLGMIWTIILR.F + 2 Oxidation (M)
1542.7956	1541.7883	1541.8301	-27.08	107 -	121	0	---	K.LVSIGAEEIVDGNVK.M
1694.8383	1693.8310	1693.9138	-48.86	421 -	435	1	---	K.DYETATLSEIKALLK.K
1749.8450	1748.8377	1748.8944	-32.46	835 -	849	1	---	K.ILAGDKNYITEDELR.R
1790.9055	1789.8982	1789.8483	27.9	199 -	214	0	---	K.DDPLTNLNTAFDVAER.F

No match to: 856.4939, 885.4522, 938.5014, 1053.6335, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1296.6643, 1316.7441, 1439.7765, 1531.7724, 1549.6584, 1563.7825, 1589.7406, 1602.7672, 1609.7890, 1710.8990, 1731.8218, 1735.8306, 1770.8924, 1780.8137, 1882.9347, 2087.0152, 2143.0538, 2247.1067

8. ALBU_MOUSE **Mass:** 70700 **Score:** 30 **Expect:** 17 **Matches:** 5

Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1439.7765	1438.7692	1438.7780	-6.10	439 -	452	0	---	K.APQVSTPTLVEAAR.N
1479.7824	1478.7751	1478.7881	-8.79	422 -	434	0	---	K.LGEYGFQNAILVR.Y
1563.7825	1562.7752	1562.7181	36.5	457 -	469	1	---	R.VGTKCCTLPEDQR.L
1609.7890	1608.7817	1608.7824	-0.41	348 -	360	0	---	K.DVFLGTFLYEYSR.R
1882.9347	1881.9274	1881.9295	-1.10	509 -	524	0	---	R.RPCFSALTVDETYVPK.E

No match to: 856.4939, 885.4522, 938.5014, 1053.6335, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1296.6643, 1308.7093, 1316.7441, 1531.7724, 1542.7956, 1549.6584, 1589.7406, 1602.7672, 1694.8383, 1710.8990, 1731.8218, 1735.8306, 1749.8450, 1770.8924, 1780.8137, 1790.9055, 2087.0152, 2143.0538, 2247.1067

9. MK15_MOUSE **Mass:** 61040 **Score:** 30 **Expect:** 17 **Matches:** 5

Mitogen-activated protein kinase 15 OS=Mus musculus GN=Mapk15 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1479.7824	1478.7751	1478.7300	30.5	506 -	520	0	---	R.MFGISVSQGAQGAAR.A
1542.7956	1541.7883	1541.7191	44.9	1 -	13	1	---	-.MCAAEVDRHVAQR.Y
1694.8383	1693.8310	1693.8900	-34.83	414 -	428	1	---	R.RQSSDPLFQLPPPGR.G
1710.8990	1709.8917	1709.8373	31.8	323 -	337	0	---	R.LPVHEGDQLSAPEYR.K
1882.9347	1881.9274	1882.0135	-45.72	61 -	76	1	---	R.EIMLLKEFGGHPNIIR.L + Oxidation (M)

No match to: 856.4939, 885.4522, 938.5014, 1053.6335, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1296.6643, 1308.7093, 1316.7441, 1439.7765, 1531.7724, 1549.6584, 1563.7825, 1589.7406, 1602.7672, 1609.7890, 1731.8218, 1735.8306, 1749.8450, 1770.8924, 1780.8137, 1790.9055, 2087.0152, 2143.0538, 2247.1067

10. EDF1_MOUSE **Mass:** 16359 **Score:** 29 **Expect:** 21 **Matches:** 3

Endothelial differentiation-related factor 1 OS=Mus musculus GN=Edf1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1053.6335	1052.6262	1052.5978	26.9	114 -	123	0	---	R.AIPNNQVLGK.I
1549.6584	1548.6511	1548.7281	-49.69	61 -	72	1	---	K.LDRETEELHHDR.V
2247.1067	2246.0994	2246.1542	-24.42	94 -	113	1	---	K.DLATKINEKPQVIADYESGR.A

No match to: 856.4939, 885.4522, 938.5014, 1098.4611, 1194.6953, 1206.6763, 1284.7246, 1296.6643, 1308.7093, 1316.7441, 1439.7765, 1479.7824, 1531.7724, 1542.7956, 1563.7825, 1589.7406, 1602.7672, 1609.7890, 1694.8383, 1710.8990, 1731.8218, 1735.8306, 1749.8450, 1770.8924, 1780.8137, 1790.9055, 1882.9347, 2087.0152, 2143.0538

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (856.4939,1+) : <no title>

Query2 (885.4522,1+) : <no title>

Query3 (938.5014,1+) : <no title>

Query4 (1053.6335,1+) : <no title>

Query5 (1098.4611,1+) : <no title>

Query6 (1194.6953,1+) : <no title>

Query7 (1206.6763,1+) : <no title>

Query8 (1284.7246,1+) : <no title>

Query9 (1296.6643,1+) : <no title>

Query10 (1308.7093,1+) : <no title>

Query11 (1316.7441,1+) : <no title>

Query12 (1439.7765,1+) : <no title>

Query13 (1479.7824,1+) : <no title>

Query14 (1531.7724,1+) : <no title>

Query15 (1542.7956,1+) : <no title>

Query16 (1549.6584,1+) : <no title>

Query17 (1563.7825,1+) : <no title>

Query18 (1589.7406,1+) : <no title>

Query19 (1602.7672,1+) : <no title>

Query20 (1609.7890,1+) : <no title>

Query21 (1694.8383,1+) : <no title>

Query22 (1710.8990,1+) : <no title>

Query23 (1731.8218,1+) : <no title>

Query24 (1735.8306,1+) : <no title>

Query25 (1749.8450,1+) : <no title>

Query26 (1770.8924,1+) : <no title>

Query27 (1780.8137,1+) : <no title>

Query28 (1790.9055,1+) : <no title>

Query29 (1882.9347,1+) : <no title>

Query30 (2087.0152,1+) : <no title>

Query31 (2143.0538,1+) : <no title>

Query32 (2247.1067,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:49:53 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

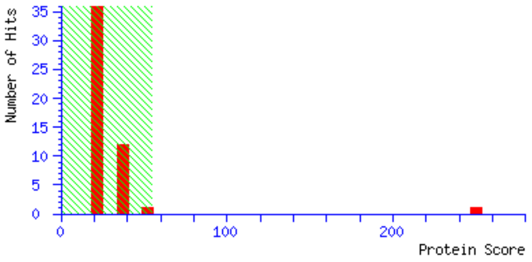
Top Score : **250 for CPNE1_MOUSE, Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**CPNE1_MOUSE**	59591	250	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1
2.	**ZN639_MOUSE**	57182	48	Zinc finger protein 639 OS=Mus musculus GN=Znf639 PE=2 SV=1
3.	**GRHL3_MOUSE**	68400	43	Grainyhead-like protein 3 homolog OS=Mus musculus GN=Grhl3 PE=2 SV=1
4.	**MYH4_MOUSE**	223632	41	Myosin-4 OS=Mus musculus GN=Myh4 PE=2 SV=1
5.	**ES8L3_MOUSE**	68572	41	Epidermal growth factor receptor kinase substrate 8-like protein 3 OS=Mus musculus GN=Eps8l3 PE=2 SV=1
6.	**COPA_MOUSE**	140011	39	Coatomer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=1
7.	**RHG22_MOUSE**	78308	38	Rho GTPase-activating protein 22 OS=Mus musculus GN=Arhgap22 PE=1 SV=2
8.	**DEPD6_MOUSE**	46603	37	DEP domain-containing mTOR-interacting protein OS=Mus musculus GN=Depdc6 PE=1 SV=2
9.	**RT33_MOUSE**	12452	35	28S ribosomal protein S33, mitochondrial OS=Mus musculus GN=Mrps33 PE=2 SV=1
10.	**SYCM_MOUSE**	61804	34	Probable cysteinyl-tRNA synthetase, mitochondrial OS=Mus musculus GN=Cars2 PE=2 SV=2

Results List

1. CPNE1_MOUSE **Mass:** 59591 **Score:** 250 **Expect:** 1.6e-021 **Matches:** 13

Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
811.4811	810.4739	810.4712	3.31	377 -	383	0	---	R.QALPQVR.L
836.4309	835.4236	835.4341	-12.46	171 -	176	0	---	K.WQLAYR.T
888.4842	887.4770	887.4726	4.95	487 -	493	1	---	R.RFQNAPR.E
990.5112	989.5040	989.5043	-0.29	400 -	408	0	25	R.FAAQAAQQR.S
1033.5244	1032.5172	1032.5274	-9.90	138 -	146	0	---	R.VVTMEVEAR.N
1136.6170	1135.6097	1135.6026	6.23	478 -	486	0	47	R.DIVQFVPYR.R
1157.5706	1156.5633	1156.5553	6.95	157 -	165	0	42	K.SDPFLEFFR.Q
1292.7062	1291.6989	1291.7037	-3.70	478 -	487	1	---	R.DIVQFVPYRR.F
1321.6803	1320.6730	1320.6575	11.7	166 -	176	1	---	R.QGDGKWQLAYR.T
1353.6625	1352.6552	1352.7088	-39.64	73 -	83	1	---	K.LRFGIYDIDNK.T
1504.8007	1503.7934	1503.7893	2.76	124 -	137	1	---	R.GTITVSAQELKDSR.V
1635.8211	1634.8138	1634.8304	-10.17	60 -	72	0	---	K.TLQIEYHFETVQK.L
1782.9728	1781.9656	1781.9577	4.43	384 -	399	0	---	R.LYGPTNFAPIINHVAR.F

No match to: 868.4404, 883.4301, 925.4755, 1196.5533, 1284.7291, 1409.7053, 1439.7852, 1479.7914, 1572.8078, 1609.7918, 1657.8209, 1684.8962, 2263.0358, 2301.0336

2. ZN639_MOUSE **Mass:** 57182 **Score:** 48 **Expect:** 0.23 **Matches:** 6

Zinc finger protein 639 OS=Mus musculus GN=Znf639 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
925.4755	924.4682	924.4375	33.3	1 -	7	1	---	-.MNEYPKK.R + Oxidation (M)
1157.5706	1156.5633	1156.6200	-49.00	182 -	192	0	---	K.GQALNVTAQQK.W
1504.8007	1503.7934	1503.8198	-17.51	193 -	205	1	---	K.WPLLRANSSGLYK.C
1635.8211	1634.8138	1634.7974	10.0	240 -	253	0	---	K.ESFSTNMLLIEHAK.L + Oxidation (M)
1657.8209	1656.8137	1656.8736	-36.18	448 -	461	1	---	K.IHLDFKHSADLPHK.C
2263.0358	2262.0285	2262.0674	-17.19	392 -	410	1	---	R.HVAIEHTKIFPHVCDDCGK.G

No match to: 811.4811, 836.4309, 868.4404, 883.4301, 888.4842, 990.5112, 1033.5244, 1136.6170, 1196.5533, 1284.7291, 1292.7062, 1321.6803, 1353.6625, 1409.7053, 1439.7852, 1479.7914, 1572.8078, 1609.7918, 1684.8962, 1782.9728, 2301.0336

3. GRHL3_MOUSE **Mass:** 68400 **Score:** 43 **Expect:** 0.83 **Matches:** 6

Grainyhead-like protein 3 homolog OS=Mus musculus GN=Grhl3 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1033.5244	1032.5172	1032.5676	-48.85	74 -	83	1	---	K.RILSSSTGGR.N
1196.5533	1195.5461	1195.5543	-6.88	245 -	255	0	---	K.AGESPMAYLNK.G + Oxidation (M)
1321.6803	1320.6730	1320.6925	-14.78	34 -	45	0	---	K.TYLENPLTAATK.A
1353.6625	1352.6552	1352.6507	3.36	1 -	11	1	---	-.MSNELDFRSVR.L
1479.7914	1478.7841	1478.7803	2.57	279 -	291	1	---	K.VKSVVMVVFDNDK.V
2301.0336	2300.0263	2300.0386	-5.33	15 -	33	1	---	K.NDPVSFQKFPYSNEDEAWK.T

No match to: 811.4811, 836.4309, 868.4404, 883.4301, 888.4842, 925.4755, 990.5112, 1136.6170, 1157.5706, 1284.7291, 1292.7062, 1409.7053, 1439.7852, 1504.8007, 1572.8078, 1609.7918, 1635.8211, 1657.8209, 1684.8962, 1782.9728, 2263.0358

4. MYH4_MOUSE **Mass:** 223632 **Score:** 41 **Expect:** 1.2 **Matches:** 12

Myosin-4 OS=Mus musculus GN=Myh4 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
888.4842	887.4770	887.4712	6.46	1535 -	1541	1	---	K.KQIDQEK.S
990.5112	989.5040	989.5029	1.08	865 -	873	1	---	K.EDLAKSEAK.R
1033.5244	1032.5172	1032.5386	-20.74	1359 -	1367	1	---	K.AELQRAMSK.A
1136.6170	1135.6097	1135.6237	-12.37	407 -	416	1	---	R.VKVGNEYVTK.G
1321.6803	1320.6730	1320.6319	31.1	355 -	366	0	---	K.LTGAVMHYGNMK.F
1353.6625	1352.6552	1352.6217	24.8	355 -	366	0	---	K.LTGAVMHYGNMK.F + 2 Oxidation (M)
1409.7053	1408.6981	1408.6578	28.6	1762 -	1774	0	---	K.AITDAAMMAEELK.K + Oxidation (M)
1479.7914	1478.7841	1478.7980	-9.40	387 -	400	0	---	K.AAYLTSLNSADLLK.A
1572.8078	1571.8005	1571.8089	-5.34	1681 -	1693	1	---	R.RANLMQAEIEELR.A
1609.7918	1608.7845	1608.7738	6.61	876 -	888	1	---	K.ELEEKMVALMQEK.N + 2 Oxidation (M)
1635.8211	1634.8138	1634.7934	12.5	1294 -	1307	1	---	R.QLDEKDAMVSQLSR.G + Oxidation (M)
1684.8962	1683.8889	1683.9155	-15.79	1565 -	1578	1	---	R.IQLELNQVKSEIDR.K

No match to: 811.4811, 836.4309, 868.4404, 883.4301, 925.4755, 1157.5706, 1196.5533, 1284.7291, 1292.7062, 1439.7852, 1504.8007, 1657.8209, 1782.9728, 2263.0358, 2301.0336

5. ES8L3_MOUSE **Mass:** 68572 **Score:** 41 **Expect:** 1.3 **Matches:** 6

Epidermal growth factor receptor kinase substrate 8-like protein 3 OS=Mus musculus GN=Eps8l3 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
836.4309	835.4236	835.3970	31.9	1 -	7	0	---	-.MSRPSSR.A + Oxidation (M)
1033.5244	1032.5172	1032.4732	42.5	31 -	38	0	---	R.VEHLMTCK.L + Oxidation (M)
1321.6803	1320.6730	1320.6826	-7.30	223 -	234	0	---	R.EPNGFTLPPPPR.R
1439.7852	1438.7779	1438.7456	22.4	74 -	85	0	---	R.DGWLHLLDIETK.E
1572.8078	1571.8005	1571.7912	5.93	31 -	43	1	---	R.VEHLMTCKLGTQR.V
1684.8962	1683.8889	1683.8654	14.0	458 -	471	1	---	R.AALKMQVLYEFEAR.N + Oxidation (M)

No match to: 811.4811, 868.4404, 883.4301, 888.4842, 925.4755, 990.5112, 1136.6170, 1157.5706, 1196.5533, 1284.7291, 1292.7062, 1353.6625, 1409.7053, 1479.7914, 1504.8007, 1609.7918, 1635.8211, 1657.8209, 1782.9728, 2263.0358, 2301.0336

6. COPA_MOUSE **Mass:** 140011 **Score:** 39 **Expect:** 2 **Matches:** 4

Coatomer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
990.5112	989.5040	989.5406	-37.07	424 -	431	1	25	R.NRFAVLDR.M
1479.7914	1478.7841	1478.7253	39.8	468 -	480	0	---	R.DADSITLFDVQQK.R
1635.8211	1634.8138	1634.8264	-7.71	468 -	481	1	---	R.DADSITLFDVQQKR.T
1657.8209	1656.8137	1656.7579	33.6	247 -	260	0	---	R.GHYNNVSCAVFHPR.Q

No match to: 811.4811, 836.4309, 868.4404, 883.4301, 888.4842, 925.4755, 1033.5244, 1136.6170, 1157.5706, 1196.5533, 1284.7291, 1292.7062, 1321.6803, 1353.6625, 1409.7053, 1439.7852, 1504.8007, 1572.8078, 1609.7918, 1684.8962, 1782.9728, 2263.0358, 2301.0336

7. RHG22_MOUSE **Mass:** 78308 **Score:** 38 **Expect:** 2.5 **Matches:** 7

Rho GTPase-activating protein 22 OS=Mus musculus GN=Arhgap22 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
883.4301	882.4228	882.4521	-33.18	653 -	659	0	---	K.YAMLEIK.L + Oxidation (M)

990.5112	989.5040	989.5328	-29.11	1	9	1	---	-.MLPTASSKR.R
1033.5244	1032.5172	1032.4916	24.7	69	76	0	---	R.GDQLFYYK.D
1136.6170	1135.6097	1135.6423	-28.73	653	661	1	---	K.YAMLEIKLR.N
1292.7062	1291.6989	1291.6520	36.3	191	201	1	---	R.ERGLSEEGLFR.M
1504.8007	1503.7934	1503.7657	18.5	429	440	1	---	K.MHTLPVWKSSFR.Q + Oxidation (M)
1684.8962	1683.8889	1683.8580	18.4	107	121	1	---	K.HLFEITPGGATEREK.V

No match to: 811.4811, 836.4309, 868.4404, 888.4842, 925.4755, 1157.5706, 1196.5533, 1284.7291, 1321.6803, 1353.6625, 1409.7053, 1439.7852, 1479.7914, 1572.8078, 1609.7918, 1635.8211, 1657.8209, 1782.9728, 2263.0358, 2301.0336

8. DEPD6_MOUSE **Mass:** 46603 **Score:** 37 **Expect:** 3.2 **Matches:** 4

DEP domain-containing mTOR-interacting protein OS=Mus musculus GN=Depdc6 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
990.5112	989.5040	989.5328	-29.11	88	95	1	8	K.LMQKLADR.G + Oxidation (M)
1157.5706	1156.5633	1156.5434	17.2	258	268	0	---	K.STSFMSVSPSK.E
1635.8211	1634.8138	1634.8205	-4.12	206	218	0	---	K.HPFVDSNLLYQFR.M
2301.0336	2300.0263	2299.9207	45.9	1	25	0	---	-.MEEGSSGGSGSSDSNAGGSGGVQQR.E + Oxidation (M)

No match to: 811.4811, 836.4309, 868.4404, 883.4301, 888.4842, 925.4755, 1033.5244, 1136.6170, 1196.5533, 1284.7291, 1292.7062, 1321.6803, 1353.6625, 1409.7053, 1439.7852, 1479.7914, 1504.8007, 1572.8078, 1609.7918, 1657.8209, 1684.8962, 1782.9728, 2263.0358

9. RT33_MOUSE **Mass:** 12452 **Score:** 35 **Expect:** 4.7 **Matches:** 4

28S ribosomal protein S33, mitochondrial OS=Mus musculus GN=Mrps33 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
836.4309	835.4236	835.4334	-11.67	11	17	1	---	R.MSRLSAR.I + Oxidation (M)
883.4301	882.4228	882.4117	12.6	25	32	1	---	R.STDSKSMK.V
1409.7053	1408.6981	1408.7132	-10.78	2	13	1	---	M.SPLSEYALRMSR.L
1572.8078	1571.8005	1571.7436	36.2	1	13	1	---	-.MSPLSEYALRMSR.L + 2 Oxidation (M)

No match to: 811.4811, 868.4404, 888.4842, 925.4755, 990.5112, 1033.5244, 1136.6170, 1157.5706, 1196.5533, 1284.7291, 1292.7062, 1321.6803, 1353.6625, 1439.7852, 1479.7914, 1504.8007, 1609.7918, 1635.8211, 1657.8209, 1684.8962, 1782.9728, 2263.0358, 2301.0336

10. SYCM_MOUSE **Mass:** 61804 **Score:** 34 **Expect:** 7.1 **Matches:** 5

Probable cysteinyl-tRNA synthetase, mitochondrial OS=Mus musculus GN=Cars2 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
925.4755	924.4682	924.4222	49.8	298	305	1	---	K.GTEEKMSK.S + Oxidation (M)
1292.7062	1291.6989	1291.6707	21.9	470	479	1	---	R.CVVDELVRFR.L
1409.7053	1408.6981	1408.6617	25.8	457	469	0	---	R.QCVSGDSSTVTLR.C
1572.8078	1571.8005	1571.8532	-33.52	404	417	0	---	R.AVNTILDLVHHANR.Q
1657.8209	1656.8137	1656.8447	-18.70	319	331	1	---	K.TFSPDVFRLFCLR.T

No match to: 811.4811, 836.4309, 868.4404, 883.4301, 888.4842, 990.5112, 1033.5244, 1136.6170, 1157.5706, 1196.5533, 1284.7291, 1321.6803, 1353.6625, 1439.7852, 1479.7914, 1504.8007, 1609.7918, 1635.8211, 1684.8962, 1782.9728, 2263.0358, 2301.0336

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (811.4811,1+) : <no title>

Query2 (836.4309,1+) : <no title>

Query3 (868.4404,1+) : <no title>

Query4 (883.4301,1+) : <no title>

Query5 (888.4842,1+) : <no title>

Query6 (925.4755,1+) : <no title>

Query7 (990.5112,1+) : <no title>

Query8 (1033.5244,1+) : <no title>

Query9 (1136.6170,1+) : <no title>

Query10 (1157.5706,1+) : <no title>

Query11 (1196.5533,1+) : <no title>

Query12 (1284.7291,1+) : <no title>

Query13 (1292.7062,1+) : <no title>

Query14 (1321.6803,1+) : <no title>

Query15 (1353.6625,1+) : <no title>

Query16 (1409.7053,1+) : <no title>

Query17 (1439.7852,1+) : <no title>

Query18 (1479.7914,1+) : <no title>

Query19 (1504.8007,1+) : <no title>

Query20 (1572.8078,1+) : <no title>

Query21 (1609.7918,1+) : <no title>

Query22 (1635.8211,1+) : <no title>

Query23 (1657.8209,1+) : <no title>

Query24 (1684.8962,1+) : <no title>

Query25 (1782.9728,1+) : <no title>

Query26 (2263.0358,1+) : <no title>

Query27 (2301.0336,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : Auto submitted by BioTools

Database : SwissProt 57.15 (515203 sequences; 181334896 residues)

Taxonomy : Mus musculus (house mouse) (16230 sequences)

Timestamp : 5 Nov 2013 at 04:49:45 GMT

Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.

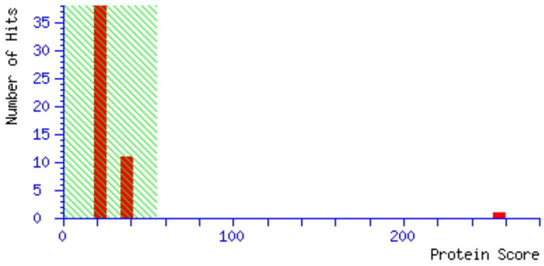
Top Score : 256 for K2C8_MOUSE, Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	K2C8_MOUSE	54531	256	Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4
2.	SERC_MOUSE	40732	41	Phosphoserine aminotransferase OS=Mus musculus GN=Psat1 PE=1 SV=1
3.	COMD9_MOUSE	22121	38	COMM domain-containing protein 9 OS=Mus musculus GN=Commd9 PE=2 SV=3
4.	CA113_MOUSE	60686	36	SH3 domain-containing protein C1orf113 homolog OS=Mus musculus PE=1 SV=1
5.	SBP1_MOUSE	53051	35	Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2
6.	SBP2_MOUSE	53147	35	Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2
7.	K2C7_MOUSE	50678	32	Keratin, type II cytoskeletal 7 OS=Mus musculus GN=Krt7 PE=1 SV=1
8.	TCEA1_MOUSE	34315	32	Transcription elongation factor A protein 1 OS=Mus musculus GN=Tcea1 PE=1 SV=2
9.	C2D1B_MOUSE	93490	31	Coiled-coil and C2 domain-containing protein 1B OS=Mus musculus GN=Cc2d1b PE=1 SV=1
10.	CUL2_MOUSE	87448	31	Cullin-2 OS=Mus musculus GN=Cul2 PE=1 SV=2

Results List

1. K2C8_MOUSE **Mass:** 54531 **Score:** 256 **Expect:** 4.1e-022 **Matches:** 17

Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
868.4504	867.4431	867.4311	13.8	302 -	308	1	---	K.HGDDLRR.T
879.4440	878.4367	878.4246	13.7	24 -	32	0	---	R.SFTSGPGAR.I
913.4604	912.4531	912.4301	25.2	41 -	49	0	---	R.VGSSSSSFR.G
1053.5652	1052.5579	1052.5250	31.2	232 -	239	0	---	R.QIHEEEIR.E
1079.5303	1078.5230	1078.5043	17.3	271 -	279	0	7	R.AQYEDIANR.S
1082.6236	1081.6163	1081.5920	22.4	108 -	116	1	---	K.FASFIDKVR.F
1113.6520	1112.6447	1112.6189	23.2	359 -	368	0	15	K.LAELEAALQR.A
1208.6187	1207.6114	1207.5867	20.5	309 -	318	1	---	R.TKTEISEMNR.N
1253.7138	1252.7065	1252.6775	23.1	84 -	94	0	---	K.LEVDPNIQAVR.T
1318.7068	1317.6996	1317.6598	30.1	259 -	270	0	22	R.SLDMDGIIAEVR.A
1334.7055	1333.6982	1333.6548	32.6	259 -	270	0	---	R.SLDMDGIIAEVR.A + Oxidation (M)
1344.7242	1343.7169	1343.6681	36.3	335 -	347	0	---	R.ASLEAAIADAEQR.G
1355.8004	1354.7931	1354.7568	26.8	323 -	334	1	---	R.LQAEIEALKGQR.A
1419.7967	1418.7894	1418.7405	34.5	220 -	231	0	55	R.LEGLTDEINFLR.Q
1426.7703	1425.7630	1425.6922	49.7	280 -	291	1	---	R.SRAEAETMYQIK.Y
1797.8904	1796.8832	1796.8250	32.3	205 -	219	1	---	K.DVDEAYMNKVELESR.L
2109.0745	2108.0672	2108.0056	29.2	240 -	258	0	---	R.ELQSQISDTSVVLSMDNSR.S

No match to: 875.4474, 1036.5448, 1051.5915, 1104.5987, 1117.6618, 1192.6491, 1213.5907, 1214.6406, 1233.6737, 1401.7850, 1454.8070, 1689.8623

2. SERC_MOUSE **Mass:** 40732 **Score:** 41 **Expect:** 1.3 **Matches:** 5

Phosphoserine aminotransferase OS=Mus musculus GN=Psat1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1036.5448	1035.5375	1035.5284	8.80	299 -	306	1	---	R.SRMNIPFR.I + Oxidation (M)
1113.6520	1112.6447	1112.5979	42.1	6 -	16	0	---	K.QVVNFGPGPAK.L
1117.6618	1116.6545	1116.6212	29.8	324 -	333	0	---	K.AVELNMISLK.G
1689.8623	1688.8550	1688.8556	-0.36	1 -	16	1	---	-.MEATKQVVNFGPGPAK.L + Oxidation (M)
2109.0745	2108.0672	2108.0750	-3.68	337 -	356	1	---	R.SVGGIRASLYNAVTTEDVEK.L

No match to: 868.4504, 875.4474, 879.4440, 913.4604, 1051.5915, 1053.5652, 1079.5303, 1082.6236, 1104.5987, 1192.6491, 1208.6187, 1213.5907, 1214.6406, 1233.6737, 1253.7138, 1318.7068, 1334.7055, 1344.7242, 1355.8004, 1401.7850, 1419.7967, 1426.7703, 1454.8070, 1797.8904

3. COMD9_MOUSE **Mass:** 22121 **Score:** 38 **Expect:** 2.7 **Matches:** 4

COMM domain-containing protein 9 OS=Mus musculus GN=Commd9 PE=2 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
879.4440	878.4367	878.4094	31.1	134 -	141	0	---	K.TSSDNISR.M
1214.6406	1213.6333	1213.6779	-36.67	188 -	198	1	---	R.IRDQLSAVANK.-
1253.7138	1252.7065	1252.6928	10.9	101 -	110	0	---	K.IIVEHISTWR.A
1334.7055	1333.6982	1333.6837	10.8	130 -	141	1	---	R.VDIKTSSDNISR.M

No match to: 868.4504, 875.4474, 913.4604, 1036.5448, 1051.5915, 1053.5652, 1079.5303, 1082.6236, 1104.5987, 1113.6520, 1117.6618, 1192.6491, 1208.6187, 1213.5907, 1233.6737, 1318.7068, 1344.7242, 1355.8004, 1401.7850, 1419.7967, 1426.7703, 1454.8070, 1689.8623, 1797.8904, 2109.0745

4. CA113_MOUSE **Mass:** 60686 **Score:** 36 **Expect:** 3.6 **Matches:** 6

SH3 domain-containing protein C1orf113 homolog OS=Mus musculus PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
875.4474	874.4402	874.4508	-12.18	416 -	422	1	---	K.DERTLNK.A
1082.6236	1081.6163	1081.5880	26.2	428 -	437	1	---	K.LPSERAGPQK.Q
1113.6520	1112.6447	1112.6553	-9.54	135 -	144	1	0	K.IISRESAPIK.E
1344.7242	1343.7169	1343.6867	22.5	1 -	11	0	---	-.MVQSELQLQPR.A + Oxidation (M)
1355.8004	1354.7931	1354.8071	-10.34	499 -	509	1	---	R.LELLELKLEQK.M
2109.0745	2108.0672	2107.9619	49.9	397 -	415	0	---	K.AEDVSAMEEANFLEEPLAK.D + Oxidation (M)

No match to: 868.4504, 879.4440, 913.4604, 1036.5448, 1051.5915, 1053.5652, 1079.5303, 1104.5987, 1117.6618, 1192.6491, 1208.6187, 1213.5907, 1214.6406, 1233.6737, 1253.7138, 1318.7068, 1334.7055, 1401.7850, 1419.7967, 1426.7703, 1454.8070, 1689.8623, 1797.8904

5. SBP1_MOUSE **Mass:** 53051 **Score:** 35 **Expect:** 5.4 **Matches:** 5

Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1051.5915	1050.5843	1050.5498	32.8	412 -	419	0	---	K.QFYPDLIR.E
1214.6406	1213.6333	1213.6204	10.7	53 -	62	0	---	K.SPQYSQVIHR.L
1233.6737	1232.6665	1232.6401	21.4	104 -	114	0	---	R.IYVVDVGSEPR.A
1454.8070	1453.7997	1453.7275	49.6	24 -	34	0	---	R.EEIVYLPCIYR.N
1689.8623	1688.8550	1688.7907	38.1	212 -	227	0	---	K.DGFNPAHVEAGLYGSR.I

No match to: 868.4504, 875.4474, 879.4440, 913.4604, 1036.5448, 1053.5652, 1079.5303, 1082.6236, 1104.5987, 1113.6520, 1117.6618, 1192.6491, 1208.6187, 1213.5907, 1253.7138, 1318.7068, 1334.7055, 1344.7242, 1355.8004, 1401.7850, 1419.7967, 1426.7703, 1797.8904, 2109.0745

6. SBP2_MOUSE **Mass:** 53147 **Score:** 35 **Expect:** 5.4 **Matches:** 5

Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1051.5915	1050.5843	1050.5498	32.8	412 -	419	0	---	K.QFYPDLIR.E
1214.6406	1213.6333	1213.6204	10.7	53 -	62	0	---	K.SPQYSQVIHR.L
1233.6737	1232.6665	1232.6401	21.4	104 -	114	0	---	R.IYVVDVGSEPR.A
1454.8070	1453.7997	1453.7275	49.6	24 -	34	0	---	R.EEIVYLPCIYR.N
1689.8623	1688.8550	1688.7907	38.1	212 -	227	0	---	K.DGFNPAHVEAGLYGSR.I

No match to: 868.4504, 875.4474, 879.4440, 913.4604, 1036.5448, 1053.5652, 1079.5303, 1082.6236, 1104.5987, 1113.6520, 1117.6618, 1192.6491, 1208.6187, 1213.5907, 1253.7138, 1318.7068, 1334.7055, 1344.7242, 1355.8004, 1401.7850, 1419.7967, 1426.7703, 1797.8904, 2109.0745

7. K2C7_MOUSE **Mass:** 50678 **Score:** 32 **Expect:** 10 **Matches:** 5

Keratin, type II cytoskeletal 7 OS=Mus musculus GN=Krt7 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1082.6236	1081.6163	1081.5920	22.4	96 -	104	1	---	K.FASFIDKVR.F
1104.5987	1103.5914	1103.5724	17.3	47 -	58	0	---	R.SAYGGPVGAGIR.E

1117.6618	1116.6545	1116.6291	22.8	134 -	143	0	---	R.IFEAQIAGLR.Q
1192.6491	1191.6419	1191.6360	4.92	32 -	42	0	---	R.SLYGLGSSRPR.V
1797.8904	1796.8832	1796.9282	-25.04	26 -	42	1	---	R.ASFGSRSLYGLGSSRPR.V

No match to: 868.4504, 875.4474, 879.4440, 913.4604, 1036.5448, 1051.5915, 1053.5652, 1079.5303, 1113.6520, 1208.6187, 1213.5907, 1214.6406, 1233.6737, 1253.7138, 1318.7068, 1334.7055, 1344.7242, 1355.8004, 1401.7850, 1419.7967, 1426.7703, 1454.8070, 1689.8623, 2109.0745

8. TCEA1_MOUSE **Mass:** 34315 **Score:** 32 **Expect:** 11 **Matches:** 4

Transcription elongation factor A protein 1 OS=Mus musculus GN=Tcea1 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
879.4440	878.4367	878.4354	1.48	12 -	18	1	---	K.MDKMVQK.K
1104.5987	1103.5914	1103.6121	-18.71	46 -	55	1	---	R.IGMSVNALRK.Q + Oxidation (M)
1113.6520	1112.6447	1112.6553	-9.54	19 -	29	1	12	K.KNAAGALDLLK.E
1355.8004	1354.7931	1354.7820	8.22	20 -	32	1	---	K.NAAGALDLLKELK.N

No match to: 868.4504, 875.4474, 913.4604, 1036.5448, 1051.5915, 1053.5652, 1079.5303, 1082.6236, 1117.6618, 1192.6491, 1208.6187, 1213.5907, 1214.6406, 1233.6737, 1253.7138, 1318.7068, 1334.7055, 1344.7242, 1401.7850, 1419.7967, 1426.7703, 1454.8070, 1689.8623, 1797.8904, 2109.0745

9. C2D1B_MOUSE **Mass:** 93490 **Score:** 31 **Expect:** 12 **Matches:** 6

Coiled-coil and C2 domain-containing protein 1B OS=Mus musculus GN=Cc2d1b PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
879.4440	878.4367	878.4246	13.7	418 -	424	0	---	K.QYQDAVR.A
1036.5448	1035.5375	1035.5686	-30.03	750 -	757	1	---	K.LNINRNHR.G
1079.5303	1078.5230	1078.5658	-39.71	286 -	295	1	---	R.EYKAAALDAK.R
1334.7055	1333.6982	1333.6837	10.8	512 -	524	1	---	K.ASSSKESLSPSVR.E
1426.7703	1425.7630	1425.8303	-47.21	559 -	571	1	---	R.VAKSLEAQIIQAR.A
2109.0745	2108.0672	2108.0329	16.3	69 -	87	1	---	K.GQAPLPMAHIEKLAADCMR.D

No match to: 868.4504, 875.4474, 913.4604, 1051.5915, 1053.5652, 1082.6236, 1104.5987, 1113.6520, 1117.6618, 1192.6491, 1208.6187, 1213.5907, 1214.6406, 1233.6737, 1253.7138, 1318.7068, 1344.7242, 1355.8004, 1401.7850, 1419.7967, 1454.8070, 1689.8623, 1797.8904

10. CUL2_MOUSE **Mass:** 87448 **Score:** 31 **Expect:** 12 **Matches:** 7

Cullin-2 OS=Mus musculus GN=Cul2 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1036.5448	1035.5375	1035.5423	-4.64	711 -	719	0	---	R.FNPSISMIK.K
1053.5652	1052.5579	1052.5324	24.2	394 -	401	1	---	K.YCDNLLKK.S
1117.6618	1116.6545	1116.6213	29.8	720 -	728	1	---	K.KCIEVLIDK.Q
1192.6491	1191.6419	1191.6798	-31.81	677 -	686	1	---	R.KMYLQAAIVR.I
1208.6187	1207.6114	1207.6271	-12.96	23 -	32	0	---	K.AVVMLEYVER.A
1454.8070	1453.7997	1453.8326	-22.67	150 -	161	0	---	K.LMVEPLQNILIR.M + Oxidation (M)
1689.8623	1688.8550	1688.9025	-28.15	415 -	428	1	---	K.LTSFITVFKYIDDK.D

No match to: 868.4504, 875.4474, 879.4440, 913.4604, 1051.5915, 1079.5303, 1082.6236, 1104.5987, 1113.6520, 1213.5907, 1214.6406, 1233.6737, 1253.7138, 1318.7068, 1334.7055, 1344.7242, 1355.8004, 1401.7850, 1419.7967, 1426.7703, 1797.8904, 2109.0745

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (868.4504,1+) : <no title>

Query2 (875.4474,1+) : <no title>

Query3 (879.4440,1+) : <no title>

Query4 (913.4604,1+) : <no title>

Query5 (1036.5448,1+) : <no title>

Query6 (1051.5915,1+) : <no title>

Query7 (1053.5652,1+) : <no title>

Query8 (1079.5303,1+) : <no title>

Query9 (1082.6236,1+) : <no title>

Query10 (1104.5987,1+) : <no title>

Query11 (1113.6520,1+) : <no title>

Query12 (1117.6618,1+) : <no title>

Query13 (1192.6491,1+) : <no title>

Query14 (1208.6187,1+) : <no title>

Query15 (1213.5907,1+) : <no title>

Query16 (1214.6406,1+) : <no title>

Query17 (1233.6737,1+) : <no title>

Query18 (1253.7138,1+) : <no title>

Query19 (1318.7068,1+) : <no title>

Query20 (1334.7055,1+) : <no title>

Query21 (1344.7242,1+) : <no title>

Query22 (1355.8004,1+) : <no title>

Query23 (1401.7850,1+) : <no title>

Query24 (1419.7967,1+) : <no title>

Query25 (1426.7703,1+) : <no title>

Query26 (1454.8070,1+) : <no title>

Query27 (1689.8623,1+) : <no title>

Query28 (1797.8904,1+) : <no title>

Query29 (2109.0745,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus. (16281 sequences)**

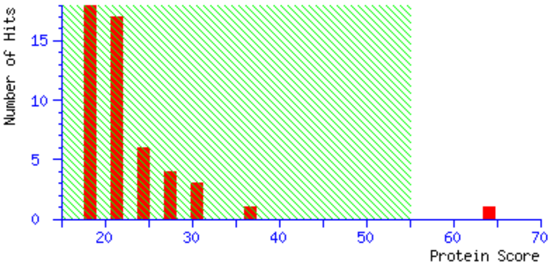
Timestamp : **22 Nov 2013 at 05:26:11 GMT**

Top Score : **64 for HNRPK_MOUSE, Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**HNRPK_MOUSE**	51230	64	Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1
2.	**BECN1_MOUSE**	52015	37	Beclin-1 OS=Mus musculus GN=Becn1 PE=1 SV=2
3.	**ZNF32_MOUSE**	31722	30	Zinc finger protein 32 OS=Mus musculus GN=Znf32 PE=2 SV=1
4.	**CJ046_MOUSE**	42364	30	Uncharacterized protein C10orf46 homolog OS=Mus musculus PE=2 SV=1
5.	**PDIP2_MOUSE**	42072	29	Polymerase delta-interacting protein 2 OS=Mus musculus GN=Poldip2 PE=2 SV=1
6.	**HIF1N_MOUSE**	40387	29	Hypoxia-inducible factor 1-alpha inhibitor OS=Mus musculus GN=Hif1an PE=2 SV=2
7.	**CCNI_MOUSE**	42861	28	Cyclin-I OS=Mus musculus GN=Ccni PE=2 SV=3
8.	**ZN516_MOUSE**	126820	27	Zinc finger protein 516 OS=Mus musculus GN=Znf516 PE=2 SV=1
9.	**CP17A_MOUSE**	58000	26	Steroid 17-alpha-hydroxylase/17,20 lyase OS=Mus musculus GN=Cyp17a1 PE=2 SV=1
10.	**NXT1_MOUSE**	16065	26	NTF2-related export protein 1 OS=Mus musculus GN=Nxt1 PE=1 SV=2

Results List

1. HNRPK_MOUSE **Mass:** 51230 **Score: 64** **Expect:** 0.0063 **Matches:** 6

Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1

Observed Mr(expt) Mr(calc) ppm Start End Miss Peptide

1053.6433	1052.6360	1052.6342	1.71	192 -	201	0	R.VVLIGGKPDR.V
1098.4711	1097.4639	1097.4448	17.4	140 -	148	0	K.GSDFDCELR.L
1194.6953	1193.6880	1193.6921	-3.40	306 -	316	0	R.NLPLPPPPPPR.G
1549.6538	1548.6465	1548.6450	1.02	180 -	191	0	K.LFQECCPHSTDR.V
1735.8135	1734.8062	1734.7995	3.90	22 -	35	1	K.RPAEDMEEEQAFKR.S
1780.8203	1779.8130	1779.7911	12.3	70 -	86	0	R.TDYNASVSVPDSSGPER.I

No match to: 812.3750, 855.4832, 856.5334, 880.4682, 885.4687, 956.5614, 1216.6740, 1308.7241, 1316.7373, 1479.7734, 1589.7422, 1731.8100, 1749.8608, 1770.8922, 1790.8887, 2248.0680

2. BECN1_MOUSE **Mass:** 52015 **Score:** 37 **Expect:** 3 **Matches:** 4

Beclin-1 OS=Mus musculus GN=Becn1 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
856.5334	855.5261	855.5079	21.3	79 -	85	1	R.RFIPPAR.M
1194.6953	1193.6880	1193.6842	3.19	426 -	435	1	K.ALKFMLTNLK.W + Oxidation (M)
1479.7734	1478.7662	1478.7551	7.46	344 -	356	1	K.SKELPLYCSGGLR.F
1790.8887	1789.8814	1789.9322	-28.41	247 -	261	1	K.SVENQVRYAQIQLDK.L

No match to: 812.3750, 855.4832, 880.4682, 885.4687, 956.5614, 1053.6433, 1098.4711, 1216.6740, 1308.7241, 1316.7373, 1549.6538, 1589.7422, 1731.8100, 1735.8135, 1749.8608, 1770.8922, 1780.8203, 2248.0680

3. ZNF32_MOUSE **Mass:** 31722 **Score:** 30 **Expect:** 17 **Matches:** 3

Zinc finger protein 32 OS=Mus musculus GN=Znf32 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
1098.4711	1097.4638	1097.4924	-26.00	136 -	144	1	K.ECGKSFSQR.G
1194.6953	1193.6880	1193.6377	42.1	171 -	180	1	R.NQSNLAVHRR.V
1790.8887	1789.8814	1789.8240	32.1	97 -	111	0	R.IHTGQKPFECTQCGK.S

No match to: 812.3750, 855.4832, 856.5334, 880.4682, 885.4687, 956.5614, 1053.6433, 1216.6740, 1308.7241, 1316.7373, 1479.7734, 1549.6538, 1589.7422, 1731.8100, 1735.8135, 1749.8608, 1770.8922, 1780.8203, 2248.0680

4. CJ046_MOUSE **Mass:** 42364 **Score:** 30 **Expect:** 17 **Matches:** 3

Uncharacterized protein C10orf46 homolog OS=Mus musculus PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
855.4832	854.4759	854.4610	17.5	195 -	201	0	K.ITSHLER.V
1780.8203	1779.8130	1779.8938	-45.36	59 -	75	0	R.ELPGGQLLAVHAGSMER.K + Oxidation (M)
2248.0680	2247.0608	2247.1286	-30.17	130 -	147	1	K.FLMNVITIEDYKSTYWPK.L

No match to: 812.3750, 856.5334, 880.4682, 885.4687, 956.5614, 1053.6433, 1098.4711, 1194.6953, 1216.6740, 1308.7241, 1316.7373, 1479.7734, 1549.6538, 1589.7422, 1731.8100, 1735.8135, 1749.8608, 1770.8922, 1790.8887

5. PDIP2_MOUSE **Mass:** 42072 **Score:** 29 **Expect:** 20 **Matches:** 3

Polymerase delta-interacting protein 2 OS=Mus musculus GN=Poldip2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Peptide**
1316.7373	1315.7300	1315.7388	-6.67	61 -	72	0	K.VLETVGVFEVPK.Q
1479.7734	1478.7662	1478.7518	9.73	130 -	141	0	K.THTYYQVLIDAR.D
1790.8887	1789.8814	1789.8231	32.6	150 -	165	0	R.SQTEAVTFLANHDDSR.A

No match to: 812.3750, 855.4832, 856.5334, 880.4682, 885.4687, 956.5614, 1053.6433, 1098.4711, 1194.6953, 1216.6740, 1308.7241, 1549.6538, 1589.7422, 1731.8100, 1735.8135, 1749.8608, 1770.8922, 1780.8203, 2248.0680

6. HIF1N_MOUSE **Mass:** 40387 **Score:** 29 **Expect:** 21 **Matches:** 3

Hypoxia-inducible factor 1-alpha inhibitor OS=Mus musculus GN=Hif1an PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
856.5334	855.5261	855.4926	39.1	132 -	138	0	K.LQAIQQR.G
1053.6433	1052.6360	1052.5913	42.5	312 -	320	1	K.AHQKVAIMR.N
1549.6538	1548.6465	1548.7202	-47.55	1 -	17	0	-.MAATAAEVAASGSGEAR.E

No match to: 812.3750, 855.4832, 880.4682, 885.4687, 956.5614, 1098.4711, 1194.6953, 1216.6740, 1308.7241, 1316.7373, 1479.7734, 1589.7422, 1731.8100, 1735.8135, 1749.8608, 1770.8922, 1780.8203, 1790.8887, 2248.0680

7. CCNI_MOUSE **Mass:** 42861 **Score:** 28 **Expect:** 28 **Matches:** 3

Cyclin-I OS=Mus musculus GN=Ccni PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1316.7373	1315.7300	1315.6707	45.1	1 -	11	1	-.MKFPGPLENQR.L
1790.8887	1789.8814	1789.8895	-4.54	86 -	100	0	K.YLNCIAISCFFLAAK.T
2248.0680	2247.0608	2247.1212	-26.88	57 -	75	0	K.YQFNLYPETFALASSLLDR.F

No match to: 812.3750, 855.4832, 856.5334, 880.4682, 885.4687, 956.5614, 1053.6433, 1098.4711, 1194.6953, 1216.6740, 1308.7241, 1479.7734, 1549.6538, 1589.7422, 1731.8100, 1735.8135, 1749.8608, 1770.8922, 1780.8203

8. ZN516_MOUSE **Mass:** 126820 **Score:** 27 **Expect:** 32 **Matches:** 4

Zinc finger protein 516 OS=Mus musculus GN=Znf516 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1194.6953	1193.6880	1193.6517	30.4	806 -	818	1	R.SGRTGPPPALGGK.E
1479.7734	1478.7662	1478.7300	24.5	705 -	717	1	K.LSDLHKEHCGVGK.R
1735.8135	1734.8062	1734.7454	35.1	1085 -	1099	0	R.TQAHQGDFVCVECGK.S
2248.0680	2247.0608	2247.1648	-46.30	946 -	968	1	K.LGGPAVGTGFTPPNKHSAPDSLK.A

No match to: 812.3750, 855.4832, 856.5334, 880.4682, 885.4687, 956.5614, 1053.6433, 1098.4711, 1216.6740, 1308.7241, 1316.7373, 1549.6538, 1589.7422, 1731.8100, 1749.8608, 1770.8922, 1780.8203, 1790.8887

9. CP17A_MOUSE **Mass:** 58000 **Score:** 26 **Expect:** 37 **Matches:** 3

Steroid 17-alpha-hydroxylase/17,20 lyase OS=Mus musculus GN=Cyp17a1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1216.6740	1215.6667	1215.6652	1.21	127 -	136	0	K.LVFSTFSLFR.D
1735.8135	1734.8062	1734.7420	37.0	403 -	415	1	K.NEWDQPDRFMPER.F + Oxidation (M)
2248.0680	2247.0608	2247.1682	-47.79	90 -	110	1	K.GKEFSGRPQMVTLGLLSDQGK.G

No match to: 812.3750, 855.4832, 856.5334, 880.4682, 885.4687, 956.5614, 1053.6433, 1098.4711, 1194.6953, 1308.7241, 1316.7373, 1479.7734, 1549.6538, 1589.7422, 1731.8100, 1749.8608, 1770.8922, 1780.8203, 1790.8887

10. NXT1_MOUSE **Mass:** 16065 **Score:** 26 **Expect:** 44 **Matches:** 2

NTF2-related export protein 1 OS=Mus musculus GN=Nxt1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide

1780.8203	1779.8130	1779.8025	5.89	16 -	30	0	R.AAEEFVNVYYTTMDK.R
1790.8887	1789.8814	1789.8127	38.4	1 -	15	1	-.MASVDFKTYVDQACR.A

No match to: 812.3750, 855.4832, 856.5334, 880.4682, 885.4687, 956.5614, 1053.6433, 1098.4711, 1194.6953, 1216.6740, 1308.7241, 1316.7373, 1479.7734, 1549.6538, 1589.7422, 1731.8100, 1735.8135, 1749.8608, 1770.8922, 2248.0680

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:49:36 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

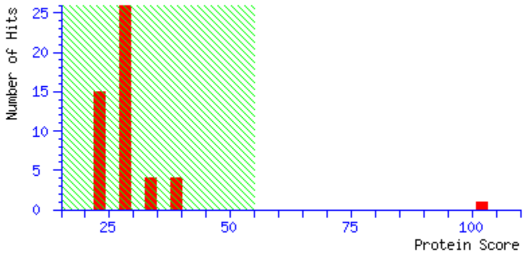
Top Score : **102 for AL1B1_MOUSE, Aldehyde dehydrogenase X, mitochondrial OS=Mus musculus GN=Aldh1b1 PE=2 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**AL1B1_MOUSE**	58087	102	Aldehyde dehydrogenase X, mitochondrial OS=Mus musculus GN=Aldh1b1 PE=2 SV=1
2.	**GTF2I_MOUSE**	112708	39	General transcription factor II-I OS=Mus musculus GN=Gtf2i PE=1 SV=3
3.	**FBX33_MOUSE**	63865	37	F-box only protein 33 OS=Mus musculus GN=Fbxo33 PE=1 SV=2
4.	**CPNE8_MOUSE**	63653	36	Copine-8 OS=Mus musculus GN=Cpne8 PE=2 SV=2
5.	**SNX25_MOUSE**	98437	36	Sorting nexin-25 OS=Mus musculus GN=Snx25 PE=2 SV=1
6.	**PSMG1_MOUSE**	33938	34	Proteasome assembly chaperone 1 OS=Mus musculus GN=Psmg1 PE=1 SV=1
7.	**GSDC2_MOUSE**	54259	34	Gasdermin-C2 OS=Mus musculus GN=Gsdmc2 PE=2 SV=2
8.	**CI128_MOUSE**	55113	33	Uncharacterized protein C9orf128 homolog OS=Mus musculus PE=2 SV=1
9.	**RS3_MOUSE**	26828	31	40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1
10.	**GIT1_MOUSE**	86046	30	ARF GTPase-activating protein GIT1 OS=Mus musculus GN=Git1 PE=1 SV=1

Results List

1. AL1B1_MOUSE **Mass:** 58087 **Score:** 102 **Expect:** 1e-006 **Matches:** 8

Aldehyde dehydrogenase X, mitochondrial OS=Mus musculus GN=Aldh1b1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
804.4269	803.4196	803.3960	29.4	386 -	392	0	---	K.LLCGGER.L
886.5074	885.5001	885.4920	9.24	432 -	438	0	---	K.IEEVIQR.A
888.4606	887.4533	887.4348	20.8	495 -	502	0	---	R.ELGEDGLR.A
1014.5913	1013.5841	1013.5869	-2.81	431 -	438	1	---	K.KIEEVIQR.A
1068.5961	1067.5889	1067.5764	11.7	444 -	453	0	10	R.YGLAAAVFTR.D
1143.5708	1142.5635	1142.5608	2.40	327 -	335	0	20	R.TFVEESIYR.E
1572.8251	1571.8178	1571.7732	28.4	41 -	53	0	---	K.LFINNEWHDAVSK.K
2561.2139	2560.2066	2560.2194	-4.99	350 -	371	1	---	K.VGNPFELDTQQGPQVDKEQFER.I

No match to: 847.4757, 896.5128, 936.4985, 1046.5972, 1091.5733, 1160.6063, 1180.6680, 1259.5844, 1425.7058, 1435.6867, 1673.8262, 1737.9358, 2689.3311

2. GTF2I_MOUSE **Mass:** 112708 **Score:** 39 **Expect:** 1.9 **Matches:** 7

General transcription factor II-I OS=Mus musculus GN=Gtf2i PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
847.4757	846.4684	846.4269	49.0	745 -	752	0	---	K.CGEALGLK.Q
886.5074	885.5001	885.5072	-7.99	186 -	192	0	---	K.RPFLEPK.K
1014.5913	1013.5841	1013.6022	-17.87	186 -	193	1	---	K.RPFLEPKK.H
1046.5972	1045.5899	1045.5669	22.0	410 -	418	0	---	R.RPSTYGIPR.L
1068.5961	1067.5889	1067.5400	45.8	346 -	353	1	---	K.VREFNFEK.W
1160.6063	1159.5990	1159.5986	0.39	562 -	570	1	---	K.EDWNVRITK.L
1425.7058	1424.6985	1424.7082	-6.75	917 -	928	1	---	K.APSYLEISSMRR.I + Oxidation (M)

No match to: 804.4269, 888.4606, 896.5128, 936.4985, 1091.5733, 1143.5708, 1180.6680, 1259.5844, 1435.6867, 1572.8251, 1673.8262, 1737.9358, 2561.2139, 2689.3311

3. FBX33_MOUSE **Mass:** 63865 **Score:** 37 **Expect:** 3.3 **Matches:** 5

F-box only protein 33 OS=Mus musculus GN=Fbxo33 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
886.5074	885.5001	885.4780	25.0	205 -	211	1	---	R.NNRNLQK.F
936.4985	935.4912	935.5262	-37.42	128 -	134	1	---	R.LEFLMRK.C
1143.5708	1142.5635	1142.6046	-35.93	379 -	387	0	1	R.VYLMVFDIK.S + Oxidation (M)
1425.7058	1424.6985	1424.7558	-40.18	116 -	127	1	---	R.ICLRVSPAEQPR.L
1673.8262	1672.8189	1672.8858	-39.98	374 -	387	1	---	K.SSSLRVYLMVFDIK.S + Oxidation (M)

No match to: 804.4269, 847.4757, 888.4606, 896.5128, 1014.5913, 1046.5972, 1068.5961, 1091.5733, 1160.6063, 1180.6680, 1259.5844, 1435.6867, 1572.8251, 1737.9358, 2561.2139, 2689.3311

4. CPNE8_MOUSE **Mass:** 63653 **Score:** 36 **Expect:** 3.6 **Matches:** 5

Copine-8 OS=Mus musculus GN=Cpne8 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
847.4757	846.4684	846.4447	28.0	454 -	461	0	---	K.ESIVNASK.L
1143.5708	1142.5635	1142.5760	-10.97	178 -	186	0	0	K.SDPFLVFYR.S
1425.7058	1424.6985	1424.6718	18.8	219 -	230	1	---	R.ALCNGDYDRTIK.V

1673.8262	1672.8189	1672.8759	-34.07	359 -	374	1	---	K.MFPALGFGAKLPPDGR.I
1737.9358	1736.9285	1736.8563	41.6	173 -	186	1	---	K.DFFGKSDPFLVFYR.S

No match to: 804.4269, 886.5074, 888.4606, 896.5128, 936.4985, 1014.5913, 1046.5972, 1068.5961, 1091.5733, 1160.6063, 1180.6680, 1259.5844, 1435.6867, 1572.8251, 2561.2139, 2689.3311

5. SNX25_MOUSE **Mass:** 98437 **Score:** 36 **Expect:** 4 **Matches:** 6

Sorting nexin-25 OS=Mus musculus GN=Snx25 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
886.5074	885.5001	885.5284	-31.87	636 -	643	1	---	K.VIDVQGKK.T
896.5128	895.5055	895.5127	-8.06	56 -	63	0	---	R.LSHVDVVK.V
1143.5708	1142.5635	1142.5832	-17.26	559 -	567	0	---	R.LSEFQNLHR.K
1160.6063	1159.5990	1159.6271	-24.20	569 -	578	1	---	K.LSECVPSLKK.V
1180.6680	1179.6608	1179.6724	-9.87	54 -	63	1	---	R.QRLSHVDVVK.V
1259.5844	1258.5771	1258.6016	-19.44	307 -	316	1	---	R.FGTYMERIDK.R

No match to: 804.4269, 847.4757, 888.4606, 936.4985, 1014.5913, 1046.5972, 1068.5961, 1091.5733, 1425.7058, 1435.6867, 1572.8251, 1673.8262, 1737.9358, 2561.2139, 2689.3311

6. PSMG1_MOUSE **Mass:** 33938 **Score:** 34 **Expect:** 6 **Matches:** 4

Proteasome assembly chaperone 1 OS=Mus musculus GN=Psmg1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
847.4757	846.4684	846.4997	-36.97	259 -	265	1	---	R.SLKCLVK.N
888.4606	887.4533	887.4097	49.1	30 -	36	1	---	R.RDTPEDR.E
1068.5961	1067.5889	1067.5652	22.2	2 -	11	0	---	M.AATFFGEVVK.A
1143.5708	1142.5635	1142.6183	-47.92	266 -	275	0	---	K.NIPESTEILK.K

No match to: 804.4269, 886.5074, 896.5128, 936.4985, 1014.5913, 1046.5972, 1091.5733, 1160.6063, 1180.6680, 1259.5844, 1425.7058, 1435.6867, 1572.8251, 1673.8262, 1737.9358, 2561.2139, 2689.3311

7. GSDC2_MOUSE **Mass:** 54259 **Score:** 34 **Expect:** 6.5 **Matches:** 4

Gasdermin-C2 OS=Mus musculus GN=Gsdmc2 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
886.5074	885.5001	885.5283	-31.84	336 -	342	1	---	K.ILDELRK.D
1014.5913	1013.5841	1013.5698	14.0	176 -	183	1	---	K.GFFKQLFK.V
2561.2139	2560.2066	2560.2124	-2.25	313 -	335	0	---	K.VLYDLMNMLELNQLGHMDGPGGK.I + Oxidation (M)
2689.3311	2688.3238	2688.3073	6.12	312 -	335	1	---	R.KVLYDLMNMLELNQLGHMDGPGGK.I + Oxidation (M)

No match to: 804.4269, 847.4757, 888.4606, 896.5128, 936.4985, 1046.5972, 1068.5961, 1091.5733, 1143.5708, 1160.6063, 1180.6680, 1259.5844, 1425.7058, 1435.6867, 1572.8251, 1673.8262, 1737.9358

8. CI128_MOUSE **Mass:** 55113 **Score:** 33 **Expect:** 8.3 **Matches:** 4

Uncharacterized protein C9orf128 homolog OS=Mus musculus PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1046.5972	1045.5899	1045.5590	29.6	296 -	304	1	---	K.RAELVEMAK.A
1091.5733	1090.5660	1090.5560	9.21	404 -	412	1	---	R.ATFDPKAWR.A
2561.2139	2560.2066	2560.1953	4.42	382 -	401	0	---	R.CLMFCFIPSRPEEVGEFWLK.K + Oxidation (M)

2689.3311	2688.3238	2688.2903	12.5	382 -	402	1	---	R.CLMFCFIPSRPEEVGEFWLKK.R + Oxidation (M)

No match to: 804.4269, 847.4757, 886.5074, 888.4606, 896.5128, 936.4985, 1014.5913, 1068.5961, 1143.5708, 1160.6063, 1180.6680, 1259.5844, 1425.7058, 1435.6867, 1572.8251, 1673.8262, 1737.9358

9. RS3_MOUSE **Mass:** 26828 **Score:** 31 **Expect:** 13 **Matches:** 4

40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
888.4606	887.4533	887.4712	-20.24	55 -	62	0	---	R.TQNVLGEK.G
896.5128	895.5055	895.4804	28.1	11 -	18	0	---	K.FVADGIFK.A
1143.5708	1142.5635	1142.5794	-13.91	188 -	197	0	---	K.IMLPWDPSGK.I
1572.8251	1571.8178	1571.7508	42.6	77 -	90	0	---	R.FGFPEGSVELYAEK.V

No match to: 804.4269, 847.4757, 886.5074, 936.4985, 1014.5913, 1046.5972, 1068.5961, 1091.5733, 1160.6063, 1180.6680, 1259.5844, 1425.7058, 1435.6867, 1673.8262, 1737.9358, 2561.2139, 2689.3311

10. GIT1_MOUSE **Mass:** 86046 **Score:** 30 **Expect:** 14 **Matches:** 5

ARF GTPase-activating protein GIT1 OS=Mus musculus GN=Git1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
847.4757	846.4684	846.4824	-16.52	341 -	347	1	---	K.LARFNAR.E
1425.7058	1424.6985	1424.6606	26.7	219 -	229	0	---	R.LVECQYELTDR.L
1572.8251	1571.8178	1571.8381	-12.94	687 -	700	0	---	K.IHLAVTEMASLFPK.R + Oxidation (M)
1673.8262	1672.8189	1672.8103	5.13	243 -	256	1	---	K.NGHYIIPQMADRSR.Q + Oxidation (M)
1737.9358	1736.9285	1736.8437	48.8	257 -	271	1	---	R.QKCMSQSLDLSELAK.A

No match to: 804.4269, 886.5074, 888.4606, 896.5128, 936.4985, 1014.5913, 1046.5972, 1068.5961, 1091.5733, 1143.5708, 1160.6063, 1180.6680, 1259.5844, 1435.6867, 2561.2139, 2689.3311

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (804.4269,1+) : <no title>
Query2 (847.4757,1+) : <no title>
Query3 (886.5074,1+) : <no title>
Query4 (888.4606,1+) : <no title>
Query5 (896.5128,1+) : <no title>
Query6 (936.4985,1+) : <no title>
Query7 (1014.5913,1+) : <no title>

Query8 (1046.5972,1+) : <no title>

Query9 (1068.5961,1+) : <no title>

Query10 (1091.5733,1+) : <no title>

Query11 (1143.5708,1+) : <no title>

Query12 (1160.6063,1+) : <no title>

Query13 (1180.6680,1+) : <no title>

Query14 (1259.5844,1+) : <no title>

Query15 (1425.7058,1+) : <no title>

Query16 (1435.6867,1+) : <no title>

Query17 (1572.8251,1+) : <no title>

Query18 (1673.8262,1+) : <no title>

Query19 (1737.9358,1+) : <no title>

Query20 (2561.2139,1+) : <no title>

Query21 (2689.3311,1+) : <no title>

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:49:16 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

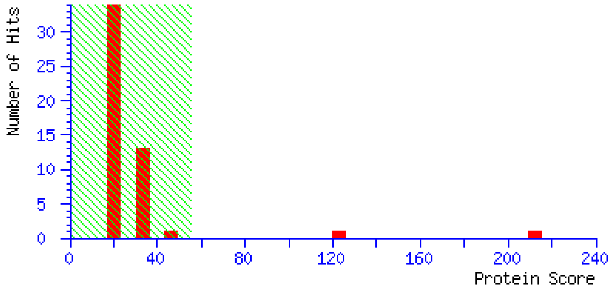
Top Score : **212 for DESM_MOUSE, Desmin OS=Mus musculus GN=Des PE=1 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**DESM_MOUSE**	53522	212	Desmin OS=Mus musculus GN=Des PE=1 SV=3
2.	**GRP78_MOUSE**	72492	128	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3
3.	**ETV6_MOUSE**	56541	42	Transcription factor ETV6 OS=Mus musculus GN=Etv6 PE=1 SV=1
4.	**LAP2_MOUSE**	158047	31	Protein LAP2 OS=Mus musculus GN=Erbb2ip PE=1 SV=2
5.	**FEZF2_MOUSE**	50154	31	Fez family zinc finger protein 2 OS=Mus musculus GN=Fezf2 PE=2 SV=1
6.	**GSTM2_MOUSE**	25871	31	Glutathione S-transferase Mu 2 OS=Mus musculus GN=Gstm2 PE=1 SV=2
7.	**PTN13_MOUSE**	272048	30	Tyrosine-protein phosphatase non-receptor type 13 OS=Mus musculus GN=Ptpn13 PE=1 SV=2
8.	**DHSO_MOUSE**	38795	30	Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3
9.	**TSSP2_MOUSE**	37400	30	Testis serine protease 2 OS=Mus musculus GN=Tessp2 PE=2 SV=1
10.	**MED28_MOUSE**	19697	29	Mediator of RNA polymerase II transcription subunit 28 OS=Mus musculus GN=Med28 PE=1 SV=2

Results List

1. DESM_MOUSE **Mass:** 53522 **Score:** 212 **Expect:** 1e-017 **Matches:** 14

Desmin OS=Mus musculus GN=Des PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
986.4493	985.4420	985.3997	42.9	318 -	324	0	---	K.QEMMEYR.H
1028.5393	1027.5320	1027.5662	-33.28	193 -	200	0	---	K.LQEEIQLR.E
1086.5430	1085.5357	1085.5829	-43.50	164 -	172	0	---	R.QVEVLTNQR.A
1101.5260	1100.5187	1100.5462	-24.95	180 -	188	0	---	R.DNLIDDLQR.L
1263.5586	1262.5513	1262.5891	-29.91	201 -	211	0	---	R.EEAENNLAAFR.A
1268.5345	1267.5272	1267.5720	-35.34	287 -	296	0	---	K.NISEAEEWYK.S
1281.6016	1280.5943	1280.6434	-38.40	395 -	405	0	---	K.MALDVEIATYR.K
1284.5249	1283.5176	1283.5703	-41.06	150 -	159	0	---	R.VAELYEEEMR.E + Oxidation (M)
1460.6973	1459.6901	1459.6725	12.0	38 -	52	1	---	R.AGFGTKGSSSSMTSR.V
1555.6449	1554.6376	1554.7063	-44.16	355 -	368	0	---	R.FASEANGYQDNIAR.L
1561.7930	1560.7857	1560.8511	-41.91	227 -	239	1	---	R.RIESLNEEIAFLK.K
1673.7965	1672.7893	1672.8532	-38.24	127 -	141	0	81	R.FLEQQNAALAAEVNR.L
1699.7946	1698.7873	1698.8537	-39.05	175 -	188	1	---	R.VDVERDNLIDDLQR.L
2755.3089	2754.3017	2754.3501	-17.57	79 -	104	0	---	R.APSYGAGELLDFSLADAVNQEFLATR.T

No match to: 1000.4384, 1002.4702, 1069.5251, 1074.5064, 1191.5963, 1211.5377, 1245.5615, 1282.5709, 1556.6900, 1588.7639, 1689.8601, 1694.7986, 1801.8408, 1860.8545, 1933.9432, 2199.8856, 2258.3810

2. GRP78_MOUSE **Mass:** 72492 **Score:** 128 **Expect:** 2.6e-009 **Matches:** 5

78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1074.5064	1073.4992	1073.5465	-44.12	525 -	533	0	---	K.ITITNDQNR.L
1191.5963	1190.5891	1190.6295	-33.99	466 -	475	0	---	K.VYEGERPLTK.D
1460.6973	1459.6901	1459.7518	-42.32	355 -	368	0	55	K.SDIDEIVLVGGSTR.I
1801.8408	1800.8336	1800.8893	-30.97	560 -	574	1	---	R.IDTRNELESYAYSLK.N
1933.9432	1932.9359	1933.0058	-36.15	476 -	493	0	44	K.DNHLLGTFDLTGIPPAPR.G

No match to: 986.4493, 1000.4384, 1002.4702, 1028.5393, 1069.5251, 1086.5430, 1101.5260, 1211.5377, 1245.5615, 1263.5586, 1268.5345, 1281.6016, 1282.5709, 1284.5249, 1555.6449, 1556.6900, 1561.7930, 1588.7639, 1673.7965, 1689.8601, 1694.7986, 1699.7946, 1860.8545, 2199.8856, 2258.3810, 2755.3089

3. ETV6_MOUSE **Mass:** 56541 **Score:** 42 **Expect:** 1.1 **Matches:** 3

Transcription factor ETV6 OS=Mus musculus GN=Etv6 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1460.6973	1459.6901	1459.7267	-25.06	2 -	14	1	24	M.SETPAQSSIKQER.I
1689.8601	1688.8528	1688.9111	-34.51	366 -	380	1	---	R.IVDPNGLARLWGNHK.N
1933.9432	1932.9359	1932.9839	-24.86	41 -	56	1	---	R.ALRMEEDSIHLPTHLR.L + Oxidation (M)

No match to: 986.4493, 1000.4384, 1002.4702, 1028.5393, 1069.5251, 1074.5064, 1086.5430, 1101.5260, 1191.5963, 1211.5377, 1245.5615, 1263.5586, 1268.5345, 1281.6016, 1282.5709, 1284.5249, 1555.6449, 1556.6900, 1561.7930, 1588.7639, 1673.7965, 1694.7986, 1699.7946, 1801.8408, 1860.8545, 2199.8856, 2258.3810, 2755.3089

4. LAP2_MOUSE **Mass:** 158047 **Score:** 31 **Expect:** 12 **Matches:** 7

Protein LAP2 OS=Mus musculus GN=Erbb2ip PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1069.5251	1068.5178	1068.5299	-11.27	535 -	544	1	---	K.TSESTTTKSK.L
1211.5377	1210.5305	1210.5578	-22.57	799 -	809	0	---	K.NEAEHIENGAK.F
1588.7639	1587.7566	1587.7641	-4.71	1008 -	1021	1	---	R.LPRSESAENHSYAK.H
1689.8601	1688.8528	1688.8556	-1.66	767 -	780	0	---	K.LVTNNIFQPEVMER.S
1694.7986	1693.7913	1693.8385	-27.86	483 -	496	1	---	R.YPTPYPDELKNMVK.T
1933.9432	1932.9359	1932.9615	-13.24	283 -	299	0	---	K.IDENQLMYLPDSIGGLR.S
2755.3089	2754.3017	2754.3685	-24.26	1123 -	1147	0	---	R.AYSIDGPNTSRPQSARPSINEIPER.T

No match to: 986.4493, 1000.4384, 1002.4702, 1028.5393, 1074.5064, 1086.5430, 1101.5260, 1191.5963, 1245.5615, 1263.5586, 1268.5345, 1281.6016, 1282.5709, 1284.5249, 1460.6973, 1555.6449, 1556.6900, 1561.7930, 1673.7965, 1699.7946, 1801.8408, 1860.8545, 2199.8856, 2258.3810

5. FEZF2_MOUSE **Mass:** 50154 **Score:** 31 **Expect:** 13 **Matches:** 5

Fez family zinc finger protein 2 OS=Mus musculus GN=Fezf2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1028.5393	1027.5320	1027.5410	-8.82	340 -	348	0	---	R.SSTLNTHIR.I
1086.5430	1085.5357	1085.5717	-33.15	260 -	270	0	---	K.LPGGSTDSKPK.N
1673.7965	1672.7893	1672.7913	-1.19	2 -	17	0	3	M.ASSASLETMVPPACPR.A
1689.8601	1688.8528	1688.7862	39.4	2 -	17	0	---	M.ASSASLETMVPPACPR.A + Oxidation (M)
2755.3089	2754.3017	2754.4158	-41.45	63 -	86	0	---	K.LLNLCSPLPCMIPLQPLGYEVPSK.T + Oxidation (M)

No match to: 986.4493, 1000.4384, 1002.4702, 1069.5251, 1074.5064, 1101.5260, 1191.5963, 1211.5377, 1245.5615, 1263.5586, 1268.5345, 1281.6016, 1282.5709, 1284.5249, 1460.6973, 1555.6449, 1556.6900, 1561.7930, 1588.7639, 1694.7986, 1699.7946, 1801.8408, 1860.8545, 1933.9432, 2199.8856, 2258.3810

6. GSTM2_MOUSE **Mass:** 25871 **Score:** 31 **Expect:** 14 **Matches:** 5

Glutathione S-transferase Mu 2 OS=Mus musculus GN=Gstm2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1086.5430	1085.5357	1085.5175	16.7	194 -	202	1	---	K.ISDYMKSSR.F
1561.7930	1560.7857	1560.8221	-23.34	124 -	136	1	---	K.KPEYLEGLPEKMK.L
1673.7965	1672.7893	1672.8566	-40.26	95 -	108	1	---	R.IRVDILENQAMDTR.I
1689.8601	1688.8528	1688.8515	0.73	95 -	108	1	---	R.IRVDILENQAMDTR.I + Oxidation (M)
1699.7946	1698.7873	1698.7858	0.90	174 -	187	1	---	K.CLDAFPNLKDFMGR.F + Oxidation (M)

No match to: 986.4493, 1000.4384, 1002.4702, 1028.5393, 1069.5251, 1074.5064, 1101.5260, 1191.5963, 1211.5377, 1245.5615, 1263.5586, 1268.5345, 1281.6016, 1282.5709, 1284.5249, 1460.6973, 1555.6449, 1556.6900, 1588.7639, 1694.7986, 1801.8408, 1860.8545, 1933.9432, 2199.8856, 2258.3810, 2755.3089

7. PTN13_MOUSE **Mass:** 272048 **Score:** 30 **Expect:** 15 **Matches:** 6

Tyrosine-protein phosphatase non-receptor type 13 OS=Mus musculus GN=Ptpn13 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1002.4702	1001.4629	1001.4930	-30.07	950 -	957	0	---	K.ASWEEKPR.G
1101.5260	1100.5187	1100.5285	-8.86	1941 -	1950	0	---	R.DGCPVVPTTR.A
1281.6016	1280.5943	1280.6109	-13.00	308 -	318	1	---	R.DISGETGRYQR.C

1460.6973	1459.6901	1459.7341	-30.14	2321	2333	0	18	R.VMALEDIQTGEVR.H
1801.8408	1800.8336	1800.8842	-28.13	762	775	1	---	K.VCQRLTEYGVHFHR.V
1860.8545	1859.8472	1859.8757	-15.33	1961	1978	0	---	K.ANGLTSMEPSGQPALMPK.N + 2 Oxidation (M)

No match to: 986.4493, 1000.4384, 1028.5393, 1069.5251, 1074.5064, 1086.5430, 1191.5963, 1211.5377, 1245.5615, 1263.5586, 1268.5345, 1282.5709, 1284.5249, 1555.6449, 1556.6900, 1561.7930, 1588.7639, 1673.7965, 1689.8601, 1694.7986, 1699.7946, 1933.9432, 2199.8856, 2258.3810, 2755.3089

8. DHSO_MOUSE **Mass:** 38795 **Score:** 30 **Expect:** 17 **Matches:** 4

Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1002.4702	1001.4629	1001.5029	-39.95	227	235	0	---	K.ETPQEIASK.V
1268.5345	1267.5272	1267.5867	-46.88	101	110	1	---	R.EVDEYCKIGR.Y
1860.8545	1859.8472	1859.9087	-33.08	92	107	1	---	R.VAIEPGVPREVDEYCK.I
1933.9432	1932.9359	1933.0303	-48.82	194	212	1	---	K.AMGAAQVVVTDLSASRLTK.A + Oxidation (M)

No match to: 986.4493, 1000.4384, 1028.5393, 1069.5251, 1074.5064, 1086.5430, 1101.5260, 1191.5963, 1211.5377, 1245.5615, 1263.5586, 1281.6016, 1282.5709, 1284.5249, 1460.6973, 1555.6449, 1556.6900, 1561.7930, 1588.7639, 1673.7965, 1689.8601, 1694.7986, 1699.7946, 1801.8408, 2199.8856, 2258.3810, 2755.3089

9. TSSP2_MOUSE **Mass:** 37400 **Score:** 30 **Expect:** 18 **Matches:** 4

Testis serine protease 2 OS=Mus musculus GN=Tessp2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
986.4493	985.4420	985.4474	-5.44	249	256	1	---	K.RGMVCGYK.E + Oxidation (M)
1191.5963	1190.5891	1190.6408	-43.43	125	134	1	---	R.IQYNVKVGDR.S
1689.8601	1688.8528	1688.8457	4.17	279	293	0	---	K.WVQVGVVSWGISCGR.K
1694.7986	1693.7913	1693.8352	-25.89	294	308	1	---	R.KGYPGVYTDVAFYSK.W

No match to: 1000.4384, 1002.4702, 1028.5393, 1069.5251, 1074.5064, 1086.5430, 1101.5260, 1211.5377, 1245.5615, 1263.5586, 1268.5345, 1281.6016, 1282.5709, 1284.5249, 1460.6973, 1555.6449, 1556.6900, 1561.7930, 1588.7639, 1673.7965, 1699.7946, 1801.8408, 1860.8545, 1933.9432, 2199.8856, 2258.3810, 2755.3089

10. MED28_MOUSE **Mass:** 19697 **Score:** 29 **Expect:** 19 **Matches:** 1

Mediator of RNA polymerase II transcription subunit 28 OS=Mus musculus GN=Med28 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1460.6973	1459.6901	1459.7267	-25.06	113	124	1	22	K.EDVSELRSELQR.K

No match to: 986.4493, 1000.4384, 1002.4702, 1028.5393, 1069.5251, 1074.5064, 1086.5430, 1101.5260, 1191.5963, 1211.5377, 1245.5615, 1263.5586, 1268.5345, 1281.6016, 1282.5709, 1284.5249, 1555.6449, 1556.6900, 1561.7930, 1588.7639, 1673.7965, 1689.8601, 1694.7986, 1699.7946, 1801.8408, 1860.8545, 1933.9432, 2199.8856, 2258.3810, 2755.3089

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (986.4493,1+) : <no title>

Query2 (1000.4384,1+) : <no title>

Query3 (1002.4702,1+) : <no title>

Query4 (1028.5393,1+) : <no title>

Query5 (1069.5251,1+) : <no title>

Query6 (1074.5064,1+) : <no title>

Query7 (1086.5430,1+) : <no title>

Query8 (1101.5260,1+) : <no title>

Query9 (1191.5963,1+) : <no title>

Query10 (1211.5377,1+) : <no title>

Query11 (1245.5615,1+) : <no title>

Query12 (1263.5586,1+) : <no title>

Query13 (1268.5345,1+) : <no title>

Query14 (1281.6016,1+) : <no title>

Query15 (1282.5709,1+) : <no title>

Query16 (1284.5249,1+) : <no title>

Query17 (1460.6973,1+) : <no title>

Query18 (1555.6449,1+) : <no title>

Query19 (1556.6900,1+) : <no title>

Query20 (1561.7930,1+) : <no title>

Query21 (1588.7639,1+) : <no title>

Query22 (1673.7965,1+) : <no title>

Query23 (1689.8601,1+) : <no title>

Query24 (1694.7986,1+) : <no title>

Query25 (1699.7946,1+) : <no title>

Query26 (1801.8408,1+) : <no title>

Query27 (1860.8545,1+) : <no title>

Query28 (1933.9432,1+) : <no title>

Query29 (2199.8856,1+) : <no title>

Query30 (2258.3810,1+) : <no title>

Query31 (2755.3089,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:49:07 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

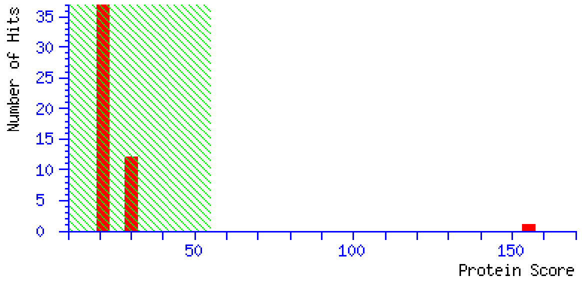
Top Score : **155 for K2C8_MOUSE, Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**K2C8_MOUSE**	54531	155	Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4
2.	**WDR44_MOUSE**	102063	32	WD repeat-containing protein 44 OS=Mus musculus GN=Wdr44 PE=1 SV=1
3.	**SMC1B_MOUSE**	145678	30	Structural maintenance of chromosomes protein 1B OS=Mus musculus GN=Smc1b PE=1 SV=1
4.	**TIMD3_MOUSE**	31428	30	Hepatitis A virus cellular receptor 2 homolog OS=Mus musculus GN=Havcr2 PE=2 SV=1
5.	**NUD10_MOUSE**	18809	30	Diphosphoinositol polyphosphate phosphohydrolase 3-alpha OS=Mus musculus GN=Nudt10 PE=2 SV=1
6.	**NUD11_MOUSE**	18809	30	Diphosphoinositol polyphosphate phosphohydrolase 3-beta OS=Mus musculus GN=Nudt11 PE=1 SV=1
7.	**GSDA3_MOUSE**	52330	28	Gasdermin-A3 OS=Mus musculus GN=Gsdma3 PE=1 SV=1
8.	**ITL1A_MOUSE**	35444	28	Intelectin-1a OS=Mus musculus GN=Itln1 PE=1 SV=1
9.	**S18L2_MOUSE**	8982	27	SS18-like protein 2 OS=Mus musculus GN=Ss18l2 PE=2 SV=1
10.	**FOXP3_MOUSE**	47886	26	Forkhead box protein P3 OS=Mus musculus GN=Foxp3 PE=2 SV=1

Results List

1. K2C8_MOUSE **Mass:** 54531 **Score:** 155 **Expect:** 5.1e-012 **Matches:** 11

Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1053.5253	1052.5180	1052.5250	-6.66	232	239	0	---	R.QIHEEEIR.E
1079.4992	1078.4919	1078.5043	-11.52	271	279	0	---	R.AQYEDIANR.S
1082.5745	1081.5672	1081.5920	-22.92	108	116	1	---	K.FASFIDKVR.F
1113.6033	1112.5961	1112.6189	-20.54	359	368	0	---	K.LAELEAALQR.A
1253.6634	1252.6562	1252.6775	-17.07	84	94	0	---	K.LEVDPNIQAVR.T
1318.6439	1317.6366	1317.6598	-17.63	259	270	0	---	R.SLDMDGIIAEVR.A
1334.6548	1333.6475	1333.6548	-5.40	259	270	0	---	R.SLDMDGIIAEVR.A + Oxidation (M)
1344.6602	1343.6529	1343.6681	-11.27	335	347	0	---	R.ASLEAAIADAEQR.G
1355.7269	1354.7196	1354.7568	-27.48	323	334	1	---	R.LQAEIEALKGQR.A
1419.7205	1418.7132	1418.7405	-19.27	220	231	0	40	R.LEGLTDEINFLR.Q
1797.8002	1796.7929	1796.8250	-17.90	205	219	1	---	K.DVDEAYMNKVELESR.L

No match to: 1040.5286, 1084.5272, 1365.6735, 1406.6671

2. WDR44_MOUSE **Mass:** 102063 **Score:** 32 **Expect:** 9.8 **Matches:** 5

WD repeat-containing protein 44 OS=Mus musculus GN=Wdr44 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1053.5253	1052.5180	1052.5516	-31.85	728	735	0	---	K.YHTQIHVR.S
1082.5745	1081.5672	1081.5404	24.8	784	793	0	---	K.GYVNSSSQIK.A
1084.5272	1083.5199	1083.5634	-40.13	775	783	1	---	R.DLSLSMKYK.G
1355.7269	1354.7196	1354.7245	-3.61	664	675	1	---	R.YFLSGSLDGKLR.L
1419.7205	1418.7132	1418.6889	17.1	562	575	0	---	R.VSPSPSQESLSSSK.S

No match to: 1040.5286, 1079.4992, 1113.6033, 1253.6634, 1318.6439, 1334.6548, 1344.6602, 1365.6735, 1406.6671, 1797.8002

3. SMC1B_MOUSE **Mass:** 145678 **Score:** 30 **Expect:** 16 **Matches:** 5

Structural maintenance of chromosomes protein 1B OS=Mus musculus GN=Smc1b PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1040.5286	1039.5213	1039.5298	-8.16	426	433	1	---	K.EQIEEHKK.R
1053.5253	1052.5180	1052.5291	-10.52	510	518	0	---	R.LYPDSVFGR.L
1318.6439	1317.6366	1317.6776	-31.10	875	886	0	---	K.EVLATQSSNIEK.I
1406.6671	1405.6598	1405.7136	-38.26	26	38	1	---	K.RFTCIIGPNGSGK.S
1419.7205	1418.7132	1418.7075	4.02	470	481	0	10	R.MSEVNEELSLIR.N

No match to: 1079.4992, 1082.5745, 1084.5272, 1113.6033, 1253.6634, 1334.6548, 1344.6602, 1355.7269, 1365.6735, 1797.8002

4. TIMD3_MOUSE **Mass:** 31428 **Score:** 30 **Expect:** 16 **Matches:** 3

Hepatitis A virus cellular receptor 2 homolog OS=Mus musculus GN=Havcr2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1082.5745	1081.5672	1081.5516	14.5	74	82	1	---	R.NVTYQKSSR.Y
1253.6634	1252.6562	1252.6048	41.0	70	79	1	---	R.TDERNVTYQK.S
1355.7269	1354.7196	1354.6769	31.5	21	32	0	---	R.SLENAYVFEVGK.N

No match to: 1040.5286, 1053.5253, 1079.4992, 1084.5272, 1113.6033, 1318.6439, 1334.6548, 1344.6602, 1365.6735, 1406.6671, 1419.7205,

1797.8002

5. NUD10_MOUSE **Mass:** 18809 **Score:** 30 **Expect:** 16 **Matches:** 3

Diphosphoinositol polyphosphate phosphohydrolase 3-alpha OS=Mus musculus GN=Nudt10 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1053.5253	1052.5180	1052.5008	16.4	19 -	26	1	---	K.RAACLCFR.S
1084.5272	1083.5199	1083.5237	-3.46	10 -	18	1	---	R.TYDPEGFKK.R
1318.6439	1317.6366	1317.6677	-23.61	79 -	89	0	---	R.LLGVFEQNQDR.K

No match to: 1040.5286, 1079.4992, 1082.5745, 1113.6033, 1253.6634, 1334.6548, 1344.6602, 1355.7269, 1365.6735, 1406.6671, 1419.7205, 1797.8002

6. NUD11_MOUSE **Mass:** 18809 **Score:** 30 **Expect:** 16 **Matches:** 3

Diphosphoinositol polyphosphate phosphohydrolase 3-beta OS=Mus musculus GN=Nudt11 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1053.5253	1052.5180	1052.5008	16.4	19 -	26	1	---	K.RAACLCFR.S
1084.5272	1083.5199	1083.5237	-3.46	10 -	18	1	---	R.TYDPEGFKK.R
1318.6439	1317.6366	1317.6677	-23.61	79 -	89	0	---	R.LLGVFEQNQDR.K

No match to: 1040.5286, 1079.4992, 1082.5745, 1113.6033, 1253.6634, 1334.6548, 1344.6602, 1355.7269, 1365.6735, 1406.6671, 1419.7205, 1797.8002

7. GSDA3_MOUSE **Mass:** 52330 **Score:** 28 **Expect:** 23 **Matches:** 3

Gasdermin-A3 OS=Mus musculus GN=Gsdma3 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1355.7269	1354.7196	1354.7146	3.68	45 -	55	1	---	K.STLFWGARYVR.T
1365.6735	1364.6662	1364.7010	-25.43	150 -	161	0	---	K.NLYVVMEAVEAK.Q
1419.7205	1418.7132	1418.6612	36.6	134 -	145	0	4	K.LSADHSFLNEMR.Y

No match to: 1040.5286, 1053.5253, 1079.4992, 1082.5745, 1084.5272, 1113.6033, 1253.6634, 1318.6439, 1334.6548, 1344.6602, 1406.6671, 1797.8002

8. ITL1A_MOUSE **Mass:** 35444 **Score:** 28 **Expect:** 23 **Matches:** 3

Intelectin-1a OS=Mus musculus GN=Itln1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1040.5286	1039.5213	1039.5338	-12.05	190 -	198	1	---	K.YPVKYGEGK.C
1082.5745	1081.5672	1081.5556	10.7	51 -	59	0	---	K.AQDGLYFLR.T
1344.6602	1343.6529	1343.6470	4.43	218 -	229	1	---	R.KTASYYSPSGQR.E

No match to: 1053.5253, 1079.4992, 1084.5272, 1113.6033, 1253.6634, 1318.6439, 1334.6548, 1355.7269, 1365.6735, 1406.6671, 1419.7205, 1797.8002

9. S18L2_MOUSE **Mass:** 8982 **Score:** 27 **Expect:** 31 **Matches:** 2

SS18-like protein 2 OS=Mus musculus GN=Ss18l2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1053.5253	1052.5180	1052.4961	20.9	34 -	41	0	---	R.CIVEYQNK.G
1334.6548	1333.6475	1333.6853	-28.29	1 -	11	0	---	-.MSVIFAPDWLR.G

No match to: 1040.5286, 1079.4992, 1082.5745, 1084.5272, 1113.6033, 1253.6634, 1318.6439, 1344.6602, 1355.7269, 1365.6735, 1406.6671, 1419.7205, 1797.8002

10. FOXP3_MOUSE **Mass:** 47886 **Score:** 26 **Expect:** 39 **Matches:** 3

Forkhead box protein P3 OS=Mus musculus GN=Foxp3 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1084.5272	1083.5199	1083.5713	-47.38	348 -	356	0	---	R.WAILEAPER.Q
1365.6735	1364.6662	1364.6143	38.1	216 -	226	0	---	K.HCQADHLLDEK.G
1419.7205	1418.7132	1418.7261	-9.12	263 -	276	1	1	K.MALAKAPSVASMDK.S

No match to: 1040.5286, 1053.5253, 1079.4992, 1082.5745, 1113.6033, 1253.6634, 1318.6439, 1334.6548, 1344.6602, 1355.7269, 1406.6671, 1797.8002

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (1040.5286,1+) : <no title>
Query2 (1053.5253,1+) : <no title>
Query3 (1079.4992,1+) : <no title>
Query4 (1082.5745,1+) : <no title>
Query5 (1084.5272,1+) : <no title>
Query6 (1113.6033,1+) : <no title>
Query7 (1253.6634,1+) : <no title>
Query8 (1318.6439,1+) : <no title>
Query9 (1334.6548,1+) : <no title>
Query10 (1344.6602,1+) : <no title>
Query11 (1355.7269,1+) : <no title>
Query12 (1365.6735,1+) : <no title>
Query13 (1406.6671,1+) : <no title>
Query14 (1419.7205,1+) : <no title>
Query15 (1797.8002,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:48:28 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

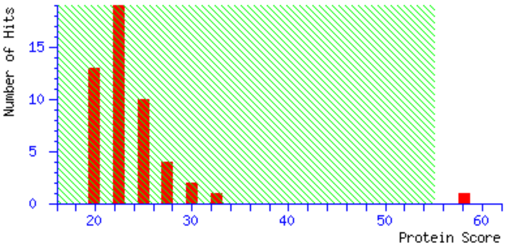
Top Score : **58 for DESM_MOUSE, Desmin OS=Mus musculus GN=Des PE=1 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**DESM_MOUSE**	53522	58	Desmin OS=Mus musculus GN=Des PE=1 SV=3
2.	**MIDA_MOUSE**	48748	32	Protein midA homolog, mitochondrial OS=Mus musculus PE=2 SV=3
3.	**F158A_MOUSE**	23058	30	UPF0172 protein FAM158A OS=Mus musculus GN=Fam158a PE=2 SV=1
4.	**ARFRP_MOUSE**	23101	29	ADP-ribosylation factor-related protein 1 OS=Mus musculus GN=Arfrp1 PE=2 SV=2
5.	**B3GN7_MOUSE**	45862	28	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 OS=Mus musculus GN=B3gnt7 PE=2 SV=2
6.	**UTP18_MOUSE**	61636	28	U3 small nucleolar RNA-associated protein 18 homolog OS=Mus musculus GN=Utp18 PE=1 SV=1
7.	**CBX8_MOUSE**	39893	27	Chromobox protein homolog 8 OS=Mus musculus GN=Cbx8 PE=1 SV=1
8.	**DGLB_MOUSE**	75168	26	Sn1-specific diacylglycerol lipase beta OS=Mus musculus GN=Daglb PE=1 SV=2
9.	**NOP2_MOUSE**	87098	26	Putative ribosomal RNA methyltransferase NOP2 OS=Mus musculus GN=Nop2 PE=2 SV=1
10.	**T132C_MOUSE**	122100	25	Transmembrane protein 132C OS=Mus musculus GN=Tmem132c PE=2 SV=3

Results List

1. DESM_MOUSE **Mass:** 53522 **Score:** 58 **Expect:** 0.025 **Matches:** 6

Desmin OS=Mus musculus GN=Des PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1028.6123	1027.6050	1027.5662	37.8	193 -	200	0	---	K.LQEEIQLR.E
1032.5788	1031.5715	1031.5360	34.4	59 -	70	0	---	R.TSGGAGGLGSLR.S
1587.8675	1586.8602	1586.7900	44.3	105 -	117	1	---	R.TNEKVELQELNDR.F
1673.9141	1672.9068	1672.8532	32.0	127 -	141	0	---	R.FLEQQNAALAAEVNR.L
2247.1875	2246.1802	2246.0927	39.0	201 -	221	1	---	R.EEAENNLAAFRADVDAATLAR.I
2755.4207	2754.4134	2754.3501	23.0	79 -	104	0	---	R.APSYGAGELLDFSLADAVNQEFLATR.T

No match to: 875.5250, 991.4878, 1023.4758, 1055.5335, 1061.5536, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1433.8186, 1995.0915, 2060.0905, 2462.3472

2. MIDA_MOUSE **Mass:** 48748 **Score:** 32 **Expect:** 10 **Matches:** 4

Protein midA homolog, mitochondrial OS=Mus musculus PE=2 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
875.5250	874.5177	874.4807	42.3	1 -	7	1	---	-.MNALVRR.C + Oxidation (M)
1055.5335	1054.5262	1054.5005	24.4	174 -	182	0	---	R.DAESLVYMK.G
1061.5536	1060.5464	1060.5699	-22.20	357 -	365	1	---	K.NMGIDVRLK.V + Oxidation (M)
2060.0905	2059.0832	2059.1037	-9.95	243 -	260	1	---	K.LRFVLAPCATPAEAFIQR.D

No match to: 991.4878, 1023.4758, 1028.6123, 1032.5788, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1433.8186, 1587.8675, 1673.9141, 1995.0915, 2247.1875, 2462.3472, 2755.4207

3. F158A_MOUSE **Mass:** 23058 **Score:** 30 **Expect:** 17 **Matches:** 3

UPF0172 protein FAM158A OS=Mus musculus GN=Fam158a PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
991.4878	990.4805	990.4804	0.11	1 -	9	0	---	-.MGEVEISAR.A
1032.5788	1031.5715	1031.5685	2.92	111 -	119	0	---	R.AVLIMLDNK.K + Oxidation (M)
1061.5536	1060.5464	1060.5488	-2.27	144 -	151	1	---	K.DKNLVMWR.D

No match to: 875.5250, 1023.4758, 1028.6123, 1055.5335, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1433.8186, 1587.8675, 1673.9141, 1995.0915, 2060.0905, 2247.1875, 2462.3472, 2755.4207

4. ARFRP_MOUSE **Mass:** 23101 **Score:** 29 **Expect:** 21 **Matches:** 3

ADP-ribosylation factor-related protein 1 OS=Mus musculus GN=Arfrp1 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
875.5250	874.5177	874.4886	33.3	190 -	196	0	---	R.NVHRPPR.Q
991.4878	990.4805	990.4844	-3.95	178 -	185	0	---	R.EGIEWMVK.C
1587.8675	1586.8602	1586.8880	-17.50	53 -	68	0	---	K.ITTTVGLNIGTVDVGK.A

No match to: 1023.4758, 1028.6123, 1032.5788, 1055.5335, 1061.5536, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1433.8186, 1673.9141, 1995.0915, 2060.0905, 2247.1875, 2462.3472, 2755.4207

5. B3GN7_MOUSE **Mass:** 45862 **Score:** 28 **Expect:** 26 **Matches:** 3

UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 OS=Mus musculus GN=B3gnt7 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**

1433.8186	1432.8114	1432.8402	-20.12	165 -	178	1	---	R.GAVRTLFLLGTASK.Q
2462.3472	2461.3399	2461.2569	33.7	195 -	214	0	---	R.LYADILQWDFLDSFFNLTLK.E
2755.4207	2754.4134	2754.3583	20.0	115 -	137	1	---	R.YFPMLLNHPEKCAGDVYMLVVVK.S + 2 Oxidation (M)

No match to: 875.5250, 991.4878, 1023.4758, 1028.6123, 1032.5788, 1055.5335, 1061.5536, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1587.8675, 1673.9141, 1995.0915, 2060.0905, 2247.1875

6. UTP18_MOUSE **Mass:** 61636 **Score:** 28 **Expect:** 29 **Matches:** 4

U3 small nucleolar RNA-associated protein 18 homolog OS=Mus musculus GN=Utp18 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1055.5335	1054.5262	1054.5083	17.0	529 -	538	0	---	R.GGYFALGNEK.G
1268.6611	1267.6538	1267.6309	18.1	529 -	540	1	---	R.GGYFALGNEKGR.A
1326.7861	1325.7788	1325.7164	47.1	23 -	36	1	---	K.ARPGSGSTPAKAAR.S
1433.8186	1432.8114	1432.7925	13.1	280 -	291	1	---	K.TNPKIQSIYLEK.F

No match to: 875.5250, 991.4878, 1023.4758, 1028.6123, 1032.5788, 1061.5536, 1168.7148, 1272.0371, 1587.8675, 1673.9141, 1995.0915, 2060.0905, 2247.1875, 2462.3472, 2755.4207

7. CBX8_MOUSE **Mass:** 39893 **Score:** 27 **Expect:** 32 **Matches:** 4

Chromobox protein homolog 8 OS=Mus musculus GN=Cbx8 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
991.4878	990.4805	990.4804	0.11	1 -	9	0	---	-.MELSAVGER.V
1028.6123	1027.6050	1027.5927	12.0	101 -	109	1	---	R.GIRIPYPGR.S
1061.5536	1060.5464	1060.5149	29.7	110 -	119	0	---	R.SPQDLASTSR.A
1673.9141	1672.9068	1672.8645	25.3	280 -	295	1	---	R.VRHSSGTPASVGSLYR.D

No match to: 875.5250, 1023.4758, 1032.5788, 1055.5335, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1433.8186, 1587.8675, 1995.0915, 2060.0905, 2247.1875, 2462.3472, 2755.4207

8. DGLB_MOUSE **Mass:** 75168 **Score:** 26 **Expect:** 39 **Matches:** 4

Sn1-specific diacylglycerol lipase beta OS=Mus musculus GN=Daglb PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1023.4758	1022.4685	1022.5042	-34.86	1 -	9	0	---	-.MPGMVLFGR.R + Oxidation (M)
1028.6123	1027.6050	1027.5774	26.8	646 -	654	1	---	R.ALDRVLADR.T
1032.5788	1031.5715	1031.5699	1.60	2 -	10	1	---	M.PGMVLFGRR.W
1673.9141	1672.9068	1672.9222	-9.24	485 -	499	0	---	K.DFVVSLILGMDVIPR.L

No match to: 875.5250, 991.4878, 1055.5335, 1061.5536, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1433.8186, 1587.8675, 1995.0915, 2060.0905, 2247.1875, 2462.3472, 2755.4207

9. NOP2_MOUSE **Mass:** 87098 **Score:** 26 **Expect:** 41 **Matches:** 4

Putative ribosomal RNA methyltransferase NOP2 OS=Mus musculus GN=Nop2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1168.7148	1167.7075	1167.7088	-1.11	227 -	236	1	---	K.RIQDIVGVLR.D
1268.6611	1267.6538	1267.6455	6.54	468 -	477	1	---	K.DIQRCAHLQK.E
1326.7861	1325.7788	1325.7554	17.6	68 -	80	1	---	K.SPGIKTLPGELSK.G
2247.1875	2246.1802	2246.1729	3.25	435 -	456	1	---	K.VVGGFDRVLLDAPCSGTGVISK.D

No match to: 875.5250, 991.4878, 1023.4758, 1028.6123, 1032.5788, 1055.5335, 1061.5536, 1272.0371, 1433.8186, 1587.8675, 1673.9141, 1995.0915, 2060.0905, 2462.3472, 2755.4207

10. T132C_MOUSE **Mass:** 122100 **Score:** 25 **Expect:** 54 **Matches:** 4

Transmembrane protein 132C OS=Mus musculus GN=Tmem132c PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1032.5788	1031.5715	1031.5328	37.5	80 -	87	0	---	R.VESFFIYK.A
1673.9141	1672.9068	1672.8818	15.0	689 -	704	1	---	K.ATSAVAMAEELLRAPK.K + Oxidation (M)
2247.1875	2246.1802	2246.1716	3.87	634 -	654	0	---	R.EVGMTTIQVLSPLSDSILAEK.T + Oxidation (M)
2755.4207	2754.4134	2754.5201	-38.75	629 -	654	1	---	R.VLVGREVGMTTIQVLSPLSDSILAEK.T

No match to: 875.5250, 991.4878, 1023.4758, 1028.6123, 1055.5335, 1061.5536, 1168.7148, 1268.6611, 1272.0371, 1326.7861, 1433.8186, 1587.8675, 1995.0915, 2060.0905, 2462.3472

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (875.5250,1+) : <no title>

Query2 (991.4878,1+) : <no title>

Query3 (1023.4758,1+) : <no title>

Query4 (1028.6123,1+) : <no title>

Query5 (1032.5788,1+) : <no title>

Query6 (1055.5335,1+) : <no title>

Query7 (1061.5536,1+) : <no title>

Query8 (1168.7148,1+) : <no title>

Query9 (1268.6611,1+) : <no title>

Query10 (1272.0371,1+) : <no title>

Query11 (1326.7861,1+) : <no title>

Query12 (1433.8186,1+) : <no title>

Query13 (1587.8675,1+) : <no title>

Query14 (1673.9141,1+) : <no title>

Query15 (1995.0915,1+) : <no title>

Query16 (2060.0905,1+) : <no title>

Query17 (2247.1875,1+) : <no title>

Query18 (2462.3472,1+) : <no title>

Query19 (2755.4207,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **IPI_mouse (59534 sequences; 26627161 residues)**

Timestamp : **5 Nov 2013 at 07:59:02 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

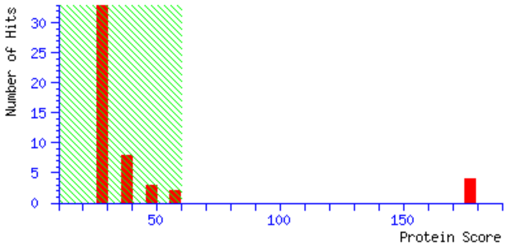
Top Score : **177 for IPI00128108, Tax_Id=10090 Gene_Symbol=Try4 trypsin 4**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 60 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**IPI00128108**	26941	177	Tax_Id=10090 Gene_Symbol=Try4 trypsin 4
2.	**IPI00759953**	26944	177	Tax_Id=10090 Gene_Symbol=Try5 trypsin 5
3.	**IPI00989590**	27961	176	Tax_Id=10090 Gene_Symbol=Try4 Uncharacterized protein
4.	**IPI00406464**	28002	176	Tax_Id=10090 Gene_Symbol=Try5 Putative uncharacterized protein
5.	**IPI01027601**	14574	60	Tax_Id=10090 Gene_Symbol=Try5 14 kDa protein
6.	**IPI00403650**	26871	54	Tax_Id=10090 Gene_Symbol=Prss2 Anionic trypsin-2
7.	**IPI00228825**	129164	44	Tax_Id=10090 Gene_Symbol=Ccdc150 Coiled-coil domain-containing protein 150
8.	**IPI00353583**	87342	43	Tax_Id=10090 Gene_Symbol=Zfp735 zinc finger protein 735
9.	**IPI00346603**	16383	43	Tax_Id=10090 Gene_Symbol=2410004P03Rik hypothetical protein LOC73667 isoform 1
10.	**IPI00465762**	32361	42	Tax_Id=10090 Gene_Symbol=Pde5a Uncharacterized protein

Results List

1. IPI00128108 **Mass:** 26941 **Score:** 177 **Expect:** 1.2e-013 **Matches:** 7

Tax_Id=10090 Gene_Symbol=Try4 trypsin 4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
871.4160	870.4087	870.4096	-1.10	96 -	102	0	---	K.HPNFNSR.T
925.4534	924.4461	924.4487	-2.86	24 -	31	0	---	K.IVGGYTCR.E
1041.6023	1040.5950	1040.5978	-2.70	113 -	122	0	42	K.LASPVTLNAR.V
1190.6305	1189.6233	1189.6376	-12.09	103 -	112	0	---	R.TLNNDIMLIK.L + Oxidation (M)
1225.6664	1224.6591	1224.6727	-11.13	93 -	102	1	---	K.IIKHPNFNSR.T
1668.7802	1667.7729	1667.8011	-16.90	179 -	193	0	---	K.ITNNMICVGFLEGGK.D + Oxidation (M)
2212.0798	2211.0725	2211.0920	-8.81	73 -	92	0	63	R.LGEHNINVLEGNEQFVNSAK.I

No match to: 834.4235, 856.4715, 883.4145, 915.3925, 921.4268, 953.4425, 1028.5634, 1069.5866, 1080.5760, 1149.5935, 1196.6219, 1207.6077, 1212.6143, 1247.6057, 1527.7594, 1571.7673, 1614.7975, 1626.7846, 1635.8649, 1690.7765, 1834.7973, 2226.0862, 2234.0797, 2249.0713, 2277.0481

2. IPI00759953 **Mass:** 26944 **Score:** 177 **Expect:** 1.2e-013 **Matches:** 7

Tax_Id=10090 Gene_Symbol=Try5 trypsin 5

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
871.4160	870.4087	870.4096	-1.10	96 -	102	0	---	K.HPNFNSR.T
925.4534	924.4461	924.4487	-2.86	24 -	31	0	---	K.IVGGYTCR.E
1041.6023	1040.5950	1040.5978	-2.70	113 -	122	0	42	K.LASPVTLNAR.V
1190.6305	1189.6233	1189.6376	-12.09	103 -	112	0	---	R.TLNNDIMLIK.L + Oxidation (M)
1225.6664	1224.6591	1224.6727	-11.13	93 -	102	1	---	K.IIKHPNFNSR.T
1668.7802	1667.7729	1667.8011	-16.90	179 -	193	0	---	K.ITNNMICVGFLEGGK.D + Oxidation (M)
2212.0798	2211.0725	2211.0920	-8.81	73 -	92	0	63	R.LGEHNINVLEGNEQFVNSAK.I

No match to: 834.4235, 856.4715, 883.4145, 915.3925, 921.4268, 953.4425, 1028.5634, 1069.5866, 1080.5760, 1149.5935, 1196.6219, 1207.6077, 1212.6143, 1247.6057, 1527.7594, 1571.7673, 1614.7975, 1626.7846, 1635.8649, 1690.7765, 1834.7973, 2226.0862, 2234.0797, 2249.0713, 2277.0481

3. IPI00989590 **Mass:** 27961 **Score:** 176 **Expect:** 1.5e-013 **Matches:** 7

Tax_Id=10090 Gene_Symbol=Try4 Uncharacterized protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
871.4160	870.4087	870.4096	-1.10	96 -	102	0	---	K.HPNFNSR.T
925.4534	924.4461	924.4487	-2.86	24 -	31	0	---	K.IVGGYTCR.E
1041.6023	1040.5950	1040.5978	-2.70	113 -	122	0	42	K.LASPVTLNAR.V
1190.6305	1189.6233	1189.6376	-12.09	103 -	112	0	---	R.TLNNDIMLIK.L + Oxidation (M)
1225.6664	1224.6591	1224.6727	-11.13	93 -	102	1	---	K.IIKHPNFNSR.T
1668.7802	1667.7729	1667.8011	-16.90	179 -	193	0	---	K.ITNNMICVGFLEGGK.D + Oxidation (M)
2212.0798	2211.0725	2211.0920	-8.81	73 -	92	0	63	R.LGEHNINVLEGNEQFVNSAK.I

No match to: 834.4235, 856.4715, 883.4145, 915.3925, 921.4268, 953.4425, 1028.5634, 1069.5866, 1080.5760, 1149.5935, 1196.6219, 1207.6077, 1212.6143, 1247.6057, 1527.7594, 1571.7673, 1614.7975, 1626.7846, 1635.8649, 1690.7765, 1834.7973, 2226.0862, 2234.0797, 2249.0713, 2277.0481

4. IPI00406464 **Mass:** 28002 **Score:** 176 **Expect:** 1.5e-013 **Matches:** 7

Tax_Id=10090 Gene_Symbol=Try5 Putative uncharacterized protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide

871.4160	870.4087	870.4096	-1.10	96 -	102	0	---	K.HPNFNSR.T
925.4534	924.4461	924.4487	-2.86	24 -	31	0	---	K.IVGGYTCR.E
1041.6023	1040.5950	1040.5978	-2.70	113 -	122	0	42	K.LASPVTLNAR.V
1190.6305	1189.6233	1189.6376	-12.09	103 -	112	0	---	R.TLNNDIMLIK.L + Oxidation (M)
1225.6664	1224.6591	1224.6727	-11.13	93 -	102	1	---	K.IIKHPNFNSR.T
1668.7802	1667.7729	1667.8011	-16.90	179 -	193	0	---	K.ITNNMICVGFLEGGK.D + Oxidation (M)
2212.0798	2211.0725	2211.0920	-8.81	73 -	92	0	63	R.LGEHNINVLEGNEQFVNSAK.I

No match to: 834.4235, 856.4715, 883.4145, 915.3925, 921.4268, 953.4425, 1028.5634, 1069.5866, 1080.5760, 1149.5935, 1196.6219, 1207.6077, 1212.6143, 1247.6057, 1527.7594, 1571.7673, 1614.7975, 1626.7846, 1635.8649, 1690.7765, 1834.7973, 2226.0862, 2234.0797, 2249.0713, 2277.0481

5. IPI01027601 **Mass:** 14574 **Score:** 60 **Expect:** 0.061 **Matches:** 2

Tax_Id=10090 Gene_Symbol=Try5 14 kDa protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.6023	1040.5950	1040.5978	-2.70	5 -	14	0	42	K.LASPVTLNAR.V
1668.7802	1667.7729	1667.8011	-16.90	71 -	85	0	---	K.ITNNMICVGFLEGGK.D + Oxidation (M)

No match to: 834.4235, 856.4715, 871.4160, 883.4145, 915.3925, 921.4268, 925.4534, 953.4425, 1028.5634, 1069.5866, 1080.5760, 1149.5935, 1190.6305, 1196.6219, 1207.6077, 1212.6143, 1225.6664, 1247.6057, 1527.7594, 1571.7673, 1614.7975, 1626.7846, 1635.8649, 1690.7765, 1834.7973, 2212.0798, 2226.0862, 2234.0797, 2249.0713, 2277.0481

6. IPI00403650 **Mass:** 26871 **Score:** 54 **Expect:** 0.22 **Matches:** 2

Tax_Id=10090 Gene_Symbol=Prss2 Anionic trypsin-2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
925.4534	924.4461	924.4487	-2.86	24 -	31	0	---	K.IVGGYTCR.E
1041.6023	1040.5950	1040.5978	-2.70	113 -	122	0	42	K.LASPVTLNAR.V

No match to: 834.4235, 856.4715, 871.4160, 883.4145, 915.3925, 921.4268, 953.4425, 1028.5634, 1069.5866, 1080.5760, 1149.5935, 1190.6305, 1196.6219, 1207.6077, 1212.6143, 1225.6664, 1247.6057, 1527.7594, 1571.7673, 1614.7975, 1626.7846, 1635.8649, 1668.7802, 1690.7765, 1834.7973, 2212.0798, 2226.0862, 2234.0797, 2249.0713, 2277.0481

7. IPI00228825 **Mass:** 129164 **Score:** 44 **Expect:** 2.7 **Matches:** 10

Tax_Id=10090 Gene_Symbol=Ccdc150 Coiled-coil domain-containing protein 150

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1069.5866	1068.5793	1068.5273	48.6	570 -	578	1	---	K.NMLAYEKGK.L + Oxidation (M)
1080.5760	1079.5687	1079.5723	-3.37	268 -	276	0	---	R.QQVHALQEK.C
1196.6219	1195.6146	1195.5907	20.0	962 -	971	0	---	R.FVSEMNTLQK.E
1212.6143	1211.6070	1211.5856	17.7	962 -	971	0	---	R.FVSEMNTLQK.E + Oxidation (M)
1225.6664	1224.6591	1224.5986	49.4	550 -	560	1	---	K.ATSDYQGKVEK.A
1527.7594	1526.7521	1526.7473	3.20	119 -	130	0	---	R.MCYLENLIQSLK.M + Oxidation (M)
1635.8649	1634.8577	1634.8740	-9.98	834 -	847	1	---	K.VEAELHAERIEALR.K
1690.7765	1689.7692	1689.8396	-41.64	626 -	639	1	---	K.AYLEQTEAHLKEMK.S
2226.0862	2225.0789	2225.1804	-45.63	147 -	166	1	---	K.TAFLNDQLNIIQGEHSKGLK.L
2249.0713	2248.0640	2248.1310	-29.79	91 -	110	0	---	K.AISPIPNEVICPESPGNLWR.N

No match to: 834.4235, 856.4715, 871.4160, 883.4145, 915.3925, 921.4268, 925.4534, 953.4425, 1028.5634, 1041.6023, 1149.5935, 1190.6305, 1207.6077, 1247.6057, 1571.7673, 1614.7975, 1626.7846, 1668.7802, 1834.7973, 2212.0798, 2234.0797, 2277.0481

8. IPI00353583 **Mass:** 87342 **Score:** 43 **Expect:** 2.7 **Matches:** 7

Tax_Id=10090 Gene_Symbol=Zfp735 zinc finger protein 735

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1041.6023	1040.5950	1040.5767	17.6	456 -	464	1	---	K.HSKYKPPGK.C
1149.5935	1148.5863	1148.5826	3.21	267 -	276	0	---	R.VNDNNIGYIK.N
1527.7594	1526.7521	1526.7954	-28.31	603 -	615	1	---	K.SFTQSSSLKIHHR.I
1614.7975	1613.7903	1613.7542	22.4	465 -	478	0	---	K.CSSKPSGLMVFETR.G + Oxidation (M)
1635.8649	1634.8577	1634.8277	18.3	575 -	587	1	---	K.YFTRSSNLQVHQR.V
1668.7802	1667.7729	1667.7144	35.1	252 -	266	0	---	K.LGIYHMGSSCGNSNR.V + Oxidation (M)
1834.7973	1833.7900	1833.8250	-19.09	616 -	630	1	---	R.IHTGDKPYRCNECGK.C

No match to: 834.4235, 856.4715, 871.4160, 883.4145, 915.3925, 921.4268, 925.4534, 953.4425, 1028.5634, 1069.5866, 1080.5760, 1190.6305, 1196.6219, 1207.6077, 1212.6143, 1225.6664, 1247.6057, 1571.7673, 1626.7846, 1690.7765, 2212.0798, 2226.0862, 2234.0797, 2249.0713, 2277.0481

9. IPI00346603 **Mass:** 16383 **Score:** 43 **Expect:** 2.9 **Matches:** 4

Tax_Id=10090 Gene_Symbol=2410004P03Rik hypothetical protein LOC73667 isoform 1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
921.4268	920.4195	920.4239	-4.85	82 -	89	0	---	K.DYDPLGNK.K
1196.6219	1195.6146	1195.6197	-4.22	140 -	149	1	---	K.RKPDDELQPV.-
1626.7846	1625.7773	1625.7661	6.89	125 -	138	0	---	K.ALGHMDFFFVEGTR.K
2226.0862	2225.0789	2225.1012	-10.01	40 -	60	0	---	R.ALAGGCQGTPALGVQQDQLWR.E

No match to: 834.4235, 856.4715, 871.4160, 883.4145, 915.3925, 925.4534, 953.4425, 1028.5634, 1041.6023, 1069.5866, 1080.5760, 1149.5935, 1190.6305, 1207.6077, 1212.6143, 1225.6664, 1247.6057, 1527.7594, 1571.7673, 1614.7975, 1635.8649, 1668.7802, 1690.7765, 1834.7973, 2212.0798, 2234.0797, 2249.0713, 2277.0481

10. IPI00465762 **Mass:** 32361 **Score:** 42 **Expect:** 3.9 **Matches:** 6

Tax_Id=10090 Gene_Symbol=Pde5a Uncharacterized protein

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1080.5760	1079.5687	1079.5434	23.5	1 -	9	1	---	-.MLPFGDKTR.D + Oxidation (M)
1190.6305	1189.6233	1189.6199	2.83	221 -	230	0	---	K.TQSILCMPIK.N
1196.6219	1195.6146	1195.6383	-19.79	89 -	98	1	---	K.KEQMPLTPPR.F
1212.6143	1211.6070	1211.6332	-21.64	89 -	98	1	---	K.KEQMPLTPPR.F + Oxidation (M)
1527.7594	1526.7521	1526.6936	38.3	8 -	19	1	---	K.TRDMVNAWFSER.V + Oxidation (M)
1690.7765	1689.7692	1689.7920	-13.49	143 -	156	1	---	R.YSLFLVCEDSSKDK.F

No match to: 834.4235, 856.4715, 871.4160, 883.4145, 915.3925, 921.4268, 925.4534, 953.4425, 1028.5634, 1041.6023, 1069.5866, 1149.5935, 1207.6077, 1225.6664, 1247.6057, 1571.7673, 1614.7975, 1626.7846, 1635.8649, 1668.7802, 1834.7973, 2212.0798, 2226.0862, 2234.0797, 2249.0713, 2277.0481

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (834.4235,1+) : <no title>

Query2 (856.4715,1+) : <no title>

Query3 (871.4160,1+) : <no title>

Query4 (883.4145,1+) : <no title>

Query5 (915.3925,1+) : <no title>

Query6 (921.4268,1+) : <no title>

Query7 (925.4534,1+) : <no title>

Query8 (953.4425,1+) : <no title>

Query9 (1028.5634,1+) : <no title>

Query10 (1041.6023,1+) : <no title>

Query11 (1069.5866,1+) : <no title>

Query12 (1080.5760,1+) : <no title>

Query13 (1149.5935,1+) : <no title>

Query14 (1190.6305,1+) : <no title>

Query15 (1196.6219,1+) : <no title>

Query16 (1207.6077,1+) : <no title>

Query17 (1212.6143,1+) : <no title>

Query18 (1225.6664,1+) : <no title>

Query19 (1247.6057,1+) : <no title>

Query20 (1527.7594,1+) : <no title>

Query21 (1571.7673,1+) : <no title>

Query22 (1614.7975,1+) : <no title>

Query23 (1626.7846,1+) : <no title>

Query24 (1635.8649,1+) : <no title>

Query25 (1668.7802,1+) : <no title>

Query26 (1690.7765,1+) : <no title>

Query27 (1834.7973,1+) : <no title>

Query28 (2212.0798,1+) : <no title>

Query29 (2226.0862,1+) : <no title>

Query30 (2234.0797,1+) : <no title>

Query31 (2249.0713,1+) : <no title>

Query32 (2277.0481,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : Auto submitted by BioTools

Database : SwissProt 57.15 (515203 sequences; 181334896 residues)

Taxonomy : Mus. (16281 sequences)

Timestamp : 22 Nov 2010 at 05:08:11 GMT

Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.

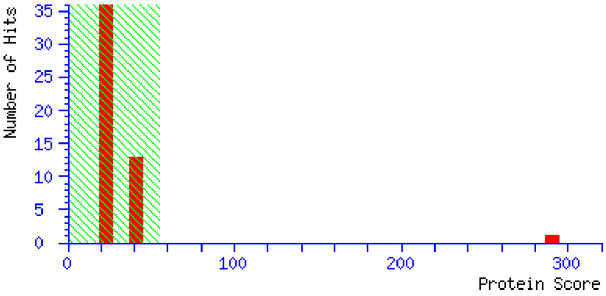
Top Score : 290 for DCTN2_MOUSE, Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**DCTN2_MOUSE**	44204	290	Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3
2.	**EF2_MOUSE**	96222	48	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2
3.	**LYPA1_MOUSE**	25014	41	Acyl-protein thioesterase 1 OS=Mus musculus GN=Lypla1 PE=1 SV=1
4.	**DOK5_MOUSE**	35887	38	Docking protein 5 OS=Mus musculus GN=Dok5 PE=1 SV=1
5.	**RGS5_MOUSE**	21243	36	Regulator of G-protein signaling 5 OS=Mus musculus GN=Rgs5 PE=2 SV=2
6.	**LITD1_MOUSE**	88705	36	LINE-1 type transposase domain-containing protein 1 OS=Mus musculus GN=L1td1 PE=2 SV=1
7.	**ECE1_MOUSE**	87815	35	Endothelin-converting enzyme 1 OS=Mus musculus GN=Ece1 PE=1 SV=1
8.	**ZNF32_MOUSE**	31722	35	Zinc finger protein 32 OS=Mus musculus GN=Znf32 PE=2 SV=1
9.	**UN45A_MOUSE**	104579	35	Protein unc-45 homolog A OS=Mus musculus GN=Unc45a PE=1 SV=2
10.	**ADCK3_MOUSE**	72154	33	Chaperone activity of bc1 complex-like, mitochondrial OS=Mus musculus GN=Cabc1 PE=2 SV=2

Results List

1. <u>DCTN2_MOUSE</u> **Mass:** 44204 **Score:** 290 **Expect:** 1.6e-025 **Matches:** 9

Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1031.5698	1030.5625	1030.5659	-3.24	232 -	240	0	---	R.LTELEATVR.C
1187.6731	1186.6658	1186.6670	-0.95	231 -	240	1	---	K.RLTELEATVR.C
1286.6832	1285.6760	1285.6779	-1.49	310 -	319	0	94	K.VHQLYETIQR.W
1582.8429	1581.8357	1581.8515	-10.00	320 -	333	0	---	R.WSPVASTLPELVQR.L
1591.8073	1590.8001	1590.8036	-2.20	367 -	380	0	---	K.DNTALLTQVQTTMR.E
1598.8709	1597.8636	1597.8675	-2.42	269 -	283	0	100	K.VSALDLAVLDQVEAR.L
1614.8438	1613.8365	1613.8876	-31.62	126 -	140	1	---	K.ESATEEKLTPVVLAK.Q
1706.8285	1705.8212	1705.8271	-3.45	381 -	396	0	---	R.ENLATVEGNFASIDAR.M
2445.1896	2444.1823	2444.1932	-4.43	299 -	319	1	---	K.ASVEDADTQNKVHQLYETIQR.W

No match to: 856.5338, 880.4595, 964.5179, 969.5360, 1075.5849, 1138.5175, 1208.5276, 1238.6039, 1300.6947, 1642.8340, 1688.8164, 1742.8382, 1790.8980, 1837.1934, 1852.9114, 1870.9342, 2143.0553

2. <u>EF2_MOUSE</u> **Mass:** 96222 **Score:** 48 **Expect:** 0.27 **Matches:** 8

Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4595	879.4522	879.4194	37.4	253 -	259	1	---	K.VEDMMKK.L
969.5360	968.5287	968.5403	-12.02	717 -	726	0	---	R.GGGQIIPTAR.R
1138.5175	1137.5103	1137.5091	1.05	639 -	647	0	---	K.YEWDVAEAR.K
1208.5276	1207.5204	1207.4961	20.1	689 -	698	0	---	K.EGALCEENMR.G
1238.6039	1237.5966	1237.6125	-12.84	1 -	10	0	---	-.MVNFTVDQIR.A + Oxidation (M)
1642.8340	1641.8267	1641.7565	42.8	387 -	400	1	---	K.SCDPKGPLMMYISK.M + Oxidation (M)
1742.8382	1741.8309	1741.8311	-0.12	634 -	647	1	---	R.YLAEKYEWDVAEAR.K
2143.0553	2142.0480	2142.0705	-10.50	606 -	625	1	---	K.ARPFPDGLAEDIDKGEVSAR.Q

No match to: 856.5338, 964.5179, 1031.5698, 1075.5849, 1187.6731, 1286.6832, 1300.6947, 1582.8429, 1591.8073, 1598.8709, 1614.8438, 1688.8164, 1706.8285, 1790.8980, 1837.1934, 1852.9114, 1870.9342, 2445.1896

3. <u>LYPA1_MOUSE</u> **Mass:** 25014 **Score:** 41 **Expect:** 1.3 **Matches:** 4

Acyl-protein thioesterase 1 OS=Mus musculus GN=Lypla1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1187.6731	1186.6658	1186.6710	-4.34	191 -	201	0	---	K.ALINPANVTFK.I
1642.8340	1641.8267	1641.8937	-40.83	91 -	105	1	---	K.QAAETVKALIDQEVK.N
1742.8382	1741.8309	1741.8062	14.2	2 -	18	0	---	M.CGNNMSAPMPAVVPAAR.K
1870.9342	1869.9269	1869.9012	13.8	2 -	19	1	---	M.CGNNMSAPMPAVVPAARK.A

No match to: 856.5338, 880.4595, 964.5179, 969.5360, 1031.5698, 1075.5849, 1138.5175, 1208.5276, 1238.6039, 1286.6832, 1300.6947, 1582.8429, 1591.8073, 1598.8709, 1614.8438, 1688.8164, 1706.8285, 1790.8980, 1837.1934, 1852.9114, 2143.0553, 2445.1896

4. <u>DOK5_MOUSE</u> **Mass:** 35887 **Score:** 38 **Expect:** 2.3 **Matches:** 5

Docking protein 5 OS=Mus musculus GN=Dok5 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1138.5175	1137.5103	1137.5488	-33.91	1 -	10	0	---	-.MASNFNDIVK.Q

1208.5276	1207.5204	1207.5689	-40.23	106	115	0	---	K.VLQMECVGTR.I + Oxidation (M)
1582.8429	1581.8357	1581.8490	-8.42	21	32	1	---	R.LGIYQRCWLVFK.K
1688.8164	1687.8091	1687.7698	23.3	201	214	0	---	R.MCETGEGLFIFQTR.D
1706.8285	1705.8212	1705.7849	21.3	187	200	1	---	R.YGRDTTWFTFEAGR.M

No match to: 856.5338, 880.4595, 964.5179, 969.5360, 1031.5698, 1075.5849, 1187.6731, 1238.6039, 1286.6832, 1300.6947, 1591.8073, 1598.8709, 1614.8438, 1642.8340, 1742.8382, 1790.8980, 1837.1934, 1852.9114, 1870.9342, 2143.0553, 2445.1896

5. RGS5_MOUSE **Mass:** 21243 **Score:** 36 **Expect:** 3.8 **Matches:** 4

Regulator of G-protein signaling 5 OS=Mus musculus GN=Rgs5 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
964.5179	963.5106	963.5138	-3.28	150	157	1	---	R.SFDLAQKR.I
1075.5849	1074.5776	1074.5498	25.9	170	177	1	---	R.FVRSEFYK.E
1706.8285	1705.8212	1705.8345	-7.80	128	141	1	---	K.EVNIDHFTKDITMK.N + Oxidation (M)
1742.8382	1741.8309	1741.8426	-6.71	1	15	1	---	-.MCKGLAALPHSCLER.A

No match to: 856.5338, 880.4595, 969.5360, 1031.5698, 1138.5175, 1187.6731, 1208.5276, 1238.6039, 1286.6832, 1300.6947, 1582.8429, 1591.8073, 1598.8709, 1614.8438, 1642.8340, 1688.8164, 1790.8980, 1837.1934, 1852.9114, 1870.9342, 2143.0553, 2445.1896

6. LITD1_MOUSE **Mass:** 88705 **Score:** 36 **Expect:** 4.2 **Matches:** 5

LINE-1 type transposase domain-containing protein 1 OS=Mus musculus GN=L1td1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1138.5175	1137.5103	1137.5639	-47.16	147	157	1	---	R.GGEALRGEHGR.C
1286.6832	1285.6760	1285.7289	-41.15	538	548	1	---	R.GVISVIRQMQR.E
1598.8709	1597.8637	1597.8788	-9.45	708	722	1	9	K.IRLTADLSPGTIDAR.S
1706.8285	1705.8212	1705.8522	-18.19	524	537	1	---	K.EADLILETEENFKR.G
1790.8980	1789.8907	1789.9284	-21.05	231	245	1	---	K.ELEPELQCSVKLAFK.C

No match to: 856.5338, 880.4595, 964.5179, 969.5360, 1031.5698, 1075.5849, 1187.6731, 1208.5276, 1238.6039, 1300.6947, 1582.8429, 1591.8073, 1614.8438, 1642.8340, 1688.8164, 1742.8382, 1837.1934, 1852.9114, 1870.9342, 2143.0553, 2445.1896

7. ECE1_MOUSE **Mass:** 87815 **Score:** 35 **Expect:** 4.7 **Matches:** 7

Endothelin-converting enzyme 1 OS=Mus musculus GN=Ece1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1138.5175	1137.5103	1137.4873	20.2	483	490	1	---	K.WMDEETRR.S + Oxidation (M)
1187.6731	1186.6658	1186.6631	2.31	195	204	0	---	R.AKPLMELIEK.L + Oxidation (M)
1598.8709	1597.8636	1597.8538	6.17	276	289	0	---	K.VLTGYLNYMVQLGK.L
1614.8438	1613.8365	1613.8487	-7.54	276	289	0	---	K.VLTGYLNYMVQLGK.L + Oxidation (M)
1706.8285	1705.8212	1705.8212	-0.01	618	630	1	---	R.EYDKDGNLRPWWK.N
1742.8382	1741.8309	1741.8102	11.9	387	399	0	---	K.CLLNNYMMWNLVR.K + Oxidation (M)
1870.9342	1869.9269	1869.9052	11.6	387	400	1	---	K.CLLNNYMMWNLVRK.T + Oxidation (M)

No match to: 856.5338, 880.4595, 964.5179, 969.5360, 1031.5698, 1075.5849, 1208.5276, 1238.6039, 1286.6832, 1300.6947, 1582.8429, 1591.8073, 1642.8340, 1688.8164, 1790.8980, 1837.1934, 1852.9114, 2143.0553, 2445.1896

8. ZNF32_MOUSE **Mass:** 31722 **Score:** 35 **Expect:** 5 **Matches:** 4

Zinc finger protein 32 OS=Mus musculus GN=Znf32 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
964.5179	963.5106	963.4808	31.0	265 -	272	1	---	R.SCSQRLTL.-
1591.8073	1590.8001	1590.7613	24.4	2 -	15	0	---	M.FGFPTATLLDCHGR.Y
1706.8285	1705.8212	1705.7552	38.7	237 -	251	0	---	K.VHTGETPYLCGQCGK.S
1790.8980	1789.8907	1789.8240	37.3	97 -	111	0	---	R.IHTGQKPFECTQCGK.S

No match to: 856.5338, 880.4595, 969.5360, 1031.5698, 1075.5849, 1138.5175, 1187.6731, 1208.5276, 1238.6039, 1286.6832, 1300.6947, 1582.8429, 1598.8709, 1614.8438, 1642.8340, 1688.8164, 1742.8382, 1837.1934, 1852.9114, 1870.9342, 2143.0553, 2445.1896

9. UN45A_MOUSE **Mass:** 104579 **Score:** 35 **Expect:** 5.5 **Matches:** 7

Protein unc-45 homolog A OS=Mus musculus GN=Unc45a PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
964.5179	963.5106	963.5025	8.39	26 -	33	1	---	R.KEGNELFK.C
969.5360	968.5287	968.4974	32.3	63 -	70	1	---	R.NRAACHLK.L
1031.5698	1030.5625	1030.5295	32.1	84 -	93	1	---	K.AIEKDGGDVK.A
1075.5849	1074.5776	1074.5934	-14.69	627 -	635	1	---	K.DKPSFVRAR.V
1582.8429	1581.8357	1581.7929	27.1	639 -	653	0	---	K.LLAAGVVSAMTCMVK.T + 2 Oxidation (M)
1688.8164	1687.8091	1687.8199	-6.41	915 -	930	1	---	K.GEESPVTRAAAACLEK.A
1790.8980	1789.8907	1789.9574	-37.25	822 -	836	1	---	K.LLVLYSGEDDELLRR.A

No match to: 856.5338, 880.4595, 1138.5175, 1187.6731, 1208.5276, 1238.6039, 1286.6832, 1300.6947, 1591.8073, 1598.8709, 1614.8438, 1642.8340, 1706.8285, 1742.8382, 1837.1934, 1852.9114, 1870.9342, 2143.0553, 2445.1896

10. ADCK3_MOUSE **Mass:** 72154 **Score:** 33 **Expect:** 7.4 **Matches:** 5

Chaperone activity of bc1 complex-like, mitochondrial OS=Mus musculus GN=Cabc1 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1075.5849	1074.5776	1074.6219	-41.25	260 -	268	1	---	R.IVSTLCKVR.G
1286.6832	1285.6760	1285.6626	10.4	525 -	536	1	---	R.AAADQDREAVLK.K
1591.8073	1590.8001	1590.8473	-29.70	2 -	17	1	---	M.AAMLGDAIMVAKGLAK.L + 2 Oxidation (M)
1706.8285	1705.8212	1705.8929	-42.01	1 -	17	1	---	-.MAAMLGDAIMVAKGLAK.L + Oxidation (M)
1742.8382	1741.8309	1741.8709	-22.98	42 -	57	0	---	R.ALQSTAVEQFSMVFGK.V

No match to: 856.5338, 880.4595, 964.5179, 969.5360, 1031.5698, 1138.5175, 1187.6731, 1208.5276, 1238.6039, 1300.6947, 1582.8429, 1598.8709, 1614.8438, 1642.8340, 1688.8164, 1790.8980, 1837.1934, 1852.9114, 1870.9342, 2143.0553, 2445.1896

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (856.5338,1+) : <no title>

Query2 (880.4595,1+) : <no title>

Query3 (964.5179,1+) : <no title>

Query4 (969.5360,1+) : <no title>

Query5 (1031.5698,1+) : <no title>

Query6 (1075.5849,1+) : <no title>

Query7 (1138.5175,1+) : <no title>

Query8 (1187.6731,1+) : <no title>

Query9 (1208.5276,1+) : <no title>

Query10 (1238.6039,1+) : <no title>

Query11 (1286.6832,1+) : <no title>

Query12 (1300.6947,1+) : <no title>

Query13 (1582.8429,1+) : <no title>

Query14 (1591.8073,1+) : <no title>

Query15 (1598.8709,1+) : <no title>

Query16 (1614.8438,1+) : <no title>

Query17 (1642.8340,1+) : <no title>

Query18 (1688.8164,1+) : <no title>

Query19 (1706.8285,1+) : <no title>

Query20 (1742.8382,1+) : <no title>

Query21 (1790.8980,1+) : <no title>

Query22 (1837.1934,1+) : <no title>

Query23 (1852.9114,1+) : <no title>

Query24 (1870.9342,1+) : <no title>

Query25 (2143.0553,1+) : <no title>

Query26 (2445.1896,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus. (16281 sequences)**

Timestamp : **22 Nov 2013 at 05:07:53 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

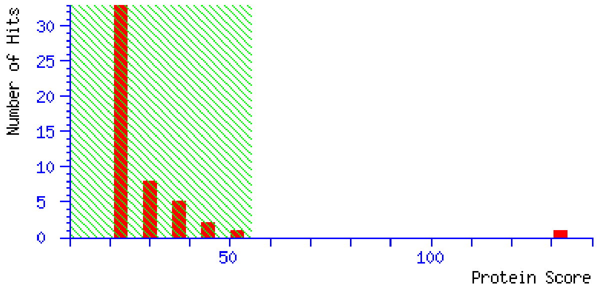
Top Score : **132 for PRDX2_MOUSE, Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**PRDX2_MOUSE**	21936	132	Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3
2.	**RASL1_MOUSE**	90285	49	RasGAP-activating-like protein 1 OS=Mus musculus GN=Rasal1 PE=2 SV=1
3.	**WN10A_MOUSE**	47793	48	Protein Wnt-10a OS=Mus musculus GN=Wnt10a PE=2 SV=1
4.	**CA158_MOUSE**	22924	47	Uncharacterized protein C1orf158 homolog OS=Mus musculus PE=2 SV=1
5.	**WDR93_MOUSE**	79715	38	WD repeat-containing protein 93 OS=Mus musculus GN=Wdr93 PE=2 SV=1
6.	**DOCK5_MOUSE**	215405	36	Dedicator of cytokinesis protein 5 OS=Mus musculus GN=Dock5 PE=1 SV=1
7.	**FHAD1_MOUSE**	164538	36	Forkhead-associated domain-containing protein 1 OS=Mus musculus GN=Fhad1 PE=2 SV=1
8.	**TBB5_MOUSE**	50095	35	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1
9.	**TBB2C_MOUSE**	50255	35	Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1
10.	**CSDC2_MOUSE**	16931	33	Cold shock domain-containing protein C2 OS=Mus musculus GN=Csdc2 PE=2 SV=1

Results List

1. PRDX2_MOUSE **Mass:** 21936 **Score:** 132 **Expect:** 1e-009 **Matches:** 3

Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
937.4434	936.4361	936.4301	6.44	120 -	127	0	45	K.NDEGIAYR.G
1108.5864	1107.5791	1107.5924	-12.01	110 -	119	0	---	K.SLSQNYGVLK.N
1211.6691	1210.6618	1210.6670	-4.28	140 -	150	0	55	R.QITVNDLPVGR.S

No match to: 856.5211, 898.5019, 1028.5319, 1039.5844, 1077.5448, 1089.5870, 1130.5804, 1194.6404, 1419.7561, 1618.7694, 1728.9244, 1857.0366, 1988.9957

2. RASL1_MOUSE **Mass:** 90285 **Score:** 49 **Expect:** 0.2 **Matches:** 6

RasGAP-activating-like protein 1 OS=Mus musculus GN=Rasal1 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
898.5019	897.4946	897.4821	14.0	592 -	598	1	---	R.YFRLSGR.D
1028.5319	1027.5246	1027.5298	-5.08	188 -	197	0	---	R.EAPGTTSPLR.V
1039.5844	1038.5771	1038.6186	-39.90	11 -	20	1	---	R.VVEGRALPAK.D
1077.5448	1076.5375	1076.5251	11.5	333 -	341	0	---	R.TNDPNTLFR.S
1211.6691	1210.6618	1210.7146	-43.59	732 -	741	1	2	R.QLLLGRDQLR.L
1618.7694	1617.7621	1617.8151	-32.74	160 -	173	0	---	R.VFWGNHSLETSTIK.K

No match to: 856.5211, 937.4434, 1089.5870, 1108.5864, 1130.5804, 1194.6404, 1419.7561, 1728.9244, 1857.0366, 1988.9957

3. WN10A_MOUSE **Mass:** 47793 **Score:** 48 **Expect:** 0.25 **Matches:** 5

Protein Wnt-10a OS=Mus musculus GN=Wnt10a PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
898.5019	897.4946	897.4603	38.3	237 -	243	1	---	R.DIHARMR.L
937.4434	936.4361	936.4157	21.8	71 -	77	0	---	R.QMEVCVR.H + Oxidation (M)
1077.5448	1076.5375	1076.5219	14.5	70 -	77	1	---	R.RQMEVCVR.H
1130.5804	1129.5731	1129.5741	-0.84	233 -	241	1	---	R.EPHRDIHAR.M
1194.6404	1193.6331	1193.6081	21.0	116 -	125	0	---	K.VPYESPIFSR.G

No match to: 856.5211, 1028.5319, 1039.5844, 1089.5870, 1108.5864, 1211.6691, 1419.7561, 1618.7694, 1728.9244, 1857.0366, 1988.9957

4. CA158_MOUSE **Mass:** 22924 **Score:** 47 **Expect:** 0.34 **Matches:** 4

Uncharacterized protein C1orf158 homolog OS=Mus musculus PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
898.5019	897.4946	897.5324	-42.03	122 -	128	0	---	K.LLWLPEK.S
1089.5870	1088.5798	1088.5583	19.7	169 -	177	1	---	R.LPVCAMSRR.E
1857.0366	1856.0293	1856.0533	-12.91	178 -	193	1	---	R.EHAIPVPHPRLQPIPR.F
1988.9957	1987.9884	1987.9574	15.6	52 -	67	1	---	R.KEYVPMPDHRPDFVSR.W + Oxidation (M)

No match to: 856.5211, 937.4434, 1028.5319, 1039.5844, 1077.5448, 1108.5864, 1130.5804, 1194.6404, 1211.6691, 1419.7561, 1618.7694, 1728.9244

5. WDR93_MOUSE **Mass:** 79715 **Score:** 38 **Expect:** 2.4 **Matches:** 5

WD repeat-containing protein 93 OS=Mus musculus GN=Wdr93 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**

898.5019	897.4946	897.4630	35.3	684	690	0	---	K.YSIMLQK.E + Oxidation (M)
1039.5844	1038.5771	1038.6113	-32.95	134	141	1	---	R.IYVLEKFK.A
1077.5448	1076.5375	1076.4986	36.2	182	191	0	---	K.AINEVDDSSK.Q
1194.6404	1193.6331	1193.5962	31.0	554	564	0	---	R.SQSVTLMDVAK.A + Oxidation (M)
1211.6691	1210.6618	1210.6050	47.0	664	673	1	---	K.SIQMTKTQMK.G + Oxidation (M)

No match to: 856.5211, 937.4434, 1028.5319, 1089.5870, 1108.5864, 1130.5804, 1419.7561, 1618.7694, 1728.9244, 1857.0366, 1988.9957

6. DOCK5_MOUSE **Mass:** 215405 **Score:** 36 **Expect:** 4 **Matches:** 7

Dedicator of cytokinesis protein 5 OS=Mus musculus GN=Dock5 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1077.5448	1076.5375	1076.5098	25.7	1722	1730	1	---	K.EDSENRISK.F
1130.5804	1129.5731	1129.6131	-35.44	1844	1854	1	---	R.DSKAPPPPPPK.A
1211.6691	1210.6618	1210.6921	-25.05	405	415	0	---	K.LLPGDLTQVQK.N
1419.7561	1418.7489	1418.7994	-35.59	1831	1843	1	---	R.NSAEIAPPLPVRR.D
1728.9244	1727.9171	1727.8380	45.8	1456	1469	0	---	R.ANEVQQFSYSRPFR.K
1857.0366	1856.0293	1855.9615	36.6	320	336	0	---	R.RPFGVAVMDISDIVHGK.V + Oxidation (M)
1988.9957	1987.9884	1987.9067	41.1	1005	1019	1	---	K.DWMVMNMTQNRVFLR.A + 3 Oxidation (M)

No match to: 856.5211, 898.5019, 937.4434, 1028.5319, 1039.5844, 1089.5870, 1108.5864, 1194.6404, 1618.7694

7. FHAD1_MOUSE **Mass:** 164538 **Score:** 36 **Expect:** 4.3 **Matches:** 7

Forkhead-associated domain-containing protein 1 OS=Mus musculus GN=Fhad1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.5211	855.5139	855.5290	-17.72	1049	1055	1	---	K.VLREALR.A
1077.5448	1076.5375	1076.5536	-14.96	1033	1042	0	---	K.VAQTTGLMEK.K
1108.5864	1107.5791	1107.5594	17.8	860	868	1	---	K.TKMILTDDR.L + Oxidation (M)
1618.7694	1617.7621	1617.8396	-47.85	291	304	1	---	K.EIESMKSQINALQK.G
1728.9244	1727.9171	1727.8955	12.5	1144	1157	1	---	K.DHVNESFLELRTLR.M
1857.0366	1856.0293	1855.9787	27.3	1215	1230	1	---	K.LYTDMIKTLGSLMNIK.D + Oxidation (M)
1988.9957	1987.9884	1988.0551	-33.55	1056	1072	0	---	R.ASQEKPRPHLSTEQKPR.T

No match to: 898.5019, 937.4434, 1028.5319, 1039.5844, 1089.5870, 1130.5804, 1194.6404, 1211.6691, 1419.7561

8. TBB5_MOUSE **Mass:** 50095 **Score:** 35 **Expect:** 5.5 **Matches:** 4

Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1028.5319	1027.5246	1027.5121	12.2	351	359	0	---	K.TAVCDIPPR.G
1039.5844	1038.5771	1038.5862	-8.75	310	318	0	---	R.YLTVAAVFR.G
1077.5448	1076.5375	1076.5250	11.6	155	162	1	---	K.IREEYPDR.I
1130.5804	1129.5731	1129.5880	-13.18	242	251	0	---	R.FPGQLNADLR.K

No match to: 856.5211, 898.5019, 937.4434, 1089.5870, 1108.5864, 1194.6404, 1211.6691, 1419.7561, 1618.7694, 1728.9244, 1857.0366, 1988.9957

9. TBB2C_MOUSE **Mass:** 50255 **Score:** 35 **Expect:** 5.5 **Matches:** 4

Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1028.5319	1027.5246	1027.5121	12.2	351 -	359	0	---	K.TAVCDIPPR.G
1039.5844	1038.5771	1038.5862	-8.75	310 -	318	0	---	R.YLTVAAVFR.G
1077.5448	1076.5375	1076.5250	11.6	155 -	162	1	---	K.IREEYPDR.I
1130.5804	1129.5731	1129.5880	-13.18	242 -	251	0	---	R.FPGQLNADLR.K

No match to: 856.5211, 898.5019, 937.4434, 1089.5870, 1108.5864, 1194.6404, 1211.6691, 1419.7561, 1618.7694, 1728.9244, 1857.0366, 1988.9957

10. CSDC2_MOUSE **Mass:** 16931 **Score:** 33 **Expect:** 8.5 **Matches:** 2

Cold shock domain-containing protein C2 OS=Mus musculus GN=Csdc2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1194.6404	1193.6331	1193.6590	-21.70	118 -	127	1	---	K.ICPIPPKNQK.F
1211.6691	1210.6618	1210.6571	3.92	34 -	44	1	11	R.IWERGGGIAPR.D

No match to: 856.5211, 898.5019, 937.4434, 1028.5319, 1039.5844, 1077.5448, 1089.5870, 1108.5864, 1130.5804, 1419.7561, 1618.7694, 1728.9244, 1857.0366, 1988.9957

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (856.5211,1+) : <no title>
Query2 (898.5019,1+) : <no title>
Query3 (937.4434,1+) : <no title>
Query4 (1028.5319,1+) : <no title>
Query5 (1039.5844,1+) : <no title>
Query6 (1077.5448,1+) : <no title>
Query7 (1089.5870,1+) : <no title>
Query8 (1108.5864,1+) : <no title>
Query9 (1130.5804,1+) : <no title>
Query10 (1194.6404,1+) : <no title>
Query11 (1211.6691,1+) : <no title>
Query12 (1419.7561,1+) : <no title>
Query13 (1618.7694,1+) : <no title>
Query14 (1728.9244,1+) : <no title>
Query15 (1857.0366,1+) : <no title>
Query16 (1988.9957,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : Auto submitted by BioTools

Database : SwissProt 57.15 (515203 sequences; 181334896 residues)

Taxonomy : Mus. (16281 sequences)

Timestamp : 22 Nov 2013 at 05:07:33 GMT

Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.

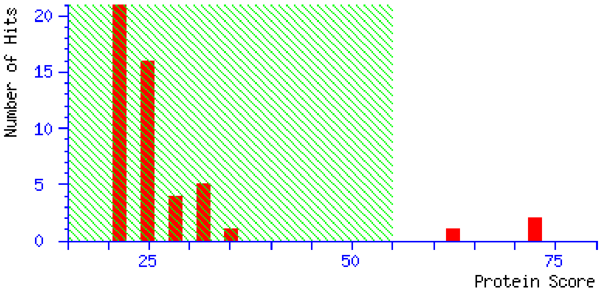
Top Score : 72 for GSTA2_MOUSE, Glutathione S-transferase A2 OS=Mus musculus GN=Gsta2 PE=1 SV=2

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant ($p<0.05$).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**GSTA2_MOUSE**	25631	72	Glutathione S-transferase A2 OS=Mus musculus GN=Gsta2 PE=1 SV=2
2.	**GSTA1_MOUSE**	25706	72	Glutathione S-transferase A1 OS=Mus musculus GN=Gsta1 PE=1 SV=2
3.	**GSTA3_MOUSE**	25401	62	Glutathione S-transferase A3 OS=Mus musculus GN=Gsta3 PE=1 SV=2
4.	**TOP3A_MOUSE**	114168	34	DNA topoisomerase 3-alpha OS=Mus musculus GN=Top3a PE=1 SV=1
5.	**SAM12_MOUSE**	18462	33	Sterile alpha motif domain-containing protein 12 OS=Mus musculus GN=Samd12 PE=2 SV=1
6.	**TLR12_MOUSE**	101079	32	Toll-like receptor 12 OS=Mus musculus GN=Tlr12 PE=2 SV=1
7.	**DPOLN_MOUSE**	97640	32	DNA polymerase nu OS=Mus musculus GN=Poln PE=2 SV=2
8.	**MA6D1_MOUSE**	20648	31	MAP6 domain-containing protein 1 OS=Mus musculus GN=Map6d1 PE=1 SV=1
9.	**PKHA8_MOUSE**	58552	30	Pleckstrin homology domain-containing family A member 8 OS=Mus musculus GN=Plekha8 PE=2 SV=2
10.	**TOP1_MOUSE**	91275	30	DNA topoisomerase 1 OS=Mus musculus GN=Top1 PE=1 SV=2

Results List

1. GSTA2_MOUSE **Mass:** 25631 **Score:** 72 **Expect:** 0.00092 **Matches:** 3

Glutathione S-transferase A2 OS=Mus musculus GN=Gsta2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
921.4534	920.4461	920.4320	15.3	14 -	20	1	---	R.GRMECIR.W
937.4602	936.4530	936.4269	27.8	14 -	20	1	---	R.GRMECIR.W + Oxidation (M)
1245.6144	1244.6071	1244.5898	13.9	142 -	152	0	54	K.SHGQDYLVGNR.L

No match to: 828.4596, 856.5372, 880.4954, 889.4679, 1028.6035, 1090.6051, 1227.6053, 1283.5883, 1315.7014, 1388.7675, 1426.7122, 1432.7362, 1448.7130, 1516.7498, 2247.1165

2. GSTA1_MOUSE **Mass:** 25706 **Score:** 72 **Expect:** 0.00092 **Matches:** 3

Glutathione S-transferase A1 OS=Mus musculus GN=Gsta1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
921.4534	920.4461	920.4320	15.3	14 -	20	1	---	R.GRMECIR.W
937.4602	936.4530	936.4269	27.8	14 -	20	1	---	R.GRMECIR.W + Oxidation (M)
1245.6144	1244.6071	1244.5898	13.9	142 -	152	0	54	K.SHGQDYLVGNR.L

No match to: 828.4596, 856.5372, 880.4954, 889.4679, 1028.6035, 1090.6051, 1227.6053, 1283.5883, 1315.7014, 1388.7675, 1426.7122, 1432.7362, 1448.7130, 1516.7498, 2247.1165

3. GSTA3_MOUSE **Mass:** 25401 **Score:** 62 **Expect:** 0.0098 **Matches:** 1

Glutathione S-transferase A3 OS=Mus musculus GN=Gsta3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1245.6144	1244.6071	1244.5898	13.9	142 -	152	0	54	K.SHGQDYLVGNR.L

No match to: 828.4596, 856.5372, 880.4954, 889.4679, 921.4534, 937.4602, 1028.6035, 1090.6051, 1227.6053, 1283.5883, 1315.7014, 1388.7675, 1426.7122, 1432.7362, 1448.7130, 1516.7498, 2247.1165

4. TOP3A_MOUSE **Mass:** 114168 **Score:** 34 **Expect:** 7.3 **Matches:** 5

DNA topoisomerase 3-alpha OS=Mus musculus GN=Top3a PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.5372	855.5299	855.5079	25.7	752 -	758	1	---	R.FPRALPR.A
1028.6035	1027.5962	1027.6390	-41.62	820 -	828	1	---	R.EAVLLTVRK.Q
1388.7675	1387.7603	1387.7168	31.3	968 -	981	1	2	K.RPRAGSSDAGSTVK.K
1426.7122	1425.7049	1425.6962	6.08	121 -	131	1	---	K.YCPENFIDIKK.T
2247.1165	2246.1093	2246.0711	17.0	639 -	657	1	---	R.TEMAQQEEIYPAMPEPVRK.C

No match to: 828.4596, 880.4954, 889.4679, 921.4534, 937.4602, 1090.6051, 1227.6053, 1245.6144, 1283.5883, 1315.7014, 1432.7362, 1448.7130, 1516.7498

5. SAM12_MOUSE **Mass:** 18462 **Score:** 33 **Expect:** 8.5 **Matches:** 3

Sterile alpha motif domain-containing protein 12 OS=Mus musculus GN=Samd12 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1090.6051	1089.5978	1089.5819	14.6	42 -	50	1	---	R.TFQKVPDQK.G
1432.7362	1431.7289	1431.7569	-19.56	56 -	69	1	---	R.LQGEAETAKSATVK.L
1516.7498	1515.7425	1515.7780	-23.43	26 -	39	0	---	K.LQIEGEGVESQSIK.N

No match to: 828.4596, 856.5372, 880.4954, 889.4679, 921.4534, 937.4602, 1028.6035, 1227.6053, 1245.6144, 1283.5883, 1315.7014,

1388.7675, 1426.7122, 1448.7130, 2247.1165

6. TLR12_MOUSE **Mass:** 101079 **Score:** 32 **Expect:** 11 **Matches:** 5

Toll-like receptor 12 OS=Mus musculus GN=Tlr12 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
828.4596	827.4523	827.4541	-2.22	672 -	677	0	---	K.TYIYIR.D
1090.6051	1089.5978	1089.5488	44.9	628 -	636	0	---	K.DLMLQDSLR.E
1245.6144	1244.6071	1244.5761	24.9	39 -	47	1	---	R.YFTFCRHSK.L
1426.7122	1425.7049	1425.6864	13.0	759 -	769	0	---	R.FLFDVFVSHCR.Q
1516.7498	1515.7425	1515.8045	-40.91	501 -	515	0	---	K.LGSQNASGVFPALQK.L

No match to: 856.5372, 880.4954, 889.4679, 921.4534, 937.4602, 1028.6035, 1227.6053, 1283.5883, 1315.7014, 1388.7675, 1432.7362, 1448.7130, 2247.1165

7. DPOLN_MOUSE **Mass:** 97640 **Score:** 32 **Expect:** 12 **Matches:** 6

DNA polymerase nu OS=Mus musculus GN=Poln PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
828.4596	827.4523	827.4766	-29.38	136 -	141	1	---	K.RQHFLK.E
889.4679	888.4606	888.4739	-14.94	209 -	216	0	---	K.AQLMDALK.Q
921.4534	920.4461	920.4637	-19.17	238 -	245	0	---	K.EALTCTVK.G
1245.6144	1244.6071	1244.6071	0.04	442 -	451	1	---	K.IPVDKEEMER.T
1388.7675	1387.7603	1387.7671	-4.93	782 -	795	0	---	R.ISTAVATSPTLTAR.L
1426.7122	1425.7049	1425.6776	19.1	650 -	661	0	---	R.DDVFSTLTSQWK.D

No match to: 856.5372, 880.4954, 937.4602, 1028.6035, 1090.6051, 1227.6053, 1283.5883, 1315.7014, 1432.7362, 1448.7130, 1516.7498, 2247.1165

8. MA6D1_MOUSE **Mass:** 20648 **Score:** 31 **Expect:** 14 **Matches:** 3

MAP6 domain-containing protein 1 OS=Mus musculus GN=Map6d1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
828.4596	827.4523	827.4250	33.0	50 -	58	0	---	R.GNPSVAGAR.E
889.4679	888.4606	888.4276	37.1	2 -	8	0	---	M.AWPCISR.L
921.4534	920.4461	920.4828	-39.92	72 -	79	1	---	R.DFGVRTAR.A

No match to: 856.5372, 880.4954, 937.4602, 1028.6035, 1090.6051, 1227.6053, 1245.6144, 1283.5883, 1315.7014, 1388.7675, 1426.7122, 1432.7362, 1448.7130, 1516.7498, 2247.1165

9. PKHA8_MOUSE **Mass:** 58552 **Score:** 30 **Expect:** 15 **Matches:** 4

Pleckstrin homology domain-containing family A member 8 OS=Mus musculus GN=Plekha8 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4954	879.4881	879.4484	45.2	115 -	121	1	---	K.TKMSELR.L + Oxidation (M)
889.4679	888.4606	888.4739	-14.95	359 -	366	0	---	K.MDLVGNIK.K
1028.6035	1027.5962	1027.6066	-10.16	349 -	358	0	---	K.LGPTVFAPVK.M
1388.7675	1387.7603	1387.7585	1.23	440 -	450	1	---	K.TLRQHHGWVVR.G

No match to: 828.4596, 856.5372, 921.4534, 937.4602, 1090.6051, 1227.6053, 1245.6144, 1283.5883, 1315.7014, 1426.7122, 1432.7362, 1448.7130, 1516.7498, 2247.1165

10. TOP1_MOUSE **Mass:** 91275 **Score:** 30 **Expect:** 17 **Matches:** 6

DNA topoisomerase 1 OS=Mus musculus GN=Top1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
828.4596	827.4523	827.4541	-2.24	738 -	744	0	---	K.WGVPIEK.I
889.4679	888.4606	888.4552	6.05	329 -	335	1	---	K.IKEENEK.L
1283.5883	1282.5810	1282.6405	-46.33	606 -	617	0	---	K.ELTAPDENVPAK.I
1432.7362	1431.7289	1431.7101	13.1	379 -	390	0	---	R.IMPEDIIINCSK.D
1448.7130	1447.7057	1447.7051	0.47	379 -	390	0	---	R.IMPEDIIINCSK.D + Oxidation (M)
2247.1165	2246.1093	2246.0565	23.5	255 -	273	1	---	K.AEEVATFFAKMLDHEYTTK.E + Oxidation (M)

No match to: 856.5372, 880.4954, 921.4534, 937.4602, 1028.6035, 1090.6051, 1227.6053, 1245.6144, 1315.7014, 1388.7675, 1426.7122, 1516.7498

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 : ±50 ppm
Fragment Mass Tolerance: ±0.6 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (828.4596,1+) : <no title>
Query2 (856.5372,1+) : <no title>
Query3 (880.4954,1+) : <no title>
Query4 (889.4679,1+) : <no title>
Query5 (921.4534,1+) : <no title>
Query6 (937.4602,1+) : <no title>
Query7 (1028.6035,1+) : <no title>
Query8 (1090.6051,1+) : <no title>
Query9 (1227.6053,1+) : <no title>
Query10 (1245.6144,1+) : <no title>
Query11 (1283.5883,1+) : <no title>
Query12 (1315.7014,1+) : <no title>
Query13 (1388.7675,1+) : <no title>
Query14 (1426.7122,1+) : <no title>
Query15 (1432.7362,1+) : <no title>
Query16 (1448.7130,1+) : <no title>
Query17 (1516.7498,1+) : <no title>
Query18 (2247.1165,1+) : <no title>

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:47:54 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

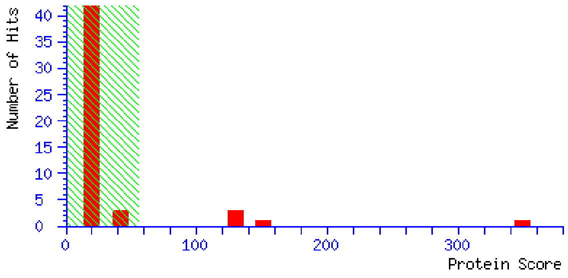
Top Score : **349 for HSP7C_MOUSE, Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**HSP7C_MOUSE**	71055	349	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1
2.	**HSP72_MOUSE**	69983	143	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=1
3.	**HS71A_MOUSE**	70321	134	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2
4.	**HS71L_MOUSE**	70992	134	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4
5.	**HS71B_MOUSE**	70418	134	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3
6.	**GRP78_MOUSE**	72492	40	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3
7.	**DNJB1_MOUSE**	38314	40	DnaJ homolog subfamily B member 1 OS=Mus musculus GN=Dnajb1 PE=2 SV=3
8.	**KCIP4_MOUSE**	28965	31	Kv channel-interacting protein 4 OS=Mus musculus GN=Kcnip4 PE=1 SV=1
9.	**FBX31_MOUSE**	57896	31	F-box only protein 31 OS=Mus musculus GN=Fbxo31 PE=1 SV=1
10.	**NEC1_MOUSE**	84749	30	Neuroendocrine convertase 1 OS=Mus musculus GN=Pcsk1 PE=1 SV=1

Results List

1. HSP7C_MOUSE **Mass:** 71055 **Score:** 349 **Expect:** 2e-031 **Matches:** 7

Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1199.6404	1198.6331	1198.6670	-28.25	160 -	171	0	92	K.DAGTIAGLNVLR.I
1228.6001	1227.5928	1227.6207	-22.77	26 -	36	0	35	K.VEIIANDQGNR.T
1410.6198	1409.6125	1409.6609	-34.31	77 -	88	1	---	R.RFDDAVVQSDMK.H
1426.5993	1425.5921	1425.6558	-44.74	77 -	88	1	---	R.RFDDAVVQSDMK.H + Oxidation (M)
1487.6625	1486.6553	1486.6940	-26.06	37 -	49	0	87	R.TTPSYVAFTDTER.L
1805.8539	1804.8466	1804.8890	-23.51	57 -	72	1	---	K.NQVAMNPTNTVFDAKR.L
1981.9716	1980.9643	1980.9905	-13.24	138 -	155	0	75	K.TVTNAVVTVPAYFNDSQR.Q

No match to: 1034.5246, 1154.6069, 1371.8288, 1443.6848, 1449.9106, 1501.6660, 1646.9416, 1701.7922

2. HSP72_MOUSE **Mass:** 69983 **Score:** 143 **Expect:** 8.1e-011 **Matches:** 3

Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1228.6001	1227.5928	1227.6207	-22.77	27 -	37	0	35	K.VEIIANDQGNR.T
1487.6625	1486.6553	1486.6940	-26.06	38 -	50	0	87	R.TTPSYVAFTDTER.L
1646.9416	1645.9343	1645.9039	18.5	95 -	109	1	---	R.VVSEGGKPKVQVEYK.G

No match to: 1034.5246, 1154.6069, 1199.6404, 1371.8288, 1410.6198, 1426.5993, 1443.6848, 1449.9106, 1501.6660, 1701.7922, 1805.8539, 1981.9716

3. HS71A_MOUSE **Mass:** 70321 **Score:** 134 **Expect:** 6.5e-010 **Matches:** 2

Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1228.6001	1227.5928	1227.6207	-22.77	26 -	36	0	35	K.VEIIANDQGNR.T
1487.6625	1486.6553	1486.6940	-26.06	37 -	49	0	87	R.TTPSYVAFTDTER.L

No match to: 1034.5246, 1154.6069, 1199.6404, 1371.8288, 1410.6198, 1426.5993, 1443.6848, 1449.9106, 1501.6660, 1646.9416, 1701.7922, 1805.8539, 1981.9716

4. HS71L_MOUSE **Mass:** 70992 **Score:** 134 **Expect:** 6.5e-010 **Matches:** 2

Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1228.6001	1227.5928	1227.6207	-22.77	28 -	38	0	35	K.VEIIANDQGNR.T
1487.6625	1486.6553	1486.6940	-26.06	39 -	51	0	87	R.TTPSYVAFTDTER.L

No match to: 1034.5246, 1154.6069, 1199.6404, 1371.8288, 1410.6198, 1426.5993, 1443.6848, 1449.9106, 1501.6660, 1646.9416, 1701.7922, 1805.8539, 1981.9716

5. HS71B_MOUSE **Mass:** 70418 **Score:** 134 **Expect:** 6.5e-010 **Matches:** 2

Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1228.6001	1227.5928	1227.6207	-22.77	26 -	36	0	35	K.VEIIANDQGNR.T
1487.6625	1486.6553	1486.6940	-26.06	37 -	49	0	87	R.TTPSYVAFTDTER.L

No match to: 1034.5246, 1154.6069, 1199.6404, 1371.8288, 1410.6198, 1426.5993, 1443.6848, 1449.9106, 1501.6660, 1646.9416, 1701.7922, 1805.8539, 1981.9716

6. GRP78_MOUSE **Mass:** 72492 **Score:** 40 **Expect:** 1.5 **Matches:** 1

78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1228.6001	1227.5928	1227.6207	-22.77	51 -	61	0	35	R.VEIIANDQGNR.I

No match to: 1034.5246, 1154.6069, 1199.6404, 1371.8288, 1410.6198, 1426.5993, 1443.6848, 1449.9106, 1487.6625, 1501.6660, 1646.9416, 1701.7922, 1805.8539, 1981.9716

7. DNJB1_MOUSE **Mass:** 38314 **Score:** 40 **Expect:** 1.7 **Matches:** 4

DnaJ homolog subfamily B member 1 OS=Mus musculus GN=Dnajb1 PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1034.5246	1033.5173	1033.5080	9.04	38 -	46	1	---	K.EPGAEEKFK.E
1154.6069	1153.5996	1153.6356	-31.21	241 -	249	1	---	K.DKPHNIFKR.D
1199.6404	1198.6331	1198.5982	29.1	4 -	13	0	7	K.DYYQTLGLAR.G
1228.6001	1227.5928	1227.5673	20.8	110 -	119	0	---	R.NPFDTFFGQR.N

No match to: 1371.8288, 1410.6198, 1426.5993, 1443.6848, 1449.9106, 1487.6625, 1501.6660, 1646.9416, 1701.7922, 1805.8539, 1981.9716

8. KCIP4_MOUSE **Mass:** 28965 **Score:** 31 **Expect:** 13 **Matches:** 3

Kv channel-interacting protein 4 OS=Mus musculus GN=Kcnip4 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1701.7922	1700.7849	1700.8001	-8.92	173 -	186	1	---	K.DGYITKEEMLDIMK.A + Oxidation (M)
1805.8539	1804.8466	1804.8562	-5.32	187 -	201	1	---	K.AIYDMMGKCTYPVLK.E + Oxidation (M)
1981.9716	1980.9643	1980.9463	9.10	219 -	235	1	---	K.NKDGVVTIDEFIESCQK.D

No match to: 1034.5246, 1154.6069, 1199.6404, 1228.6001, 1371.8288, 1410.6198, 1426.5993, 1443.6848, 1449.9106, 1487.6625, 1501.6660, 1646.9416

9. FBX31_MOUSE **Mass:** 57896 **Score:** 31 **Expect:** 14 **Matches:** 5

F-box only protein 31 OS=Mus musculus GN=Fbxo31 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1034.5246	1033.5173	1033.5226	-5.12	110 -	118	0	---	K.LEITGVSCR.D
1154.6069	1153.5996	1153.6244	-21.49	86 -	94	0	---	R.ILHTDTIWR.R
1199.6404	1198.6331	1198.6571	-20.00	198 -	208	0	---	K.GPHNGHIQIVK.R
1410.6198	1409.6125	1409.6431	-21.70	186 -	197	1	---	R.KSATVECMYGHK.G
1426.5993	1425.5921	1425.6381	-32.27	186 -	197	1	---	R.KSATVECMYGHK.G + Oxidation (M)

No match to: 1228.6001, 1371.8288, 1443.6848, 1449.9106, 1487.6625, 1501.6660, 1646.9416, 1701.7922, 1805.8539, 1981.9716

10. NEC1_MOUSE **Mass:** 84749 **Score:** 30 **Expect:** 15 **Matches:** 4

Neuroendocrine convertase 1 OS=Mus musculus GN=Pcsk1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1034.5246	1033.5173	1033.4975	19.2	429 -	438	0	---	K.NGAGLMVNSR.F + Oxidation (M)
1154.6069	1153.5996	1153.5880	10.1	287 -	296	1	---	K.AFEYGVKQGR.Q
1443.6848	1442.6776	1442.6394	26.4	212 -	224	0	---	R.CAGEIAMQANNHK.C
1981.9716	1980.9643	1981.0204	-28.30	429 -	447	1	---	K.NGAGLMVNSRFGFGLLNAK.A + Oxidation (M)

No match to: 1199.6404, 1228.6001, 1371.8288, 1410.6198, 1426.5993, 1449.9106, 1487.6625, 1501.6660, 1646.9416, 1701.7922, 1805.8539

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (1034.5246,1+) : <no title>

Query2 (1154.6069,1+) : <no title>

Query3 (1199.6404,1+) : <no title>

Query4 (1228.6001,1+) : <no title>

Query5 (1371.8288,1+) : <no title>

Query6 (1410.6198,1+) : <no title>

Query7 (1426.5993,1+) : <no title>

Query8 (1443.6848,1+) : <no title>

Query9 (1449.9106,1+) : <no title>

Query10 (1487.6625,1+) : <no title>

Query11 (1501.6660,1+) : <no title>

Query12 (1646.9416,1+) : <no title>

Query13 (1701.7922,1+) : <no title>

Query14 (1805.8539,1+) : <no title>

Query15 (1981.9716,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:47:44 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

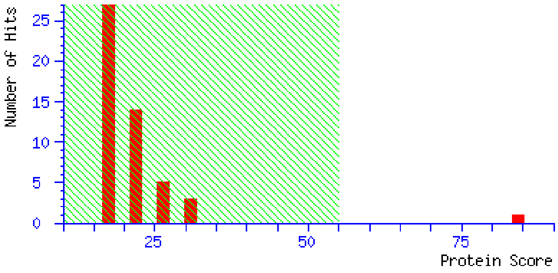
Top Score : **84 for TAGL_MOUSE, Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	**Mass**	**Score**	**Description**
1.	**TAGL_MOUSE**	22618	84	Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3
2.	**KCTD6_MOUSE**	27835	32	BTB/POZ domain-containing protein KCTD6 OS=Mus musculus GN=Kctd6 PE=2 SV=1
3.	**ACES_MOUSE**	68525	31	Acetylcholinesterase OS=Mus musculus GN=Ache PE=1 SV=1
4.	**FKBP5_MOUSE**	51504	30	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Mus musculus GN=Fkbp5 PE=1 SV=1
5.	**CCD27_MOUSE**	74004	26	Coiled-coil domain-containing protein 27 OS=Mus musculus GN=Ccdc27 PE=2 SV=1
6.	**SLUR1_MOUSE**	12578	26	Secreted Ly-6/uPAR-related protein 1 OS=Mus musculus GN=Slurp1 PE=2 SV=1
7.	**ID3_MOUSE**	13366	25	DNA-binding protein inhibitor ID-3 OS=Mus musculus GN=Id3 PE=1 SV=1
8.	**SHAN2_MOUSE**	159394	25	SH3 and multiple ankyrin repeat domains protein 2 OS=Mus musculus GN=Shank2 PE=1 SV=1
9.	**ACAD8_MOUSE**	45789	25	Isobutyryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acad8 PE=2 SV=2
10.	**GPC5_MOUSE**	64891	23	Glypican-5 OS=Mus musculus GN=Gpc5 PE=2 SV=1

Results List

1. TAGL_MOUSE **Mass:** 22618 **Score:** 84 **Expect:** 6.2e-005 **Matches:** 3

Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
806.3523	805.3450	805.3752	-37.48	122 -	128	0	---	K.DMAAVQR.T + Oxidation (M)
854.3754	853.3681	853.3752	-8.30	5 -	12	0	---	K.GPSYGMSR.E
1210.5286	1209.5213	1209.5513	-24.80	21 -	29	1	56	K.KYDEELEER.L

No match to: 856.5218, 896.4893, 1044.5397, 1224.5362, 1243.5824, 1266.5792, 1289.5312, 1552.7751, 1568.6779, 2112.3339, 2126.9883

2. KCTD6_MOUSE **Mass:** 27835 **Score:** 32 **Expect:** 9.3 **Matches:** 3

BTB/POZ domain-containing protein KCTD6 OS=Mus musculus GN=Kctd6 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
806.3523	805.3450	805.3211	29.7	166 -	171	0	---	K.HMMDTR.D + Oxidation (M)
1224.5362	1223.5289	1223.5571	-23.04	51 -	60	0	---	R.DPQGNYFIDR.D
1266.5792	1265.5719	1265.6047	-25.91	207 -	216	1	---	R.NTRVHHMSER.A

No match to: 854.3754, 856.5218, 896.4893, 1044.5397, 1210.5286, 1243.5824, 1289.5312, 1552.7751, 1568.6779, 2112.3339, 2126.9883

3. ACES_MOUSE **Mass:** 68525 **Score:** 31 **Expect:** 13 **Matches:** 2

Acetylcholinesterase OS=Mus musculus GN=Ache PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.5218	855.5146	855.5039	12.5	45 -	52	1	---	R.GGQLRGIR.L
2126.9883	2125.9810	2126.0249	-20.65	285 -	305	0	17	R.LVGCPPGGAGGNDTELIACLR.T

No match to: 806.3523, 854.3754, 896.4893, 1044.5397, 1210.5286, 1224.5362, 1243.5824, 1266.5792, 1289.5312, 1552.7751, 1568.6779, 2112.3339

4. FKBP5_MOUSE **Mass:** 51504 **Score:** 30 **Expect:** 15 **Matches:** 5

Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Mus musculus GN=Fkbp5 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1044.5397	1043.5325	1043.5222	9.82	407 -	414	1	---	R.RVYANMFK.K + Oxidation (M)
1224.5362	1223.5289	1223.5492	-16.59	253 -	262	1	---	K.AKESWEMDTK.E
1289.5312	1288.5239	1288.5354	-8.89	441 -	451	0	---	K.QHESQAMEEGK.A + Oxidation (M)
1552.7751	1551.7678	1551.7239	28.3	358 -	371	0	---	R.GEAQLLMNDFESAK.G
1568.6779	1567.6706	1567.7188	-30.71	358 -	371	0	---	R.GEAQLLMNDFESAK.G + Oxidation (M)

No match to: 806.3523, 854.3754, 856.5218, 896.4893, 1210.5286, 1243.5824, 1266.5792, 2112.3339, 2126.9883

5. CCD27_MOUSE **Mass:** 74004 **Score:** 26 **Expect:** 39 **Matches:** 2

Coiled-coil domain-containing protein 27 OS=Mus musculus GN=Ccdc27 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1243.5824	1242.5751	1242.5728	1.88	308 -	320	0	---	K.SSEGPPEEAAAAK.L
2126.9883	2125.9810	2126.0603	-37.32	308 -	328	1	11	K.SSEGPPEEAAAAKLSRPSQSK.T

No match to: 806.3523, 854.3754, 856.5218, 896.4893, 1044.5397, 1210.5286, 1224.5362, 1266.5792, 1289.5312, 1552.7751, 1568.6779, 2112.3339

6. SLUR1_MOUSE **Mass:** 12578 **Score:** 26 **Expect:** 43 **Matches:** 2

Secreted Ly-6/uPAR-related protein 1 OS=Mus musculus GN=Slurp1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
854.3754	853.3681	853.3310	43.6	45 -	51	0	---	K.MEDTACK.T
1568.6779	1567.6706	1567.6793	-5.50	39 -	51	1	---	K.NIAQCKMEDTACK.T

No match to: 806.3523, 856.5218, 896.4893, 1044.5397, 1210.5286, 1224.5362, 1243.5824, 1266.5792, 1289.5312, 1552.7751, 2112.3339, 2126.9883

7. ID3_MOUSE **Mass:** 13366 **Score:** 25 **Expect:** 47 **Matches:** 1

DNA-binding protein inhibitor ID-3 OS=Mus musculus GN=Id3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
2126.9883	2125.9810	2125.9707	4.83	3 -	20	1	13	K.ALSPVRGCYEAVCCLSER.S

No match to: 806.3523, 854.3754, 856.5218, 896.4893, 1044.5397, 1210.5286, 1224.5362, 1243.5824, 1266.5792, 1289.5312, 1552.7751, 1568.6779, 2112.3339

8. SHAN2_MOUSE **Mass:** 159394 **Score:** 25 **Expect:** 49 **Matches:** 5

SH3 and multiple ankyrin repeat domains protein 2 OS=Mus musculus GN=Shank2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
806.3523	805.3450	805.3566	-14.35	210 -	216	0	---	R.DSQAETR.A
856.5218	855.5146	855.4967	20.9	459 -	466	0	---	K.GPFLGLPR.G
1044.5397	1043.5325	1043.5838	-49.15	490 -	498	0	---	R.QFLAPPMLK.F
1266.5792	1265.5719	1265.5922	-15.99	1286 -	1297	0	---	R.SPEVMSTVSGTR.S + Oxidation (M)
1552.7751	1551.7678	1551.8256	-37.25	395 -	408	0	---	K.DKPEEIVPASKPSR.T

No match to: 854.3754, 896.4893, 1210.5286, 1224.5362, 1243.5824, 1289.5312, 1568.6779, 2112.3339, 2126.9883

9. ACAD8_MOUSE **Mass:** 45789 **Score:** 25 **Expect:** 55 **Matches:** 3

Isobutyryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acad8 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
896.4893	895.4820	895.4552	30.0	49 -	56	0	---	K.VAFDFAAR.E
1044.5397	1043.5325	1043.5148	16.9	234 -	242	0	---	K.VGWNSQPTR.A
1210.5286	1209.5213	1209.5369	-12.93	343 -	353	0	---	R.EDAVALCSMAK.L + Oxidation (M)

No match to: 806.3523, 854.3754, 856.5218, 1224.5362, 1243.5824, 1266.5792, 1289.5312, 1552.7751, 1568.6779, 2112.3339, 2126.9883

10. GPC5_MOUSE **Mass:** 64891 **Score:** 23 **Expect:** 76 **Matches:** 3

Glypican-5 OS=Mus musculus GN=Gpc5 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
854.3754	853.3681	853.3640	4.85	358 -	364	0	---	R.CTFDPSK.E
1266.5792	1265.5719	1265.6186	-36.88	73 -	82	1	---	K.MEERYQIAAR.Q
2126.9883	2125.9810	2126.0176	-17.24	515 -	532	1	---	R.TLKITNWMPDSMNFSDVK.Q

No match to: 806.3523, 856.5218, 896.4893, 1044.5397, 1210.5286, 1224.5362, 1243.5824, 1289.5312, 1552.7751, 1568.6779, 2112.3339

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (806.3523,1+) : <no title>

Query2 (854.3754,1+) : <no title>

Query3 (856.5218,1+) : <no title>

Query4 (896.4893,1+) : <no title>

Query5 (1044.5397,1+) : <no title>

Query6 (1210.5286,1+) : <no title>

Query7 (1224.5362,1+) : <no title>

Query8 (1243.5824,1+) : <no title>

Query9 (1266.5792,1+) : <no title>

Query10 (1289.5312,1+) : <no title>

Query11 (1552.7751,1+) : <no title>

Query12 (1568.6779,1+) : <no title>

Query13 (2112.3339,1+) : <no title>

Query14 (2126.9883,1+) : <no title>

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

Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**

Taxonomy : **Mus musculus (house mouse) (16230 sequences)**

Timestamp : **5 Nov 2013 at 04:47:35 GMT**

Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**

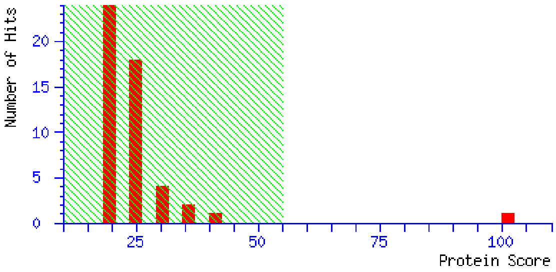
Top Score : **101 for MSS4_MOUSE, Guanine nucleotide exchange factor MSS4 OS=Mus musculus GN=Rabif PE=2 SV=1**

Mascot Score Histogram

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.

Protein scores greater than 55 are significant (p<0.05).

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Index

	Accession	Mass	Score	Description
1.	**MSS4_MOUSE**	14248	101	Guanine nucleotide exchange factor MSS4 OS=Mus musculus GN=Rabif PE=2 SV=1
2.	**LSP1_MOUSE**	36806	42	Lymphocyte-specific protein 1 OS=Mus musculus GN=Lsp1 PE=1 SV=2
3.	**MICA2_MOUSE**	111200	34	Protein MICAL-2 OS=Mus musculus GN=Mical2 PE=1 SV=1
4.	**SMOC1_MOUSE**	52298	33	SPARC-related modular calcium-binding protein 1 OS=Mus musculus GN=Smoc1 PE=2 SV=2
5.	**NSUN5_MOUSE**	51568	32	Putative methyltransferase NSUN5 OS=Mus musculus GN=Nsun5 PE=2 SV=2
6.	**THEM5_MOUSE**	28132	30	Thioesterase superfamily member 5 OS=Mus musculus GN=Them5 PE=2 SV=1
7.	**AP1S2_MOUSE**	19145	29	AP-1 complex subunit sigma-2 OS=Mus musculus GN=Ap1s2 PE=2 SV=1
8.	**MCEM1_MOUSE**	20693	29	Mast cell-expressed membrane protein 1 homolog OS=Mus musculus GN=Mcemp1 PE=2 SV=1
9.	**MUTYH_MOUSE**	58378	28	A/G-specific adenine DNA glycosylase OS=Mus musculus GN=Mutyh PE=2 SV=1
10.	**NAR2B_MOUSE**	33354	26	T-cell ecto-ADP-ribosyltransferase 2 OS=Mus musculus GN=Art2b PE=2 SV=1

Results List

1. MSS4_MOUSE **Mass:** 14248 **Score:** 101 **Expect:** 1.3e-006 **Matches:** 4

Guanine nucleotide exchange factor MSS4 OS=Mus musculus GN=Rabif PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1007.4878	1006.4805	1006.5270	-46.17	42 -	49	0	---	R.QLFLPSMR.K + Oxidation (M)
1098.5401	1097.5328	1097.5505	-16.15	111 -	119	0	---	K.NSFYVALER.V
1163.5807	1162.5735	1162.6281	-46.99	41 -	49	1	---	R.RQLFLPSMR.K + Oxidation (M)
1188.6346	1187.6273	1187.6663	-32.78	30 -	40	0	49	R.VLQPGTALFSR.R

No match to: 842.4617, 856.4699, 868.3781, 874.4405, 976.4259, 990.4526, 999.3938, 1073.5232, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

2. LSP1_MOUSE **Mass:** 36806 **Score:** 42 **Expect:** 1.1 **Matches:** 2

Lymphocyte-specific protein 1 OS=Mus musculus GN=Lsp1 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
842.4617	841.4544	841.4294	29.8	2 -	9	0	28	M.AEAAIDPR.C
874.4405	873.4332	873.4192	16.0	48 -	54	0	---	R.QLQDQDK.D

No match to: 856.4699, 868.3781, 976.4259, 990.4526, 999.3938, 1007.4878, 1073.5232, 1098.5401, 1163.5807, 1188.6346, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

3. MICA2_MOUSE **Mass:** 111200 **Score:** 34 **Expect:** 5.8 **Matches:** 2

Protein MICAL-2 OS=Mus musculus GN=Mical2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
842.4617	841.4544	841.4810	-31.58	872 -	878	0	27	K.ALSWPLR.L
874.4405	873.4332	873.4385	-6.04	617 -	622	0	---	K.FYELFR.G

No match to: 856.4699, 868.3781, 976.4259, 990.4526, 999.3938, 1007.4878, 1073.5232, 1098.5401, 1163.5807, 1188.6346, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

4. SMOC1_MOUSE **Mass:** 52298 **Score:** 33 **Expect:** 7.9 **Matches:** 4

SPARC-related modular calcium-binding protein 1 OS=Mus musculus GN=Smoc1 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
842.4617	841.4544	841.4956	-48.94	1 -	7	1	---	-.MLPARVR.L
1007.4878	1006.4805	1006.4607	19.6	310 -	318	0	---	K.SVEADDPFK.D
1163.5807	1162.5735	1162.5619	9.97	440 -	451	0	---	K.EGGSLGSFPQGK.R
1864.8827	1863.8754	1863.9149	-21.20	433 -	451	1	---	K.GCLGVSKEGGSLGSFPQGK.R

No match to: 856.4699, 868.3781, 874.4405, 976.4259, 990.4526, 999.3938, 1073.5232, 1098.5401, 1188.6346, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1903.7803, 1919.7831

5. NSUN5_MOUSE **Mass:** 51568 **Score:** 32 **Expect:** 9.8 **Matches:** 3

Putative methyltransferase NSUN5 OS=Mus musculus GN=Nsun5 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1098.5401	1097.5328	1097.5366	-3.48	156 -	164	1	---	K.RQGFSYQGR.A
1163.5807	1162.5735	1162.5652	7.08	454 -	465	1	---	R.KAAVGASMQPST.- + Oxidation (M)
1188.6346	1187.6273	1187.6808	-45.05	263 -	273	1	11	K.RLAAMATLVAR.A + Oxidation (M)

No match to: 842.4617, 856.4699, 868.3781, 874.4405, 976.4259, 990.4526, 999.3938, 1007.4878, 1073.5232, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

6. THEM5_MOUSE **Mass:** 28132 **Score:** 30 **Expect:** 16 **Matches:** 2

Thioesterase superfamily member 5 OS=Mus musculus GN=Them5 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4617	841.4544	841.4480	7.64	21 -	27	0	13	R.SPCLLPR.V
1487.6658	1486.6585	1486.6908	-21.71	214 -	225	1	---	K.LYMSCIAQSRDK.Q + Oxidation (M)

No match to: 856.4699, 868.3781, 874.4405, 976.4259, 990.4526, 999.3938, 1007.4878, 1073.5232, 1098.5401, 1163.5807, 1188.6346, 1198.6754, 1213.5130, 1760.7450, 1864.8827, 1903.7803, 1919.7831

7. AP1S2_MOUSE **Mass:** 19145 **Score:** 29 **Expect:** 19 **Matches:** 2

AP-1 complex subunit sigma-2 OS=Mus musculus GN=Ap1s2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1007.4878	1006.4805	1006.5124	-31.66	18 -	25	0	---	K.WYVPLSDK.E
1188.6346	1187.6273	1187.5831	37.2	1 -	9	0	10	-.MQFMLLFSR.Q + Oxidation (M)

No match to: 842.4617, 856.4699, 868.3781, 874.4405, 976.4259, 990.4526, 999.3938, 1073.5232, 1098.5401, 1163.5807, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

8. MCEM1_MOUSE **Mass:** 20693 **Score:** 29 **Expect:** 21 **Matches:** 3

Mast cell-expressed membrane protein 1 homolog OS=Mus musculus GN=Mcemp1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
856.4699	855.4626	855.4450	20.5	176 -	183	1	---	K.KAQPQPST.-
990.4526	989.4453	989.4236	21.9	1 -	9	0	---	-.MHASASQDK.N + Oxidation (M)
1188.6346	1187.6273	1187.6510	-19.92	40 -	50	1	---	K.LSQSTPTKQAK.F

No match to: 842.4617, 868.3781, 874.4405, 976.4259, 999.3938, 1007.4878, 1073.5232, 1098.5401, 1163.5807, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

9. MUTYH_MOUSE **Mass:** 58378 **Score:** 28 **Expect:** 29 **Matches:** 2

A/G-specific adenine DNA glycosylase OS=Mus musculus GN=Mutyh PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4617	841.4544	841.4559	-1.70	80 -	85	1	17	K.RDLPWR.N
976.4259	975.4186	975.4370	-18.79	90 -	97	1	---	K.EEANSDRR.A

No match to: 856.4699, 868.3781, 874.4405, 990.4526, 999.3938, 1007.4878, 1073.5232, 1098.5401, 1163.5807, 1188.6346, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

10. NAR2B_MOUSE **Mass:** 33354 **Score:** 26 **Expect:** 40 **Matches:** 3

T-cell ecto-ADP-ribosyltransferase 2 OS=Mus musculus GN=Art2b PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
990.4526	989.4453	989.4528	-7.61	150 -	157	0	---	K.VMFEYTGK.G + Oxidation (M)
1007.4878	1006.4805	1006.4508	29.5	116 -	123	0	---	K.SPDNFHYK.A
1188.6346	1187.6273	1187.5823	38.0	162 -	172	0	---	R.FGQFSSSSLTK.R

No match to: 842.4617, 856.4699, 868.3781, 874.4405, 976.4259, 999.3938, 1073.5232, 1098.5401, 1163.5807, 1198.6754, 1213.5130, 1487.6658, 1760.7450, 1864.8827, 1903.7803, 1919.7831

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 : ±50 ppm

Fragment Mass Tolerance: ±0.6 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (842.4617,1+) : <no title>

Query2 (856.4699,1+) : <no title>

Query3 (868.3781,1+) : <no title>

Query4 (874.4405,1+) : <no title>

Query5 (976.4259,1+) : <no title>

Query6 (990.4526,1+) : <no title>

Query7 (999.3938,1+) : <no title>

Query8 (1007.4878,1+) : <no title>

Query9 (1073.5232,1+) : <no title>

Query10 (1098.5401,1+) : <no title>

Query11 (1163.5807,1+) : <no title>

Query12 (1188.6346,1+) : <no title>

Query13 (1198.6754,1+) : <no title>

Query14 (1213.5130,1+) : <no title>

Query15 (1487.6658,1+) : <no title>

Query16 (1760.7450,1+) : <no title>

Query17 (1864.8827,1+) : <no title>

Query18 (1903.7803,1+) : <no title>

Query19 (1919.7831,1+) : <no title>

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