Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

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

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

Timestamp : **20 May 2013 at 01:32:42 GMT**

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

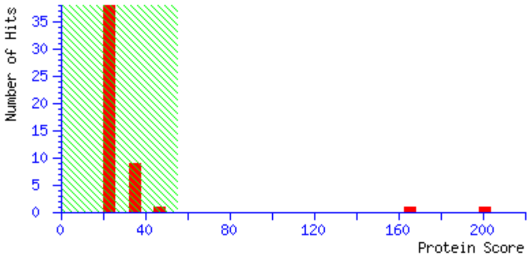
Top Score : **201 for PDIA4_MOUSE, Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=2**

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.	PDIA4_MOUSE	72271	201	Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=2
2.	MYH11_MOUSE	227743	161	Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1
3.	DIAP3_MOUSE	134684	44	Protein diaphanous homolog 3 OS=Mus musculus GN=Diaph3 PE=2 SV=1
4.	CENPE_MOUSE	287830	40	Centromere-associated protein E OS=Mus musculus GN=Cenpe PE=1 SV=1
5.	G6PD2_MOUSE	59601	37	Glucose-6-phosphate 1-dehydrogenase 2 OS=Mus musculus GN=G6pd2 PE=2 SV=3
6.	AGO1_MOUSE	98236	31	Protein argonaute-1 OS=Mus musculus GN=Eif2c1 PE=1 SV=1
7.	KIF5A_MOUSE	117745	31	Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3
8.	IGSF2_MOUSE	115331	31	Immunoglobulin superfamily member 2 OS=Mus musculus GN=Cd101 PE=2 SV=1
9.	CA194_MOUSE	18977	31	Uncharacterized protein C1orf194 homolog OS=Mus musculus PE=2 SV=1
10.	K1C42_MOUSE	50444	31	Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1

Results List

1. PDIA4_MOUSE **Mass:** 72271 **Score:** 201 **Expect:** 1.3e-016 **Matches:** 13

Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1131.6385	1130.6312	1130.5832	42.4	606 -	615	1	---	K.NPIKFEGGNR.D
1178.6233	1177.6160	1177.5629	45.1	254 -	263	0	48	K.GRPFDYNGPR.E
1282.7234	1281.7161	1281.6717	34.6	239 -	249	1	30	K.RFDVSGYPTLK.I
1306.7133	1305.7060	1305.6639	32.3	527 -	537	1	---	K.TFDAIVMDPKK.D + Acetyl (N-term)
1313.7090	1312.7017	1312.6564	34.5	329 -	339	0	---	K.FHHTFSPEIAK.F
1501.7919	1500.7846	1500.7321	35.0	610 -	622	1	---	K.FEGGNRDLEHLSK.F
1542.8306	1541.8233	1541.8242	-0.59	240 -	252	1	---	R.FDVSGYPTLKIFR.K
1686.7837	1685.7764	1685.7243	30.9	479 -	492	0	74	K.FAMEPEEFDSDTLR.E
1755.9363	1754.9290	1754.8879	23.4	590 -	605	1	---	K.VEGFPTIYFAPSGDKK.N
1783.9123	1782.9050	1782.8498	30.9	266 -	281	0	---	K.YGIVDYMIEQSGPPSK.E
1848.9479	1847.9406	1847.8842	30.5	325 -	339	1	---	R.EDYKFHHTFSPEIAK.F
2125.1398	2124.1325	2124.0680	30.4	405 -	421	0	---	K.RPLVVVYYSVDFSFDYR.A
2509.2482	2508.2409	2508.1519	35.5	479 -	499	1	---	K.FAMEPEEFDSDTLREFVTAFK.K

No match to: 804.4492, 826.4234, 832.4631, 848.4022, 1067.5555, 1116.6465, 1128.6199, 1148.6414, 1164.0126, 1195.6317, 1198.7511, 1335.7076, 1347.6645, 1470.8558, 1516.7607, 1556.8506, 1570.8644, 1598.9730, 1629.8798, 1701.7970, 1714.8275, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1773.9612, 1777.9562, 1790.9478, 1805.9222, 1818.9186, 1858.0026, 1902.0480, 1913.0184, 2003.0379, 2017.0528, 2039.0068, 2146.1285, 2175.1341, 2303.2357, 2374.1478, 2451.1595, 2691.3565

2. MYH11_MOUSE **Mass:** 227743 **Score:** 161 **Expect:** 1.3e-012 **Matches:** 23

Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
826.4234	825.4161	825.3942	26.5	138 -	143	0	---	K.IVDMYK.G + Acetyl (N-term); Oxidation (M)
1306.7133	1305.7060	1305.6499	42.9	1650 -	1659	1	---	K.LQAQMKDFQR.E + Acetyl (N-term)
1335.7076	1334.7004	1334.7129	-9.37	818 -	828	1	---	K.VIQRNCAAYLK.L
1347.6645	1346.6573	1346.6718	-10.76	415 -	426	0	---	K.EQADFAIEALAK.A + Acetyl (N-term)
1470.8558	1469.8485	1469.8089	26.9	1851 -	1862	1	---	K.LKEVLLQVEDER.K
1501.7919	1500.7846	1500.8082	-15.72	810 -	821	1	---	R.QQQLTAMKVIQR.N + Acetyl (N-term); Oxidation (M)
1516.7607	1515.7534	1515.6801	48.4	1579 -	1590	1	---	R.DLQARDEQNEEK.R + Acetyl (N-term)
1542.8306	1541.8233	1541.7685	35.5	1823 -	1835	0	39	K.IAQLEEQVEQEAR.E
1556.8506	1555.8434	1555.8093	21.9	55 -	68	1	---	K.GDEVVVELVENGKK.V + Acetyl (N-term)
1570.8644	1569.8571	1569.8184	24.6	1032 -	1044	1	---	K.HESMISELEVRLK.K
1629.8798	1628.8725	1628.8257	28.8	1491 -	1504	1	---	R.ALEEALEAKEELER.T
1686.7837	1685.7764	1685.8584	-48.64	1227 -	1241	1	---	K.QTLEKENADLAGELR.V
1773.9612	1772.9539	1772.8904	35.8	1762 -	1777	0	---	K.ATLQAEQLSNELATER.S
1777.9562	1776.9489	1776.9008	27.1	130 -	143	1	---	K.YLPIYSEKIVDMYK.G + Oxidation (M)
1818.9186	1817.9113	1817.8894	12.1	1008 -	1023	1	---	R.VSDLTTNLAEEEEKAK.N + Acetyl (N-term)
1858.0026	1856.9953	1856.9731	12.0	1622 -	1638	1	---	K.LEGDLKDLELQADSAIK.G
1902.0480	1901.0407	1900.9854	29.1	1761 -	1777	1	---	R.KATLQAEQLSNELATER.S
1913.0184	1912.0111	1911.9538	30.0	1425 -	1440	0	74	R.LQQELDDLVVDLDNQR.Q
2003.0379	2002.0306	2001.9677	31.4	1684 -	1701	0	---	K.SLEADLMQLQEDLAAAER.A
2125.1398	2124.1325	2124.0442	41.6	625 -	644	1	---	R.IVGLDQMAKMTESSLPSASK.T + 2 Oxidation (M)
2175.1341	2174.1268	2174.0702	26.0	1705 -	1724	1	---	K.QADLEKEELAEELASSLSGR.N

2451.1595	2450.1523	2450.0577	38.6	1738	1758	0	---	R.IAQLEEELEEEQGNMEAMSDR.V
2509.2482	2508.2409	2508.2107	12.0	483	501	0	---	K.LQQLFNHTMFILEQEEYQR.E + Acetyl (N-term)

No match to: 804.4492, 832.4631, 848.4022, 1067.5555, 1116.6465, 1128.6199, 1131.6385, 1148.6414, 1164.0126, 1178.6233, 1195.6317, 1198.7511, 1282.7234, 1313.7090, 1598.9730, 1701.7970, 1714.8275, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1755.9363, 1783.9123, 1790.9478, 1805.9222, 1848.9479, 2017.0528, 2039.0068, 2146.1285, 2303.2357, 2374.1478, 2691.3565

3. DIAP3_MOUSE **Mass:** 134684 **Score:** 44 **Expect:** 0.62 **Matches:** 19

Protein diaphanous homolog 3 OS=Mus musculus GN=Diaph3 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
804.4492	803.4419	803.4025	49.1	999	1005	1	---	R.EAAEKEK.R
832.4631	831.4559	831.4385	20.9	900	906	1	---	K.NVKQMGR.Q
848.4022	847.3950	847.4334	-45.37	900	906	1	---	K.NVKQMGR.Q + Oxidation (M)
1067.5555	1066.5483	1066.5811	-30.82	302	310	0	---	R.FFSIVEGLR.H
1128.6199	1127.6126	1127.6451	-28.80	65	73	0	---	K.ERPPLPHLK.T + Acetyl (N-term)
1178.6233	1177.6160	1177.5801	30.5	618	626	0	---	K.EFKPEISMR.R + Acetyl (N-term)
1282.7234	1281.7161	1281.6976	14.5	221	230	1	---	K.TQHKVIQCLR.A
1306.7133	1305.7060	1305.6751	23.7	617	626	1	---	K.KEFKPEISMR.R + Acetyl (N-term)
1313.7090	1312.7017	1312.7350	-25.38	358	369	1	---	K.GIKNDGLDIQLK.V
1470.8558	1469.8485	1469.8024	31.3	1069	1081	0	---	R.QSLSPMSQRPVLK.V
1542.8306	1541.8233	1541.7581	42.3	131	143	1	---	K.KEMVMQYINTASK.T
1701.7970	1700.7897	1700.8048	-8.87	255	269	1	---	K.AMDPRQPAMMADVVK.L + Acetyl (N-term)
1773.9612	1772.9539	1772.9308	13.0	513	527	1	---	R.EAKINELQAELQAFK.S + Acetyl (N-term)
1858.0026	1856.9953	1856.9057	48.2	970	984	1	---	K.KVSVEEFFNDLNNFR.T
1902.0480	1901.0407	1901.0887	-25.21	412	427	0	---	R.AEGHFLSILQHLLLIR.N + Acetyl (N-term)
1913.0184	1912.0111	1912.0200	-4.66	1066	1081	1	---	K.DIRQSLSPMSQRPVLK.V + Acetyl (N-term); Oxidation (M)
2003.0379	2002.0306	2001.9499	40.3	132	148	1	---	K.EMVMQYINTASKTGSLR.S + Acetyl (N-term); 2 Oxidation (M)
2451.1595	2450.1523	2450.2284	-31.07	718	738	0	---	R.TMILEVDETQLSESMIQNLIK.H + Oxidation (M)
2509.2482	2508.2409	2508.2339	2.81	718	738	0	---	R.TMILEVDETQLSESMIQNLIK.H + Acetyl (N-term); 2 Oxidation (M)

No match to: 826.4234, 1116.6465, 1131.6385, 1148.6414, 1164.0126, 1195.6317, 1198.7511, 1335.7076, 1347.6645, 1501.7919, 1516.7607, 1556.8506, 1570.8644, 1598.9730, 1629.8798, 1686.7837, 1714.8275, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1755.9363, 1777.9562, 1783.9123, 1790.9478, 1805.9222, 1818.9186, 1848.9479, 2017.0528, 2039.0068, 2125.1398, 2146.1285, 2175.1341, 2303.2357, 2374.1478, 2691.3565

4. CENPE_MOUSE **Mass:** 287830 **Score:** 40 **Expect:** 1.6 **Matches:** 27

Centromere-associated protein E OS=Mus musculus GN=Cenpe PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
804.4492	803.4419	803.4177	30.1	181	187	0	---	K.WLATGEK.N
826.4234	825.4161	825.4531	-44.78	1773	1779	0	---	R.IAHMNLK.E
832.4631	831.4559	831.4338	26.6	649	655	0	---	R.SENLELK.E
1128.6199	1127.6126	1127.6550	-37.56	843	852	1	---	R.LKQEIGALSK.E + Acetyl (N-term)
1131.6385	1130.6312	1130.5931	33.7	1817	1825	1	---	K.VQELKTSER.Q + Acetyl (N-term)
1178.6233	1177.6160	1177.5914	20.9	252	260	1	---	R.LKEGCFINR.N + Acetyl (N-term)
1195.6317	1194.6244	1194.6105	11.6	833	842	1	---	R.HAGVLEERER.L
1282.7234	1281.7161	1281.7193	-2.51	109	118	1	1	R.AIHDIFQRIK.K + Acetyl (N-term)

1313.7090	1312.7017	1312.7350	-25.36	711	721	1	---	K.GLLSNLELEKR.I + Acetyl (N-term)
1335.7076	1334.7004	1334.6718	21.4	1241	1250	0	---	K.EYQEIITELR.G + Acetyl (N-term)
1347.6645	1346.6573	1346.7081	-37.78	692	702	0	---	K.ELQLAFQEISK.L + Acetyl (N-term)
1501.7919	1500.7846	1500.8082	-15.70	149	160	1	---	K.MKPLIIREDTNR.T + Oxidation (M)
1516.7607	1515.7534	1515.7537	-0.21	975	986	1	---	K.QHQETINMLKMK.A + Oxidation (M)
1542.8306	1541.8233	1541.7694	35.0	975	986	1	---	K.QHQETINMLKMK.A + Acetyl (N-term)
1570.8644	1569.8571	1569.8726	-9.85	1716	1728	1	---	K.LELTQQLNENLKK.I
1701.7970	1700.7897	1700.7862	2.08	550	563	0	---	R.DQEMQLMHEVSNLK.N
1727.8389	1726.8316	1726.7719	34.6	2142	2155	0	---	R.ITAMINESTEFEER.S + Acetyl (N-term); Oxidation (M)
1755.9363	1754.9290	1754.8588	40.0	272	287	1	---	K.LSDGQVGGFINYRDSK.L
1777.9562	1776.9489	1776.8907	32.8	2127	2141	1	---	K.ENKSIGLVNNFYHSR.I
1783.9123	1782.9050	1782.9013	2.09	1626	1640	0	---	R.VAHVHLEEHQETINK.L
1805.9222	1804.9149	1804.8843	17.0	331	346	0	---	K.NTPYVNEVSNDEALLK.R
1848.9479	1847.9406	1847.9265	7.67	591	605	1	---	K.EEQIKNLQEYIDAQK.S
1913.0184	1912.0111	1912.0088	1.23	2258	2273	1	6	K.ILSLKATVEHQEEMIR.L + Oxidation (M)
2017.0528	2016.0455	2015.9872	28.9	2203	2221	1	---	R.DSERPQAASGAEQLTSKNK.I
2146.1285	2145.1212	2145.0922	13.5	1311	1329	1	---	R.TVHSMTMEGIEIGNLRLTK.K + Oxidation (M)
2175.1341	2174.1268	2174.1252	0.73	1843	1861	1	---	K.EQGLTLSKIEMENLNLAQK.I + Oxidation (M)
2303.2357	2302.2284	2302.1290	43.2	161	180	0	---	R.TVYVSDLTEEVVYTAEMALK.W + Acetyl (N-term)

No match to: 848.4022, 1067.5555, 1116.6465, 1148.6414, 1164.0126, 1198.7511, 1306.7133, 1470.8558, 1556.8506, 1598.9730, 1629.8798, 1686.7837, 1714.8275, 1723.6200, 1724.6029, 1745.5866, 1773.9612, 1790.9478, 1818.9186, 1858.0026, 1902.0480, 2003.0379, 2039.0068, 2125.1398, 2374.1478, 2451.1595, 2509.2482, 2691.3565

5. G6PD2_MOUSE **Mass:** 59601 **Score:** 37 **Expect:** 3.5 **Matches:** 9

Glucose-6-phosphate 1-dehydrogenase 2 OS=Mus musculus GN=G6pd2 PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1306.7133	1305.7060	1305.6421	49.0	206	215	0	---	K.EMVQNLMVLR.F + Acetyl (N-term); 2 Oxidation (M)
1501.7919	1500.7846	1500.7837	0.60	346	357	1	---	K.NERWDGVPFILR.C
1686.7837	1685.7764	1685.7463	17.9	394	407	0	---	R.MQPNEAVYTTMMTK.K + Acetyl (N-term)
1701.7970	1700.7897	1700.7247	38.2	153	166	0	---	K.NIQETCMSQTGFNR.I + Oxidation (M)
1755.9363	1754.9290	1754.9104	10.6	371	384	1	---	R.LQFRDIPGDIFHQK.C + Acetyl (N-term)
1790.9478	1789.9406	1789.8999	22.7	83	97	1	---	K.QSEPFFKATPEERPK.L
2175.1341	2174.1268	2174.0864	18.6	199	215	1	---	R.IDHYLDKEMVQNLMVLR.F + Acetyl (N-term); Oxidation (M)
2374.1478	2373.1405	2373.0835	24.0	408	427	0	---	K.KPGMFFNPEESELDLTYGNK.Y + Acetyl (N-term); Oxidation (M)
2509.2482	2508.2409	2508.2076	13.3	440	459	1	---	R.LILDVFCGCQMHFVRTDELR.E

No match to: 804.4492, 826.4234, 832.4631, 848.4022, 1067.5555, 1116.6465, 1128.6199, 1131.6385, 1148.6414, 1164.0126, 1178.6233, 1195.6317, 1198.7511, 1282.7234, 1313.7090, 1335.7076, 1347.6645, 1470.8558, 1516.7607, 1542.8306, 1556.8506, 1570.8644, 1598.9730, 1629.8798, 1714.8275, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1773.9612, 1777.9562, 1783.9123, 1805.9222, 1818.9186, 1848.9479, 1858.0026, 1902.0480, 1913.0184, 2003.0379, 2017.0528, 2039.0068, 2125.1398, 2146.1285, 2303.2357, 2451.1595, 2691.3565

6. AGO1_MOUSE **Mass:** 98236 **Score:** 31 **Expect:** 12 **Matches:** 10

Protein argonaute-1 OS=Mus musculus GN=Eif2c1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1067.5555	1066.5483	1066.5342	13.2	277	284	1	---	K.YRVCNVTR.R

1516.7607	1515.7534	1515.7140	26.0	424	436	0	---	R.AIATPNQGVWDMR.G + Acetyl (N-term); Oxidation (M)
1701.7970	1700.7897	1700.8304	-23.94	424	438	1	---	R.AIATPNQGVWDMRGK.Q + Acetyl (N-term); Oxidation (M)
1773.9612	1772.9539	1772.9454	4.76	549	564	1	---	K.NAVKTSPQTLSNLCLK.I
1777.9562	1776.9489	1776.8750	41.6	533	548	0	---	R.VGDTLLGMATQCVQVK.N + Acetyl (N-term); Oxidation (M)
1848.9479	1847.9406	1847.8988	22.6	492	507	1	---	K.YAQGADSVEPMFRHLK.N
1858.0026	1856.9953	1857.0030	-4.13	553	568	1	---	K.TSPQTLSNLCLKINVK.L + Acetyl (N-term)
2303.2357	2302.2284	2302.2321	-1.59	667	686	0	---	R.DGVPEGQLPQILHYELLAIR.D + Acetyl (N-term)
2451.1595	2450.1523	2450.2594	-43.74	582	605	0	---	R.SAVFQQPVIFLGADVTHPPAGDGK.K
2509.2482	2508.2409	2508.1378	41.1	813	835	1	---	R.YHLVDKEHDSGEGSHISGQSNGR.D

No match to: 804.4492, 826.4234, 832.4631, 848.4022, 1116.6465, 1128.6199, 1131.6385, 1148.6414, 1164.0126, 1178.6233, 1195.6317, 1198.7511, 1282.7234, 1306.7133, 1313.7090, 1335.7076, 1347.6645, 1470.8558, 1501.7919, 1542.8306, 1556.8506, 1570.8644, 1598.9730, 1629.8798, 1686.7837, 1714.8275, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1755.9363, 1783.9123, 1790.9478, 1805.9222, 1818.9186, 1902.0480, 1913.0184, 2003.0379, 2017.0528, 2039.0068, 2125.1398, 2146.1285, 2175.1341, 2374.1478, 2691.3565

7. KIF5A_MOUSE **Mass:** 117745 **Score:** 31 **Expect:** 12 **Matches:** 14

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
826.4234	825.4161	825.4021	17.0	275	280	0	---	K.SYVPYR.D + Acetyl (N-term)
848.4022	847.3950	847.3923	3.14	502	508	0	---	K.SQEVEEK.S
1131.6385	1130.6312	1130.6118	17.2	547	556	0	---	R.IAEVLNGLMR.D + Oxidation (M)
1178.6233	1177.6160	1177.6091	5.83	893	901	1	---	R.YQQEVDRIK.E
1313.7090	1312.7017	1312.7285	-20.39	546	556	1	---	K.RIAEVLNGLMR.D + Acetyl (N-term)
1470.8558	1469.8485	1469.8089	26.9	733	744	1	---	K.DLNQKLQLELEK.L
1516.7607	1515.7534	1515.7780	-16.24	239	253	1	---	K.VSKTGAEGAVLDEAK.N + Acetyl (N-term)
1629.8798	1628.8725	1628.8369	21.9	509	522	0	---	K.SQQNQLLVDELSQK.V
1701.7970	1700.7897	1700.7312	34.4	812	827	0	---	K.SAEMEPEDSGGIHSQK.Q
1783.9123	1782.9050	1782.8253	44.7	605	617	1	---	R.CRQLENLQVECHR.K + Acetyl (N-term)
1818.9186	1817.9113	1817.8935	9.83	173	188	0	---	R.FVSSPEEILDVIDEGK.S + Acetyl (N-term)
1902.0480	1901.0407	1900.9782	32.9	572	588	0	---	K.LPVEISGAIEEEFTVAR.L + Acetyl (N-term)
1913.0184	1912.0111	1911.9174	49.0	469	485	1	---	R.ELSHLQSENDAAKDEVK.E
2691.3565	2690.3492	2690.3286	7.66	486	508	1	---	K.EVLQALEELAVNYDQKSQEVEEK.S

No match to: 804.4492, 832.4631, 1067.5555, 1116.6465, 1128.6199, 1148.6414, 1164.0126, 1195.6317, 1198.7511, 1282.7234, 1306.7133, 1335.7076, 1347.6645, 1501.7919, 1542.8306, 1556.8506, 1570.8644, 1598.9730, 1686.7837, 1714.8275, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1755.9363, 1773.9612, 1777.9562, 1790.9478, 1805.9222, 1848.9479, 1858.0026, 2003.0379, 2017.0528, 2039.0068, 2125.1398, 2146.1285, 2175.1341, 2303.2357, 2374.1478, 2451.1595, 2509.2482

8. IGSF2_MOUSE **Mass:** 115331 **Score:** 31 **Expect:** 13 **Matches:** 13

Immunoglobulin superfamily member 2 OS=Mus musculus GN=Cd101 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
832.4631	831.4559	831.4425	16.0	1012	1018	0	---	K.ALWVGMR.K
1116.6465	1115.6392	1115.6550	-14.12	1000	1009	1	---	K.LSQLSLSAKK.E + Acetyl (N-term)
1131.6385	1130.6312	1130.5906	35.9	1010	1018	1	---	K.EKALWVGMR.K + Acetyl (N-term)
1178.6233	1177.6160	1177.6237	-6.57	537	546	1	---	K.SSLRVNLMSR.Q + Oxidation (M)
1306.7133	1305.7060	1305.6928	10.1	89	98	1	---	R.VQSKEIYIER.L + Acetyl (N-term)

1347.6645	1346.6573	1346.6255	23.6	77 -	88	0	---	K.DAGFSYAVYAQR.V
1542.8306	1541.8233	1541.7798	28.3	407 -	420	1	0	R.EPAARSVTVSAEQR.T + Acetyl (N-term)
1714.8275	1713.8202	1713.8475	-15.93	310 -	324	0	---	R.DGNPQLQGVWFLNGK.E + Acetyl (N-term)
1790.9478	1789.9406	1789.8893	28.6	939 -	953	1	---	K.WINQASGESQRMVLR.V + Oxidation (M)
2039.0068	2037.9995	2038.0241	-12.06	547 -	563	0	---	R.QPQVMLAHTFHLSCVVR.A + Oxidation (M)
2175.1341	2174.1268	2174.0698	26.2	571 -	589	0	---	K.LPFSVTWQFQPAGSGAFHR.L + Acetyl (N-term)
2374.1478	2373.1405	2373.0940	19.6	494 -	514	1	---	R.LEIASAMVTDSGTYECRVSER.L
2691.3565	2690.3492	2690.2507	36.6	34 -	57	1	---	R.AEGYPVSIRCTVSGHQGPSTQDFR.W + Acetyl (N-term)

No match to: 804.4492, 826.4234, 848.4022, 1067.5555, 1128.6199, 1148.6414, 1164.0126, 1195.6317, 1198.7511, 1282.7234, 1313.7090, 1335.7076, 1470.8558, 1501.7919, 1516.7607, 1556.8506, 1570.8644, 1598.9730, 1629.8798, 1686.7837, 1701.7970, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1755.9363, 1773.9612, 1777.9562, 1783.9123, 1805.9222, 1818.9186, 1848.9479, 1858.0026, 1902.0480, 1913.0184, 2003.0379, 2017.0528, 2125.1398, 2146.1285, 2303.2357, 2451.1595, 2509.2482

9. CA194_MOUSE **Mass:** 18977 **Score:** 31 **Expect:** 14 **Matches:** 5

Uncharacterized protein C1orf194 homolog OS=Mus musculus PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1067.5555	1066.5483	1066.5560	-7.22	19 -	27	0	---	K.HLGNLWASK.K + Acetyl (N-term)
1195.6317	1194.6244	1194.6509	-22.18	19 -	28	1	---	K.HLGNLWASKK.S + Acetyl (N-term)
1542.8306	1541.8233	1541.7838	25.6	2 -	14	0	---	M.LQPQETFSNPALR.D + Acetyl (N-term)
1714.8275	1713.8202	1713.8951	-43.69	75 -	89	1	---	R.LATLYNHHTGAFKNK.T
2691.3565	2690.3492	2690.3161	12.3	33 -	56	1	---	K.NPAHLAQQQDPWSRLSSTPTATSR.S + Acetyl (N-term)

No match to: 804.4492, 826.4234, 832.4631, 848.4022, 1116.6465, 1128.6199, 1131.6385, 1148.6414, 1164.0126, 1178.6233, 1198.7511, 1282.7234, 1306.7133, 1313.7090, 1335.7076, 1347.6645, 1470.8558, 1501.7919, 1516.7607, 1556.8506, 1570.8644, 1598.9730, 1629.8798, 1686.7837, 1701.7970, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1755.9363, 1773.9612, 1777.9562, 1783.9123, 1790.9478, 1805.9222, 1818.9186, 1848.9479, 1858.0026, 1902.0480, 1913.0184, 2003.0379, 2017.0528, 2039.0068, 2125.1398, 2146.1285, 2175.1341, 2303.2357, 2374.1478, 2451.1595, 2509.2482

10. K1C42_MOUSE **Mass:** 50444 **Score:** 31 **Expect:** 14 **Matches:** 8

Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1148.6414	1147.6341	1147.6349	-0.74	105 -	113	1	---	R.LATYLDRVR.A + Acetyl (N-term)
1178.6233	1177.6160	1177.5874	24.3	420 -	429	1	---	R.EGMVTSRQVR.T + Oxidation (M)
1542.8306	1541.8233	1541.8049	11.9	427 -	439	1	---	R.QVRTIVEEVQDGK.V + Acetyl (N-term)
1556.8506	1555.8434	1555.8205	14.7	112 -	125	1	---	R.VRALEEANADLEVK.I
1570.8644	1569.8571	1569.8362	13.3	114 -	127	1	---	R.ALEEANADLEVKIR.E
1773.9612	1772.9539	1772.8727	45.8	1 -	17	1	---	-.MASTTSVRQFSTSGSVK.G
2003.0379	2002.0306	2002.0517	-10.53	315 -	331	1	---	R.RSVQNLEIELQSQLSMK.A
2303.2357	2302.2284	2302.2090	8.46	203 -	222	1	---	R.VLDELTLARADLEMQIESLK.E + Oxidation (M)

No match to: 804.4492, 826.4234, 832.4631, 848.4022, 1067.5555, 1116.6465, 1128.6199, 1131.6385, 1164.0126, 1195.6317, 1198.7511, 1282.7234, 1306.7133, 1313.7090, 1335.7076, 1347.6645, 1470.8558, 1501.7919, 1516.7607, 1598.9730, 1629.8798, 1686.7837, 1701.7970, 1714.8275, 1723.6200, 1724.6029, 1727.8389, 1745.5866, 1755.9363, 1777.9562, 1783.9123, 1790.9478, 1805.9222, 1818.9186, 1848.9479, 1858.0026, 1902.0480, 1913.0184, 2017.0528, 2039.0068, 2125.1398, 2146.1285, 2175.1341, 2374.1478, 2451.1595, 2509.2482, 2691.3565

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (804.4492,1+) : <no title>

Query2 (826.4234,1+) : <no title>

Query3 (832.4631,1+) : <no title>

Query4 (848.4022,1+) : <no title>

Query5 (1067.5555,1+) : <no title>

Query6 (1116.6465,1+) : <no title>

Query7 (1128.6199,1+) : <no title>

Query8 (1131.6385,1+) : <no title>

Query9 (1148.6414,1+) : <no title>

Query10 (1164.0126,1+) : <no title>

Query11 (1178.6233,1+) : <no title>

Query12 (1195.6317,1+) : <no title>

Query13 (1198.7511,1+) : <no title>

Query14 (1282.7234,1+) : <no title>

Query15 (1306.7133,1+) : <no title>

Query16 (1313.7090,1+) : <no title>

Query17 (1335.7076,1+) : <no title>

Query18 (1347.6645,1+) : <no title>

Query19 (1470.8558,1+) : <no title>

Query20 (1501.7919,1+) : <no title>

Query21 (1516.7607,1+) : <no title>

Query22 (1542.8306,1+) : <no title>

Query23 (1556.8506,1+) : <no title>

Query24 (1570.8644,1+) : <no title>

Query25 (1598.9730,1+) : <no title>

Query26 (1629.8798,1+) : <no title>

Query27 (1686.7837,1+) : <no title>

Query28 (1701.7970,1+) : <no title>

Query29 (1714.8275,1+) : <no title>

Query30 (1723.6200,1+) : <no title>

Query31 (1724.6029,1+) : <no title>

Query32 (1727.8389,1+) : <no title>

Query33 (1745.5866,1+) : <no title>

Query34 (1755.9363,1+) : <no title>

Query35 (1773.9612,1+) : <no title>

Query36 (1777.9562,1+) : <no title>

Query37 (1783.9123,1+) : <no title>

Query38 (1790.9478,1+) : <no title>

Query39 (1805.9222,1+) : <no title>

Query40 (1818.9186,1+) : <no title>

Query41 (1848.9479,1+) : <no title>

Query42 (1858.0026,1+) : <no title>

Query43 (1902.0480,1+) : <no title>

Query44 (1913.0184,1+) : <no title>

Query45 (2003.0379,1+) : <no title>

Query46 (2017.0528,1+) : <no title>

Query47 (2039.0068,1+) : <no title>

Query48 (2125.1398,1+) : <no title>

Query49 (2146.1285,1+) : <no title>

Query50 (2175.1341,1+) : <no title>

Query51 (2303.2357,1+) : <no title>

Query52 (2374.1478,1+) : <no title>

Query53 (2451.1595,1+) : <no title>

Query54 (2509.2482,1+) : <no title>

Query55 (2691.3565,1+) : <no title>

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

Mascot Search Results

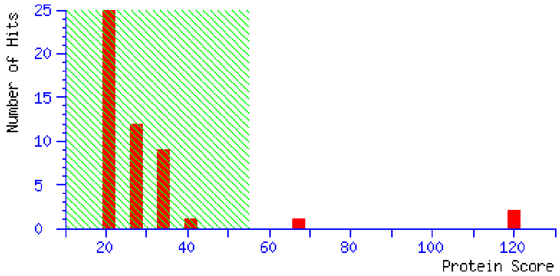
User :
Email :
Search title : **Auto submitted by BioTools**
Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**
Taxonomy : **Mus. (16281 sequences)**
Timestamp : **20 May 2013 at 01:32:50 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **120 for HS71A_MOUSE, Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a 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.	**HS71A_MOUSE**	70321	120	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2
2.	**HS71B_MOUSE**	70418	119	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3
3.	**HS71L_MOUSE**	70992	66	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4
4.	**U5S1_MOUSE**	110261	41	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1
5.	**ECHA_MOUSE**	83302	37	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1
6.	**TARA_MOUSE**	225171	36	TRIO and F-actin-binding protein OS=Mus musculus GN=Triobp PE=1 SV=3
7.	**HSP7C_MOUSE**	71055	34	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1
8.	**PARVG_MOUSE**	37610	34	Gamma-parvin OS=Mus musculus GN=Parvg PE=1 SV=1
9.	**TTC23_MOUSE**	55372	32	Tetratricopeptide repeat protein 23 OS=Mus musculus GN=Ttc23 PE=2 SV=1
10.	**NRAP_MOUSE**	196735	32	Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap PE=1 SV=2

Results List

1. HS71A_MOUSE **Mass:** 70321 **Score:** 120 **Expect:** 1.6e-008 **Matches:** 13

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**
804.4262	803.4190	803.4389	-24.78	501 -	507	0	---	K.ITITNDK.G
832.4582	831.4509	831.4450	7.13	251 -	257	1	---	K.KDISQNK.R
1109.6245	1108.6173	1108.5665	45.8	349 -	357	0	---	K.LLQDFFNGR.D
1183.6895	1182.6822	1182.6397	36.0	459 -	469	0	---	R.FELSGIPPAPR.G
1197.7358	1196.7286	1196.6877	34.1	160 -	171	0	---	K.DAGVIAGLNVLR.I
1390.7797	1389.7725	1389.7405	23.0	237 -	247	1	---	R.LVSHFVEEFKR.K
1465.8545	1464.8472	1464.8049	28.9	329 -	342	0	---	K.AQIHDLVLVGGSTR.I
1487.7390	1486.7317	1486.6940	25.3	37 -	49	0	7	R.TTPSYVAFTDTER.L
1542.7924	1541.7851	1541.7296	36.0	300 -	311	1	---	R.ARFEELCSDLFR.G
1675.7697	1674.7625	1674.7234	23.3	221 -	236	0	---	K.ATAGDTHLGGEDFDNR.L
1687.9394	1686.9321	1686.8940	22.6	172 -	187	0	14	R.IINEPTAAAIAYGLDR.T
2774.3263	2773.3190	2773.3195	-0.20	424 -	447	0	---	K.QTQTFTTYSDNQPGVLIQVYEGER.A
2981.4769	2980.4696	2980.4553	4.79	273 -	299	0	---	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A

No match to: 1110.6181, 1210.6660, 1428.7622, 1480.8111, 1502.7816, 1552.8628, 1592.9945, 1653.8659, 1710.9420, 1751.9679, 1776.9783, 1782.9238, 1982.0462, 2691.2918

2. HS71B_MOUSE **Mass:** 70418 **Score:** 119 **Expect:** 2e-008 **Matches:** 13

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
804.4262	803.4190	803.4389	-24.78	501 -	507	0	---	K.ITITNDK.G
832.4582	831.4509	831.4450	7.13	251 -	257	1	---	K.KDISQNK.R
1109.6245	1108.6173	1108.5665	45.8	349 -	357	0	---	K.LLQDFFNGR.D
1183.6895	1182.6822	1182.6397	36.0	459 -	469	0	---	R.FELSGIPPAPR.G
1197.7358	1196.7286	1196.6877	34.1	160 -	171	0	---	K.DAGVIAGLNVLR.I
1390.7797	1389.7725	1389.7405	23.0	237 -	247	1	---	R.LVSHFVEEFKR.K
1465.8545	1464.8472	1464.8049	28.9	329 -	342	0	---	K.AQIHDLVLVGGSTR.I
1487.7390	1486.7317	1486.6940	25.3	37 -	49	0	7	R.TTPSYVAFTDTER.L
1542.7924	1541.7851	1541.7296	36.0	300 -	311	1	---	R.ARFEELCSDLFR.G
1675.7697	1674.7625	1674.7234	23.3	221 -	236	0	---	K.ATAGDTHLGGEDFDNR.L
1687.9394	1686.9321	1686.8940	22.6	172 -	187	0	14	R.IINEPTAAAIAYGLDR.T
2774.3263	2773.3190	2773.3195	-0.20	424 -	447	0	---	K.QTQTFTTYSDNQPGVLIQVYEGER.A
2981.4769	2980.4696	2980.4553	4.79	273 -	299	0	---	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A

No match to: 1110.6181, 1210.6660, 1428.7622, 1480.8111, 1502.7816, 1552.8628, 1592.9945, 1653.8659, 1710.9420, 1751.9679, 1776.9783, 1782.9238, 1982.0462, 2691.2918

3. HS71L_MOUSE **Mass:** 70992 **Score:** 66 **Expect:** 0.0045 **Matches:** 10

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
804.4262	803.4190	803.4389	-24.78	503 -	509	0	---	K.ITITNDK.G
832.4582	831.4509	831.4450	7.13	253 -	259	1	---	K.KDISQNK.R
1183.6895	1182.6822	1182.6397	36.0	461 -	471	0	---	R.FDLTGIPPAPR.G
1197.7358	1196.7286	1196.6877	34.1	162 -	173	0	---	K.DAGVIAGLNVLR.I
1390.7797	1389.7725	1389.7405	23.0	239 -	249	1	---	R.LVSHFVEEFKR.K
1465.8545	1464.8472	1464.8413	4.04	331 -	344	1	---	K.AKIHDIVLVGGSTR.I
1480.8111	1479.8038	1479.7834	13.8	348 -	359	1	---	K.VQKLLQDYFNGR.D
1487.7390	1486.7317	1486.6940	25.3	39 -	51	0	7	R.TTPSYVAFTDTER.L
1675.7697	1674.7625	1674.7234	23.3	223 -	238	0	---	K.ATAGDTHLGGEDFDNR.L
2774.3263	2773.3190	2773.3956	-27.63	360 -	386	1	---	R.DLNKSINPDEAVAYGAAVQAAILMGDK.S

No match to: 1109.6245, 1110.6181, 1210.6660, 1428.7622, 1502.7816, 1542.7924, 1552.8628, 1592.9945, 1653.8659, 1687.9394, 1710.9420, 1751.9679, 1776.9783, 1782.9238, 1982.0462, 2691.2918, 2981.4769

4. U5S1_MOUSE **Mass:** 110261 **Score:** 41 **Expect:** 1.4 **Matches:** 9

116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
832.4582	831.4509	831.4636	-15.27	602 -	608	1	---	K.MLDGLRK.V
1428.7622	1427.7549	1427.7693	-10.09	682 -	693	1	---	K.NKITMIAEPLEK.G + Acetyl (N-term)
1480.8111	1479.8038	1479.7319	48.6	951 -	962	0	---	K.FFDDPMLLELAK.Q + Acetyl (N-term)
1502.7816	1501.7743	1501.8253	-33.93	790 -	802	0	---	K.ILDAVVAQEPLHR.G + Acetyl (N-term)

1542.7924	1541.7851	1541.7872	-1.33	775	787	1	---	R.EGPLCDELIRNVK.F
1552.8628	1551.8555	1551.8232	20.8	813	825	1	---	R.RVVYSAFLMATPR.L + Acetyl (N-term)
1710.9420	1709.9347	1709.9928	-33.96	177	193	1	---	R.GVGIKSTPVTVVLPDTK.G
1776.9783	1775.9710	1776.0073	-20.44	262	276	1	---	R.LILELKLPPTDAYYK.L
2981.4769	2980.4696	2980.4616	2.68	422	447	1	---	K.FFGEFTGFVDMCVQHIPSPKVGAKPK.I + Acetyl (N-term); Oxidation (M)

No match to: 804.4262, 1109.6245, 1110.6181, 1183.6895, 1197.7358, 1210.6660, 1390.7797, 1465.8545, 1487.7390, 1592.9945, 1653.8659, 1675.7697, 1687.9394, 1751.9679, 1782.9238, 1982.0462, 2691.2918, 2774.3263

5. ECHA_MOUSE **Mass:** 83302 **Score:** 37 **Expect:** 3.4 **Matches:** 7

Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
832.4582	831.4509	831.4702	-23.13	285	291	1	---	K.TVEEKVK.K
1183.6895	1182.6822	1182.6245	48.9	28	38	0	---	R.SFTTSSALLTR.T
1428.7622	1427.7549	1427.7732	-12.79	54	66	1	---	R.INSPNSKVNTLNK.E
1776.9783	1775.9710	1775.9166	30.6	391	406	1	---	K.DTTVTGLGRGQQQVFK.G + Acetyl (N-term)
1982.0462	1981.0390	1980.9835	28.0	188	205	1	---	R.LPKMVGVPAAFDMMLTGR.N + 3 Oxidation (M)
2774.3263	2773.3190	2773.4255	-38.41	133	159	0	---	K.SPKPVVAAISGSCLGGGLELAIACQYR.I
2981.4769	2980.4696	2980.6168	-49.39	354	383	1	---	K.FGAPQKNVQQLAILGAGLMGAGIAQVSVDK.G

No match to: 804.4262, 1109.6245, 1110.6181, 1197.7358, 1210.6660, 1390.7797, 1465.8545, 1480.8111, 1487.7390, 1502.7816, 1542.7924, 1552.8628, 1592.9945, 1653.8659, 1675.7697, 1687.9394, 1710.9420, 1751.9679, 1782.9238, 2691.2918

6. TARA_MOUSE **Mass:** 225171 **Score:** 36 **Expect:** 4 **Matches:** 12

TRIO and F-actin-binding protein OS=Mus musculus GN=Triobp PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
804.4262	803.4190	803.3960	28.6	1949	1954	0	---	K.EVQCLR.D
832.4582	831.4509	831.4199	37.4	207	214	1	---	R.GDTAGQRK.E
1109.6245	1108.6173	1108.5625	49.4	737	746	1	---	R.DAPRATSPPR.H + Acetyl (N-term)
1210.6660	1209.6587	1209.6829	-20.04	1394	1405	1	---	K.RPAEGKAGSPLK.G
1487.7390	1486.7317	1486.7813	-33.38	1997	2009	1	---	R.LAMAALQEKEAVR.N + Acetyl (N-term); Oxidation (M)
1502.7816	1501.7743	1501.7929	-12.39	1458	1469	1	---	K.KHWFVLTDSSLK.Y + Acetyl (N-term)
1542.7924	1541.7851	1541.7395	29.6	1511	1524	0	---	K.DAVYTLSAMTSGIR.R + Acetyl (N-term); Oxidation (M)
1675.7697	1674.7625	1674.7380	14.6	496	509	1	---	R.DNPRTSCTSQNTPR.T + Acetyl (N-term)
1687.9394	1686.9321	1686.8550	45.7	1070	1084	1	0	K.AQIERHLESGHTGPR.Q
1710.9420	1709.9347	1709.9060	16.8	1009	1024	1	---	R.QSSPAPSRQVTKPSAK.Q + Acetyl (N-term)
1782.9238	1781.9165	1781.9424	-14.55	1229	1244	1	---	R.DLLGLLRAPEDGAWTR.L
2981.4769	2980.4696	2980.4355	11.4	1109	1135	1	---	K.SWGSQKEGPSLGGWPELEGPSLEGIWR.G + Acetyl (N-term)

No match to: 1110.6181, 1183.6895, 1197.7358, 1390.7797, 1428.7622, 1465.8545, 1480.8111, 1552.8628, 1592.9945, 1653.8659, 1751.9679, 1776.9783, 1982.0462, 2691.2918, 2774.3263

7. HSP7C_MOUSE **Mass:** 71055 **Score:** 34 **Expect:** 6 **Matches:** 6

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

804.4262	803.4190	803.4389	-24.78	501 -	507	0	---	K.ITITNDK.G
1480.8111	1479.8038	1479.7470	38.4	300 -	311	1	---	R.ARFEELNADLFR.G
1487.7390	1486.7317	1486.6940	25.3	37 -	49	0	7	R.TTPSYVAFTDTER.L
1653.8659	1652.8586	1652.8246	20.6	89 -	102	0	---	K.HWPFMVVNDAGRPK.V
1982.0462	1981.0390	1980.9905	24.4	138 -	155	0	---	K.TVTNAVVTVPAYFNDSQR.Q
2774.3263	2773.3190	2773.3195	-0.20	424 -	447	0	---	K.QTQTFTTYSDNQPGVLIQVYEGER.A

No match to: 832.4582, 1109.6245, 1110.6181, 1183.6895, 1197.7358, 1210.6660, 1390.7797, 1428.7622, 1465.8545, 1502.7816, 1542.7924, 1552.8628, 1592.9945, 1675.7697, 1687.9394, 1710.9420, 1751.9679, 1776.9783, 1782.9238, 2691.2918, 2981.4769

8. PARVG_MOUSE **Mass:** 37610 **Score:** 34 **Expect:** 7.3 **Matches:** 5

Gamma-parvin OS=Mus musculus GN=Parvg PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
832.4582	831.4509	831.4450	7.13	301 -	307	1	---	K.DAKSTLR.I + Acetyl (N-term)
1653.8659	1652.8586	1652.7767	49.5	316 -	331	1	---	K.HSLRAEGGGAHHATPN.- + Acetyl (N-term)
1710.9420	1709.9347	1709.9101	14.4	209 -	223	0	---	K.VHAVQEAIVSFVNQK.L + Acetyl (N-term)
1751.9679	1750.9607	1750.9215	22.4	1 -	14	0	---	-.MELEFLYDLLQLPK.E
2774.3263	2773.3190	2773.4248	-38.15	260 -	283	0	---	K.EFYLTPSSPTEMLHNVTLALDLLK.D + Acetyl (N-term)

No match to: 804.4262, 1109.6245, 1110.6181, 1183.6895, 1197.7358, 1210.6660, 1390.7797, 1428.7622, 1465.8545, 1480.8111, 1487.7390, 1502.7816, 1542.7924, 1552.8628, 1592.9945, 1675.7697, 1687.9394, 1776.9783, 1782.9238, 1982.0462, 2691.2918, 2981.4769

9. TTC23_MOUSE **Mass:** 55372 **Score:** 32 **Expect:** 9.2 **Matches:** 6

Tetratricopeptide repeat protein 23 OS=Mus musculus GN=Ttc23 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1109.6245	1108.6173	1108.5652	47.0	212 -	220	0	---	K.ALEYTEITK.D + Acetyl (N-term)
1428.7622	1427.7549	1427.7620	-4.95	439 -	451	0	---	K.TLATQHTIDTLSK.I
1480.8111	1479.8038	1479.7834	13.8	190 -	201	1	---	K.LSFAQLYQGQKR.S + Acetyl (N-term)
1653.8659	1652.8586	1652.7828	45.9	116 -	129	0	---	K.EILANSIESPCHNK.T + Acetyl (N-term)
1776.9783	1775.9710	1775.8914	44.8	403 -	420	1	---	R.ALGRADLAQGNNSGAYAK.L
2774.3263	2773.3190	2773.2535	23.6	1 -	25	0	---	-.MQESQDTHMSSHLDEVVAAVSVTSK.N + Acetyl (N-term); Oxidation (M)

No match to: 804.4262, 832.4582, 1110.6181, 1183.6895, 1197.7358, 1210.6660, 1390.7797, 1465.8545, 1487.7390, 1502.7816, 1542.7924, 1552.8628, 1592.9945, 1675.7697, 1687.9394, 1710.9420, 1751.9679, 1782.9238, 1982.0462, 2691.2918, 2981.4769

10. NRAP_MOUSE **Mass:** 196735 **Score:** 32 **Expect:** 10 **Matches:** 11

Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
804.4262	803.4190	803.4025	20.5	591 -	598	0	---	R.ALGATDSK.L + Acetyl (N-term)
1109.6245	1108.6173	1108.5876	26.7	1652 -	1660	1	---	K.YKSDLNLTR.G
1502.7816	1501.7743	1501.7123	41.3	653 -	664	0	---	K.LHDYTVLPEDMK.T + Acetyl (N-term)
1542.7924	1541.7851	1541.8090	-15.48	1453 -	1466	0	---	K.FTTVVDSPDLIHAK.E
1653.8659	1652.8586	1652.8344	14.6	166 -	180	1	---	K.GSFPAMITPAYQRAK.A + Oxidation (M)
1687.9394	1686.9321	1686.8829	29.2	199 -	213	0	---	R.VSTFTPVADTPELLR.A + Acetyl (N-term)
1710.9420	1709.9347	1709.9135	12.4	1175 -	1190	1	---	R.GVPCVVPGTLEIEGRK.K
1751.9679	1750.9607	1750.9941	-19.10	591 -	607	1	---	R.ALGATDSKLLHSLQVAK.M

1982.0462	1981.0390	1980.9662	36.7	623 - 638	1	---	K.THFNLPMDMVNLRHAK.K + Acetyl (N-term); Oxidation (M)
2691.2918	2690.2845	2690.3300	-16.89	1210 - 1232	1	---	K.YTAVTDTPNLLHAKYSNQITNER.L + Acetyl (N-term)
2981.4769	2980.4696	2980.5076	-12.76	1000 - 1025	1	---	K.HHYTQTADLPEVLLAKLNAMNISETR.Y + Oxidation (M)

No match to: 832.4582, 1110.6181, 1183.6895, 1197.7358, 1210.6660, 1390.7797, 1428.7622, 1465.8545, 1480.8111, 1487.7390, 1552.8628, 1592.9945, 1675.7697, 1776.9783, 1782.9238, 2774.3263

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (804.4262,1+) : <no title>

Query2 (832.4582,1+) : <no title>

Query3 (1109.6245,1+) : <no title>

Query4 (1110.6181,1+) : <no title>

Query5 (1183.6895,1+) : <no title>

Query6 (1197.7358,1+) : <no title>

Query7 (1210.6660,1+) : <no title>

Query8 (1390.7797,1+) : <no title>

Query9 (1428.7622,1+) : <no title>

Query10 (1465.8545,1+) : <no title>

Query11 (1480.8111,1+) : <no title>

Query12 (1487.7390,1+) : <no title>

Query13 (1502.7816,1+) : <no title>

Query14 (1542.7924,1+) : <no title>

Query15 (1552.8628,1+) : <no title>

Query16 (1592.9945,1+) : <no title>

Query17 (1653.8659,1+) : <no title>

Query18 (1675.7697,1+) : <no title>

Query19 (1687.9394,1+) : <no title>

Query20 (1710.9420,1+) : <no title>

Query21 (1751.9679,1+) : <no title>

Query22 (1776.9783,1+) : <no title>

Query23 (1782.9238,1+) : <no title>

Query24 (1982.0462,1+) : <no title>

Query25 (2691.2918,1+) : <no title>

Query26 (2774.3263,1+) : <no title>

Query27 (2981.4769,1+) : <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 : **20 May 2013 at 01:32:58 GMT**

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

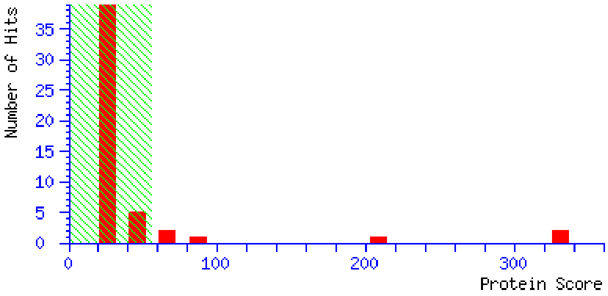
Top Score : **331 for HS71A_MOUSE, Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2**

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.	**HS71A_MOUSE**	70321	331	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2
2.	**HS71B_MOUSE**	70418	330	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3
3.	**HS71L_MOUSE**	70992	200	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4
4.	**HSP7C_MOUSE**	71055	90	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1
5.	**HSP72_MOUSE**	69983	71	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=1
6.	**ALBU_MOUSE**	70700	71	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3
7.	**NRAP_MOUSE**	196735	50	Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap PE=1 SV=2
8.	**NIBAN_MOUSE**	103440	45	Protein Niban OS=Mus musculus GN=Niban PE=1 SV=2
9.	**MOB2_MOUSE**	27176	43	Mps one binder kinase activator-like 2 OS=Mus musculus GN=Mob2 PE=2 SV=1
10.	**UBA6_MOUSE**	119430	37	Ubiquitin-like modifier-activating enzyme 6 OS=Mus musculus GN=Uba6 PE=2 SV=1

Results List

1. HS71A_MOUSE **Mass:** 70321 **Score:** 331 **Expect:** 1.3e-029 **Matches:** 20

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**
1017.5586	1016.5513	1016.5614	-10.00	501	509	1	---	K.ITITNDKGR.L
1109.5740	1108.5667	1108.5665	0.17	349	357	0	---	K.LLQDFFNGR.D
1137.5575	1136.5502	1136.5462	3.58	525	533	1	---	R.YKAEDEVQR.D
1183.6450	1182.6378	1182.6397	-1.64	459	469	0	---	R.FELSGIPPAPR.G
1197.6930	1196.6858	1196.6877	-1.64	160	171	0	54	K.DAGVIAGLNVLR.I
1228.6365	1227.6292	1227.6207	6.88	26	36	0	---	K.VEIIANDQGNR.T
1315.6157	1314.6084	1314.5914	12.9	302	311	0	---	R.FEELCSDLFR.G
1390.7523	1389.7450	1389.7405	3.28	237	247	1	41	R.LVSHFVEEFKR.K
1465.8145	1464.8072	1464.8049	1.60	329	342	0	---	K.AQIHDLVLVGGSTR.I
1487.7107	1486.7035	1486.6940	6.36	37	49	0	58	R.TTPSYVAFTDTER.L
1542.7437	1541.7364	1541.7296	4.41	300	311	1	---	R.ARFEELCSDLFR.G
1666.8360	1665.8287	1665.8264	1.43	89	102	0	---	K.HWPFQVVNDGDKPK.V
1675.7421	1674.7348	1674.7234	6.81	221	236	0	---	K.ATAGDTHLGGEDFDNR.L
1687.9037	1686.8964	1686.8940	1.40	172	187	0	36	R.IINEPTAAAIAYGLDR.T
1814.9604	1813.9531	1813.9435	5.32	57	72	1	---	K.NQVALNPQNTVFDAKR.L
2232.1237	2231.1164	2231.0416	33.6	540	559	1	---	K.NALESYAFNMKSAVEDEGLK.G + Oxidation (M)
2774.3164	2773.3092	2773.3195	-3.74	424	447	0	---	K.QTQTFTTYSDNQPGVLIQVYEGER.A
2975.4818	2974.4745	2974.4825	-2.66	129	155	0	---	K.EIAEAYLGHPVTNAVITVPAYFNDSQR.Q
2981.4505	2980.4432	2980.4553	-4.07	273	299	0	---	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A
3234.6126	3233.6053	3233.6179	-3.88	127	155	1	---	K.MKEIAEAYLGHPVTNAVITVPAYFNDSQR.Q

No match to: 1033.4768, 1110.5576, 1208.6312, 1250.6984, 1367.7083, 1380.6566, 1439.7722, 1455.8158, 1479.7960, 1481.7844, 1512.8508, 1516.7153, 1552.8426, 1609.7908, 1653.8350, 1662.8532, 1681.8354, 1882.9362, 1901.9165, 1981.9916, 2033.0248, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2804.3653

2. HS71B_MOUSE **Mass:** 70418 **Score:** 330 **Expect:** 1.6e-029 **Matches:** 20

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**
1017.5586	1016.5513	1016.5614	-10.00	501	509	1	---	K.ITITNDKGR.L
1109.5740	1108.5667	1108.5665	0.17	349	357	0	---	K.LLQDFFNGR.D
1137.5575	1136.5502	1136.5462	3.58	525	533	1	---	R.YKAEDEVQR.D
1183.6450	1182.6378	1182.6397	-1.64	459	469	0	---	R.FELSGIPPAPR.G
1197.6930	1196.6858	1196.6877	-1.64	160	171	0	54	K.DAGVIAGLNVLR.I
1228.6365	1227.6292	1227.6207	6.88	26	36	0	---	K.VEIIANDQGNR.T
1315.6157	1314.6084	1314.5914	12.9	302	311	0	---	R.FEELCSDLFR.G
1390.7523	1389.7450	1389.7405	3.28	237	247	1	41	R.LVSHFVEEFKR.K
1465.8145	1464.8072	1464.8049	1.60	329	342	0	---	K.AQIHDLVLVGGSTR.I
1487.7107	1486.7035	1486.6940	6.36	37	49	0	58	R.TTPSYVAFTDTER.L
1542.7437	1541.7364	1541.7296	4.41	300	311	1	---	R.ARFEELCSDLFR.G
1666.8360	1665.8287	1665.8264	1.43	89	102	0	---	K.HWPFQVVNDGDKPK.V
1675.7421	1674.7348	1674.7234	6.81	221	236	0	---	K.ATAGDTHLGGEDFDNR.L
1687.9037	1686.8964	1686.8940	1.40	172	187	0	36	R.IINEPTAAAIAYGLDR.T

1814.9604	1813.9531	1813.9435	5.32	57	-	72	1	---	K.NQVALNPQNTVFDAKR.L
2232.1237	2231.1164	2231.0416	33.6	540	-	559	1	---	K.NALESYAFNMKSAVEDEGLK.G + Oxidation (M)
2774.3164	2773.3092	2773.3195	-3.74	424	-	447	0	---	K.QTQTFTTYSDNQPGVLIQVYEGER.A
2975.4818	2974.4745	2974.4825	-2.66	129	-	155	0	---	K.EIAEAYLGHPVTNAVITVPAYFNDSQR.Q
2981.4505	2980.4432	2980.4553	-4.07	273	-	299	0	---	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A
3234.6126	3233.6053	3233.6179	-3.88	127	-	155	1	---	K.MKEIAEAYLGHPVTNAVITVPAYFNDSQR.Q

No match to: 1033.4768, 1110.5576, 1208.6312, 1250.6984, 1367.7083, 1380.6566, 1439.7722, 1455.8158, 1479.7960, 1481.7844, 1512.8508, 1516.7153, 1552.8426, 1609.7908, 1653.8350, 1662.8532, 1681.8354, 1882.9362, 1901.9165, 1981.9916, 2033.0248, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2804.3653

3. HS71L_MOUSE **Mass:** 70992 **Score:** 200 **Expect:** 1.6e-016 **Matches:** 11

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
1017.5586	1016.5513	1016.5614	-10.00	503	-	511	1	---	K.ITITNDKGR.L
1137.5575	1136.5502	1136.5098	35.6	527	-	535	1	---	R.YKAEDEGQR.E + Acetyl (N-term)
1183.6450	1182.6378	1182.6397	-1.65	461	-	471	0	---	R.FDLTGIPPAPR.G
1197.6930	1196.6858	1196.6877	-1.64	162	-	173	0	54	K.DAGVIAGLNVLR.I
1228.6365	1227.6292	1227.6207	6.88	28	-	38	0	---	K.VEIIANDQGNR.T
1390.7523	1389.7450	1389.7405	3.28	239	-	249	1	41	R.LVSHFVEEFKR.K
1465.8145	1464.8072	1464.8413	-23.23	331	-	344	1	---	K.AKIHDIVLVGGSTR.I
1487.7107	1486.7035	1486.6940	6.36	39	-	51	0	58	R.TTPSYVAFTDTER.L
1675.7421	1674.7348	1674.7234	6.81	223	-	238	0	---	K.ATAGDTHLGGEDFDNR.L
2774.3164	2773.3092	2773.3956	-31.17	360	-	386	1	---	R.DLNKSINPDEAVAYGAAVQAAILMGDK.S
2975.4818	2974.4745	2974.4958	-7.13	472	-	499	1	---	R.GVPQIEVTFDIDANGILNVTAMDKSTGK.A + Acetyl (N-term)

No match to: 1033.4768, 1109.5740, 1110.5576, 1208.6312, 1250.6984, 1315.6157, 1367.7083, 1380.6566, 1439.7722, 1455.8158, 1479.7960, 1481.7844, 1512.8508, 1516.7153, 1542.7437, 1552.8426, 1609.7908, 1653.8350, 1662.8532, 1666.8360, 1681.8354, 1687.9037, 1814.9604, 1882.9362, 1901.9165, 1981.9916, 2033.0248, 2232.1237, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2804.3653, 2981.4505, 3234.6126

4. HSP7C_MOUSE **Mass:** 71055 **Score:** 90 **Expect:** 1.8e-005 **Matches:** 8

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
1017.5586	1016.5513	1016.5614	-10.00	501	-	509	1	---	K.ITITNDKGR.L
1197.6930	1196.6858	1196.6554	25.4	459	-	469	0	5	K.FELTGIPPAPR.G
1228.6365	1227.6292	1227.6207	6.88	26	-	36	0	---	K.VEIIANDQGNR.T
1481.7844	1480.7771	1480.7998	-15.33	329	-	342	0	---	K.SQIHDIVLVGGSTR.I
1487.7107	1486.7035	1486.6940	6.36	37	-	49	0	58	R.TTPSYVAFTDTER.L
1653.8350	1652.8277	1652.8246	1.92	89	-	102	0	---	K.HWPFMVVNDAGRPK.V
1981.9916	1980.9844	1980.9905	-3.11	138	-	155	0	---	K.TVTNAVVTVPAYFNDSQR.Q
2774.3164	2773.3092	2773.3195	-3.74	424	-	447	0	---	K.QTQTFTTYSDNQPGVLIQVYEGER.A

No match to: 1033.4768, 1109.5740, 1110.5576, 1137.5575, 1183.6450, 1208.6312, 1250.6984, 1315.6157, 1367.7083, 1380.6566, 1390.7523, 1439.7722, 1455.8158, 1465.8145, 1479.7960, 1512.8508, 1516.7153, 1542.7437, 1552.8426, 1609.7908, 1662.8532, 1666.8360, 1675.7421, 1681.8354, 1687.9037, 1814.9604, 1882.9362, 1901.9165, 2033.0248, 2232.1237, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2804.3653, 2975.4818, 2981.4505, 3234.6126

5. HSP72_MOUSE **Mass:** 69983 **Score:** 71 **Expect:** 0.0012 **Matches:** 6

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
1017.5586	1016.5513	1016.5614	-10.00	504 -	512	1	---	K.ITITNDKGR.L
1183.6450	1182.6378	1182.6397	-1.65	462 -	472	0	---	K.FDLTGIPPAPR.G
1228.6365	1227.6292	1227.6207	6.88	27 -	37	0	---	K.VEIIANDQGNR.T
1367.7083	1366.7010	1366.6802	15.2	128 -	139	1	---	K.MKEIAEAYLGGK.V + Acetyl (N-term); Oxidation (M)
1487.7107	1486.7035	1486.6940	6.36	38 -	50	0	58	R.TTPSYVAFTDTER.L
1662.8532	1661.8459	1661.7831	37.8	58 -	71	0	---	K.NQVAMNPTNTIFDR.K + Acetyl (N-term)

No match to: 1033.4768, 1109.5740, 1110.5576, 1137.5575, 1197.6930, 1208.6312, 1250.6984, 1315.6157, 1380.6566, 1390.7523, 1439.7722, 1455.8158, 1465.8145, 1479.7960, 1481.7844, 1512.8508, 1516.7153, 1542.7437, 1552.8426, 1609.7908, 1653.8350, 1666.8360, 1675.7421, 1681.8354, 1687.9037, 1814.9604, 1882.9362, 1901.9165, 1981.9916, 2033.0248, 2232.1237, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2774.3164, 2804.3653, 2975.4818, 2981.4505, 3234.6126

6. ALBU_MOUSE **Mass:** 70700 **Score:** 71 **Expect:** 0.0013 **Matches:** 14

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1017.5586	1016.5513	1016.5291	21.8	89 -	97	0	---	K.SLHTLFGDK.L
1250.6984	1249.6912	1249.7142	-18.46	559 -	569	1	---	K.HKPKATAEQLK.T
1439.7722	1438.7649	1438.7780	-9.11	439 -	452	0	---	K.APQVSTPTLVEAAR.N
1455.8158	1454.8085	1454.7994	6.28	361 -	372	1	---	R.RHPDYSVSLLLR.L
1479.7960	1478.7887	1478.7881	0.39	422 -	434	0	---	K.LGEYGFQNAILVR.Y
1481.7844	1480.7771	1480.7885	-7.73	439 -	452	0	---	K.APQVSTPTLVEAAR.N + Acetyl (N-term)
1609.7908	1608.7835	1608.7824	0.68	348 -	360	0	---	K.DVFLGTFLYEYSR.R
1662.8532	1661.8459	1661.8447	0.76	470 -	483	0	---	R.LPCVEDYLSAILNR.V
1681.8354	1680.8281	1680.8359	-4.63	243 -	257	0	---	R.LSQTFPNADFAEITK.L
1882.9362	1881.9289	1881.9295	-0.29	509 -	524	0	---	R.RPCFSALTVDETYVPK.E
1901.9165	1900.9092	1900.8890	10.6	153 -	168	0	---	K.ENPTTFMGHYLHEVAR.R
1981.9916	1980.9844	1980.9211	31.9	585 -	602	1	---	K.AADKDTCFSTEGPNLVTR.C
2650.3123	2649.3050	2649.1761	48.7	563 -	584	1	---	K.ATAEQLKTVMDDFAQFLDTCCK.A + Acetyl (N-term); Oxidation (M)
2804.3653	2803.3580	2803.3013	20.3	287 -	309	1	---	K.YMCENQATISSKLQTCCDKPLLK.K + Oxidation (M)

No match to: 1033.4768, 1109.5740, 1110.5576, 1137.5575, 1183.6450, 1197.6930, 1208.6312, 1228.6365, 1315.6157, 1367.7083, 1380.6566, 1390.7523, 1465.8145, 1487.7107, 1512.8508, 1516.7153, 1542.7437, 1552.8426, 1653.8350, 1666.8360, 1675.7421, 1687.9037, 1814.9604, 2033.0248, 2232.1237, 2691.2971, 2748.3236, 2757.3156, 2774.3164, 2975.4818, 2981.4505, 3234.6126

7. NRAP_MOUSE **Mass:** 196735 **Score:** 50 **Expect:** 0.17 **Matches:** 19

Nebulin-related-anchoring protein OS=Mus musculus GN=Nrap PE=1 SV=2

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

1017.5586	1016.5513	1016.5251	25.8	589	-	598	1	---	K.GRALGATDSK.L + Acetyl (N-term)
1109.5740	1108.5667	1108.5876	-18.87	1652	-	1660	1	---	K.YKSDLNLTR.G
1228.6365	1227.6292	1227.6360	-5.54	1399	-	1408	1	---	K.KAHALQSEFR.Y + Acetyl (N-term)
1315.6157	1314.6084	1314.6172	-6.72	1500	-	1510	1	---	R.ARMNAMHLSDK.V + Acetyl (N-term)
1439.7722	1438.7649	1438.7238	28.5	1016	-	1027	1	---	K.LNAMNISETRYK.E
1481.7844	1480.7771	1480.7344	28.9	1016	-	1027	1	---	K.LNAMNISETRYK.E + Acetyl (N-term)
1542.7437	1541.7364	1541.8090	-47.05	1453	-	1466	0	---	K.FTTVVDSPDLIHAK.E
1653.8350	1652.8277	1652.8344	-4.05	166	-	180	1	---	K.GSFPAMITPAYQRAK.A + Oxidation (M)
1666.8360	1665.8287	1665.8470	-10.94	555	-	569	1	---	K.GFEMKLDAMSLLAAK.A + Acetyl (N-term)
1681.8354	1680.8281	1680.7777	30.0	724	-	738	1	---	K.FTSVADSSQMEHAKK.S + Oxidation (M)
1687.9037	1686.8964	1686.8829	8.03	199	-	213	0	---	R.VSTFTPVADTPELLR.A + Acetyl (N-term)
1882.9362	1881.9289	1881.8527	40.5	144	-	159	1	---	R.MVEARQSLGEGYTEDR.E + Acetyl (N-term)
1901.9165	1900.9092	1900.9101	-0.48	1160	-	1174	1	---	K.LQSENLYRSDLNFMR.G + Oxidation (M)
1981.9916	1980.9844	1980.9662	9.16	623	-	638	1	---	K.THFNLPMDMVNLRHAK.K + Acetyl (N-term); Oxidation (M)
2650.3123	2649.3050	2649.2540	19.2	860	-	881	1	---	K.GFEDTRSQCHISLDMVHLVHAR.Q + Acetyl (N-term)
2691.2971	2690.2898	2690.3300	-14.93	1210	-	1232	1	---	K.YTAVTDTPNLLHAKYSNQITNER.L + Acetyl (N-term)
2748.3236	2747.3164	2747.2288	31.9	1346	-	1368	1	---	K.EAASSQAQCHLPMDMMYLVHARK.A + Acetyl (N-term); 2 Oxidation (M)
2757.3156	2756.3083	2756.3617	-19.35	1078	-	1102	1	---	R.SLEDDLSLAHSVHATSLQSDVNYKK.G
2981.4505	2980.4432	2980.5076	-21.62	1000	-	1025	1	---	K.HHYTQTADLPEVLLAKLNAMNISETR.Y + Oxidation (M)

No match to: 1033.4768, 1110.5576, 1137.5575, 1183.6450, 1197.6930, 1208.6312, 1250.6984, 1367.7083, 1380.6566, 1390.7523, 1455.8158, 1465.8145, 1479.7960, 1487.7107, 1512.8508, 1516.7153, 1552.8426, 1609.7908, 1662.8532, 1675.7421, 1814.9604, 2033.0248, 2232.1237, 2774.3164, 2804.3653, 2975.4818, 3234.6126

8. NIBAN_MOUSE **Mass:** 103440 **Score:** 45 **Expect:** 0.51 **Matches:** 7

Protein Niban OS=Mus musculus GN=Niban PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1033.4768	1032.4696	1032.4665	2.98	27 -	34	0	---	K.NFSPYYSR.Q
1208.6312	1207.6239	1207.6019	18.2	186 -	195	0	---	K.FSALLNDCIR.H
1380.6566	1379.6493	1379.6405	6.41	35 -	45	0	---	R.QYSVAFCNHVR.S
1512.8508	1511.8436	1511.8361	4.91	426 -	437	1	---	R.FRFPHVDLVVQR.T
1552.8426	1551.8353	1551.8238	7.40	160 -	171	0	33	K.AFPVYLWQPYLR.H
1662.8532	1661.8459	1661.8049	24.7	21 -	34	1	---	K.TEASIKNFSPYYSR.Q
2033.0248	2032.0175	2032.0054	5.96	204 -	220	0	---	K.QTTFEAQAFLEAVQFFR.Q

No match to: 1017.5586, 1109.5740, 1110.5576, 1137.5575, 1183.6450, 1197.6930, 1228.6365, 1250.6984, 1315.6157, 1367.7083, 1390.7523, 1439.7722, 1455.8158, 1465.8145, 1479.7960, 1481.7844, 1487.7107, 1516.7153, 1542.7437, 1609.7908, 1653.8350, 1666.8360, 1675.7421, 1681.8354, 1687.9037, 1814.9604, 1882.9362, 1901.9165, 1981.9916, 2232.1237, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2774.3164, 2804.3653, 2975.4818, 2981.4505, 3234.6126

9. MOB2_MOUSE **Mass:** 27176 **Score:** 43 **Expect:** 0.76 **Matches:** 7

Mps one binder kinase activator-like 2 OS=Mus musculus GN=Mob2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1017.5586	1016.5513	1016.5178	32.9	188 -	195	0	---	R.EFNLLDPK.E + Acetyl (N-term)
1137.5575	1136.5502	1136.5358	12.7	1 -	9	1	---	-.MDWLMGKSK.A + Acetyl (N-term)
1367.7083	1366.7010	1366.7568	-40.82	10 -	22	1	---	K.AKPNGKKPAAEEK.K
1439.7722	1438.7649	1438.7344	21.2	135 -	146	1	---	R.EFPSSFESLVKK.I + Acetyl (N-term)
1681.8354	1680.8281	1680.8359	-4.63	121 -	134	1	---	K.LVTDEDVFPTKYGR.E + Acetyl (N-term)
1687.9037	1686.8964	1686.8253	42.1	132 -	145	1	---	K.YGREFPSSFESLVK.K + Acetyl (N-term)
1901.9165	1900.9092	1900.8699	20.7	105 -	120	0	---	K.CTAPQYVDFVMSSVQK.L + Acetyl (N-term)

No match to: 1033.4768, 1109.5740, 1110.5576, 1183.6450, 1197.6930, 1208.6312, 1228.6365, 1250.6984, 1315.6157, 1380.6566, 1390.7523, 1455.8158, 1465.8145, 1479.7960, 1481.7844, 1487.7107, 1512.8508, 1516.7153, 1542.7437, 1552.8426, 1609.7908, 1653.8350, 1662.8532, 1666.8360, 1675.7421, 1814.9604, 1882.9362, 1981.9916, 2033.0248, 2232.1237, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2774.3164, 2804.3653, 2975.4818, 2981.4505, 3234.6126

10. UBA6_MOUSE **Mass:** 119430 **Score:** 37 **Expect:** 3 **Matches:** 8

Ubiquitin-like modifier-activating enzyme 6 OS=Mus musculus GN=Uba6 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1208.6312	1207.6239	1207.5986	21.0	948 -	957	0	---	R.NGISFTIWDR.W
1439.7722	1438.7649	1438.7014	44.1	840 -	851	0	---	K.SDLQMTVLSFEK.D + Acetyl (N-term)
1487.7107	1486.7035	1486.7160	-8.42	49 -	61	1	18	R.YVLGDTAMQKMAK.S + 2 Oxidation (M)
1662.8532	1661.8459	1661.8546	-5.20	777 -	791	0	---	K.DLSVNSLMDILSEVK.I
1681.8354	1680.8281	1680.8148	7.95	659 -	672	0	---	K.FWQAYPSAEDVLQK.I
1981.9916	1980.9844	1981.0421	-29.16	730 -	746	1	---	K.DGSLFWQSPKRPPSPIK.F + Acetyl (N-term)
2232.1237	2231.1164	2231.1732	-25.45	673 -	691	1	---	K.IQNGQSLEGCFQVIKLLSR.R + Acetyl (N-term)
3234.6126	3233.6053	3233.6240	-5.76	764 -	791	1	---	K.LYATVYCIPFSEKDLSVNSLMDILSEVK.I

No match to: 1017.5586, 1033.4768, 1109.5740, 1110.5576, 1137.5575, 1183.6450, 1197.6930, 1228.6365, 1250.6984, 1315.6157, 1367.7083, 1380.6566, 1390.7523, 1455.8158, 1465.8145, 1479.7960, 1481.7844, 1512.8508, 1516.7153, 1542.7437, 1552.8426, 1609.7908, 1653.8350, 1666.8360, 1675.7421, 1687.9037, 1814.9604, 1882.9362, 1901.9165, 2033.0248, 2650.3123, 2691.2971, 2748.3236, 2757.3156, 2774.3164, 2804.3653, 2975.4818, 2981.4505

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (1017.5586,1+) : <no title>
Query2 (1033.4768,1+) : <no title>
Query3 (1109.5740,1+) : <no title>
Query4 (1110.5576,1+) : <no title>
Query5 (1137.5575,1+) : <no title>
Query6 (1183.6450,1+) : <no title>
Query7 (1197.6930,1+) : <no title>
Query8 (1208.6312,1+) : <no title>
Query9 (1228.6365,1+) : <no title>
Query10 (1250.6984,1+) : <no title>
Query11 (1315.6157,1+) : <no title>
Query12 (1367.7083,1+) : <no title>
Query13 (1380.6566,1+) : <no title>
Query14 (1390.7523,1+) : <no title>
Query15 (1439.7722,1+) : <no title>
Query16 (1455.8158,1+) : <no title>
Query17 (1465.8145,1+) : <no title>
Query18 (1479.7960,1+) : <no title>
Query19 (1481.7844,1+) : <no title>
Query20 (1487.7107,1+) : <no title>
Query21 (1512.8508,1+) : <no title>
Query22 (1516.7153,1+) : <no title>
Query23 (1542.7437,1+) : <no title>
Query24 (1552.8426,1+) : <no title>
Query25 (1609.7908,1+) : <no title>
Query26 (1653.8350,1+) : <no title>
Query27 (1662.8532,1+) : <no title>
Query28 (1666.8360,1+) : <no title>
Query29 (1675.7421,1+) : <no title>
Query30 (1681.8354,1+) : <no title>
Query31 (1687.9037,1+) : <no title>
Query32 (1814.9604,1+) : <no title>
Query33 (1882.9362,1+) : <no title>
Query34 (1901.9165,1+) : <no title>
Query35 (1981.9916,1+) : <no title>
Query36 (2033.0248,1+) : <no title>
Query37 (2232.1237,1+) : <no title>
Query38 (2650.3123,1+) : <no title>
Query39 (2691.2971,1+) : <no title>
Query40 (2748.3236,1+) : <no title>
Query41 (2757.3156,1+) : <no title>
Query42 (2774.3164,1+) : <no title>
Query43 (2804.3653,1+) : <no title>
Query44 (2975.4818,1+) : <no title>

Query45 (2981.4505,1+) : <no title>

Query46 (3234.6126,1+) : <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 : **20 May 2013 at 01:33:23 GMT**

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

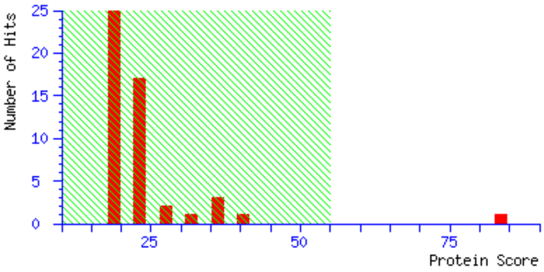
Top Score : **84 for ODO2_MOUSE, Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1**

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.	**ODO2_MOUSE**	49306	84	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1
2.	**RASL2_MOUSE**	91087	40	Ras GTPase-activating protein 4 OS=Mus musculus GN=Rasa4 PE=2 SV=1
3.	**TDGF1_MOUSE**	19539	36	Teratocarcinoma-derived growth factor OS=Mus musculus GN=Tdgf1 PE=1 SV=1
4.	**EBP2_MOUSE**	34795	35	Probable rRNA-processing protein EBP2 OS=Mus musculus GN=Ebna1bp2 PE=2 SV=1
5.	**NLE1_MOUSE**	53628	34	Notchless protein homolog 1 OS=Mus musculus GN=Nle1 PE=2 SV=3
6.	**ICAL_MOUSE**	85099	31	Calpastatin OS=Mus musculus GN=Cast PE=1 SV=2
7.	**GLTL1_MOUSE**	63721	27	Putative polypeptide N-acetylgalactosaminyltransferase-like protein 1 OS=Mus musculus GN=Galntl1 PE=2 SV=1
8.	**SYT1_MOUSE**	47730	25	Synaptotagmin-1 OS=Mus musculus GN=Syt1 PE=1 SV=1
9.	**GLO2_MOUSE**	34519	25	Hydroxyacylglutathione hydrolase, mitochondrial OS=Mus musculus GN=Hagh PE=2 SV=2
10.	**GSTK1_MOUSE**	25801	24	Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gstk1 PE=1 SV=3

Results List

1. ODO2_MOUSE **Mass:** 49306 **Score:** 84 **Expect:** 7.1e-005 **Matches:** 6

Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
1189.6680	1188.6607	1188.6503	8.78	135	-	145	0	---	K.VEGGTPLFTLR.K
1419.7576	1418.7503	1418.7405	6.87	314	-	326	0	34	R.DYIDISVAVATPR.G
1454.6781	1453.6708	1453.6507	13.8	335	-	346	0	---	R.NVETMNYADIER.T
1979.9956	1978.9883	1978.9757	6.35	411	-	426	0	---	K.VEVRPMMYVALTYDHR.L
2248.0877	2247.0805	2247.1019	-9.56	69	-	89	0	---	K.NDVITVQTPAFAESVTEGDVR.W
2691.2968	2690.2896	2690.3188	-10.86	69	-	92	1	---	K.NDVITVQTPAFAESVTEGDVRWEK.A

No match to: 871.3026, 946.5851, 1167.6630, 1268.6204, 1338.8396, 1371.8134, 1587.8222, 1666.0132, 2748.3054

2. RASL2_MOUSE **Mass:** 91087 **Score:** 40 **Expect:** 1.5 **Matches:** 6

Ras GTPase-activating protein 4 OS=Mus musculus GN=Rasa4 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
946.5851	945.5778	945.5647	13.8	312	-	320	0	---	K.LFLGQGLAK.D
1419.7576	1418.7503	1418.7592	-6.26	533	-	544	1	---	R.QGVAQLKDFIMK.L + Acetyl (N-term)
1454.6781	1453.6708	1453.6759	-3.53	21	-	33	0	---	K.DITGSSDPYCIVK.V
1666.0132	1665.0059	1664.9508	33.1	417	-	431	1	---	R.AHLVALLSAICRSVR.T
2691.2968	2690.2896	2690.3340	-16.52	191	-	214	1	---	K.GASEALLVEAWDWDLVSRNDFLGK.V
2748.3054	2747.2982	2747.3304	-11.72	100	-	123	0	---	K.GFSGWTHLVEVDPNEEVQGEIHLR.L

No match to: 871.3026, 1167.6630, 1189.6680, 1268.6204, 1338.8396, 1371.8134, 1587.8222, 1979.9956, 2248.0877

3. TDGF1_MOUSE **Mass:** 19539 **Score:** 36 **Expect:** 4.5 **Matches:** 3

Teratocarcinoma-derived growth factor OS=Mus musculus GN=Tdgf1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
1979.9956	1978.9883	1979.0476	-29.99	47	-	64	1	---	R.SFQFVPSVGIQNSKSLNK.T
2691.2968	2690.2896	2690.3778	-32.80	1	-	26	0	---	-.MGYFSSSVVLLVAISSAFEFGPVAGR.D
2748.3054	2747.2982	2747.2679	11.0	147	-	170	0	---	R.TPCQTPSVTTTFMLAGACLFLDMK.V + Acetyl (N-term); Oxidation (M)

No match to: 871.3026, 946.5851, 1167.6630, 1189.6680, 1268.6204, 1338.8396, 1371.8134, 1419.7576, 1454.6781, 1587.8222, 1666.0132, 2248.0877

4. EBP2_MOUSE **Mass:** 34795 **Score:** 35 **Expect:** 5 **Matches:** 4

Probable rRNA-processing protein EBP2 OS=Mus musculus GN=Ebna1bp2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
1189.6680	1188.6607	1188.6172	36.6	154	-	163	1	---	K.LQTKQAAMEK.S + Acetyl (N-term)
1587.8222	1586.8149	1586.7940	13.2	210	-	222	0	---	K.LDFLEGDQKPVER.S + Acetyl (N-term)
2248.0877	2247.0805	2246.9936	38.7	132	-	149	1	---	K.RPTDYFAEMAKSDQQMQK.I + Acetyl (N-term); 2 Oxidation (M)

2748.3054	2747.2982	2747.3978	-36.26	70 -	94	1	---	R.LDVTLGPVPEVSETQPTPQNQDQKK.G

No match to: 871.3026, 946.5851, 1167.6630, 1268.6204, 1338.8396, 1371.8134, 1419.7576, 1454.6781, 1666.0132, 1979.9956, 2691.2968

5. NLE1_MOUSE **Mass:** 53628 **Score:** 34 **Expect:** 5.8 **Matches:** 4

Notchless protein homolog 1 OS=Mus musculus GN=Nle1 PE=2 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1268.6204	1267.6131	1267.6044	6.86	128 -	139	0	---	K.YLASGSGDTTVR.F + Acetyl (N-term)
1419.7576	1418.7503	1418.6903	42.3	225 -	237	1	5	K.DGSVRVWDTTAGR.C
1587.8222	1586.8149	1586.7722	26.9	1 -	16	0	---	-.MAAAVVEEAAAGDVQR.L
2691.2968	2690.2896	2690.3334	-16.29	102 -	127	1	---	R.AVTRCTSSLEGHSEAVISVAFSPTGK.Y

No match to: 871.3026, 946.5851, 1167.6630, 1189.6680, 1338.8396, 1371.8134, 1454.6781, 1666.0132, 1979.9956, 2248.0877, 2748.3054

6. ICAL_MOUSE **Mass:** 85099 **Score:** 31 **Expect:** 12 **Matches:** 5

Calpastatin OS=Mus musculus GN=Cast PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1167.6630	1166.6557	1166.6659	-8.75	706 -	715	1	---	K.DKPEKPPTKK.T
1189.6680	1188.6607	1188.6139	39.4	279 -	288	1	---	K.EGTIPPEYRK.L
1979.9956	1978.9883	1978.9960	-3.88	113 -	129	1	---	K.TESKKPQSSEQPVVHEK.K + Acetyl (N-term)
2248.0877	2247.0805	2247.0880	-3.34	22 -	41	1	---	R.HTQEHVNEKNIGSSSKPGEK.K + Acetyl (N-term)
2748.3054	2747.2982	2747.3250	-9.76	505 -	530	1	---	K.GVVPEDAVETLAGSLGTREADPEHEK.T + Acetyl (N-term)

No match to: 871.3026, 946.5851, 1268.6204, 1338.8396, 1371.8134, 1419.7576, 1454.6781, 1587.8222, 1666.0132, 2691.2968

7. GLTL1_MOUSE **Mass:** 63721 **Score:** 27 **Expect:** 33 **Matches:** 4

Putative polypeptide N-acetylgalactosaminyltransferase-like protein 1 OS=Mus musculus GN=Galntl1 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1371.8134	1370.8061	1370.7810	18.4	289 -	301	0	---	R.TPVIAGGIFVIDK.S + Acetyl (N-term)
1587.8222	1586.8149	1586.7729	26.5	380 -	392	0	---	K.QYYYEARPSAIGK.A + Acetyl (N-term)
2248.0877	2247.0805	2247.1436	-28.12	466 -	485	0	---	K.SPPPAQAWLFSDHLIQQQGK.C
2691.2968	2690.2896	2690.2575	11.9	437 -	461	0	---	K.QGVNCLESQGQNTAGDLLLGMGICR.G

No match to: 871.3026, 946.5851, 1167.6630, 1189.6680, 1268.6204, 1338.8396, 1419.7576, 1454.6781, 1666.0132, 1979.9956, 2748.3054

8. SYT1_MOUSE **Mass:** 47730 **Score:** 25 **Expect:** 48 **Matches:** 4

Synaptotagmin-1 OS=Mus musculus GN=Syt1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1268.6204	1267.6131	1267.5768	28.7	389 -	398	0	---	R.HWSDMLANPR.R + Acetyl (N-term)
1419.7576	1418.7503	1418.7657	-10.88	355 -	366	0	---	K.VQVVVTVLDYDK.I + Acetyl (N-term)
1454.6781	1453.6708	1453.7201	-33.95	376 -	388	0	---	K.VFVGYNSTGAELR.H + Acetyl (N-term)
2691.2968	2690.2896	2690.4214	-48.99	399 -	421	1	---	R.RPIAQWHTLQVEEEVDAMLAVKK.-

No match to: 871.3026, 946.5851, 1167.6630, 1189.6680, 1338.8396, 1371.8134, 1587.8222, 1666.0132, 1979.9956, 2248.0877, 2748.3054

9. GLO2_MOUSE **Mass:** 34519 **Score:** 25 **Expect:** 53 **Matches:** 3

Hydroxyacylglutathione hydrolase, mitochondrial OS=Mus musculus GN=Hagh PE=2 SV=2

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

1189.6680	1188.6607	1188.6172	36.6	42	-	51	0	---	K.NLTVQQDIMK.V
2248.0877	2247.0805	2247.0994	-8.43	212	-	230	1	---	R.LPPDTKVYCGHEYTVNNLK.F
2691.2968	2690.2896	2690.2574	12.0	253	-	275	0	---	K.YAIGEPTVPSTLAEEFTYNPFMR.V + Acetyl (N-term); Oxidation (M)

No match to: 871.3026, 946.5851, 1167.6630, 1268.6204, 1338.8396, 1371.8134, 1419.7576, 1454.6781, 1587.8222, 1666.0132, 1979.9956, 2748.3054

10. GSTK1_MOUSE **Mass:** 25801 **Score:** 24 **Expect:** 60 **Matches:** 3

Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gstk1 PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Ions**	**Peptide**
1268.6204	1267.6131	1267.5979	12.0	50	-	61	0	---	K.DSGNQPPAMVPR.K
1454.6781	1453.6708	1453.6983	-18.97	50	-	62	1	---	K.DSGNQPPAMVPRK.G + Acetyl (N-term); Oxidation (M)
2748.3054	2747.2982	2747.3589	-22.10	168	-	193	1	---	K.LIENTDAACKYGAFGLPTTVAHVDGK.T

No match to: 871.3026, 946.5851, 1167.6630, 1189.6680, 1338.8396, 1371.8134, 1419.7576, 1587.8222, 1666.0132, 1979.9956, 2248.0877, 2691.2968

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (871.3026,1+) : <no title>

Query2 (946.5851,1+) : <no title>

Query3 (1167.6630,1+) : <no title>

Query4 (1189.6680,1+) : <no title>

Query5 (1268.6204,1+) : <no title>

Query6 (1338.8396,1+) : <no title>

Query7 (1371.8134,1+) : <no title>

Query8 (1419.7576,1+) : <no title>

Query9 (1454.6781,1+) : <no title>

Query10 (1587.8222,1+) : <no title>

Query11 (1666.0132,1+) : <no title>

Query12 (1979.9956,1+) : <no title>

Query13 (2248.0877,1+) : <no title>

Query14 (2691.2968,1+) : <no title>

Query15 (2748.3054,1+) : <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 : **20 Jun 2013 at 07:31:47 GMT**

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

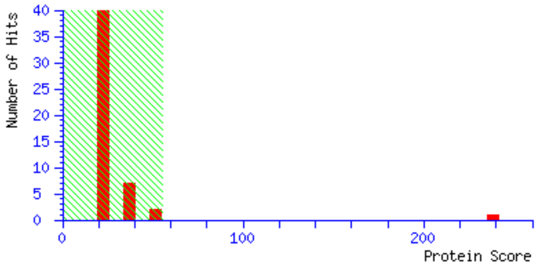
Top Score : **238 for K2C8_MOUSE, Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4**

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	238	Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4
2.	**PRAM_MOUSE**	75844	47	PML-RARA-regulated adapter molecule 1 OS=Mus musculus GN=Pram1 PE=1 SV=1
3.	**K2C71_MOUSE**	57860	45	Keratin, type II cytoskeletal 71 OS=Mus musculus GN=Krt71 PE=1 SV=1
4.	**SPI2_MOUSE**	45861	42	Serpin I2 OS=Mus musculus GN=Serpini2 PE=1 SV=1
5.	**MYT1L_MOUSE**	135041	36	Myelin transcription factor 1-like protein OS=Mus musculus GN=Myt1l PE=2 SV=2
6.	**RDH13_MOUSE**	36726	33	Retinol dehydrogenase 13 OS=Mus musculus GN=Rdh13 PE=2 SV=1
7.	**CC112_MOUSE**	52745	31	Coiled-coil domain-containing protein 112 OS=Mus musculus GN=Ccdc112 PE=2 SV=2
8.	**GDF9_MOUSE**	50358	31	Growth/differentiation factor 9 OS=Mus musculus GN=Gdf9 PE=2 SV=2
9.	**K1C19_MOUSE**	44515	30	Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1
10.	**PLIN1_MOUSE**	55904	30	Perilipin-1 OS=Mus musculus GN=Plin1 PE=1 SV=2

Results List

1. K2C8_MOUSE **Mass:** 54531 **Score:** 238 **Expect:** 2.6e-020 **Matches:** 18

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**
868.4658	867.4586	867.4311	31.7	302	308	1	---	K.HGDDLRR.T
932.4739	931.4666	931.4610	5.97	400	407	0	---	K.LLEGEESR.L
1053.5428	1052.5355	1052.5250	9.95	232	239	0	---	R.QIHEEEIR.E
1079.4970	1078.4898	1078.5043	-13.48	271	279	0	---	R.AQYEDIANR.S
1082.5796	1081.5723	1081.5920	-18.26	108	116	1	---	K.FASFIDKVR.F
1113.6071	1112.5998	1112.6189	-17.20	359	368	0	15	K.LAELEAALQR.A
1208.5919	1207.5847	1207.5867	-1.65	309	318	1	---	R.TKTEISEMNR.N
1253.6564	1252.6491	1252.6775	-22.68	84	94	0	---	K.LEVDPNIQAVR.T
1318.6479	1317.6406	1317.6598	-14.58	259	270	0	34	R.SLDMDGIIAEVR.A
1334.6706	1333.6633	1333.6548	6.40	259	270	0	---	R.SLDMDGIIAEVR.A + Oxidation (M)
1344.6612	1343.6539	1343.6681	-10.50	335	347	0	---	R.ASLEAAIADAEQR.G
1355.7412	1354.7339	1354.7568	-16.90	323	334	1	---	R.LQAEIEALKGQR.A
1419.7340	1418.7267	1418.7405	-9.76	220	231	0	36	R.LEGLTDEINFLR.Q
1426.7080	1425.7007	1425.6922	5.99	280	291	1	---	R.SRAEAETMYQIK.Y
1435.8002	1434.7929	1434.8082	-10.65	388	399	1	---	K.LALDIEITTYRK.L
1797.8345	1796.8272	1796.8250	1.22	205	219	1	---	K.DVDEAYMNKVELESR.L
1973.9912	1972.9839	1972.9887	-2.43	335	353	1	---	R.ASLEAAIADAEQRGEMAIK.D
2109.0014	2107.9942	2108.0056	-5.40	240	258	0	---	R.ELQSQISDTSVVLSMDNSR.S

No match to: 995.6173, 1011.6164, 1029.5812, 1041.5766, 1148.6981, 1266.7140, 1303.6221, 1328.6632, 1330.6862, 1365.7061, 1401.7146, 1406.7604, 1447.7314, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 1572.8528

2. PRAM_MOUSE **Mass:** 75844 **Score:** 47 **Expect:** 0.31 **Matches:** 8

PML-RARA-regulated adapter molecule 1 OS=Mus musculus GN=Pram1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1082.5796	1081.5723	1081.6033	-28.64	378	386	1	---	R.KFLQPQHGK.F
1208.5919	1207.5847	1207.5689	13.0	599	608	1	---	K.MMIDPNAKTR.R + 2 Oxidation (M)
1266.7140	1265.7068	1265.7132	-5.08	105	115	0	---	R.KPLHPEFTGLK.K
1303.6221	1302.6149	1302.6456	-23.58	40	50	0	---	K.FPQTELSEQPK.K
1330.6862	1329.6789	1329.6598	14.3	330	341	1	---	R.ASSEPEVCKVPK.K
1419.7340	1418.7267	1418.7630	-25.60	318	329	1	---	K.KHPQLQPSDLTR.A
1447.7314	1446.7241	1446.7871	-43.55	587	598	1	---	K.FKFEGEIVIHTK.M
1797.8345	1796.8272	1796.8581	-17.18	247	262	0	---	R.ELDSHSPQPDISTFPK.N

No match to: 868.4658, 932.4739, 995.6173, 1011.6164, 1029.5812, 1041.5766, 1053.5428, 1079.4970, 1113.6071, 1148.6981, 1253.6564, 1318.6479, 1328.6632, 1334.6706, 1344.6612, 1355.7412, 1365.7061, 1401.7146, 1406.7604, 1426.7080, 1435.8002, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 1572.8528, 1973.9912, 2109.0014

3. K2C71_MOUSE **Mass:** 57860 **Score:** 45 **Expect:** 0.51 **Matches:** 7

Keratin, type II cytoskeletal 71 OS=Mus musculus GN=Krt71 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
932.4739	931.4666	931.4723	-6.11	384	392	1	---	R.GDSALKDAR.A
1082.5796	1081.5723	1081.5920	-18.26	142	150	1	---	K.FASFIDKVR.F
1318.6479	1317.6406	1317.6888	-36.57	344	354	1	2	K.NTKNEITELTR.F

1401.7146	1400.7073	1400.7147	-5.30	295	306	0	---	R.NLDLDSIIDEVR.A
1572.8528	1571.8455	1571.7687	48.9	412	423	1	---	R.MLREYQELMSLK.L + 2 Oxidation (M)
1797.8345	1796.8272	1796.9169	-49.92	328	343	1	---	K.FQELQLAAGRHGDDLK.N
1973.9912	1972.9839	1972.9425	21.0	55	74	1	---	R.SITLNMASGSGKNGGFGFGR.N + Oxidation (M)

No match to: 868.4658, 995.6173, 1011.6164, 1029.5812, 1041.5766, 1053.5428, 1079.4970, 1113.6071, 1148.6981, 1208.5919, 1253.6564, 1266.7140, 1303.6221, 1328.6632, 1330.6862, 1334.6706, 1344.6612, 1355.7412, 1365.7061, 1406.7604, 1419.7340, 1426.7080, 1435.8002, 1447.7314, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 2109.0014

4. SPI2_MOUSE **Mass:** 45861 **Score:** 42 **Expect:** 1 **Matches:** 6

Serpin I2 OS=Mus musculus GN=Serpini2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.5766	1040.5693	1040.5212	46.2	380	388	0	---	R.TESILFMGK.V + Oxidation (M)
1208.5919	1207.5847	1207.5941	-7.80	207	217	1	---	K.DGSTVKVPMMK.A + Oxidation (M)
1330.6862	1329.6789	1329.6889	-7.50	389	400	1	---	K.VTDPDIQTTKGR.D
1344.6612	1343.6539	1343.5915	46.5	196	206	1	---	K.EDTEMTDFTKK.D
1447.7314	1446.7241	1446.7653	-28.49	377	388	1	---	K.HIRTESILFMGK.V + Oxidation (M)
1797.8345	1796.8272	1796.8767	-27.53	162	176	1	---	K.IKNMFSEEEFGPLTR.L

No match to: 868.4658, 932.4739, 995.6173, 1011.6164, 1029.5812, 1053.5428, 1079.4970, 1082.5796, 1113.6071, 1148.6981, 1253.6564, 1266.7140, 1303.6221, 1318.6479, 1328.6632, 1334.6706, 1355.7412, 1365.7061, 1401.7146, 1406.7604, 1419.7340, 1426.7080, 1435.8002, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 1572.8528, 1973.9912, 2109.0014

5. MYT1L_MOUSE **Mass:** 135041 **Score:** 36 **Expect:** 4.6 **Matches:** 7

Myelin transcription factor 1-like protein OS=Mus musculus GN=Myt1l PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1208.5919	1207.5847	1207.5721	10.4	670	680	1	---	R.DISPKGYDDAK.R
1318.6479	1317.6406	1317.6048	27.2	1056	1067	0	---	R.ASNGIENDEEIK.Q
1334.6706	1333.6633	1333.7275	-48.15	1042	1053	1	---	K.AKLSGEQMLTIK.Q + Oxidation (M)
1365.7061	1364.6989	1364.6540	32.8	1028	1040	1	---	R.SLSGCPRATSAMK.K
1419.7340	1418.7267	1418.7551	-20.05	1044	1055	1	7	K.LSGEQMLTIKQR.A + Oxidation (M)
1447.7314	1446.7241	1446.7202	2.68	248	260	0	---	K.SELSLDLDSDVVR.E
2109.0014	2107.9942	2108.0307	-17.31	1092	1109	1	---	R.TQITTMESNLKTIEEENK.V

No match to: 868.4658, 932.4739, 995.6173, 1011.6164, 1029.5812, 1041.5766, 1053.5428, 1079.4970, 1082.5796, 1113.6071, 1148.6981, 1253.6564, 1266.7140, 1303.6221, 1328.6632, 1330.6862, 1344.6612, 1355.7412, 1401.7146, 1406.7604, 1426.7080, 1435.8002, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 1572.8528, 1797.8345, 1973.9912

6. RDH13_MOUSE **Mass:** 36726 **Score:** 33 **Expect:** 7.4 **Matches:** 5

Retinol dehydrogenase 13 OS=Mus musculus GN=Rdh13 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1029.5812	1028.5739	1028.5978	-23.26	53	61	1	---	K.QTALELAKR.G
1041.5766	1040.5693	1040.5727	-3.21	84	92	1	---	R.GETLNPRVR.A
1330.6862	1329.6789	1329.7075	-21.49	118	129	0	---	R.VDILVNNAAVMR.C + Oxidation (M)
1334.6706	1333.6633	1333.5972	49.5	194	204	1	---	K.YDTKAAYCQSK.L
2109.0014	2107.9942	2108.0949	-47.79	309	328	1	---	R.LWTESARLVGLAMAHGSPGR.G

No match to: 868.4658, 932.4739, 995.6173, 1011.6164, 1053.5428, 1079.4970, 1082.5796, 1113.6071, 1148.6981, 1208.5919, 1253.6564, 1266.7140, 1303.6221, 1318.6479, 1328.6632, 1344.6612, 1355.7412, 1365.7061, 1401.7146, 1406.7604, 1419.7340, 1426.7080, 1435.8002, 1447.7314, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 1572.8528, 1797.8345, 1973.9912

7. CC112_MOUSE **Mass:** 52745 **Score:** 31 **Expect:** 13 **Matches:** 6

Coiled-coil domain-containing protein 112 OS=Mus musculus GN=Ccdc112 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
995.6173	994.6101	994.5811	29.1	362 -	369	1	---	R.DLHKLELK.I
1041.5766	1040.5693	1040.5767	-7.08	434 -	442	1	---	R.AIPTWRQGI.-
1318.6479	1317.6406	1317.6816	-31.12	145 -	155	0	---	R.TLPEQVVEFEK.F
1406.7604	1405.7532	1405.7677	-10.37	316 -	326	1	---	K.LLLESYTQQRR.E
1484.7771	1483.7698	1483.7711	-0.84	210 -	220	1	---	K.WYQKFLTLEEK.K
1797.8345	1796.8272	1796.9156	-49.18	246 -	262	1	---	K.VDTVPLPSQSKAEDSPK.Q

No match to: 868.4658, 932.4739, 1011.6164, 1029.5812, 1053.5428, 1079.4970, 1082.5796, 1113.6071, 1148.6981, 1208.5919, 1253.6564, 1266.7140, 1303.6221, 1328.6632, 1330.6862, 1334.6706, 1344.6612, 1355.7412, 1365.7061, 1401.7146, 1419.7340, 1426.7080, 1435.8002, 1447.7314, 1461.7788, 1471.7802, 1497.7773, 1508.8584, 1572.8528, 1973.9912, 2109.0014

8. GDF9_MOUSE **Mass:** 50358 **Score:** 31 **Expect:** 14 **Matches:** 5

Growth/differentiation factor 9 OS=Mus musculus GN=Gdf9 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
932.4739	931.4666	931.4837	-18.34	85 -	91	1	---	R.ALYYMKK.L + Oxidation (M)
1041.5766	1040.5693	1040.5688	0.48	147 -	155	0	---	R.VTAMEHLLK.S
1406.7604	1405.7532	1405.7024	36.1	223 -	234	0	---	R.SIHLSVNFTCTK.D
1484.7771	1483.7698	1483.7493	13.8	79 -	90	1	---	K.LQPDSRALYYMK.K
1508.8584	1507.8512	1507.7817	46.1	397 -	410	0	---	K.LDPSVPRPSCVPGK.Y

No match to: 868.4658, 995.6173, 1011.6164, 1029.5812, 1053.5428, 1079.4970, 1082.5796, 1113.6071, 1148.6981, 1208.5919, 1253.6564, 1266.7140, 1303.6221, 1318.6479, 1328.6632, 1330.6862, 1334.6706, 1344.6612, 1355.7412, 1365.7061, 1401.7146, 1419.7340, 1426.7080, 1435.8002, 1447.7314, 1461.7788, 1471.7802, 1497.7773, 1572.8528, 1797.8345, 1973.9912, 2109.0014

9. K1C19_MOUSE **Mass:** 44515 **Score:** 30 **Expect:** 14 **Matches:** 5

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**
1029.5812	1028.5739	1028.5866	-12.35	192 -	200	0	---	R.VLDELTLAR.T
1041.5766	1040.5693	1040.5978	-27.38	154 -	162	0	---	K.IVLQIDNAR.L
1303.6221	1302.6149	1302.6205	-4.30	52 -	64	0	---	R.FVTSSSGSYGGVR.G
1365.7061	1364.6989	1364.7048	-4.35	374 -	384	1	---	K.SRLEQEIATYR.S
1973.9912	1972.9839	1973.0615	-39.32	304 -	320	1	---	R.RTLQGLEIELQSQLSMK.A

No match to: 868.4658, 932.4739, 995.6173, 1011.6164, 1053.5428, 1079.4970, 1082.5796, 1113.6071, 1148.6981, 1208.5919, 1253.6564, 1266.7140, 1318.6479, 1328.6632, 1330.6862, 1334.6706, 1344.6612, 1355.7412, 1401.7146, 1406.7604, 1419.7340, 1426.7080, 1435.8002, 1447.7314, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 1572.8528, 1797.8345, 2109.0014

10. PLIN1_MOUSE **Mass:** 55904 **Score:** 30 **Expect:** 15 **Matches:** 5

Perilipin-1 OS=Mus musculus GN=Plin1 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1303.6221	1302.6149	1302.6391	-18.57	231 -	241	0	---	R.HTMQTTAWALK.Q + Oxidation (M)
1318.6479	1317.6406	1317.6776	-28.06	129 -	141	0	---	R.NSISVPIASTSDK.V
1344.6612	1343.6539	1343.6317	16.6	420 -	431	1	---	R.DIDNPSAEAERK.G
1401.7146	1400.7073	1400.7511	-31.26	172 -	186	0	---	R.LASGGADLALGSIEK.V
2109.0014	2107.9942	2108.0837	-42.47	490 -	507	1	---	R.RVSDSFFRPSVMEPILGR.A + Oxidation (M)

No match to: 868.4658, 932.4739, 995.6173, 1011.6164, 1029.5812, 1041.5766, 1053.5428, 1079.4970, 1082.5796, 1113.6071, 1148.6981, 1208.5919, 1253.6564, 1266.7140, 1328.6632, 1330.6862, 1334.6706, 1355.7412, 1365.7061, 1406.7604, 1419.7340, 1426.7080, 1435.8002, 1447.7314, 1461.7788, 1471.7802, 1484.7771, 1497.7773, 1508.8584, 1572.8528, 1797.8345, 1973.9912

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 (868.4658,1+) : <no title>
Query2 (932.4739,1+) : <no title>
Query3 (995.6173,1+) : <no title>
Query4 (1011.6164,1+) : <no title>
Query5 (1029.5812,1+) : <no title>
Query6 (1041.5766,1+) : <no title>
Query7 (1053.5428,1+) : <no title>
Query8 (1079.4970,1+) : <no title>
Query9 (1082.5796,1+) : <no title>
Query10 (1113.6071,1+) : <no title>
Query11 (1148.6981,1+) : <no title>
Query12 (1208.5919,1+) : <no title>
Query13 (1253.6564,1+) : <no title>
Query14 (1266.7140,1+) : <no title>
Query15 (1303.6221,1+) : <no title>
Query16 (1318.6479,1+) : <no title>
Query17 (1328.6632,1+) : <no title>
Query18 (1330.6862,1+) : <no title>
Query19 (1334.6706,1+) : <no title>
Query20 (1344.6612,1+) : <no title>
Query21 (1355.7412,1+) : <no title>
Query22 (1365.7061,1+) : <no title>
Query23 (1401.7146,1+) : <no title>

Query24 (1406.7604,1+) : <no title>

Query25 (1419.7340,1+) : <no title>

Query26 (1426.7080,1+) : <no title>

Query27 (1435.8002,1+) : <no title>

Query28 (1447.7314,1+) : <no title>

Query29 (1461.7788,1+) : <no title>

Query30 (1471.7802,1+) : <no title>

Query31 (1484.7771,1+) : <no title>

Query32 (1497.7773,1+) : <no title>

Query33 (1508.8584,1+) : <no title>

Query34 (1572.8528,1+) : <no title>

Query35 (1797.8345,1+) : <no title>

Query36 (1973.9912,1+) : <no title>

Query37 (2109.0014,1+) : <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 : **20 May 2013 at 01:33:47 GMT**

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

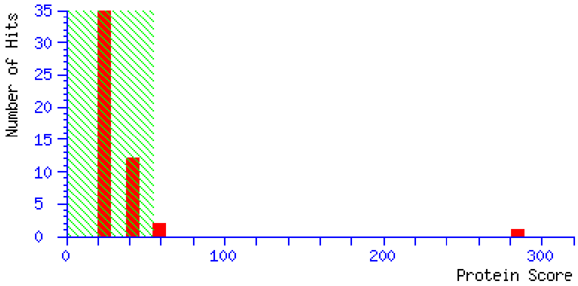
Top Score : **285 for K1C18_MOUSE, Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5**

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.	**K1C18_MOUSE**	47509	285	Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5
2.	**RSSA_MOUSE**	32931	64	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4
3.	**K1C19_MOUSE**	44515	56	Keratin, type I cytoskeletal 19 OS=Mus musculus GN=Krt19 PE=2 SV=1
4.	**FYCO1_MOUSE**	164060	38	FYVE and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Fyco1 PE=1 SV=1
5.	**HS3SB_MOUSE**	43641	37	Heparan sulfate glucosamine 3-O-sulfotransferase 3B1 OS=Mus musculus GN=Hs3st3b1 PE=2 SV=1
6.	**ARHG3_MOUSE**	60230	37	Rho guanine nucleotide exchange factor 3 OS=Mus musculus GN=Arhgef3 PE=1 SV=1
7.	**NDKM_MOUSE**	20707	36	Nucleoside diphosphate kinase, mitochondrial OS=Mus musculus GN=Nme4 PE=1 SV=1
8.	**CA194_MOUSE**	18977	35	Uncharacterized protein C1orf194 homolog OS=Mus musculus PE=2 SV=1
9.	**ALAT1_MOUSE**	55905	35	Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=2 SV=3
10.	**RM47_MOUSE**	29992	35	39S ribosomal protein L47, mitochondrial OS=Mus musculus GN=Mrpl47 PE=2 SV=2

Results List

1. K1C18_MOUSE **Mass:** 47509 **Score:** 285 **Expect:** 5.1e-025 **Matches:** 19

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

924.5554	923.5482	923.5188	31.8	104 -	110	1	---	K.IREHLEK.K
1004.5424	1003.5351	1003.5046	30.4	92 -	99	1	---	K.SLETENRR.L
1020.5184	1019.5112	1019.4884	22.4	411 -	419	0	---	R.VVSETNDTR.V
1032.5694	1031.5621	1031.5248	36.2	181 -	189	0	---	K.VVDDTNITR.L
1041.6334	1040.6261	1040.5978	27.2	143 -	151	0	52	R.IVLQIDNAR.L
1065.5734	1064.5661	1064.5502	15.0	366 -	374	0	---	K.LEAEIATYR.R
1121.5294	1120.5221	1120.4819	35.9	74 -	82	0	---	K.ETMQDLNDR.L
1148.6002	1147.5929	1147.5721	18.1	284 -	293	0	---	R.DAETTLTELR.R
1160.6539	1159.6467	1159.6197	23.2	180 -	189	1	---	R.KVVDDTNITR.L
1239.6715	1238.6643	1238.6329	25.3	159 -	168	1	10	R.VKYETELAMR.Q
1240.6244	1239.6171	1239.6208	-2.97	169 -	179	0	---	R.QSVESDIHGLR.K
1255.6655	1254.6583	1254.6278	24.3	159 -	168	1	---	R.VKYETELAMR.Q + Oxidation (M)
1281.6652	1280.6579	1280.6434	11.3	159 -	168	1	---	R.VKYETELAMR.Q + Acetyl (N-term)
1292.7494	1291.7421	1291.7136	22.1	364 -	374	1	25	K.VKLEAEIATYR.R
1305.6937	1304.6864	1304.6473	30.0	131 -	142	0	33	R.AQIFANSVDNAR.I
1368.7634	1367.7562	1367.7157	29.6	169 -	180	1	---	R.QSVESDIHGLRK.V
1419.7856	1418.7783	1418.7405	26.7	352 -	363	0	---	R.QAQEYEALLNIK.V
1785.9151	1784.9079	1784.8653	23.9	308 -	323	0	48	K.NQNINLENSLGDVEAR.Y
2380.2064	2379.1991	2379.2216	-9.46	326 -	346	0	---	K.AQMEQLNGVLLHLESELAQTR.A

No match to: 834.3310, 912.5618, 1012.5287, 1203.6746, 1223.6482, 1268.6342, 1351.7259, 1441.7466, 1556.8021, 1561.8613, 1571.8028, 1614.8077, 1633.9167, 1673.8781, 1698.8648, 1740.9933, 1799.9349, 2081.0386, 2395.2224, 2691.2733, 2749.3154, 2773.3573, 2784.3592, 2996.4764

2. RSSA_MOUSE **Mass:** 32931 **Score:** 64 **Expect:** 0.0058 **Matches:** 9

40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
912.5618	911.5546	911.5440	11.6	121 -	128	0	---	R.LLVVTDPR.A
1203.6746	1202.6673	1202.6408	22.1	90 -	102	0	---	K.FAAATGATPIAGR.F
1305.6937	1304.6864	1304.7340	-36.43	42 -	52	1	---	R.KSDGIYIINLK.R + Acetyl (N-term)
1614.8077	1613.8004	1613.7959	2.78	167 -	180	0	---	K.GAHSVGLMWWMLAR.E
1698.8648	1697.8575	1697.8526	2.92	103 -	117	0	---	R.FTPGTFTNQIQAAFR.E
1740.9933	1739.9860	1739.9417	25.4	64 -	80	0	---	R.AIVAIENPADVSVISSR.N
2081.0386	2080.0313	2080.0490	-8.50	103 -	120	1	---	R.FTPGTFTNQIQAAFREPR.L
2773.3573	2772.3501	2772.3694	-6.96	18 -	41	1	---	K.FLAAGTHLGGTNLDFQMEQYIYKR.K
2996.4764	2995.4691	2995.4709	-0.60	129 -	155	0	---	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y

No match to: 834.3310, 924.5554, 1004.5424, 1012.5287, 1020.5184, 1032.5694, 1041.6334, 1065.5734, 1121.5294, 1148.6002, 1160.6539, 1223.6482, 1239.6715, 1240.6244, 1255.6655, 1268.6342, 1281.6652, 1292.7494, 1351.7259, 1368.7634, 1419.7856, 1441.7466, 1556.8021, 1561.8613, 1571.8028, 1633.9167, 1673.8781, 1785.9151, 1799.9349, 2380.2064, 2395.2224, 2691.2733, 2749.3154, 2784.3592

3. K1C19_MOUSE **Mass:** 44515 **Score:** 56 **Expect:** 0.038 **Matches:** 2

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**
1032.5694	1031.5621	1031.5433	18.2	368 -	375	1	---	K.QLMDIKSR.L + Acetyl (N-term)
1041.6334	1040.6261	1040.5978	27.2	154 -	162	0	52	K.IVLQIDNAR.L

No match to: 834.3310, 912.5618, 924.5554, 1004.5424, 1012.5287, 1020.5184, 1065.5734, 1121.5294, 1148.6002, 1160.6539, 1203.6746, 1223.6482, 1239.6715, 1240.6244, 1255.6655, 1268.6342, 1281.6652, 1292.7494, 1305.6937, 1351.7259, 1368.7634, 1419.7856, 1441.7466, 1556.8021, 1561.8613, 1571.8028, 1614.8077, 1633.9167, 1673.8781, 1698.8648, 1740.9933, 1785.9151, 1799.9349, 2081.0386, 2380.2064, 2395.2224, 2691.2733, 2749.3154, 2773.3573, 2784.3592, 2996.4764

4. FYCO1_MOUSE **Mass:** 164060 **Score:** 38 **Expect:** 2.8 **Matches:** 15

FYVE and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Fyco1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1020.5184	1019.5112	1019.4706	39.8	588 -	595	0	---	K.ELQNMVDR.N + Oxidation (M)
1032.5694	1031.5621	1031.5248	36.2	301 -	310	0	---	K.QGDVSQATVK.K
1041.6334	1040.6261	1040.6230	3.02	1100 -	1107	1	---	R.LIELLRDK.D + Acetyl (N-term)
1065.5734	1064.5661	1064.5138	49.1	1114 -	1122	0	---	K.SDALEFQQK.L
1121.5294	1120.5221	1120.5764	-48.47	603 -	611	0	---	K.LQALQTDYK.A + Acetyl (N-term)
1148.6002	1147.5929	1147.6349	-36.64	90 -	98	1	---	R.FVRSISELR.T + Acetyl (N-term)
1160.6539	1159.6467	1159.6197	23.2	301 -	311	1	---	K.QGDVSQATVKK.L
1441.7466	1440.7394	1440.7824	-29.87	442 -	454	1	---	K.DVVPLQEELSGKK.Q
1556.8021	1555.7948	1555.7525	27.2	529 -	540	1	---	K.QLMQERDHLSQR.V + Oxidation (M)
1614.8077	1613.8004	1613.8559	-34.41	265 -	278	1	---	R.MLVSRQGGQLQVEK.E + Acetyl (N-term)
1673.8781	1672.8709	1672.8090	37.0	989 -	1002	0	---	R.AQLEEQGQQLQMTK.E + Acetyl (N-term)
1698.8648	1697.8575	1697.9312	-43.38	766 -	780	1	---	R.DKLQSQLGVAETVLR.E + Acetyl (N-term)
2380.2064	2379.1991	2379.2243	-10.60	279 -	300	0	---	K.EMGYLAVEDSIGLVSLVAELQK.Q + Oxidation (M)
2395.2224	2394.2151	2394.2139	0.54	462 -	482	1	---	R.RQLQESLAHLSSVEEELAEAR.Q
2691.2733	2690.2660	2690.2462	7.38	1013 -	1035	1	---	K.AAMEEKLNCTSSHLAECQATLLR.K + Acetyl (N-term); Oxidation (M)

No match to: 834.3310, 912.5618, 924.5554, 1004.5424, 1012.5287, 1203.6746, 1223.6482, 1239.6715, 1240.6244, 1255.6655, 1268.6342, 1281.6652, 1292.7494, 1305.6937, 1351.7259, 1368.7634, 1419.7856, 1561.8613, 1571.8028, 1633.9167, 1740.9933, 1785.9151, 1799.9349, 2081.0386, 2749.3154, 2773.3573, 2784.3592, 2996.4764

5. HS3SB_MOUSE **Mass:** 43641 **Score:** 37 **Expect:** 3 **Matches:** 10

Heparan sulfate glucosamine 3-O-sulfotransferase 3B1 OS=Mus musculus GN=Hs3st3b1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1012.5287	1011.5214	1011.5025	18.7	201 -	208	0	---	K.TPSYFVTR.E + Acetyl (N-term)
1148.6002	1147.5929	1147.6271	-29.79	191 -	200	1	---	R.TLKGQITMEK.T
1160.6539	1159.6467	1159.6019	38.6	209 -	219	1	---	R.EAPARISAMSK.D
1239.6715	1238.6643	1238.6619	1.94	92 -	104	1	---	R.APPANSLAAGKDK.T
1240.6244	1239.6171	1239.6030	11.4	340 -	351	0	---	K.AEGSGKPHCLGK.T
1268.6342	1267.6270	1267.6296	-2.07	234 -	244	0	---	R.AISDYTQTLSK.R + Acetyl (N-term)
1281.6652	1280.6579	1280.6724	-11.31	92 -	104	1	---	R.APPANSLAAGKDK.T + Acetyl (N-term)
1368.7634	1367.7562	1367.6980	42.6	339 -	351	1	---	K.KAEGSGKPHCLGK.T
1419.7856	1418.7783	1418.7129	46.2	180 -	190	1	---	K.GLAWYRDLMPR.T + Acetyl (N-term)
1799.9349	1798.9276	1798.8924	19.6	194 -	208	1	---	K.GQITMEKTPSYFVTR.E + Acetyl (N-term)

No match to: 834.3310, 912.5618, 924.5554, 1004.5424, 1020.5184, 1032.5694, 1041.6334, 1065.5734, 1121.5294, 1203.6746, 1223.6482, 1255.6655, 1292.7494, 1305.6937, 1351.7259, 1441.7466, 1556.8021, 1561.8613, 1571.8028, 1614.8077, 1633.9167, 1673.8781, 1698.8648, 1740.9933, 1785.9151, 2081.0386, 2380.2064, 2395.2224, 2691.2733, 2749.3154, 2773.3573, 2784.3592, 2996.4764

6. ARHG3_MOUSE **Mass:** 60230 **Score:** 37 **Expect:** 3 **Matches:** 8

Rho guanine nucleotide exchange factor 3 OS=Mus musculus GN=Arhgef3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1121.5294	1120.5221	1120.5625	-36.05	401	410	1	---	R.GAFSNNERVK.N
1240.6244	1239.6171	1239.6571	-32.30	74	84	0	---	R.SESRPDILAPR.A
1419.7856	1418.7783	1418.7405	26.7	314	324	1	---	K.ERLLYLEEGQK.D + Acetyl (N-term)
1441.7466	1440.7394	1440.7222	11.9	229	239	1	---	K.QDHRVQDFLQR.C
1571.8028	1570.7956	1570.8507	-35.12	248	259	1	---	R.KLDLWNFLDIPR.S + Acetyl (N-term)
1740.9933	1739.9860	1739.9067	45.6	74	88	1	---	R.SESRPDILAPRAWSR.N
2380.2064	2379.1991	2379.2144	-6.45	102	121	1	---	K.LWSETFDVCVNQVLTAKEIK.R
2996.4764	2995.4691	2995.5210	-17.33	445	474	1	---	R.QAKETVLSAAGQAGLLDSEGLVQGPGTENR.E

No match to: 834.3310, 912.5618, 924.5554, 1004.5424, 1012.5287, 1020.5184, 1032.5694, 1041.6334, 1065.5734, 1148.6002, 1160.6539, 1203.6746, 1223.6482, 1239.6715, 1255.6655, 1268.6342, 1281.6652, 1292.7494, 1305.6937, 1351.7259, 1368.7634, 1556.8021, 1561.8613, 1614.8077, 1633.9167, 1673.8781, 1698.8648, 1785.9151, 1799.9349, 2081.0386, 2395.2224, 2691.2733, 2749.3154, 2773.3573, 2784.3592

7. NDKM_MOUSE **Mass:** 20707 **Score:** 36 **Expect:** 4.4 **Matches:** 4

Nucleoside diphosphate kinase, mitochondrial OS=Mus musculus GN=Nme4 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.6334	1040.6261	1040.6455	-18.60	51	59	1	11	R.RLVGTVIQR.F
1673.8781	1672.8709	1672.8242	27.9	72	85	0	---	K.MLQAPESILAEHYR.D + Oxidation (M)
1785.9151	1784.9079	1784.8363	40.1	121	137	0	---	R.AMIGHTDSTEAAPGTIR.G + Acetyl (N-term); Oxidation (M)
2784.3592	2783.3520	2783.3297	8.00	121	146	1	---	R.AMIGHTDSTEAAPGTIRGDFSVHISR.N + Acetyl (N-term); Oxidation (M)

No match to: 834.3310, 912.5618, 924.5554, 1004.5424, 1012.5287, 1020.5184, 1032.5694, 1065.5734, 1121.5294, 1148.6002, 1160.6539, 1203.6746, 1223.6482, 1239.6715, 1240.6244, 1255.6655, 1268.6342, 1281.6652, 1292.7494, 1305.6937, 1351.7259, 1368.7634, 1419.7856, 1441.7466, 1556.8021, 1561.8613, 1571.8028, 1614.8077, 1633.9167, 1698.8648, 1740.9933, 1799.9349, 2081.0386, 2380.2064, 2395.2224, 2691.2733, 2749.3154, 2773.3573, 2996.4764

8. CA194_MOUSE **Mass:** 18977 **Score:** 35 **Expect:** 4.7 **Matches:** 5

Uncharacterized protein C1orf194 homolog OS=Mus musculus PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1020.5184	1019.5112	1019.5247	-13.31	47	56	0	---	R.LSSTPTATSR.S
1239.6715	1238.6643	1238.6183	37.1	59	68	1	---	R.DTFFDSKIPK.D + Acetyl (N-term)
1305.6937	1304.6864	1304.6684	13.8	47	58	1	---	R.LSSTPTATSRSR.D + Acetyl (N-term)
1673.8781	1672.8709	1672.8243	27.9	1	14	0	---	-.MLQPQETFSNPALR.D + Acetyl (N-term)
2691.2733	2690.2660	2690.3161	-18.60	33	56	1	---	K.NPAHLAQQQDPWSRLSSTPTATSR.S + Acetyl (N-term)

No match to: 834.3310, 912.5618, 924.5554, 1004.5424, 1012.5287, 1032.5694, 1041.6334, 1065.5734, 1121.5294, 1148.6002, 1160.6539, 1203.6746, 1223.6482, 1240.6244, 1255.6655, 1268.6342, 1281.6652, 1292.7494, 1351.7259, 1368.7634, 1419.7856, 1441.7466, 1556.8021, 1561.8613, 1571.8028, 1614.8077, 1633.9167, 1698.8648, 1740.9933, 1785.9151, 1799.9349, 2081.0386, 2380.2064, 2395.2224, 2749.3154, 2773.3573, 2784.3592, 2996.4764

9. ALAT1_MOUSE **Mass:** 55905 **Score:** 35 **Expect:** 4.8 **Matches:** 4

Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=2 SV=3

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

912.5618	911.5546	911.5804	-28.32	479 -	485	1	---	R.VLLEKLR.H + Acetyl (N-term)
1041.6334	1040.6261	1040.6091	16.4	170 -	179	1	23	K.LLVAGEGRAR.T
1121.5294	1120.5221	1120.5733	-45.65	339 -	347	1	---	K.QMAKLMSVR.L + Acetyl (N-term); Oxidation (M)
2773.3573	2772.3501	2772.4116	-22.21	143 -	169	1	---	R.RDGGIPADPNNIFLSTGASDAIVTMLK.L

No match to: 834.3310, 924.5554, 1004.5424, 1012.5287, 1020.5184, 1032.5694, 1065.5734, 1148.6002, 1160.6539, 1203.6746, 1223.6482, 1239.6715, 1240.6244, 1255.6655, 1268.6342, 1281.6652, 1292.7494, 1305.6937, 1351.7259, 1368.7634, 1419.7856, 1441.7466, 1556.8021, 1561.8613, 1571.8028, 1614.8077, 1633.9167, 1673.8781, 1698.8648, 1740.9933, 1785.9151, 1799.9349, 2081.0386, 2380.2064, 2395.2224, 2691.2733, 2749.3154, 2784.3592, 2996.4764

10. RM47_MOUSE **Mass:** 29992 **Score:** 35 **Expect:** 5.3 **Matches:** 7

39S ribosomal protein L47, mitochondrial OS=Mus musculus GN=Mrpl47 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1121.5294	1120.5221	1120.5070	13.4	137 -	146	0	---	K.VVDSMDNVDK.V
1203.6746	1202.6673	1202.6554	9.93	2 -	12	1	---	M.AATSLVGICRR.A
1268.6342	1267.6270	1267.6343	-5.78	124 -	133	1	---	R.QRLPMPSPER.L + Acetyl (N-term); Oxidation (M)
1305.6937	1304.6864	1304.6646	16.8	112 -	122	0	---	R.NMLLTLEQEAK.R + Oxidation (M)
1561.8613	1560.8540	1560.7911	40.3	201 -	212	1	---	R.FFAMPYVDRFIR.L
1799.9349	1798.9276	1798.9617	-18.96	96 -	109	1	---	K.SNEDLHKLWYVLLK.E + Acetyl (N-term)
2395.2224	2394.2151	2394.2478	-13.64	44 -	63	1	---	K.NTPHVTSFLQCKLLHTTLSR.K + Acetyl (N-term)

No match to: 834.3310, 912.5618, 924.5554, 1004.5424, 1012.5287, 1020.5184, 1032.5694, 1041.6334, 1065.5734, 1148.6002, 1160.6539, 1223.6482, 1239.6715, 1240.6244, 1255.6655, 1281.6652, 1292.7494, 1351.7259, 1368.7634, 1419.7856, 1441.7466, 1556.8021, 1571.8028, 1614.8077, 1633.9167, 1673.8781, 1698.8648, 1740.9933, 1785.9151, 2081.0386, 2380.2064, 2691.2733, 2749.3154, 2773.3573, 2784.3592, 2996.4764

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (834.3310,1+) : <no title>

Query2 (912.5618,1+) : <no title>

Query3 (924.5554,1+) : <no title>

Query4 (1004.5424,1+) : <no title>

Query5 (1012.5287,1+) : <no title>

Query6 (1020.5184,1+) : <no title>

Query7 (1032.5694,1+) : <no title>

Query8 (1041.6334,1+) : <no title>

Query9 (1065.5734,1+) : <no title>

Query10 (1121.5294,1+) : <no title>

Query11 (1148.6002,1+) : <no title>

Query12 (1160.6539,1+) : <no title>

Query13 (1203.6746,1+) : <no title>

Query14 (1223.6482,1+) : <no title>

Query15 (1239.6715,1+) : <no title>

Query16 (1240.6244,1+) : <no title>

Query17 (1255.6655,1+) : <no title>

Query18 (1268.6342,1+) : <no title>

Query19 (1281.6652,1+) : <no title>

Query20 (1292.7494,1+) : <no title>

Query21 (1305.6937,1+) : <no title>

Query22 (1351.7259,1+) : <no title>

Query23 (1368.7634,1+) : <no title>

Query24 (1419.7856,1+) : <no title>

Query25 (1441.7466,1+) : <no title>

Query26 (1556.8021,1+) : <no title>

Query27 (1561.8613,1+) : <no title>

Query28 (1571.8028,1+) : <no title>

Query29 (1614.8077,1+) : <no title>

Query30 (1633.9167,1+) : <no title>

Query31 (1673.8781,1+) : <no title>

Query32 (1698.8648,1+) : <no title>

Query33 (1740.9933,1+) : <no title>

Query34 (1785.9151,1+) : <no title>

Query35 (1799.9349,1+) : <no title>

Query36 (2081.0386,1+) : <no title>

Query37 (2380.2064,1+) : <no title>

Query38 (2395.2224,1+) : <no title>

Query39 (2691.2733,1+) : <no title>

Query40 (2749.3154,1+) : <no title>

Query41 (2773.3573,1+) : <no title>

Query42 (2784.3592,1+) : <no title>

Query43 (2996.4764,1+) : <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 : **20 May 2013 at 01:33:56 GMT**

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

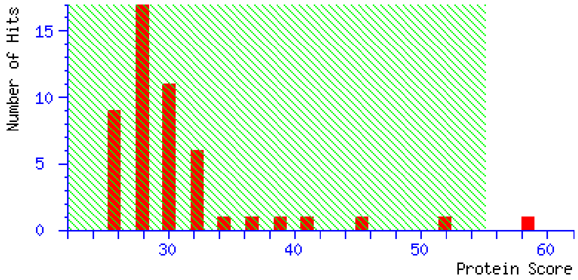
Top Score : **58 for FPPS_MOUSE, Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1**

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.	**FPPS_MOUSE**	40898	58	Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1
2.	**CSN4_MOUSE**	46541	51	COP9 signalosome complex subunit 4 OS=Mus musculus GN=Cops4 PE=1 SV=1
3.	**PUS3_MOUSE**	56138	44	tRNA pseudouridine synthase 3 OS=Mus musculus GN=Pus3 PE=1 SV=2
4.	**RT33_MOUSE**	12452	42	28S ribosomal protein S33, mitochondrial OS=Mus musculus GN=Mrps33 PE=2 SV=1
5.	**RAB21_MOUSE**	24490	39	Ras-related protein Rab-21 OS=Mus musculus GN=Rab21 PE=1 SV=4
6.	**GRID1_MOUSE**	113142	37	Glutamate receptor delta-1 subunit OS=Mus musculus GN=Grid1 PE=1 SV=1
7.	**ELL2_MOUSE**	72681	35	RNA polymerase II elongation factor ELL2 OS=Mus musculus GN=Ell2 PE=2 SV=1
8.	**ENC1_MOUSE**	67240	33	Ectoderm-neural cortex protein 1 OS=Mus musculus GN=Enc1 PE=2 SV=1
9.	**CKP2L_MOUSE**	83689	32	Cytoskeleton-associated protein 2-like OS=Mus musculus GN=Ckap2l PE=2 SV=1
10.	**ZUFSP_MOUSE**	66863	32	Zinc finger with UFM1-specific peptidase domain protein OS=Mus musculus GN=Zufsp PE=2 SV=2

Results List

1. FPPS_MOUSE **Mass:** 40898 **Score:** 58 **Expect:** 0.024 **Matches:** 6

Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1074.5422	1073.5349	1073.5465	-10.80	76 -	84	1	---	K.KQDAESLQR.A
1377.7060	1376.6988	1376.7048	-4.40	32 -	44	0	---	K.ELGHPEIGDAIAR.L
1433.7494	1432.7421	1432.7319	7.12	267 -	277	0	12	K.CSWLVVQCLLR.A
1948.0534	1947.0461	1947.0425	1.87	27 -	44	1	---	K.VLTEKELGHPEIGDAIAR.L
2672.2597	2671.2524	2671.2442	3.09	303 -	324	1	---	K.ALYEALDLQSAFFKYEEDSYNR.L
3177.6461	3176.6388	3176.6328	1.89	114 -	141	0	---	R.GQICWYQKPGIGLDAINDALLLEASIYR.L

No match to: 1076.4446, 1130.5526, 1216.6058, 1249.5702, 1359.7067, 1416.7192, 1487.8390, 1489.7779, 1501.7393, 1510.7817, 1515.7510, 1637.8400, 1679.8974, 1701.9053, 1790.8998, 2691.2894, 2748.3168

2. CSN4_MOUSE **Mass:** 46541 **Score:** 51 **Expect:** 0.13 **Matches:** 7

COP9 signalosome complex subunit 4 OS=Mus musculus GN=Cops4 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1130.5526	1129.5454	1129.5767	-27.77	108 -	116	0	---	R.QHLASIYEK.E + Acetyl (N-term)
1377.7060	1376.6988	1376.7300	-22.67	96 -	107	0	---	R.VISFEEQVASIR.Q
1433.7494	1432.7421	1432.7344	5.41	335 -	347	1	---	K.AEKIASQMITEGR.M
1515.7510	1514.7437	1514.7147	19.2	7 -	20	0	---	R.QDLAQLMNSSGSHK.D
1679.8974	1678.8901	1678.9254	-20.99	122 -	137	0	---	R.NAAQVLVGIPLETGQK.Q + Acetyl (N-term)
1701.9053	1700.8981	1700.8886	5.58	83 -	95	1	---	K.EVYHFTLEKIQPR.V + Acetyl (N-term)
1948.0534	1947.0461	1946.9857	31.1	228 -	244	1	---	K.HALHCTILASAGQQRSR.M + Acetyl (N-term)

No match to: 1074.5422, 1076.4446, 1216.6058, 1249.5702, 1359.7067, 1416.7192, 1487.8390, 1489.7779, 1501.7393, 1510.7817, 1637.8400, 1790.8998, 2672.2597, 2691.2894, 2748.3168, 3177.6461

3. PUS3_MOUSE **Mass:** 56138 **Score:** 44 **Expect:** 0.6 **Matches:** 7

tRNA pseudouridine synthase 3 OS=Mus musculus GN=Pus3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1074.5422	1073.5349	1073.5506	-14.58	399 -	408	0	---	K.HTSAFVEGVK.M
1359.7067	1358.6995	1358.6751	17.9	470 -	481	0	---	R.VCIIDAEINSIA.- + Acetyl (N-term)
1377.7060	1376.6988	1376.6871	8.48	399 -	410	1	---	K.HTSAFVEGVKMR.T + Oxidation (M)
1416.7192	1415.7119	1415.7004	8.14	32 -	43	1	---	K.EQANNIKDSSIR.E + Acetyl (N-term)
1489.7779	1488.7706	1488.7433	18.3	103 -	114	1	---	R.LVESRQTSNYHR.C
1515.7510	1514.7437	1514.7762	-21.46	469 -	481	1	---	K.RVCIIDAEINSIA.- + Acetyl (N-term)
2748.3168	2747.3096	2747.2715	13.9	70 -	93	0	---	K.IAYLGWGYQGFASQENTSNTIEEK.L + Acetyl (N-term)

No match to: 1076.4446, 1130.5526, 1216.6058, 1249.5702, 1433.7494, 1487.8390, 1501.7393, 1510.7817, 1637.8400, 1679.8974, 1701.9053, 1790.8998, 1948.0534, 2672.2597, 2691.2894, 3177.6461

4. RT33_MOUSE **Mass:** 12452 **Score:** 42 **Expect:** 1.1 **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
1359.7067	1358.6995	1358.7446	-33.19	33 -	44	0	---	K.VVSLFSEQPLAK.K + Acetyl (N-term)
1487.8390	1486.8317	1486.8395	-5.22	33 -	45	1	---	K.VVSLFSEQPLAKK.K + Acetyl (N-term)

1679.8974	1678.8901	1678.8964	-3.72	30	44	1	---	K.SMKVVSLFSEQPLAK.K + Oxidation (M)
2691.2894	2690.2821	2690.2223	22.2	46	66	1	---	K.KETYDWYPNHNTYFALMGNLR.F + Acetyl (N-term); Oxidation (M)

No match to: 1074.5422, 1076.4446, 1130.5526, 1216.6058, 1249.5702, 1377.7060, 1416.7192, 1433.7494, 1489.7779, 1501.7393, 1510.7817, 1515.7510, 1637.8400, 1701.9053, 1790.8998, 1948.0534, 2672.2597, 2748.3168, 3177.6461

5. RAB21_MOUSE **Mass:** 24490 **Score:** 39 **Expect:** 2.2 **Matches:** 5

Ras-related protein Rab-21 OS=Mus musculus GN=Rab21 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1216.6058	1215.5985	1215.5956	2.42	188	200	1	---	R.AKGNGSSQAGAAR.R + Acetyl (N-term)
1249.5702	1248.5629	1248.5656	-2.14	178	187	0	---	R.MIETAQVDER.A + Acetyl (N-term); Oxidation (M)
1359.7067	1358.6995	1358.7558	-41.46	46	57	0	---	K.HITTLQASFLTK.K
1487.8390	1486.8317	1486.8508	-12.78	46	58	1	---	K.HITTLQASFLTKK.L
1790.8998	1789.8926	1789.8889	2.07	117	131	1	---	R.KMLGNEICLCIVGNK.I + Acetyl (N-term)

No match to: 1074.5422, 1076.4446, 1130.5526, 1377.7060, 1416.7192, 1433.7494, 1489.7779, 1501.7393, 1510.7817, 1515.7510, 1637.8400, 1679.8974, 1701.9053, 1948.0534, 2672.2597, 2691.2894, 2748.3168, 3177.6461

6. GRID1_MOUSE **Mass:** 113142 **Score:** 37 **Expect:** 3.3 **Matches:** 8

Glutamate receptor delta-1 subunit OS=Mus musculus GN=Grid1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1130.5526	1129.5454	1129.5992	-47.69	354	363	1	---	R.KSTKPWNGGR.S
1359.7067	1358.6995	1358.6792	14.9	536	546	0	---	R.YMDYSVGILIK.K + Acetyl (N-term); Oxidation (M)
1416.7192	1415.7119	1415.6438	48.1	343	353	0	---	K.WHSMASLNCIR.K + Acetyl (N-term)
1433.7494	1432.7421	1432.7133	20.1	372	384	0	---	K.GHITGLTGVMEFR.E + Oxidation (M)
1501.7393	1500.7321	1500.7467	-9.74	420	433	0	---	K.GLNGSLQERPMGSR.L
1515.7510	1514.7437	1514.7803	-24.12	535	546	1	---	K.RYMDYSVGILIK.K + Acetyl (N-term); Oxidation (M)
1790.8998	1789.8926	1789.9145	-12.25	355	370	1	---	K.STKPWNGGRSMLDTIK.K
2748.3168	2747.3096	2747.3840	-27.12	983	1009	0	---	K.TPIPMSFQPVPGGVLPEALDTSHGTSI.-

No match to: 1074.5422, 1076.4446, 1216.6058, 1249.5702, 1377.7060, 1487.8390, 1489.7779, 1510.7817, 1637.8400, 1679.8974, 1701.9053, 1948.0534, 2672.2597, 2691.2894, 3177.6461

7. ELL2_MOUSE **Mass:** 72681 **Score:** 35 **Expect:** 4.9 **Matches:** 5

RNA polymerase II elongation factor ELL2 OS=Mus musculus GN=Ell2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1074.5422	1073.5349	1073.5717	-34.24	281	289	0	---	R.QTLDLELSR.K
1216.6058	1215.5985	1215.5844	11.7	291	301	0	---	K.LNPSQNASTSR.S + Acetyl (N-term)
1416.7192	1415.7119	1415.6939	12.7	1	14	1	14	-.MAAGGAAGLREEQR.Y
1501.7393	1500.7321	1500.7208	7.49	599	610	1	---	K.IKQSSPNYHEEK.Y + Acetyl (N-term)
1679.8974	1678.8901	1678.9366	-27.67	239	254	0	---	K.NSLGAILQQVANLNPK.D

No match to: 1076.4446, 1130.5526, 1249.5702, 1359.7067, 1377.7060, 1433.7494, 1487.8390, 1489.7779, 1510.7817, 1515.7510, 1637.8400, 1701.9053, 1790.8998, 1948.0534, 2672.2597, 2691.2894, 2748.3168, 3177.6461

8. ENC1_MOUSE **Mass:** 67240 **Score:** 33 **Expect:** 7.6 **Matches:** 6

Ectoderm-neural cortex protein 1 OS=Mus musculus GN=Enc1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1074.5422	1073.5349	1073.4924	39.6	1 -	9	0	---	-.MSVSVHENR.K + Oxidation (M)
1249.5702	1248.5629	1248.5849	-17.59	70 -	80	0	---	R.YFEAMFSGGLK.E
1377.7060	1376.6988	1376.7663	-49.08	319 -	330	1	---	K.EIIPKADIPSPR.K + Acetyl (N-term)
1679.8974	1678.8901	1678.8791	6.59	11 -	25	1	---	K.SRASSGSINIYLFHK.S
1701.9053	1700.8981	1700.8709	16.0	540 -	553	1	---	K.LYVVGGYFGIQRCK.T + Acetyl (N-term)
2748.3168	2747.3096	2747.3323	-8.29	110 -	133	0	---	R.VIINEENAESLLEAGDMLEFQDIR.D

No match to: 1076.4446, 1130.5526, 1216.6058, 1359.7067, 1416.7192, 1433.7494, 1487.8390, 1489.7779, 1501.7393, 1510.7817, 1515.7510, 1637.8400, 1790.8998, 1948.0534, 2672.2597, 2691.2894, 3177.6461

9. CKP2L_MOUSE **Mass:** 83689 **Score:** 32 **Expect:** 9.4 **Matches:** 7

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
1130.5526	1129.5454	1129.5437	1.43	138 -	146	0	---	R.QCPDIQELK.T
1249.5702	1248.5629	1248.6020	-31.29	523 -	532	0	---	K.IDSTLTECLR.L + Acetyl (N-term)
1359.7067	1358.6995	1358.6864	9.62	138 -	148	1	---	R.QCPDIQELKTK.Q
1377.7060	1376.6988	1376.6969	1.31	522 -	532	1	---	K.KIDSTLTECLR.L + Acetyl (N-term)
1416.7192	1415.7119	1415.7270	-10.61	446 -	459	1	---	R.KGAPSATQTHPHGK.K
1501.7393	1500.7321	1500.6878	29.5	1 -	15	0	---	-.MVGPGPTASAAAEER.W + Acetyl (N-term); Oxidation (M)
1637.8400	1636.8327	1636.8757	-26.27	255 -	268	0	---	K.SRPRPTVADSTRPR.E + Acetyl (N-term)

No match to: 1074.5422, 1076.4446, 1216.6058, 1433.7494, 1487.8390, 1489.7779, 1510.7817, 1515.7510, 1679.8974, 1701.9053, 1790.8998, 1948.0534, 2672.2597, 2691.2894, 2748.3168, 3177.6461

10. ZUFSP_MOUSE **Mass:** 66863 **Score:** 32 **Expect:** 10 **Matches:** 4

Zinc finger with UFM1-specific peptidase domain protein OS=Mus musculus GN=Zufsp PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1130.5526	1129.5454	1129.5702	-22.02	439 -	446	1	---	K.CRIIDFHK.S + Acetyl (N-term)
1216.6058	1215.5985	1215.5996	-0.91	65 -	75	0	---	K.LAAVQYGHSDR.K
1433.7494	1432.7421	1432.7092	23.0	525 -	536	1	16	K.QDMEASSLRQLR.K
1790.8998	1789.8926	1789.8339	32.8	161 -	175	1	---	K.IEGCSQDMEIHVKTK.H + Oxidation (M)

No match to: 1074.5422, 1076.4446, 1249.5702, 1359.7067, 1377.7060, 1416.7192, 1487.8390, 1489.7779, 1501.7393, 1510.7817, 1515.7510, 1637.8400, 1679.8974, 1701.9053, 1948.0534, 2672.2597, 2691.2894, 2748.3168, 3177.6461

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (1074.5422,1+) : <no title>

Query2 (1076.4446,1+) : <no title>

Query3 (1130.5526,1+) : <no title>

Query4 (1216.6058,1+) : <no title>

Query5 (1249.5702,1+) : <no title>

Query6 (1359.7067,1+) : <no title>

Query7 (1377.7060,1+) : <no title>

Query8 (1416.7192,1+) : <no title>

Query9 (1433.7494,1+) : <no title>

Query10 (1487.8390,1+) : <no title>

Query11 (1489.7779,1+) : <no title>

Query12 (1501.7393,1+) : <no title>

Query13 (1510.7817,1+) : <no title>

Query14 (1515.7510,1+) : <no title>

Query15 (1637.8400,1+) : <no title>

Query16 (1679.8974,1+) : <no title>

Query17 (1701.9053,1+) : <no title>

Query18 (1790.8998,1+) : <no title>

Query19 (1948.0534,1+) : <no title>

Query20 (2672.2597,1+) : <no title>

Query21 (2691.2894,1+) : <no title>

Query22 (2748.3168,1+) : <no title>

Query23 (3177.6461,1+) : <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 : **20 May 2013 at 02:36:18 GMT**

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

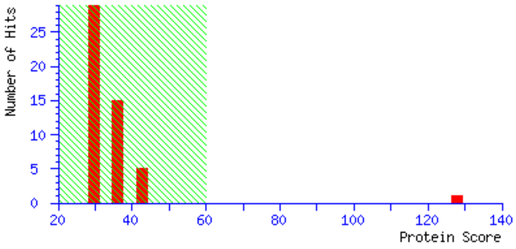
Top Score : **128 for IPI00828912, Tax_Id=10090 Gene_Symbol=1810030J14Rik mucosal pentraxin precursor**

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.	**IPI00828912**	24679	128	Tax_Id=10090 Gene_Symbol=1810030J14Rik mucosal pentraxin precursor
2.	**IPI00918331**	68855	44	Tax_Id=10090 Gene_Symbol=Brwd1 Uncharacterized protein
3.	**IPI00886417**	46246	44	Tax_Id=10090 Gene_Symbol=Brwd1 Uncharacterized protein
4.	**IPI00987122**	20749	42	Tax_Id=10090 Gene_Symbol=Gm6744 uncharacterized protein C3orf24 homolog
5.	**IPI00989199**	20849	41	Tax_Id=10090 Gene_Symbol=Gm6744 uncharacterized protein C3orf24 homolog
6.	**IPI00885883**	20677	40	Tax_Id=10090 Gene_Symbol=Dohh Uncharacterized protein
7.	**IPI00380894**	59017	37	Tax_Id=10090 Gene_Symbol=Shisa6 Protein shisa-6 homolog
8.	**IPI00970738**	27889	37	Tax_Id=10090 Gene_Symbol=Ccdc127 Uncharacterized protein
9.	**IPI00131843**	30661	36	Tax_Id=10090 Gene_Symbol=Ccdc127 Isoform 1 of Coiled-coil domain-containing protein 127
10.	**IPI00112297**	27692	36	Tax_Id=10090 Gene_Symbol=Ces7 Uncharacterized protein

Results List

1. IPI00828912 **Mass:** 24679 **Score:** 128 **Expect:** 9.4e-009 **Matches:** 4

Tax_Id=10090 Gene_Symbol=1810030J14Rik mucosal pentraxin precursor

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1051.5584	1050.5511	1050.5458	5.06	103 -	112	0	25	K.APTNLPDPAR.I
2082.0179	2081.0106	2081.0218	-5.37	58 -	74	0	30	K.TFTDLTRPYSIFSYNTR.N
2483.2254	2482.2181	2482.2533	-14.18	167 -	187	0	---	K.QSFVGEIWDVSLWDHVVPLEK.V
2590.2700	2589.2627	2589.2798	-6.61	113 -	135	0	33	R.ICVNWESGSGIAEFWLNGKPLGR.K

No match to: 987.5062, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2020.0256, 2036.0083, 2045.0380, 2067.3556, 2505.2273, 2572.2604, 2605.2673, 2691.2646, 2748.2878

2. IPI00918331 **Mass:** 68855 **Score:** 44 **Expect:** 2.4 **Matches:** 6

Tax_Id=10090 Gene_Symbol=Brwd1 Uncharacterized protein

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
987.5062	986.4989	986.5257	-27.20	433 -	441	1	---	R.RSGQVEGVR.Q
2020.0256	2019.0183	2019.0135	2.36	206 -	223	0	1	R.IMLSAGHDGSIFIWDITK.G + Oxidation (M)
2036.0083	2035.0010	2035.0197	-9.15	120 -	135	1	---	R.FEQLEWRSILLDMSAR.I + Acetyl (N-term)
2483.2254	2482.2181	2482.1726	18.3	73 -	93	1	---	R.MYFLGFDAPEKIAELESHTDK.V + Acetyl (N-term)
2572.2604	2571.2531	2571.2639	-4.22	152 -	174	0	---	K.VTMIAWNQDDSTVVTAVNDHVLK.V + Oxidation (M)
2590.2700	2589.2627	2589.1765	33.3	84 -	105	1	---	K.IAELESHTDKVDSIQFCNNGDR.F + Acetyl (N-term)

No match to: 1051.5584, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2045.0380, 2067.3556, 2082.0179, 2505.2273, 2605.2673, 2691.2646, 2748.2878

3. IPI00886417 **Mass:** 46246 **Score:** 44 **Expect:** 2.6 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Brwd1 Uncharacterized protein

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
2020.0256	2019.0183	2019.0135	2.36	195 -	212	0	1	R.IMLSAGHDGSIFIWDITK.G + Oxidation (M)
2036.0083	2035.0010	2035.0197	-9.15	109 -	124	1	---	R.FEQLEWRSILLDMSAR.I + Acetyl (N-term)
2483.2254	2482.2181	2482.1726	18.3	62 -	82	1	---	R.MYFLGFDAPEKIAELESHTDK.V + Acetyl (N-term)
2572.2604	2571.2531	2571.2639	-4.22	141 -	163	0	---	K.VTMIAWNQDDSTVVTAVNDHVLK.V + Oxidation (M)
2590.2700	2589.2627	2589.1765	33.3	73 -	94	1	---	K.IAELESHTDKVDSIQFCNNGDR.F + Acetyl (N-term)

No match to: 987.5062, 1051.5584, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2045.0380, 2067.3556, 2082.0179, 2505.2273, 2605.2673, 2691.2646, 2748.2878

4. IPI00987122 **Mass:** 20749 **Score:** 42 **Expect:** 3.8 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Gm6744 uncharacterized protein C3orf24 homolog

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
2020.0256	2019.0183	2018.9983	9.93	64 -	81	1	---	R.MEAVKGSELSGYLPQPQK.G + Acetyl (N-term); Oxidation (M)
2505.2273	2504.2200	2504.2610	-16.34	22 -	41	1	---	R.HTTPIFPPRHPFMVLPCFPR.S + Acetyl (N-term); Oxidation (M)
2590.2700	2589.2627	2589.2474	5.90	1 -	21	0	---	-.MAGYQLWSPWNPLDESLQWLR.H
2605.2673	2604.2600	2604.2854	-9.74	42 -	63	1	---	R.SSSDLEVQQCFREVAVILETPR.M + Acetyl (N-term)

No match to: 987.5062, 1051.5584, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2036.0083, 2045.0380, 2067.3556, 2082.0179, 2483.2254, 2572.2604, 2691.2646, 2748.2878

5. IPI00989199 **Mass:** 20849 **Score:** 41 **Expect:** 5.1 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Gm6744 uncharacterized protein C3orf24 homolog

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
2020.0256	2019.0183	2018.9983	9.93	64 -	81	1	---	R.MEAVKGSELSGYLPQPQK.G + Acetyl (N-term); Oxidation (M)
2505.2273	2504.2200	2504.2610	-16.34	22 -	41	1	---	R.HTTPIFPPRHPFMVLPCFPR.S + Acetyl (N-term); Oxidation (M)
2590.2700	2589.2627	2589.2474	5.90	1 -	21	0	---	-.MAGYQLWSPWNPLDESLQWLR.H
2605.2673	2604.2600	2604.2854	-9.74	42 -	63	1	---	R.SSSDLEVQQCFREVAVILETPR.M + Acetyl (N-term)

No match to: 987.5062, 1051.5584, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2036.0083, 2045.0380, 2067.3556, 2082.0179, 2483.2254, 2572.2604, 2691.2646, 2748.2878

6. IPI00885883 **Mass:** 20677 **Score:** 40 **Expect:** 6.5 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Dohh Uncharacterized protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1051.5584	1050.5511	1050.5280	21.9	179 -	188	1	---	R.AMFALRNVGG.- + Oxidation (M)
1558.8171	1557.8099	1557.8151	-3.35	164 -	176	0	---	R.EALLDEARPLFER.Y
2082.0179	2081.0106	2081.0827	-34.63	70 -	88	0	---	R.AIPVLADVLQDTSQEPMVR.H
2483.2254	2482.2181	2482.1620	22.6	46 -	66	1	---	R.GFEDSSALLKHELAYCLGQMR.D + Acetyl (N-term); Oxidation (M)

No match to: 987.5062, 1113.5603, 1927.0615, 1999.0384, 2020.0256, 2036.0083, 2045.0380, 2067.3556, 2505.2273, 2572.2604, 2590.2700, 2605.2673, 2691.2646, 2748.2878

7. IPI00380894 **Mass:** 59017 **Score:** 37 **Expect:** 12 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Shisa6 Protein shisa-6 homolog

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1113.5603	1112.5530	1112.6050	-46.75	39 -	49	1	---	R.TLNAGAVGGRR.A + Acetyl (N-term)
1558.8171	1557.8099	1557.7675	27.2	164 -	177	1	---	K.VVSPGPENKYDPEK.D
2590.2700	2589.2627	2589.2857	-8.87	227 -	249	1	---	R.QQGPIPIAHCERETISAIDTSPK.E + Acetyl (N-term)
2691.2646	2690.2573	2690.2772	-7.39	499 -	520	1	---	R.RHNTVEQLHYIPGHHTCYTASK.T + Acetyl (N-term)
2748.2878	2747.2806	2747.2755	1.83	466 -	491	1	---	R.MTKMHSHPSASNNSYATLGQSQTAAK.R

No match to: 987.5062, 1051.5584, 1927.0615, 1999.0384, 2020.0256, 2036.0083, 2045.0380, 2067.3556, 2082.0179, 2483.2254, 2505.2273, 2572.2604, 2605.2673

8. IPI00970738 **Mass:** 27889 **Score:** 37 **Expect:** 13 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Ccdc127 Uncharacterized protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
987.5062	986.4989	986.5396	-41.26	181 -	188	1	---	R.SARLELEK.S + Acetyl (N-term)
2036.0083	2035.0010	2034.9806	10.1	1 -	17	0	---	-.MNNLNDPPNWNIRPNAR.A
2572.2604	2571.2531	2571.2527	0.17	194 -	217	1	---	R.TSVDPVAADLEMAAGLSDIFKHDK.H + Acetyl (N-term)
2605.2673	2604.2600	2604.3827	-47.13	26 -	46	1	---	K.WNYALLVPMLGLAAFRWIWSR.E + Acetyl (N-term)

No match to: 1051.5584, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2020.0256, 2045.0380, 2067.3556, 2082.0179, 2483.2254, 2505.2273, 2590.2700, 2691.2646, 2748.2878

9. IPI00131843 **Mass:** 30661 **Score:** 36 **Expect:** 16 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Ccdc127 Isoform 1 of Coiled-coil domain-containing protein 127

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
987.5062	986.4989	986.5396	-41.26	181 -	188	1	---	R.SARLELEK.S + Acetyl (N-term)
2036.0083	2035.0010	2034.9806	10.1	1 -	17	0	---	-.MNNLNDPPNWNIRPNAR.A
2572.2604	2571.2531	2571.2527	0.17	194 -	217	1	---	R.TSVDPVAADLEMAAGLSDIFKHDK.H + Acetyl (N-term)

2605.2673	2604.2600	2604.3827	-47.13	26 -	46	1	---	K.WNYALLVPMLGLAAFRWIWSR.E + Acetyl (N-term)

No match to: 1051.5584, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2020.0256, 2045.0380, 2067.3556, 2082.0179, 2483.2254, 2505.2273, 2590.2700, 2691.2646, 2748.2878

10. IPI00112297 **Mass:** 27692 **Score:** 36 **Expect:** 17 **Matches:** 3

Tax_Id=10090 Gene_Symbol=Ces7 Uncharacterized protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
2082.0179	2081.0106	2080.9987	5.75	138 -	155	1	---	K.GDVVMFEEATEEEKLLSR.K
2590.2700	2589.2627	2589.2681	-2.10	1 -	22	0	8	-.MSSMVLFISITCLYVFSSFSVR.T + Oxidation (M)
2605.2673	2604.2600	2604.2458	5.45	129 -	151	1	---	R.FVFGGPFLKGDVVMFEEATEEEK.L

No match to: 987.5062, 1051.5584, 1113.5603, 1558.8171, 1927.0615, 1999.0384, 2020.0256, 2036.0083, 2045.0380, 2067.3556, 2483.2254, 2505.2273, 2572.2604, 2691.2646, 2748.2878

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Acetyl (N-term),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ±50 ppm
Fragment Mass Tolerance: ±0.5 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (987.5062,1+) : <no title>
Query2 (1051.5584,1+) : <no title>
Query3 (1113.5603,1+) : <no title>
Query4 (1558.8171,1+) : <no title>
Query5 (1927.0615,1+) : <no title>
Query6 (1999.0384,1+) : <no title>
Query7 (2020.0256,1+) : <no title>
Query8 (2036.0083,1+) : <no title>
Query9 (2045.0380,1+) : <no title>
Query10 (2067.3556,1+) : <no title>
Query11 (2082.0179,1+) : <no title>
Query12 (2483.2254,1+) : <no title>
Query13 (2505.2273,1+) : <no title>
Query14 (2572.2604,1+) : <no title>
Query15 (2590.2700,1+) : <no title>
Query16 (2605.2673,1+) : <no title>
Query17 (2691.2646,1+) : <no title>
Query18 (2748.2878,1+) : <no title>

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

MATRIX SCIENCE Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

Database : **IPI_mouse (59534 sequences; 26627161 residues)**

Timestamp : **20 May 2013 at 02:36:23 GMT**

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

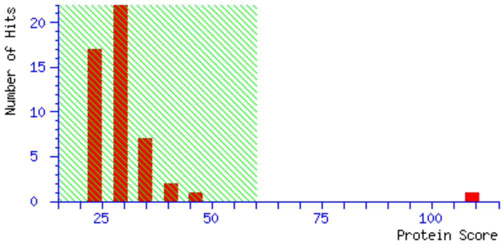
Top Score : **109 for IPI00828912, Tax_Id=10090 Gene_Symbol=1810030J14Rik mucosal pentraxin precursor**

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.	**IPI00828912**	24679	109	Tax_Id=10090 Gene_Symbol=1810030J14Rik mucosal pentraxin precursor
2.	**IPI00970738**	27889	44	Tax_Id=10090 Gene_Symbol=Ccdc127 Uncharacterized protein
3.	**IPI00131843**	30661	43	Tax_Id=10090 Gene_Symbol=Ccdc127 Isoform 1 of Coiled-coil domain-containing protein 127
4.	**IPI00136152**	12409	40	Tax_Id=10090 Gene_Symbol=5430411C19Rik Putative uncharacterized protein
5.	**IPI00515393**	71996	37	Tax_Id=10090 Gene_Symbol=Rpa1 replication protein A 70 kDa DNA-binding subunit isoform 1
6.	**IPI00975060**	128420	37	Tax_Id=10090 Gene_Symbol=Kif1a Uncharacterized protein (Fragment)
7.	**IPI00895307**	76327	36	Tax_Id=10090 Gene_Symbol=Ccdc30 Isoform 2 of Coiled-coil domain-containing protein 30
8.	**IPI00224237**	105043	35	Tax_Id=10090 Gene_Symbol=Tmtc3 Isoform 1 of Transmembrane and TPR repeat-containing protein 3
9.	**IPI00649923**	14695	34	Tax_Id=10090 Gene_Symbol=Tgtp2;Tgtp1 Uncharacterized protein
10.	**IPI01027494**	14245	33	Tax_Id=10090 Gene_Symbol=Wdfy3 Protein

Results List

1. IPI00828912 **Mass:** 24679 **Score:** 109 **Expect:** 7.5e-007 **Matches:** 2

Tax_Id=10090 Gene_Symbol=1810030J14Rik mucosal pentraxin precursor

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
2082.0797	2081.0725	2081.0218	24.3	58 -	74	0	57	K.TFTDLTRPYSIFSYNTR.N
2590.3160	2589.3087	2589.2798	11.2	113 -	135	0	32	R.ICVNWESGSGIAEFWLNGKPLGR.K

No match to: 987.5855, 1113.1180, 1113.6457, 1247.6863, 2020.0703, 2036.0456, 2045.8648, 2067.3899, 2505.2555, 2572.2969, 2592.2864

2. IPI00970738 **Mass:** 27889 **Score:** 44 **Expect:** 2.2 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Ccdc127 Uncharacterized protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
987.5855	986.5783	986.5396	39.2	181 -	188	1	---	R.SARLELEK.S + Acetyl (N-term)
2036.0456	2035.0383	2034.9806	28.4	1 -	17	0	---	-.MNNLNDPPNWNIRPNAR.A
2572.2969	2571.2896	2571.2527	14.4	194 -	217	1	---	R.TSVDPVAADLEMAAGLSDIFKHDK.H + Acetyl (N-term)
2592.2864	2591.2791	2591.2225	21.9	2 -	25	1	---	M.NNLNDPPNWNIRPNARADGGDGSK.W

No match to: 1113.1180, 1113.6457, 1247.6863, 2020.0703, 2045.8648, 2067.3899, 2082.0797, 2505.2555, 2590.3160

3. IPI00131843 **Mass:** 30661 **Score:** 43 **Expect:** 3.1 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Ccdc127 Isoform 1 of Coiled-coil domain-containing protein 127

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
987.5855	986.5783	986.5396	39.2	181 -	188	1	---	R.SARLELEK.S + Acetyl (N-term)
2036.0456	2035.0383	2034.9806	28.4	1 -	17	0	---	-.MNNLNDPPNWNIRPNAR.A
2572.2969	2571.2896	2571.2527	14.4	194 -	217	1	---	R.TSVDPVAADLEMAAGLSDIFKHDK.H + Acetyl (N-term)
2592.2864	2591.2791	2591.2225	21.9	2 -	25	1	---	M.NNLNDPPNWNIRPNARADGGDGSK.W

No match to: 1113.1180, 1113.6457, 1247.6863, 2020.0703, 2045.8648, 2067.3899, 2082.0797, 2505.2555, 2590.3160

4. IPI00136152 **Mass:** 12409 **Score:** 40 **Expect:** 6.4 **Matches:** 3

Tax_Id=10090 Gene_Symbol=5430411C19Rik Putative uncharacterized protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
2020.0703	2019.0630	2018.9765	42.9	1 -	19	0	---	-.MSQPDALCSQSTAQALLAK.N
2036.0456	2035.0383	2035.0633	-12.28	49 -	65	1	---	K.SHRACEEILPSQQLVLR.L
2082.0797	2081.0725	2080.9881	40.5	20 -	38	1	---	K.NASVSSVLAMRSCDLSEQK.F

No match to: 987.5855, 1113.1180, 1113.6457, 1247.6863, 2045.8648, 2067.3899, 2505.2555, 2572.2969, 2590.3160, 2592.2864

5. IPI00515393 **Mass:** 71996 **Score:** 37 **Expect:** 11 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Rpa1 replication protein A 70 kDa DNA-binding subunit isoform 1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
987.5855	986.5783	986.5509	27.8	233 -	240	1	---	R.VTNKSQIR.T + Acetyl (N-term)
1247.6863	1246.6790	1246.6306	38.9	520 -	529	0	---	K.VIDQQNGLYR.C + Acetyl (N-term)
2020.0703	2019.0630	2019.0160	23.3	247 -	264	1	---	R.GEGKLFSLELVDESGEIR.A + Acetyl (N-term)
2082.0797	2081.0725	2081.0476	11.9	92 -	109	1	---	R.MQPKPHGNPYGEQSVLRK.L + Oxidation (M)
2505.2555	2504.2482	2504.3023	-21.61	188 -	213	0	---	K.AYGASKPFGKPAGTGLLQPSGGTQSK.V

No match to: 1113.1180, 1113.6457, 2036.0456, 2045.8648, 2067.3899, 2572.2969, 2590.3160, 2592.2864

6. IPI00975060 **Mass:** 128420 **Score:** 37 **Expect:** 11 **Matches:** 7

Tax_Id=10090 Gene_Symbol=Kif1a Uncharacterized protein (Fragment)

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
987.5855	986.5783	986.5913	-13.20	1 -	8	0	---	-.SVLTWLLR.E
1113.6457	1112.6384	1112.6454	-6.32	839 -	846	1	---	K.TRHYLLLR.E + Acetyl (N-term)
2020.0703	2019.0630	2019.0306	16.1	95 -	114	0	---	K.LTNALVGMSPSSSLSALSSR.A + Acetyl (N-term)
2036.0456	2035.0383	2035.0255	6.26	95 -	114	0	---	K.LTNALVGMSPSSSLSALSSR.A + Acetyl (N-term); Oxidation (M)
2045.8648	2044.8575	2044.9313	-36.07	308 -	325	0	---	R.TPCAETPAEPVDWAFAQR.E
2572.2969	2571.2896	2571.1852	40.6	684 -	704	0	---	R.TFYQFEAAWDSSMHNSLLLNR.V + Acetyl (N-term)
2592.2864	2591.2791	2591.2321	18.1	712 -	733	0	---	K.IYMTLSAYIEMENCTQPAVITK.D + Oxidation (M)

No match to: 1113.1180, 1247.6863, 2067.3899, 2082.0797, 2505.2555, 2590.3160

7. IPI00895307 **Mass:** 76327 **Score:** 36 **Expect:** 16 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Ccdc30 Isoform 2 of Coiled-coil domain-containing protein 30

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1113.6457	1112.6384	1112.6077	27.6	144 -	152	0	---	R.LDEEILALR.N + Acetyl (N-term)
1247.6863	1246.6790	1246.6517	21.9	126 -	136	1	---	K.LKESGTTDLQR.A
2020.0703	2019.0630	2019.0194	21.6	499 -	515	1	---	R.KLLEQVTDQEELICSSK.C
2036.0456	2035.0383	2034.9429	46.9	164 -	180	1	---	K.YLTSGEKTSCQHQGELR.E + Acetyl (N-term)
2590.3160	2589.3087	2589.3546	-17.70	476 -	497	1	---	K.IEMEKVFQGQIMAQNDILLLEK.R

No match to: 987.5855, 1113.1180, 2045.8648, 2067.3899, 2082.0797, 2505.2555, 2572.2969, 2592.2864

8. IPI00224237 **Mass:** 105043 **Score:** 35 **Expect:** 17 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Tmtc3 Isoform 1 of Transmembrane and TPR repeat-containing protein 3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
987.5855	986.5783	986.5582	20.3	581 -	588	1	---	K.MNKPLKAK.E + Acetyl (N-term); Oxidation (M)
2505.2555	2504.2482	2504.3611	-45.08	528 -	549	1	---	R.IAPNHLNVYINLANLIRANESR.L
2572.2969	2571.2896	2571.3842	-36.80	637 -	659	1	---	K.LALFNSAILMQESGEVKLRPEAR.K
2592.2864	2591.2791	2591.3894	-42.56	124 -	148	0	12	R.SSMIAALLFAVHPIHTEAVTGVVGR.A + Oxidation (M)

No match to: 1113.1180, 1113.6457, 1247.6863, 2020.0703, 2036.0456, 2045.8648, 2067.3899, 2082.0797, 2590.3160

9. IPI00649923 **Mass:** 14695 **Score:** 34 **Expect:** 26 **Matches:** 3

Tax_Id=10090 Gene_Symbol=Tgtp2;Tgtp1 Uncharacterized protein

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1113.6457	1112.6384	1112.6917	-47.92	41 -	50	1	---	K.AVSVIEKVLR.D
1247.6863	1246.6790	1246.6227	45.2	85 -	97	0	---	K.GAAPTGAIETTMK.R
2590.3160	2589.3087	2589.2771	12.2	17 -	37	1	---	R.ESKIISEYDITLIMTYIEENK.L + Acetyl (N-term); Oxidation (M)

No match to: 987.5855, 1113.1180, 2020.0703, 2036.0456, 2045.8648, 2067.3899, 2082.0797, 2505.2555, 2572.2969, 2592.2864

10. IPI01027494 **Mass:** 14245 **Score:** 33 **Expect:** 32 **Matches:** 2

Tax_Id=10090 Gene_Symbol=Wdfy3 Protein

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
2082.0797	2081.0725	2081.0258	22.4	31 -	47	1	---	R.NQQVMCEAGLHARLLQR.C + Acetyl (N-term); Oxidation (M)
2592.2864	2591.2791	2591.2009	30.2	48 -	69	1	10	R.CGAALADEDHSLHPPLQRMFER.L + Acetyl (N-term)

No match to: 987.5855, 1113.1180, 1113.6457, 1247.6863, 2020.0703, 2036.0456, 2045.8648, 2067.3899, 2505.2555, 2572.2969, 2590.3160

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (987.5855,1+) : <no title>

Query2 (1113.1180,1+) : <no title>

Query3 (1113.6457,1+) : <no title>

Query4 (1247.6863,1+) : <no title>

Query5 (2020.0703,1+) : <no title>

Query6 (2036.0456,1+) : <no title>

Query7 (2045.8648,1+) : <no title>

Query8 (2067.3899,1+) : <no title>

Query9 (2082.0797,1+) : <no title>

Query10 (2505.2555,1+) : <no title>

Query11 (2572.2969,1+) : <no title>

Query12 (2590.3160,1+) : <no title>

Query13 (2592.2864,1+) : <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 : **20 May 2013 at 01:34:21 GMT**

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

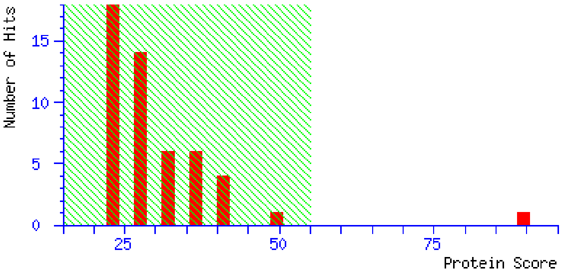
Top Score : **90 for 1433Z_MOUSE, 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1**

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.	**1433Z_MOUSE**	27925	90	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1
2.	**1433B_MOUSE**	28183	50	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3
3.	**1433F_MOUSE**	28365	43	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2
4.	**ODO2_MOUSE**	49306	41	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1
5.	**PMS2_MOUSE**	96192	39	Mismatch repair endonuclease PMS2 OS=Mus musculus GN=Pms2 PE=1 SV=1
6.	**CR034_MOUSE**	103669	39	Uncharacterized protein C18orf34 homolog OS=Mus musculus PE=2 SV=1
7.	**EGFR_MOUSE**	138187	37	Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=1
8.	**1433E_MOUSE**	29326	36	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1
9.	**DIDO1_MOUSE**	248621	35	Death-inducer obliterator 1 OS=Mus musculus GN=Dido1 PE=1 SV=4
10.	**1433G_MOUSE**	28456	35	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2

Results List

1. 1433Z_MOUSE **Mass:** 27925 **Score:** 90 **Expect:** 1.8e-005 **Matches:** 7

14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
804.4280	803.4207	803.4025	22.7	69 -	75	1	---	K.TEGAEKK.Q + Acetyl (N-term)
1108.5937	1107.5864	1107.5495	33.3	159 -	167	0	---	K.EMQPTHPIR.L
1124.5862	1123.5789	1123.5444	30.7	159 -	167	0	---	K.EMQPTHPIR.L + Oxidation (M)
1189.6879	1188.6806	1188.6536	22.7	213 -	222	0	24	K.DSTLIMQLLR.D
1548.7299	1547.7226	1547.7063	10.5	28 -	41	0	19	K.SVTEQGAELSNEER.N
2160.1359	2159.1286	2159.1143	6.62	86 -	103	1	---	K.IETELRDICNDVLSLLEK.F
2317.2136	2316.2064	2316.2041	0.96	168 -	187	0	---	R.LGLALNFSVFYYEILNSPEK.A

No match to: 848.3718, 854.4174, 932.5303, 1352.6935, 1419.7566, 1440.7325, 1557.9011, 1576.7662, 2062.9930, 2331.2228, 2339.2135, 2355.1820, 2691.2805, 2748.3076, 2780.4173

2. 1433B_MOUSE **Mass:** 28183 **Score:** 50 **Expect:** 0.17 **Matches:** 5

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
1108.5937	1107.5864	1107.5495	33.3	161 -	169	0	---	K.EMQPTHPIR.L
1124.5862	1123.5789	1123.5444	30.7	161 -	169	0	---	K.EMQPTHPIR.L + Oxidation (M)
1189.6879	1188.6806	1188.6536	22.7	215 -	224	0	24	K.DSTLIMQLLR.D
1419.7566	1418.7494	1418.7518	-1.69	59 -	70	1	---	R.SSWRVISSIEQK.T
2317.2136	2316.2064	2316.2041	0.96	170 -	189	0	---	R.LGLALNFSVFYYEILNSPEK.A

No match to: 804.4280, 848.3718, 854.4174, 932.5303, 1352.6935, 1440.7325, 1548.7299, 1557.9011, 1576.7662, 2062.9930, 2160.1359, 2331.2228, 2339.2135, 2355.1820, 2691.2805, 2748.3076, 2780.4173

3. 1433F_MOUSE **Mass:** 28365 **Score:** 43 **Expect:** 0.85 **Matches:** 3

14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1108.5937	1107.5864	1107.5448	37.6	133 -	142	0	---	R.YLAEVASGEK.K + Acetyl (N-term)
1189.6879	1188.6806	1188.6536	22.7	218 -	227	0	24	K.DSTLIMQLLR.D
1419.7566	1418.7494	1418.7518	-1.69	58 -	69	1	---	R.SSWRVISSIEQK.T

No match to: 804.4280, 848.3718, 854.4174, 932.5303, 1124.5862, 1352.6935, 1440.7325, 1548.7299, 1557.9011, 1576.7662, 2062.9930, 2160.1359, 2317.2136, 2331.2228, 2339.2135, 2355.1820, 2691.2805, 2748.3076, 2780.4173

4.

ODO2_MOUSE **Mass:** 49306 **Score:** 41 **Expect:** 1.3 **Matches:** 7

Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
854.4174	853.4101	853.4518	-48.90	219 -	225	1	2	K.GLRSEHR.E
1189.6879	1188.6806	1188.6503	25.5	135 -	145	0	---	K.VEGGTPLFTLR.K
1419.7566	1418.7494	1418.7405	6.22	314 -	326	0	---	R.DYIDISVAVATPR.G
1576.7662	1575.7589	1575.7827	-15.12	15 -	28	1	---	R.SLSAFQKGNCPLGR.R + Acetyl (N-term)
2339.2135	2338.2062	2338.1110	40.7	335 -	354	1	---	R.NVETMNYADIERTINELGEK.A

2355.1820	2354.1747	2354.1060	29.2	335 -	354	1	---	R.NVETMNYADIERTINELGEK.A + Oxidation (M)
2691.2805	2690.2732	2690.3188	-16.94	69 -	92	1	---	K.NDVITVQTPAFAESVTEGDVRWEK.A

No match to: 804.4280, 848.3718, 932.5303, 1108.5937, 1124.5862, 1352.6935, 1440.7325, 1548.7299, 1557.9011, 2062.9930, 2160.1359, 2317.2136, 2331.2228, 2748.3076, 2780.4173

5. PMS2_MOUSE **Mass:** 96192 **Score:** 39 **Expect:** 2.1 **Matches:** 8

Mismatch repair endonuclease PMS2 OS=Mus musculus GN=Pms2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
804.4280	803.4207	803.3926	35.0	638 -	643	0	---	K.HELSYR.K
848.3718	847.3646	847.4035	-45.98	408 -	414	1	---	K.STADEKR.V + Acetyl (N-term)
932.5303	931.5230	931.4875	38.1	638 -	644	1	---	K.HELSYRK.F
1440.7325	1439.7252	1439.6602	45.1	357 -	369	0	---	K.TSLIGMFDSDANK.L + Acetyl (N-term)
1548.7299	1547.7226	1547.7185	2.68	211 -	224	1	---	K.RHAVVCTSGTSGMK.E + Acetyl (N-term); Oxidation (M)
2317.2136	2316.2064	2316.1534	22.9	668 -	687	0	---	K.SMFAEMEILGQFNLGFIVTK.L + Acetyl (N-term)
2331.2228	2330.2155	2330.1763	16.8	180 -	199	1	---	K.EYSKMVQVLQAYCIISAGVR.V + Oxidation (M)
2748.3076	2747.3003	2747.3914	-33.16	664 -	687	1	---	K.EISKSMFAEMEILGQFNLGFIVTK.L + Oxidation (M)

No match to: 854.4174, 1108.5937, 1124.5862, 1189.6879, 1352.6935, 1419.7566, 1557.9011, 1576.7662, 2062.9930, 2160.1359, 2339.2135, 2355.1820, 2691.2805, 2780.4173

6. CR034_MOUSE **Mass:** 103669 **Score:** 39 **Expect:** 2.2 **Matches:** 5

Uncharacterized protein C18orf34 homolog OS=Mus musculus PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
804.4280	803.4207	803.4211	-0.49	23 -	28	0	---	K.TCLQIK.E + Acetyl (N-term)
1189.6879	1188.6806	1188.6284	43.9	673 -	681	1	22	K.EIRIMNLER.T + Oxidation (M)
1419.7566	1418.7494	1418.7405	6.23	425 -	436	1	---	K.KTWDIELSNVSK.D
1548.7299	1547.7226	1547.7315	-5.72	377 -	389	0	---	R.ETQSTTNELENLK.K + Acetyl (N-term)
2160.1359	2159.1286	2159.0609	31.4	554 -	570	0	---	R.LYAIEETQFIEMQEFIR.R

No match to: 848.3718, 854.4174, 932.5303, 1108.5937, 1124.5862, 1352.6935, 1440.7325, 1557.9011, 1576.7662, 2062.9930, 2317.2136, 2331.2228, 2339.2135, 2355.1820, 2691.2805, 2748.3076, 2780.4173

7. EGFR_MOUSE **Mass:** 138187 **Score:** 37 **Expect:** 3.2 **Matches:** 6

Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1189.6879	1188.6806	1188.6350	38.4	347 -	357	0	12	K.DTLSINATNIK.H
1352.6935	1351.6862	1351.7169	-22.73	965 -	975	1	---	R.ELILEFSKMAR.D + Oxidation (M)
2317.2136	2316.2064	2316.2089	-1.09	358 -	377	1	---	K.HFKYCTAISGDLHILPVAFK.G
2331.2228	2330.2155	2330.1035	48.1	54 -	72	0	---	R.MYNNCEVVLGNLEITYVQR.N + Oxidation (M)
2339.2135	2338.2062	2338.3121	-45.31	430 -	451	1	---	R.TKQHGQFSLAVVGLNITSLGLR.S
2780.4173	2779.4100	2779.3341	27.3	1034 -	1059	1	---	R.TPLLSSLSATSNNSTVACINRNGSCR.V

No match to: 804.4280, 848.3718, 854.4174, 932.5303, 1108.5937, 1124.5862, 1419.7566, 1440.7325, 1548.7299, 1557.9011, 1576.7662, 2062.9930, 2160.1359, 2355.1820, 2691.2805, 2748.3076

8. 1433E_MOUSE **Mass:** 29326 **Score:** 36 **Expect:** 3.7 **Matches:** 2

14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1189.6879	1188.6806	1188.6536	22.7	216 -	225	0	24	K.DSTLIMQLLR.D
2331.2228	2330.2155	2330.1947	8.95	171 -	190	0	---	R.LGLALNFSVFYYEILNSPDR.A

No match to: 804.4280, 848.3718, 854.4174, 932.5303, 1108.5937, 1124.5862, 1352.6935, 1419.7566, 1440.7325, 1548.7299, 1557.9011, 1576.7662, 2062.9930, 2160.1359, 2317.2136, 2339.2135, 2355.1820, 2691.2805, 2748.3076, 2780.4173

9. DIDO1_MOUSE **Mass:** 248621 **Score:** 35 **Expect:** 4.8 **Matches:** 11

Death-inducer obliterator 1 OS=Mus musculus GN=Dido1 PE=1 SV=4

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Ions**	**Peptide**
804.4280	803.4207	803.3926	35.0	2178	-	2183	1	---	R.AKEWDR.S
848.3718	847.3646	847.3936	-34.31	2180	-	2185	1	---	K.EWDRSR.E
932.5303	931.5230	931.5338	-11.58	780	-	787	1	---	R.TKLLNESK.K
1352.6935	1351.6862	1351.7500	-47.18	381	-	393	0	---	K.IFQPVVEAPGAPK.C
1419.7566	1418.7494	1418.7042	31.9	1035	-	1047	0	---	R.SPPEGDTTLFLSR.L
1557.9011	1556.8938	1556.8384	35.5	571	-	585	0	---	K.LPPYSNMAGAKPAIK.K
2062.9930	2061.9857	2062.0405	-26.56	763	-	779	1	---	K.ELSMWTEKPTKSVIESR.T + Acetyl (N-term)
2317.2136	2316.2064	2316.1233	35.9	2103	-	2123	1	---	R.FEAGSKEKPLDEPEAQGLESR.Q
2339.2135	2338.2062	2338.1720	14.6	1916	-	1938	1	---	R.GGPPPSQFGAQRGPPPGHFVGPR.G + Acetyl (N-term)
2691.2805	2690.2732	2690.2644	3.26	38	-	61	1	---	R.EGAGDTEVDPSEQQPQQHNLSLRR.S
2780.4173	2779.4100	2779.3375	26.1	1345	-	1369	1	---	K.GEDTMSAAPLLDPIVQQFGQFSKDK.A + Acetyl (N-term); Oxidation (M)

No match to: 854.4174, 1108.5937, 1124.5862, 1189.6879, 1440.7325, 1548.7299, 1576.7662, 2160.1359, 2331.2228, 2355.1820, 2748.3076

10. 1433G_MOUSE **Mass:** 28456 **Score:** 35 **Expect:** 5.3 **Matches:** 2

14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1189.6879	1188.6806	1188.6536	22.7	218 -	227	0	24	K.DSTLIMQLLR.D
1419.7566	1418.7494	1418.7518	-1.69	58 -	69	1	---	R.SSWRVISSIEQK.T

No match to: 804.4280, 848.3718, 854.4174, 932.5303, 1108.5937, 1124.5862, 1352.6935, 1440.7325, 1548.7299, 1557.9011, 1576.7662, 2062.9930, 2160.1359, 2317.2136, 2331.2228, 2339.2135, 2355.1820, 2691.2805, 2748.3076, 2780.4173

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Acetyl (N-term),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ±50 ppm
Fragment Mass Tolerance: ±0.5 Da
Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (804.4280,1+) : <no title>

Query2 (848.3718,1+) : <no title>

Query3 (854.4174,1+) : <no title>

Query4 (932.5303,1+) : <no title>

Query5 (1108.5937,1+) : <no title>

Query6 (1124.5862,1+) : <no title>

Query7 (1189.6879,1+) : <no title>

Query8 (1352.6935,1+) : <no title>

Query9 (1419.7566,1+) : <no title>

Query10 (1440.7325,1+) : <no title>

Query11 (1548.7299,1+) : <no title>

Query12 (1557.9011,1+) : <no title>

Query13 (1576.7662,1+) : <no title>

Query14 (2062.9930,1+) : <no title>

Query15 (2160.1359,1+) : <no title>

Query16 (2317.2136,1+) : <no title>

Query17 (2331.2228,1+) : <no title>

Query18 (2339.2135,1+) : <no title>

Query19 (2355.1820,1+) : <no title>

Query20 (2691.2805,1+) : <no title>

Query21 (2748.3076,1+) : <no title>

Query22 (2780.4173,1+) : <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 : **20 May 2013 at 01:29:19 GMT**

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

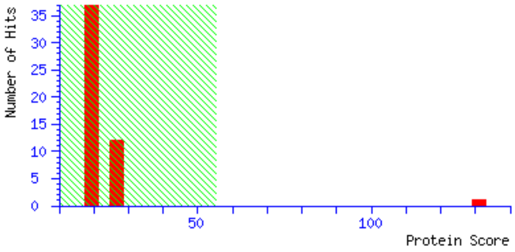
Top Score : **131 for GRP78_MOUSE, 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3**

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.	GRP78_MOUSE	72492	131	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3
2.	PRS10_MOUSE	44430	30	26S protease regulatory subunit S10B OS=Mus musculus GN=Psmc6 PE=1 SV=1
3.	FA18B_MOUSE	23575	30	Protein FAM18B OS=Mus musculus GN=Fam18b PE=1 SV=1
4.	P3C2A_MOUSE	192462	28	Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Mus musculus GN=Pik3c2a PE=1 SV=2
5.	IL18_MOUSE	22349	28	Interleukin-18 OS=Mus musculus GN=Il18 PE=1 SV=2
6.	TRHDE_MOUSE	117897	27	Thyrotropin-releasing hormone-degrading ectoenzyme OS=Mus musculus GN=Trhde PE=2 SV=1
7.	KLDC9_MOUSE	38845	25	Kelch domain-containing protein 9 OS=Mus musculus GN=Klhdc9 PE=2 SV=1
8.	TSYL5_MOUSE	44504	25	Testis-specific Y-encoded-like protein 5 OS=Mus musculus GN=Tspyl5 PE=2 SV=2
9.	KCD12_MOUSE	36155	25	BTB/POZ domain-containing protein KCTD12 OS=Mus musculus GN=Kctd12 PE=1 SV=1
10.	MCF2L_MOUSE	130493	24	Guanine nucleotide exchange factor DBS OS=Mus musculus GN=Mcf2l PE=1 SV=1

Results List

1. GRP78_MOUSE **Mass:** 72492 **Score:** 131 **Expect:** 1.3e-009 **Matches:** 9

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
1191.6687	1190.6615	1190.6295	26.8	466 -	475	0	---	K.VYEGERPLTK.D
1217.6661	1216.6588	1216.6234	29.1	187 -	198	0	---	K.DAGTIAGLNVMR.I
1512.8098	1511.8026	1511.7442	38.6	326 -	337	1	---	R.AKFEELNMDLFR.S
1566.8356	1565.8283	1565.7726	35.6	62 -	75	0	---	R.ITPSYVAFTPEGER.L
1588.9333	1587.9260	1587.8468	49.9	354 -	368	1	---	K.KSDIDEIVLVGGSTR.I
1816.0400	1815.0327	1814.9890	24.1	199 -	215	1	---	R.IINEPTAAAIAYGLDKR.E
1888.0319	1887.0246	1886.9639	32.1	166 -	182	0	---	K.VTHAVVTVPAYFNDAQR.Q
1934.0600	1933.0527	1933.0058	24.3	476 -	493	0	38	K.DNHLLGTFDLTGIPPAPR.G
1999.1357	1998.1284	1998.0786	24.9	494 -	511	0	---	R.GVPQIEVTFEIDVNGILR.V

No match to: 997.5797, 1460.8365, 2691.3421

2. PRS10_MOUSE **Mass:** 44430 **Score:** 30 **Expect:** 17 **Matches:** 4

26S protease regulatory subunit S10B OS=Mus musculus GN=Psmc6 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1191.6687	1190.6615	1190.6547	5.70	380 -	389	1	---	K.LESKLDYKPV.-
1460.8365	1459.8293	1459.8762	-32.17	310 -	322	1	---	R.LDILKIHAGPITK.H + Acetyl (N-term)
1816.0400	1815.0327	1814.9713	33.8	169 -	185	1	---	K.GCLLYGPPGTGKTLLAR.A + Acetyl (N-term)
1888.0319	1887.0246	1887.0578	-17.58	299 -	314	1	---	K.IHIDLPNEQARLDILK.I

No match to: 997.5797, 1217.6661, 1512.8098, 1566.8356, 1588.9333, 1934.0600, 1999.1357, 2691.3421

3. FA18B_MOUSE **Mass:** 23575 **Score:** 30 **Expect:** 17 **Matches:** 3

Protein FAM18B OS=Mus musculus GN=Fam18b PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1217.6661	1216.6588	1216.5989	49.3	102 -	110	1	---	K.SHWVFESRK.S + Acetyl (N-term)
1816.0400	1815.0327	1814.9733	32.7	31 -	44	1	---	K.IRHPVASFFHLFFR.V + Acetyl (N-term)
1888.0319	1887.0246	1886.9560	36.3	181 -	196	1	---	K.NLTSMATSYLGKQFLR.Q + Acetyl (N-term); Oxidation (M)

No match to: 997.5797, 1191.6687, 1460.8365, 1512.8098, 1566.8356, 1588.9333, 1934.0600, 1999.1357, 2691.3421

4. P3C2A_MOUSE **Mass:** 192462 **Score:** 28 **Expect:** 23 **Matches:** 6

Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Mus musculus GN=Pik3c2a PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1217.6661	1216.6588	1216.6598	-0.78	1072 -	1081	1	---	R.QVVLQKSMER.V
1512.8098	1511.8026	1511.8235	-13.87	226 -	238	1	---	K.LFEKIASTSEFLK.N
1566.8356	1565.8283	1565.7990	18.7	1436 -	1447	1	---	K.YNPDKHYIYVVR.I
1888.0319	1887.0246	1886.9825	22.3	905 -	920	1	---	K.HPNCLPKILASAPNWK.W + Acetyl (N-term)
1934.0600	1933.0527	1932.9649	45.5	1139 -	1154	1	---	K.VGEDLRQDMLALQMIK.I + Acetyl (N-term); 2 Oxidation (M)
2691.3421	2690.3348	2690.4142	-29.49	927 -	949	0	---	K.TYSLLHQWPPLCPLAALELLDAK.F + Acetyl (N-term)

No match to: 997.5797, 1191.6687, 1460.8365, 1588.9333, 1816.0400, 1999.1357

5. IL18_MOUSE **Mass:** 22349 **Score:** 28 **Expect:** 28 **Matches:** 3

Interleukin-18 OS=Mus musculus GN=Il18 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1191.6687	1190.6615	1190.6547	5.70	163 -	172	1	---	K.EDDAFKLILK.K
1217.6661	1216.6588	1216.7027	-36.05	93 -	104	1	---	R.GLAVTLSVKDSK.M
1460.8365	1459.8293	1459.7783	34.9	49 -	60	1	---	R.NINDQVLFVDKR.Q

No match to: 997.5797, 1512.8098, 1566.8356, 1588.9333, 1816.0400, 1888.0319, 1934.0600, 1999.1357, 2691.3421

6. TRHDE_MOUSE **Mass:** 117897 **Score:** 27 **Expect:** 35 **Matches:** 5

Thyrotropin-releasing hormone-degrading ectoenzyme OS=Mus musculus GN=Trhde PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1191.6687	1190.6615	1190.6520	7.95	29 -	38	1	---	R.TTERHIAVHK.R
1460.8365	1459.8293	1459.7572	49.4	262 -	274	0	---	R.FLGVTQFSPTHAR.K
1512.8098	1511.8026	1511.8460	-28.73	180 -	192	1	---	R.YVVLHASRVAVEK.V + Acetyl (N-term)
1566.8356	1565.8283	1565.7694	37.6	816 -	828	1	---	R.REVIMLACSFGNK.H + Acetyl (N-term)
1588.9333	1587.9260	1587.8522	46.5	262 -	275	1	---	R.FLGVTQFSPTHARK.A

No match to: 997.5797, 1217.6661, 1816.0400, 1888.0319, 1934.0600, 1999.1357, 2691.3421

7. KLDC9_MOUSE **Mass:** 38845 **Score:** 25 **Expect:** 50 **Matches:** 3

Kelch domain-containing protein 9 OS=Mus musculus GN=Klhdc9 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1217.6661	1216.6588	1216.6346	19.9	1 -	11	1	---	-.MAGVQTLGRAR.G + Acetyl (N-term); Oxidation (M)
1566.8356	1565.8283	1565.7800	30.9	338 -	350	0	---	R.TASPQVCILEFFI.- + Acetyl (N-term)
2691.3421	2690.3348	2690.2660	25.6	315 -	337	1	---	R.VGHRTCLWNDQLYLVGGFGEDGR.T + Acetyl (N-term)

No match to: 997.5797, 1191.6687, 1460.8365, 1512.8098, 1588.9333, 1816.0400, 1888.0319, 1934.0600, 1999.1357

8. TSYL5_MOUSE **Mass:** 44504 **Score:** 25 **Expect:** 55 **Matches:** 3

Testis-specific Y-encoded-like protein 5 OS=Mus musculus GN=Tspyl5 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1191.6687	1190.6615	1190.6407	17.4	396 -	406	1	---	K.LSPAPAVRQPN.- + Acetyl (N-term)
1566.8356	1565.8283	1565.8301	-1.17	110 -	125	0	---	R.LTSDTSFVGTVGALAK.L
2691.3421	2690.3348	2690.2891	17.0	180 -	205	1	---	K.MTEKHAGAGSPATVGSMDTLETVQLK.L + 2 Oxidation (M)

No match to: 997.5797, 1217.6661, 1460.8365, 1512.8098, 1588.9333, 1816.0400, 1888.0319, 1934.0600, 1999.1357

9. KCD12_MOUSE **Mass:** 36155 **Score:** 25 **Expect:** 56 **Matches:** 3

BTB/POZ domain-containing protein KCTD12 OS=Mus musculus GN=Kctd12 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
997.5797	996.5725	996.5280	44.6	91 -	97	0	---	R.YILDYLR.D + Acetyl (N-term)
1888.0319	1887.0246	1886.9864	20.3	128 -	145	1	---	R.RLGAPQQPGPGPPPPHSR.R + Acetyl (N-term)
1934.0600	1933.0527	1932.9945	30.1	113 -	127	1	---	R.LQREAEYFELPELVR.R + Acetyl (N-term)

No match to: 1191.6687, 1217.6661, 1460.8365, 1512.8098, 1566.8356, 1588.9333, 1816.0400, 1999.1357, 2691.3421

10. MCF2L_MOUSE **Mass:** 130493 **Score:** 24 **Expect:** 65 **Matches:** 5

Guanine nucleotide exchange factor DBS OS=Mus musculus GN=Mcf2l PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
1191.6687	1190.6615	1190.6183	36.3	511	-	519	0	---	K.IQELNEIYK.E + Acetyl (N-term)
1217.6661	1216.6588	1216.6234	29.1	944	-	953	0	---	K.VLTSQLQACR.E + Acetyl (N-term)
1512.8098	1511.8026	1511.7943	5.44	410	-	422	0	---	R.ALSLEGQQLIENR.H + Acetyl (N-term)
1888.0319	1887.0246	1887.0690	-23.55	561	-	577	0	---	K.QTRPVQPVAPRPEALTK.S
2691.3421	2690.3348	2690.2615	27.3	696	-	718	1	---	R.NIPAGVESCIDCPELVGRCFLER.M

No match to: 997.5797, 1460.8365, 1566.8356, 1588.9333, 1816.0400, 1934.0600, 1999.1357

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (997.5797,1+) : <no title>

Query2 (1191.6687,1+) : <no title>

Query3 (1217.6661,1+) : <no title>

Query4 (1460.8365,1+) : <no title>

Query5 (1512.8098,1+) : <no title>

Query6 (1566.8356,1+) : <no title>

Query7 (1588.9333,1+) : <no title>

Query8 (1816.0400,1+) : <no title>

Query9 (1888.0319,1+) : <no title>

Query10 (1934.0600,1+) : <no title>

Query11 (1999.1357,1+) : <no title>

Query12 (2691.3421,1+) : <no title>

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

MATRIX SCIENCE Mascot Search Results

User :

Email :

Search title : **Auto submitted by BioTools**

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

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

Timestamp : **20 May 2013 at 01:29:44 GMT**

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

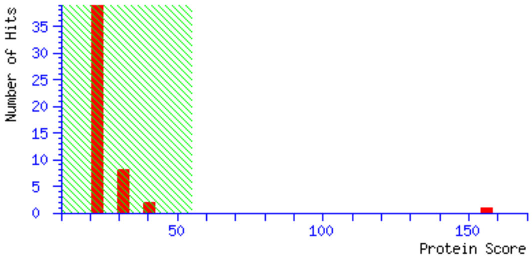
Top Score : **156 for VIME_MOUSE, Vimentin OS=Mus musculus GN=Vim PE=1 SV=3**

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.	**VIME_MOUSE**	53712	156	Vimentin OS=Mus musculus GN=Vim PE=1 SV=3
2.	**CCD42_MOUSE**	37965	37	Coiled-coil domain-containing protein 42A OS=Mus musculus GN=Ccdc42 PE=2 SV=2
3.	**CCD56_MOUSE**	11979	36	Coiled-coil domain-containing protein 56 OS=Mus musculus GN=Ccdc56 PE=2 SV=1
4.	**SPIN1_MOUSE**	29738	33	Spindlin-1 OS=Mus musculus GN=Spin1 PE=1 SV=2
5.	**GEMI5_MOUSE**	169080	33	Gem-associated protein 5 OS=Mus musculus GN=Gemin5 PE=1 SV=1
6.	**HBAZ_MOUSE**	16338	32	Hemoglobin subunit zeta OS=Mus musculus GN=Hbz PE=2 SV=2
7.	**MBL1_MOUSE**	25836	30	Mannose-binding protein A OS=Mus musculus GN=Mbl1 PE=2 SV=1
8.	**KRT36_MOUSE**	54011	29	Keratin, type I cuticular Ha6 OS=Mus musculus GN=Krt36 PE=1 SV=1
9.	**ANXA2_MOUSE**	38937	29	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2
10.	**MEP1B_MOUSE**	80467	28	Meprin A subunit beta OS=Mus musculus GN=Mep1b PE=1 SV=1

Results List

1. VIME_MOUSE **Mass:** 53712 **Score:** 156 **Expect:** 4.1e-012 **Matches:** 16

Vimentin OS=Mus musculus GN=Vim PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1046.5487	1045.5414	1045.5226	18.0	189 -	196	0	---	K.LQEEMLQR.E
1081.5468	1080.5395	1080.4948	41.4	314 -	321	1	---	K.QESNEYRR.Q
1088.5551	1087.5478	1087.5332	13.4	189 -	196	0	---	K.LQEEMLQR.E + Acetyl (N-term)
1093.5404	1092.5331	1092.5200	12.0	295 -	304	0	---	K.FADLSEAANR.N
1115.5872	1114.5799	1114.5618	16.2	105 -	113	0	---	K.VELQELNDR.F
1254.5991	1253.5918	1253.5598	25.6	146 -	155	0	---	R.LGDLYEEEMR.E
1295.6729	1294.6656	1294.6591	5.03	391 -	401	0	---	K.MALDIEIATYR.K
1296.6617	1295.6544	1295.5993	42.5	197 -	207	0	---	R.EEAESTLQSFR.Q
1423.7716	1422.7643	1422.7540	7.23	391 -	402	1	---	K.MALDIEIATYRK.L
1444.7188	1443.7116	1443.6994	8.42	51 -	64	0	10	R.SLYSSSPGGAYVTR.S
1495.7935	1494.7862	1494.7790	4.78	37 -	50	0	---	R.TYSLGSALRPSTSR.S
1557.9111	1556.9038	1556.8926	7.21	411 -	424	0	25	R.ISLPLPTFSSLNLR.E
1587.8070	1586.7997	1586.7900	6.11	101 -	113	1	---	R.TNEKVELQELNDR.F
1704.8557	1703.8484	1703.8148	19.7	171 -	184	1	---	R.VEVERDNLAEDIMR.L + Oxidation (M)
1734.8304	1733.8232	1733.8076	8.97	365 -	378	1	---	R.LQDEIQNMKEEMAR.H
2200.9913	2199.9841	2199.9742	4.48	346 -	364	0	---	R.EMEENFALEAANYQDTIGR.L

No match to: 854.3130, 1284.7435, 1513.8696, 1542.7860, 1641.7796, 1674.8641, 1723.5763, 2003.0019, 2301.0261, 2330.1460, 2691.3014, 2748.3381

2. CCD42_MOUSE **Mass:** 37965 **Score:** 37 **Expect:** 3 **Matches:** 7

Coiled-coil domain-containing protein 42A OS=Mus musculus GN=Ccdc42 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1081.5468	1080.5395	1080.5273	11.3	203 -	210	1	---	R.LARYMEEK.D + Acetyl (N-term)
1093.5404	1092.5331	1092.5419	-8.10	128 -	136	1	---	K.AKQEMMALR.L + Oxidation (M)
1444.7188	1443.7116	1443.6850	18.4	50 -	61	1	---	K.EAKIMQEAMEHK.K
1587.8070	1586.7997	1586.7545	28.5	130 -	141	1	---	K.QEMMALRLEHQK.L + Acetyl (N-term); 2 Oxidation (M)
2003.0019	2001.9946	2001.9908	1.89	88 -	103	1	---	K.AHIQKFEQFIQENDQK.R
2200.9913	2199.9841	2199.9889	-2.18	177 -	195	0	---	K.TLVSMHHDLMQSAQEGQEK.I + 2 Oxidation (M)
2301.0261	2300.0188	2300.1338	-49.99	233 -	251	1	---	R.SDVIFWESRWAHIQNTAAK.K + Acetyl (N-term)

No match to: 854.3130, 1046.5487, 1088.5551, 1115.5872, 1254.5991, 1284.7435, 1295.6729, 1296.6617, 1423.7716, 1495.7935, 1513.8696, 1542.7860, 1557.9111, 1641.7796, 1674.8641, 1704.8557, 1723.5763, 1734.8304, 2330.1460, 2691.3014, 2748.3381

3. CCD56_MOUSE **Mass:** 11979 **Score:** 36 **Expect:** 4.3 **Matches:** 4

Coiled-coil domain-containing protein 56 OS=Mus musculus GN=Ccdc56 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1081.5468	1080.5395	1080.5564	-15.59	2 -	13	0	---	M.AAPGAGDPLNAK.N
1254.5991	1253.5918	1253.6074	-12.42	1 -	13	0	---	-.MAAPGAGDPLNAK.N + Acetyl (N-term)
1542.7860	1541.7787	1541.7699	5.74	14 -	27	1	---	K.NGNAPFAQRIDPSR.E
2330.1460	2329.1388	2329.2365	-41.96	30 -	48	1	---	K.LTPAQLQFMRQVQLAQWQK.T + Oxidation (M)

No match to: 854.3130, 1046.5487, 1088.5551, 1093.5404, 1115.5872, 1284.7435, 1295.6729, 1296.6617, 1423.7716, 1444.7188, 1495.7935, 1513.8696, 1557.9111, 1587.8070, 1641.7796, 1674.8641, 1704.8557, 1723.5763, 1734.8304, 2003.0019, 2200.9913, 2301.0261, 2691.3014, 2748.3381

4. SPIN1_MOUSE **Mass:** 29738 **Score:** 33 **Expect:** 7.8 **Matches:** 6

Spindlin-1 OS=Mus musculus GN=Spin1 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1088.5551	1087.5478	1087.5775	-27.28	3 -	12	1	---	K.TPFGKTPGQR.S
1115.5872	1114.5799	1114.5407	35.2	64 -	73	0	---	R.EGNGPVTQWK.G
1295.6729	1294.6656	1294.6041	47.5	217 -	227	1	---	K.QVEYAKEDGSK.R + Acetyl (N-term)
1495.7935	1494.7862	1494.7626	15.7	52 -	63	1	---	R.NIVGCRIQHGWR.E
1674.8641	1673.8568	1673.8961	-23.49	36 -	50	1	---	K.HRTSVGPSKPVSQPR.R + Acetyl (N-term)
1734.8304	1733.8232	1733.7607	36.0	91 -	104	0	---	K.YDGFDCVYGLELNK.D + Acetyl (N-term)

No match to: 854.3130, 1046.5487, 1081.5468, 1093.5404, 1254.5991, 1284.7435, 1296.6617, 1423.7716, 1444.7188, 1513.8696, 1542.7860, 1557.9111, 1587.8070, 1641.7796, 1704.8557, 1723.5763, 2003.0019, 2200.9913, 2301.0261, 2330.1460, 2691.3014, 2748.3381

5. GEMI5_MOUSE **Mass:** 169080 **Score:** 33 **Expect:** 8.2 **Matches:** 10

Gem-associated protein 5 OS=Mus musculus GN=Gemin5 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1093.5404	1092.5331	1092.5240	8.34	672 -	679	0	---	R.EEPLFNFR.G + Acetyl (N-term)
1115.5872	1114.5799	1114.6095	-26.48	525 -	533	1	---	K.LVRDTNSIR.Y + Acetyl (N-term)
1295.6729	1294.6656	1294.6153	38.8	1408 -	1419	0	---	R.APSQPPSPTEER.N
1495.7935	1494.7862	1494.7388	31.7	1260 -	1273	1	---	R.DKLGDLSPAMAAYK.S + Oxidation (M)
1513.8696	1512.8623	1512.8048	38.0	999 -	1011	1	---	K.SNHLYREAIAVAK.A + Acetyl (N-term)
1542.7860	1541.7787	1541.8242	-29.49	534 -	545	1	---	R.YKLPVHTEISWK.G + Acetyl (N-term)
1587.8070	1586.7997	1586.8086	-5.64	845 -	858	1	---	R.SMLPLSTSLDHRSK.E + Oxidation (M)
1641.7796	1640.7723	1640.8304	-35.39	843 -	856	1	---	K.ARSMLPLSTSLDHR.S + Acetyl (N-term); Oxidation (M)
2200.9913	2199.9841	2200.0888	-47.59	911 -	928	0	---	K.GHLESGHPELFHQLMLWK.G + Acetyl (N-term)
2748.3381	2747.3308	2747.4565	-45.77	1062 -	1089	1	---	K.GDAASLRTAAELAAIAGEHELAASLALR.C

No match to: 854.3130, 1046.5487, 1081.5468, 1088.5551, 1254.5991, 1284.7435, 1296.6617, 1423.7716, 1444.7188, 1557.9111, 1674.8641, 1704.8557, 1723.5763, 1734.8304, 2003.0019, 2301.0261, 2330.1460, 2691.3014

6. HBAZ_MOUSE **Mass:** 16338 **Score:** 32 **Expect:** 10 **Matches:** 4

Hemoglobin subunit zeta OS=Mus musculus GN=Hbz PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1046.5487	1045.5414	1045.5478	-6.08	63 -	72	0	---	K.IMTAVGDAVK.S + Acetyl (N-term)
1542.7860	1541.7787	1541.8058	-17.55	101 -	113	0	---	K.LLSHCLLVTMAAR.F + Acetyl (N-term); Oxidation (M)
1674.8641	1673.8568	1673.7930	38.1	18 -	32	0	---	K.MAAQAEPIGTETLER.L + Acetyl (N-term); Oxidation (M)
2748.3381	2747.3308	2747.3332	-0.87	9 -	32	1	---	R.AIIMSMWEKMAAQAEPIGTETLER.L + Acetyl (N-term)

No match to: 854.3130, 1081.5468, 1088.5551, 1093.5404, 1115.5872, 1254.5991, 1284.7435, 1295.6729, 1296.6617, 1423.7716, 1444.7188, 1495.7935, 1513.8696, 1557.9111, 1587.8070, 1641.7796, 1704.8557, 1723.5763, 1734.8304, 2003.0019, 2200.9913, 2301.0261, 2330.1460, 2691.3014

7. MBL1_MOUSE **Mass:** 25836 **Score:** 30 **Expect:** 17 **Matches:** 6

Mannose-binding protein A OS=Mus musculus GN=Mbl1 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1046.5487	1045.5414	1045.5226	18.0	96	104	0	---	K.LANMEAEIR.I
1081.5468	1080.5395	1080.5604	-19.30	194	201	1	---	R.LTYSNWKK.D + Acetyl (N-term)
1088.5551	1087.5478	1087.5331	13.5	96	104	0	---	K.LANMEAEIR.I + Acetyl (N-term)
1115.5872	1114.5799	1114.6135	-30.09	128	136	1	---	K.KLFVTNHEK.M
1587.8070	1586.7997	1586.8603	-38.18	110	123	1	---	K.LQLTNKLHAFSMGK.K
1674.8641	1673.8568	1673.8294	16.4	91	104	1	---	R.AIEEKLANMEAEIR.I + Acetyl (N-term); Oxidation (M)

No match to: 854.3130, 1093.5404, 1254.5991, 1284.7435, 1295.6729, 1296.6617, 1423.7716, 1444.7188, 1495.7935, 1513.8696, 1542.7860, 1557.9111, 1641.7796, 1704.8557, 1723.5763, 1734.8304, 2003.0019, 2200.9913, 2301.0261, 2330.1460, 2691.3014, 2748.3381

8. KRT36_MOUSE **Mass:** 54011 **Score:** 29 **Expect:** 20 **Matches:** 5

Keratin, type I cuticular Ha6 OS=Mus musculus GN=Krt36 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1081.5468	1080.5395	1080.5451	-5.18	386	394	0	---	R.LESEIATYR.R
2003.0019	2001.9946	2002.0265	-15.95	314	330	1	---	R.RTVNSLEIELQAQQSMR.N
2200.9913	2199.9841	2200.0582	-33.72	367	383	1	---	R.CDLERQNHEYQVLLDVK.A + Acetyl (N-term)
2330.1460	2329.1388	2329.2086	-30.00	202	221	1	---	R.ILDELTLCKADLEAQVESLK.E + Acetyl (N-term)
2691.3014	2690.2941	2690.2429	19.1	2	27	1	---	M.ATQICTPTFSAGSAKGLCGTSGSFSR.I + Acetyl (N-term)

No match to: 854.3130, 1046.5487, 1088.5551, 1093.5404, 1115.5872, 1254.5991, 1284.7435, 1295.6729, 1296.6617, 1423.7716, 1444.7188, 1495.7935, 1513.8696, 1542.7860, 1557.9111, 1587.8070, 1641.7796, 1674.8641, 1704.8557, 1723.5763, 1734.8304, 2301.0261, 2748.3381

9. ANXA2_MOUSE **Mass:** 38937 **Score:** 29 **Expect:** 22 **Matches:** 6

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

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1093.5404	1092.5331	1092.5274	5.25	213	220	0	---	K.WISIMTER.S + Acetyl (N-term); Oxidation (M)
1115.5872	1114.5799	1114.5870	-6.31	38	47	0	---	R.DALNIETAVK.T + Acetyl (N-term)
1423.7716	1422.7643	1422.7211	30.4	291	302	1	---	R.IMVSRSEVDMLK.I + Oxidation (M)
1444.7188	1443.7116	1443.7293	-12.26	221	231	1	---	R.SVCHLQKVFER.Y + Acetyl (N-term)
1542.7860	1541.7787	1541.8413	-40.60	50	63	0	---	K.GVDEVTIVNILTNR.S
1674.8641	1673.8568	1673.8447	7.26	207	220	1	---	K.GTDVPKWISIMTER.S + Acetyl (N-term)

No match to: 854.3130, 1046.5487, 1081.5468, 1088.5551, 1254.5991, 1284.7435, 1295.6729, 1296.6617, 1495.7935, 1513.8696, 1557.9111, 1587.8070, 1641.7796, 1704.8557, 1723.5763, 1734.8304, 2003.0019, 2200.9913, 2301.0261, 2330.1460, 2691.3014, 2748.3381

10. MEP1B_MOUSE **Mass:** 80467 **Score:** 28 **Expect:** 24 **Matches:** 6

Meprin A subunit beta OS=Mus musculus GN=Mep1b PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1081.5468	1080.5395	1080.5676	-25.98	63	71	1	---	K.NSIIGDHKR.W + Acetyl (N-term)
1284.7435	1283.7362	1283.6874	38.0	555	566	0	---	R.GIGYGTTVFITR.E
1495.7935	1494.7862	1494.7790	4.79	57	70	1	---	K.LEANGKNSIIGDHK.R
2200.9913	2199.9841	2200.0510	-30.43	72	89	0	---	R.WPHTIPYVLEDSLEMNAK.G + Acetyl (N-term); Oxidation (M)
2691.3014	2690.2941	2690.2105	31.1	308	331	0	---	K.DSGFFMHFNTSILNEGATAMLESR.L + Oxidation (M)
2748.3381	2747.3308	2747.3681	-13.57	148	170	1	---	R.IATVQHEFLHALGFWHEQSRADR.D

No match to: 854.3130, 1046.5487, 1088.5551, 1093.5404, 1115.5872, 1254.5991, 1295.6729, 1296.6617, 1423.7716, 1444.7188, 1513.8696, 1542.7860, 1557.9111, 1587.8070, 1641.7796, 1674.8641, 1704.8557, 1723.5763, 1734.8304, 2003.0019, 2301.0261, 2330.1460

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (854.3130,1+) : <no title>

Query2 (1046.5487,1+) : <no title>

Query3 (1081.5468,1+) : <no title>

Query4 (1088.5551,1+) : <no title>

Query5 (1093.5404,1+) : <no title>

Query6 (1115.5872,1+) : <no title>

Query7 (1254.5991,1+) : <no title>

Query8 (1284.7435,1+) : <no title>

Query9 (1295.6729,1+) : <no title>

Query10 (1296.6617,1+) : <no title>

Query11 (1423.7716,1+) : <no title>

Query12 (1444.7188,1+) : <no title>

Query13 (1495.7935,1+) : <no title>

Query14 (1513.8696,1+) : <no title>

Query15 (1542.7860,1+) : <no title>

Query16 (1557.9111,1+) : <no title>

Query17 (1587.8070,1+) : <no title>

Query18 (1641.7796,1+) : <no title>

Query19 (1674.8641,1+) : <no title>

Query20 (1704.8557,1+) : <no title>

Query21 (1723.5763,1+) : <no title>

Query22 (1734.8304,1+) : <no title>

Query23 (2003.0019,1+) : <no title>

Query24 (2200.9913,1+) : <no title>

Query25 (2301.0261,1+) : <no title>

Query26 (2330.1460,1+) : <no title>

Query27 (2691.3014,1+) : <no title>

Query28 (2748.3381,1+) : <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 : **20 Jun 2013 at 07:31:12 GMT**

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

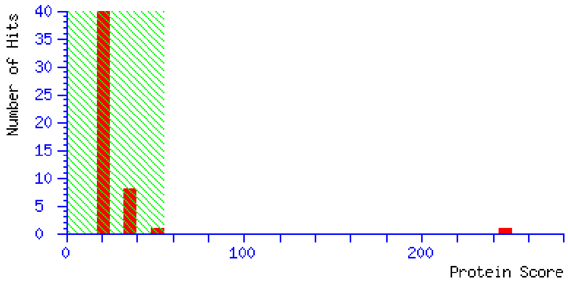
Top Score : **247 for PDIA1_MOUSE, Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1**

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	247	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1
2.	KLC1_MOUSE	61868	44	Kinesin light chain 1 OS=Mus musculus GN=Klc1 PE=1 SV=3
3.	MSRA_MOUSE	26200	37	Peptide methionine sulfoxide reductase OS=Mus musculus GN=Msra PE=1 SV=1
4.	TKN4_MOUSE	14042	34	Tachykinin-4 OS=Mus musculus GN=Tac4 PE=2 SV=1
5.	TRFL_MOUSE	79698	32	Lactotransferrin OS=Mus musculus GN=Ltf PE=2 SV=3
6.	K2C4_MOUSE	56590	31	Keratin, type II cytoskeletal 4 OS=Mus musculus GN=Krt4 PE=1 SV=2
7.	EVG1_MOUSE	24950	30	UPF0193 protein EVG1 homolog OS=Mus musculus PE=2 SV=1
8.	ANT3_MOUSE	52484	29	Antithrombin-III OS=Mus musculus GN=Serpinc1 PE=1 SV=1
9.	PTCD2_MOUSE	44443	29	Pentatricopeptide repeat-containing protein 2 OS=Mus musculus GN=Ptcd2 PE=2 SV=1
10.	CMIP_MOUSE	84217	29	C-Maf-inducing protein OS=Mus musculus GN=Cmip PE=2 SV=2

Results List

1. PDIA1_MOUSE **Mass:** 57507 **Score:** 247 **Expect:** 3.2e-021 **Matches:** 8

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
910.4453	909.4380	909.4345	3.87	447 -	454	0	---	K.FFPASADR.T
962.4547	961.4474	961.4440	3.55	341 -	347	0	---	K.ITEFCHR.F
988.5036	987.4963	987.4807	15.8	311 -	318	1	---	K.KEECPAVR.L
1002.5440	1001.5368	1001.5505	-13.74	72 -	80	1	---	K.LKAEGSEIR.L
1780.8259	1779.8186	1779.8275	-4.99	84 -	99	0	116	K.VDATEESDLAQQYGVR.G
1794.8603	1793.8530	1793.9200	-37.32	373 -	388	1	---	K.VLVGANFEEVAFDEKK.N
1833.9070	1832.8998	1832.9057	-3.24	288 -	302	0	85	K.ILFIFIDSDHTDNQR.I
1965.0339	1964.0266	1964.0367	-5.16	233 -	249	0	---	K.HNQLPLVIEFTEQTAPK.I

No match to: 849.4577, 898.5651, 904.4875, 995.6075, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1063.5526, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1123.6529, 1135.7007, 1137.6952, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1216.6582, 1219.6600, 1234.7284, 1265.7695, 1268.6940, 1319.7837, 1327.7302, 1359.7409, 1446.7783, 1508.8300, 1660.9003, 1663.9440, 1700.8843, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1987.0257, 1999.0176, 2140.1287

2. KLC1_MOUSE **Mass:** 61868 **Score:** 44 **Expect:** 0.6 **Matches:** 7

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
910.4453	909.4380	909.4668	-31.71	495 -	502	0	---	K.QGLDNVHK.Q
1002.5440	1001.5368	1001.4964	40.3	313 -	320	1	---	K.EAEPLCKR.A
1038.6180	1037.6108	1037.5618	47.2	494 -	502	1	---	R.KQGLDNVHK.Q
1327.7302	1326.7229	1326.7871	-48.34	28 -	39	1	---	K.TKQVIQGLEALK.N
1660.9003	1659.8930	1659.8944	-0.83	269 -	283	1	---	K.YKDAANLLNDALAIR.E
1780.8259	1779.8186	1779.8461	-15.43	476 -	491	1	15	R.QGKFEAAETLEEAAMR.S
2140.1287	2139.1215	2139.1357	-6.68	40 -	57	1	---	K.NEHNSILQSLLETLKCLK.K

No match to: 849.4577, 898.5651, 904.4875, 962.4547, 988.5036, 995.6075, 1011.6115, 1013.5103, 1050.6515, 1063.5526, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1123.6529, 1135.7007, 1137.6952, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1216.6582, 1219.6600, 1234.7284, 1265.7695, 1268.6940, 1319.7837, 1359.7409, 1446.7783, 1508.8300, 1663.9440, 1700.8843, 1794.8603, 1833.9070, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1987.0257, 1999.0176

3. MSRA_MOUSE **Mass:** 26200 **Score:** 37 **Expect:** 3.4 **Matches:** 5

Peptide methionine sulfoxide reductase OS=Mus musculus GN=Msra PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1123.6529	1122.6456	1122.5921	47.7	175 -	183	1	---	K.EEYQKVLSK.H
1141.5987	1140.5914	1140.6139	-19.69	28 -	38	0	---	K.VISAEEALPGR.T
1268.6940	1267.6867	1267.7248	-30.03	8 -	19	0	---	R.ALQLLSSANPVR.R
1833.9070	1832.8998	1832.8938	3.26	21 -	38	1	---	R.MGDSASKVISAEEALPGR.T + Oxidation (M)
2140.1287	2139.1215	2139.0498	33.5	85 -	104	1	---	K.GVYSTQVGFAGGHTRNPTYK.E

No match to: 849.4577, 898.5651, 904.4875, 910.4453, 962.4547, 988.5036, 995.6075, 1002.5440, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1063.5526, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1135.7007, 1137.6952, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1216.6582, 1219.6600, 1234.7284, 1265.7695, 1319.7837, 1327.7302, 1359.7409, 1446.7783, 1508.8300, 1660.9003, 1663.9440, 1700.8843, 1780.8259, 1794.8603, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1987.0257, 1999.0176

4. TKN4_MOUSE **Mass:** 14042 **Score:** 34 **Expect:** 5.9 **Matches:** 4

Tachykinin-4 OS=Mus musculus GN=Tac4 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
849.4577	848.4504	848.4505	-0.02	70 -	77	0	---	R.VGGYQLGR.I
1115.5621	1114.5549	1114.5593	-4.03	61 -	69	1	---	R.QFYGLMGKR.V + Oxidation (M)
1216.6582	1215.6509	1215.6070	36.1	59 -	68	1	---	R.TRQFYGLMGK.R + Oxidation (M)
1663.9440	1662.9367	1662.9920	-33.22	41 -	55	1	---	K.GIPVPSIELKLQELK.R

No match to: 898.5651, 904.4875, 910.4453, 962.4547, 988.5036, 995.6075, 1002.5440, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1063.5526, 1067.4996, 1079.6272, 1081.6179, 1123.6529, 1135.7007, 1137.6952, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1219.6600, 1234.7284, 1265.7695, 1268.6940, 1319.7837, 1327.7302, 1359.7409, 1446.7783, 1508.8300, 1660.9003, 1700.8843, 1780.8259, 1794.8603, 1833.9070, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1987.0257, 1999.0176, 2140.1287

5. TRFL_MOUSE **Mass:** 79698 **Score:** 32 **Expect:** 11 **Matches:** 7

Lactotransferrin OS=Mus musculus GN=Ltf PE=2 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1013.5103	1012.5031	1012.5376	-34.08	47 -	56	0	---	K.VGGPPLSCVK.K
1115.5621	1114.5549	1114.6095	-48.99	353 -	362	1	---	K.QQDVIASKAR.V
1141.5987	1140.5914	1140.6325	-36.06	47 -	57	1	---	K.VGGPPLSCVKK.S
1327.7302	1326.7229	1326.6966	19.9	423 -	434	0	---	K.CGLVPVLAENQK.S
1660.9003	1659.8930	1659.8733	11.9	104 -	117	1	---	K.EQPRTHYYAVAVVK.N
1780.8259	1779.8186	1779.8825	-35.88	654 -	668	1	---	K.TKNLLFNDNTECLAK.I
1999.0176	1998.0103	1998.0898	-39.81	622 -	638	0	---	K.VEVLQQVLLDQQVQFGR.N

No match to: 849.4577, 898.5651, 904.4875, 910.4453, 962.4547, 988.5036, 995.6075, 1002.5440, 1011.6115, 1038.6180, 1050.6515, 1063.5526, 1067.4996, 1079.6272, 1081.6179, 1123.6529, 1135.7007, 1137.6952, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1216.6582, 1219.6600, 1234.7284, 1265.7695, 1268.6940, 1319.7837, 1359.7409, 1446.7783, 1508.8300, 1663.9440, 1700.8843, 1794.8603, 1833.9070, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1987.0257, 2140.1287

6. K2C4_MOUSE **Mass:** 56590 **Score:** 31 **Expect:** 14 **Matches:** 5

Keratin, type II cytoskeletal 4 OS=Mus musculus GN=Krt4 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
988.5036	987.4963	987.5138	-17.67	51 -	59	0	---	R.SLYNLGGHK.S
1002.5440	1001.5368	1001.5393	-2.53	411 -	419	0	---	R.AELETALQK.A
1063.5526	1062.5454	1062.5604	-14.15	1 -	9	1	8	-.MIARQSSVR.G + Oxidation (M)
1327.7302	1326.7229	1326.7143	6.51	310 -	321	0	---	R.NLDLDGIIAEVR.A
1508.8300	1507.8228	1507.7743	32.1	10 -	26	1	---	R.GASRGFSSGSAIAGGVK.R

No match to: 849.4577, 898.5651, 904.4875, 910.4453, 962.4547, 995.6075, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1123.6529, 1135.7007, 1137.6952, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1216.6582, 1219.6600, 1234.7284, 1265.7695, 1268.6940, 1319.7837, 1359.7409, 1446.7783, 1660.9003, 1663.9440, 1700.8843, 1780.8259, 1794.8603, 1833.9070, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1987.0257, 1999.0176, 2140.1287

7. EVG1_MOUSE **Mass:** 24950 **Score:** 30 **Expect:** 17 **Matches:** 5

UPF0193 protein EVG1 homolog OS=Mus musculus PE=2 SV=1

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

1063.5526	1062.5454	1062.4950	47.4	49 -	56	1	---	R.HIMDTMKR.G + 2 Oxidation (M)
1219.6600	1218.6527	1218.6204	26.5	2 -	12	1	---	M.ASQERVDSVTK.G
1234.7284	1233.7211	1233.6717	40.1	126 -	136	1	---	R.LQNIFATGKDK.E
1794.8603	1793.8530	1793.8553	-1.26	42 -	55	1	---	K.LTNFQQRHIMDTMK.R + 2 Oxidation (M)
1987.0257	1986.0184	1985.9373	40.9	22 -	38	1	---	K.QAGYTPGTCELLRVMMK.E + 2 Oxidation (M)

No match to: 849.4577, 898.5651, 904.4875, 910.4453, 962.4547, 988.5036, 995.6075, 1002.5440, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1123.6529, 1135.7007, 1137.6952, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1216.6582, 1265.7695, 1268.6940, 1319.7837, 1327.7302, 1359.7409, 1446.7783, 1508.8300, 1660.9003, 1663.9440, 1700.8843, 1780.8259, 1833.9070, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1999.0176, 2140.1287

8. ANT3_MOUSE **Mass:** 52484 **Score:** 29 **Expect:** 20 **Matches:** 6

Antithrombin-III OS=Mus musculus GN=Serpinc1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
910.4453	909.4380	909.4630	-27.48	134 -	140	0	---	K.QLMEVFK.F + Oxidation (M)
1199.6618	1198.6545	1198.5982	47.0	356 -	365	1	---	R.FRTEDGFSLK.E
1359.7409	1358.7336	1358.7016	23.5	47 -	57	0	---	R.DIPVNPLCIYR.S
1508.8300	1507.8228	1507.7631	39.6	170 -	183	1	---	K.SSDLVSANRLFGDK.S
1700.8843	1699.8770	1699.8529	14.2	203 -	216	1	---	K.LQPLDFKENPEQSR.V
1999.0176	1998.0103	1997.9919	9.23	210 -	226	1	---	K.ENPEQSRVTINNWVANK.T

No match to: 849.4577, 898.5651, 904.4875, 962.4547, 988.5036, 995.6075, 1002.5440, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1063.5526, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1123.6529, 1135.7007, 1137.6952, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1205.7614, 1216.6582, 1219.6600, 1234.7284, 1265.7695, 1268.6940, 1319.7837, 1327.7302, 1446.7783, 1660.9003, 1663.9440, 1780.8259, 1794.8603, 1833.9070, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1987.0257, 2140.1287

9. PTCD2_MOUSE **Mass:** 44443 **Score:** 29 **Expect:** 20 **Matches:** 6

Pentatricopeptide repeat-containing protein 2 OS=Mus musculus GN=Ptcd2 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1216.6582	1215.6509	1215.6459	4.16	72 -	81	1	---	R.NLEEKLTQNK.L
1219.6600	1218.6527	1218.6543	-1.30	1 -	10	0	---	-.MATVFRPLER.L
1234.7284	1233.7211	1233.7081	10.6	38 -	47	1	---	K.RYLLTDNIVK.L
1319.7837	1318.7764	1318.7860	-7.28	39 -	49	1	---	R.YLLTDNIVKLK.E
1446.7783	1445.7710	1445.7912	-13.96	214 -	225	1	---	K.ICTTLREEALIK.G
1508.8300	1507.8228	1507.8068	10.6	174 -	185	1	---	K.YERALQVLIEMK.N + Oxidation (M)

No match to: 849.4577, 898.5651, 904.4875, 910.4453, 962.4547, 988.5036, 995.6075, 1002.5440, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1063.5526, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1123.6529, 1135.7007, 1137.6952, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1265.7695, 1268.6940, 1327.7302, 1359.7409, 1660.9003, 1663.9440, 1700.8843, 1780.8259, 1794.8603, 1833.9070, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1987.0257, 1999.0176, 2140.1287

10. CMIP_MOUSE **Mass:** 84217 **Score:** 29 **Expect:** 21 **Matches:** 7

C-Maf-inducing protein OS=Mus musculus GN=Cmip PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
962.4547	961.4474	961.4586	-11.64	1 -	8	1	---	-.MGAVPCRR.A + Oxidation (M)
1063.5526	1062.5454	1062.5314	13.1	9 -	17	0	---	R.ALLLCNGMR.Y + Oxidation (M)

1137.6952	1136.6879	1136.6805	6.53	36 - 45	1	---	R.TFLSKILTSK.F
1219.6600	1218.6527	1218.6325	16.6	8 - 17	1	---	R.RALLLCNGMR.Y + Oxidation (M)
1327.7302	1326.7229	1326.6714	38.8	475 - 485	0	---	R.QEVHSCLLSVR.A
1833.9070	1832.8998	1832.9818	-44.78	18 - 32	1	---	R.YKLLQEGDIQVCVIR.H
1987.0257	1986.0184	1985.9465	36.2	272 - 288	1	---	K.KFIQSMHGPTGHCPHPR.V

No match to: 849.4577, 898.5651, 904.4875, 910.4453, 988.5036, 995.6075, 1002.5440, 1011.6115, 1013.5103, 1038.6180, 1050.6515, 1067.4996, 1079.6272, 1081.6179, 1115.5621, 1123.6529, 1135.7007, 1141.5987, 1148.7229, 1155.6580, 1192.7180, 1199.6618, 1205.7614, 1216.6582, 1234.7284, 1265.7695, 1268.6940, 1319.7837, 1359.7409, 1446.7783, 1508.8300, 1660.9003, 1663.9440, 1700.8843, 1780.8259, 1794.8603, 1861.9038, 1882.1205, 1933.9415, 1947.9824, 1965.0339, 1999.0176, 2140.1287

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 (849.4577,1+) : <no title>

Query2 (898.5651,1+) : <no title>

Query3 (904.4875,1+) : <no title>

Query4 (910.4453,1+) : <no title>

Query5 (962.4547,1+) : <no title>

Query6 (988.5036,1+) : <no title>

Query7 (995.6075,1+) : <no title>

Query8 (1002.5440,1+) : <no title>

Query9 (1011.6115,1+) : <no title>

Query10 (1013.5103,1+) : <no title>

Query11 (1038.6180,1+) : <no title>

Query12 (1050.6515,1+) : <no title>

Query13 (1063.5526,1+) : <no title>

Query14 (1067.4996,1+) : <no title>

Query15 (1079.6272,1+) : <no title>

Query16 (1081.6179,1+) : <no title>

Query17 (1115.5621,1+) : <no title>

Query18 (1123.6529,1+) : <no title>

Query19 (1135.7007,1+) : <no title>

Query20 (1137.6952,1+) : <no title>

Query21 (1141.5987,1+) : <no title>

Query22 (1148.7229,1+) : <no title>

Query23 (1155.6580,1+) : <no title>

Query24 (1192.7180,1+) : <no title>

Query25 (1199.6618,1+) : <no title>

Query26 (1205.7614,1+) : <no title>

Query27 (1216.6582,1+) : <no title>

Query28 (1219.6600,1+) : <no title>

Query29 (1234.7284,1+) : <no title>

Query30 (1265.7695,1+) : <no title>

Query31 (1268.6940,1+) : <no title>

Query32 (1319.7837,1+) : <no title>

Query33 (1327.7302,1+) : <no title>

Query34 (1359.7409,1+) : <no title>

Query35 (1446.7783,1+) : <no title>

Query36 (1508.8300,1+) : <no title>

Query37 (1660.9003,1+) : <no title>

Query38 (1663.9440,1+) : <no title>

Query39 (1700.8843,1+) : <no title>

Query40 (1780.8259,1+) : <no title>

Query41 (1794.8603,1+) : <no title>

Query42 (1833.9070,1+) : <no title>

Query43 (1861.9038,1+) : <no title>

Query44 (1882.1205,1+) : <no title>

Query45 (1933.9415,1+) : <no title>

Query46 (1947.9824,1+) : <no title>

Query47 (1965.0339,1+) : <no title>

Query48 (1987.0257,1+) : <no title>

Query49 (1999.0176,1+) : <no title>

Query50 (2140.1287,1+) : <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 : **20 May 2013 at 01:29:59 GMT**

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

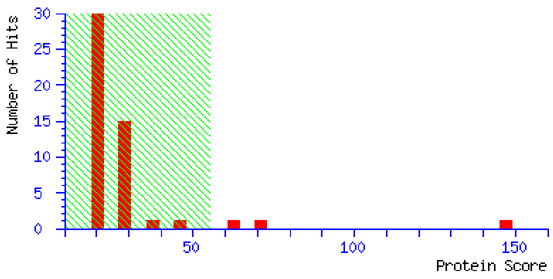
Top Score : **147 for PTRF_MOUSE, Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1**

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.	PTRF_MOUSE	43927	147	Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1
2.	A1AT3_MOUSE	45966	70	Alpha-1-antitrypsin 1-3 OS=Mus musculus GN=Serpina1c PE=1 SV=2
3.	A1AT1_MOUSE	46145	62	Alpha-1-antitrypsin 1-1 OS=Mus musculus GN=Serpina1a PE=1 SV=4
4.	TFR1_MOUSE	86076	49	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1
5.	GCNT7_MOUSE	49291	38	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7 OS=Mus musculus GN=Gcnt7 PE=2 SV=1
6.	CAND2_MOUSE	137086	33	Cullin-associated NEDD8-dissociated protein 2 OS=Mus musculus GN=Cand2 PE=1 SV=2
7.	SC6A3_MOUSE	69502	30	Sodium-dependent dopamine transporter OS=Mus musculus GN=Slc6a3 PE=1 SV=2
8.	PPM1L_MOUSE	41251	29	Protein phosphatase 1L OS=Mus musculus GN=Ppm1l PE=1 SV=1
9.	A1AT2_MOUSE	46117	29	Alpha-1-antitrypsin 1-2 OS=Mus musculus GN=Serpina1b PE=1 SV=2
10.	DCST1_MOUSE	85646	28	DC-STAMP domain-containing protein 1 OS=Mus musculus GN=Dcst1 PE=2 SV=1

Results List

1. PTRF_MOUSE **Mass:** 43927 **Score:** 147 **Expect:** 3.2e-011 **Matches:** 7

Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
1071.5989	1070.5916	1070.5913	0.30	320	-	328	0	---	K.VPPFTFHVK.K
1171.6428	1170.6355	1170.6608	-21.59	330	-	339	1	---	K.IREGEVEVLK.A
1291.6387	1290.6315	1290.6357	-3.27	302	-	312	0	49	K.SFTPDHVVYAR.S
1313.7321	1312.7248	1312.7350	-7.75	139	-	149	1	32	K.KLEVNEAELLR.R
1419.7260	1418.7187	1418.7307	-8.44	301	-	312	1	---	R.KSFTPDHVVYAR.S
1932.8634	1931.8561	1931.8418	7.39	340	-	357	0	---	K.ATEMVEVGPEDDEVGAER.G
2025.1038	2024.0965	2024.0902	3.11	63	-	80	0	15	K.IIGAVDQIQLTQAQLEER.Q

No match to: 981.5416, 1088.5817, 1093.6234, 1338.8345, 1701.5426, 1723.5341, 1724.5839, 2021.0898, 2179.1374, 2405.1854

2. A1AT3_MOUSE **Mass:** 45966 **Score:** 70 **Expect:** 0.0015 **Matches:** 4

Alpha-1-antitrypsin 1-3 OS=Mus musculus GN=Serpina1c PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
981.5416	980.5344	980.5556	-21.63	301	-	308	0	44	R.LAQIHFPR.L
1088.5817	1087.5744	1087.6060	-28.99	319	-	328	0	---	K.TLMSPLGITR.I
1171.6428	1170.6355	1170.6608	-21.60	182	-	192	1	---	K.GTQGKIVEAVK.K + Acetyl (N-term)
2405.1854	2404.1781	2404.1659	5.09	36	-	57	0	---	K.DQSPASHEIATNLGDFAISLYR.E

No match to: 1071.5989, 1093.6234, 1291.6387, 1313.7321, 1338.8345, 1419.7260, 1701.5426, 1723.5341, 1724.5839, 1932.8634, 2021.0898, 2025.1038, 2179.1374

3. A1AT1_MOUSE **Mass:** 46145 **Score:** 62 **Expect:** 0.011 **Matches:** 3

Alpha-1-antitrypsin 1-1 OS=Mus musculus GN=Serpina1a PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
981.5416	980.5344	980.5556	-21.63	301	-	308	0	44	R.LAQIHFPR.L
1088.5817	1087.5744	1087.6060	-28.99	319	-	328	0	---	K.TLMSPLGITR.I
2405.1854	2404.1781	2404.1659	5.09	36	-	57	0	---	K.DQSPASHEIATNLGDFAISLYR.E

No match to: 1071.5989, 1093.6234, 1171.6428, 1291.6387, 1313.7321, 1338.8345, 1419.7260, 1701.5426, 1723.5341, 1724.5839, 1932.8634, 2021.0898, 2025.1038, 2179.1374

4. TFR1_MOUSE **Mass:** 86076 **Score:** 49 **Expect:** 0.2 **Matches:** 6

Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
981.5416	980.5344	980.4862	49.1	669	-	675	1	---	K.TNRFVMR.E + Acetyl (N-term); Oxidation (M)
1171.6428	1170.6355	1170.6145	17.9	518	-	527	1	---	K.HPVDGKSLYR.D
1291.6387	1290.6315	1290.6568	-19.62	627	-	636	1	---	K.DLNQFKTDIR.D + Acetyl (N-term)
1932.8634	1931.8561	1931.9160	-30.97	23	-	39	1	---	R.FSLARQVDGDNSHVEMK.L
2025.1038	2024.0965	2024.0149	40.3	633	-	649	1	14	K.TDIRDMGLSLQWLYSAR.G
2405.1854	2404.1781	2404.1117	27.6	2	-	22	1	---	M.MDQARSAFSNLFGGEPLSYTR.F + Acetyl (N-term); Oxidation (M)

No match to: 1071.5989, 1088.5817, 1093.6234, 1313.7321, 1338.8345, 1419.7260, 1701.5426, 1723.5341, 1724.5839, 2021.0898, 2179.1374

5. GCNT7_MOUSE **Mass:** 49291 **Score:** 38 **Expect:** 2.4 **Matches:** 5

Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase 7 OS=Mus musculus GN=Gcnt7 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1088.5817	1087.5744	1087.5563	16.7	318	325	0	---	K.HYWVTLNR.L
1291.6387	1290.6315	1290.6172	11.0	184	193	1	---	R.RLQAEIDCMR.D
1932.8634	1931.8561	1931.9490	-48.05	326	343	1	---	R.LKDAPGATPDAGWEGHIR.A + Acetyl (N-term)
2179.1374	2178.1301	2178.0818	22.2	271	290	0	---	K.QSPPHNLTISSGSAHYALTR.K + Acetyl (N-term)
2405.1854	2404.1781	2404.2469	-28.62	6	26	1	---	R.TTKAGLVACGMICAFIFLYLR.N

No match to: 981.5416, 1071.5989, 1093.6234, 1171.6428, 1313.7321, 1338.8345, 1419.7260, 1701.5426, 1723.5341, 1724.5839, 2021.0898, 2025.1038

6. CAND2_MOUSE **Mass:** 137086 **Score:** 33 **Expect:** 8.2 **Matches:** 7

Cullin-associated NEDD8-dissociated protein 2 OS=Mus musculus GN=Cand2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1088.5817	1087.5744	1087.5873	-11.85	1163	1172	1	---	K.AGSVKQELEK.Q
1171.6428	1170.6355	1170.6794	-37.50	632	642	0	---	K.ALTLVAMSPLR.L
1291.6387	1290.6315	1290.6568	-19.63	1196	1207	0	---	K.SPTVADFSAQIR.S
1419.7260	1418.7187	1418.7518	-23.32	1195	1207	1	---	R.KSPTVADFSAQIR.S
1932.8634	1931.8561	1931.8829	-13.87	806	824	0	---	R.CVAALSAACPQEAAGTASR.L + Acetyl (N-term)
2021.0898	2020.0826	2019.9823	49.6	559	576	0	---	R.LLDPEPYVGEMSTATLAR.L + Acetyl (N-term); Oxidation (M)
2025.1038	2024.0965	2024.0976	-0.54	605	621	1	---	R.LGDDLEPTLMLLLDRLR.N + Acetyl (N-term)

No match to: 981.5416, 1071.5989, 1093.6234, 1313.7321, 1338.8345, 1701.5426, 1723.5341, 1724.5839, 2179.1374, 2405.1854

7. SC6A3_MOUSE **Mass:** 69502 **Score:** 30 **Expect:** 16 **Matches:** 4

Sodium-dependent dopamine transporter OS=Mus musculus GN=Slc6a3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
981.5416	980.5344	980.4927	42.5	228	236	0	11	R.GIDDLGPPR.W + Acetyl (N-term)
1071.5989	1070.5916	1070.5833	7.84	601	609	1	---	R.QLVDRGEVR.Q
1088.5817	1087.5744	1087.5887	-13.09	219	227	0	---	R.GVLHLHQSR.G + Acetyl (N-term)
2179.1374	2178.1301	2178.0615	31.5	509	524	1	---	K.QMTGQRPNLYWRLCWK.L + Acetyl (N-term)

No match to: 1093.6234, 1171.6428, 1291.6387, 1313.7321, 1338.8345, 1419.7260, 1701.5426, 1723.5341, 1724.5839, 1932.8634, 2021.0898, 2025.1038, 2405.1854

8. PPM1L_MOUSE **Mass:** 41251 **Score:** 29 **Expect:** 20 **Matches:** 4

Protein phosphatase 1L OS=Mus musculus GN=Ppm1l PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1419.7260	1418.7187	1418.7293	-7.48	72	84	0	---	R.LGGLDVLEAEFSK.T + Acetyl (N-term)
1932.8634	1931.8561	1931.9047	-25.15	103	118	1	---	R.DHMEDRFEVLTDLANK.T
2025.1038	2024.0965	2024.0468	24.5	1	17	1	---	-.MIEDTMTLLSLLGRIMR.Y + 2 Oxidation (M)
2405.1854	2404.1781	2404.2485	-29.29	159	178	0	---	K.ENSVLTYQTILEQQILSIDR.E + Acetyl (N-term)

No match to: 981.5416, 1071.5989, 1088.5817, 1093.6234, 1171.6428, 1291.6387, 1313.7321, 1338.8345, 1701.5426, 1723.5341, 1724.5839, 2021.0898, 2179.1374

9. A1AT2_MOUSE **Mass:** 46117 **Score:** 29 **Expect:** 21 **Matches:** 4

Alpha-1-antitrypsin 1-2 OS=Mus musculus GN=Serpina1b PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1088.5817	1087.5744	1087.6060	-28.99	319	328	0	---	K.TLMSPLGITR.I
1171.6428	1170.6355	1170.6608	-21.60	182	192	1	---	K.GTQGKIVEAVK.E + Acetyl (N-term)
2179.1374	2178.1301	2178.1718	-19.14	309	328	1	---	R.LSISGDYNLKTLMSPLGITR.I
2405.1854	2404.1781	2404.1659	5.09	36	57	0	---	K.DQSPASHEIATNLGDFAISLYR.E

No match to: 981.5416, 1071.5989, 1093.6234, 1291.6387, 1313.7321, 1338.8345, 1419.7260, 1701.5426, 1723.5341, 1724.5839, 1932.8634, 2021.0898, 2025.1038

10. DCST1_MOUSE **Mass:** 85646 **Score:** 28 **Expect:** 24 **Matches:** 5

DC-STAMP domain-containing protein 1 OS=Mus musculus GN=Dcst1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1291.6387	1290.6315	1290.6648	-25.85	617	626	0	---	R.ALFFYNEFLK.K
1313.7321	1312.7248	1312.7714	-35.48	533	544	1	10	K.VEGDSILAKLLR.K
1419.7260	1418.7187	1418.7598	-28.98	617	627	1	---	R.ALFFYNEFLKK.R
2025.1038	2024.0965	2024.0522	21.9	298	313	1	---	R.RIHLPLFNNMICVPMK.F + Acetyl (N-term)
2179.1374	2178.1301	2178.1507	-9.43	1	19	1	---	-.MAFLSSTLHSLGIFEKISR.I + Acetyl (N-term)

No match to: 981.5416, 1071.5989, 1088.5817, 1093.6234, 1171.6428, 1338.8345, 1701.5426, 1723.5341, 1724.5839, 1932.8634, 2021.0898, 2405.1854

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Acetyl (N-term),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ±50 ppm
Fragment Mass Tolerance: ±0.5 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (981.5416,1+) : <no title>
Query2 (1071.5989,1+) : <no title>
Query3 (1088.5817,1+) : <no title>
Query4 (1093.6234,1+) : <no title>
Query5 (1171.6428,1+) : <no title>
Query6 (1291.6387,1+) : <no title>
Query7 (1313.7321,1+) : <no title>
Query8 (1338.8345,1+) : <no title>
Query9 (1419.7260,1+) : <no title>
Query10 (1701.5426,1+) : <no title>
Query11 (1723.5341,1+) : <no title>
Query12 (1724.5839,1+) : <no title>

Query13 (1932.8634,1+) : <no title>

Query14 (2021.0898,1+) : <no title>

Query15 (2025.1038,1+) : <no title>

Query16 (2179.1374,1+) : <no title>

Query17 (2405.1854,1+) : <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 : **20 Jun 2013 at 07:31:03 GMT**

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

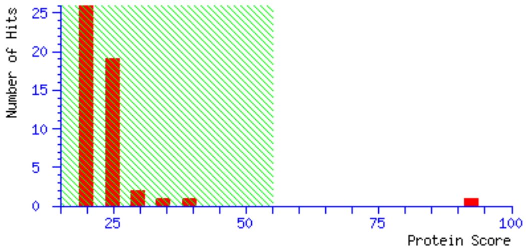
Top Score : **92 for RD23A_MOUSE, UV excision repair protein RAD23 homolog A OS=Mus musculus GN=Rad23a PE=1 SV=1**

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.	**RD23A_MOUSE**	39802	92	UV excision repair protein RAD23 homolog A OS=Mus musculus GN=Rad23a PE=1 SV=1
2.	**WDR38_MOUSE**	33715	38	WD repeat-containing protein 38 OS=Mus musculus GN=Wdr38 PE=2 SV=1
3.	**PP1A_MOUSE**	38257	35	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1
4.	**GLCTK_MOUSE**	55543	30	Glycerate kinase OS=Mus musculus GN=Glyctk PE=2 SV=1
5.	**HYEP_MOUSE**	52713	28	Epoxide hydrolase 1 OS=Mus musculus GN=Ephx1 PE=1 SV=1
6.	**SOS2_MOUSE**	154398	27	Son of sevenless homolog 2 OS=Mus musculus GN=Sos2 PE=1 SV=2
7.	**HMCS2_MOUSE**	57300	27	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2
8.	**RAB5C_MOUSE**	23626	26	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2
9.	**AP4S1_MOUSE**	16978	26	AP-4 complex subunit sigma-1 OS=Mus musculus GN=Ap4s1 PE=2 SV=1
10.	**BPI_MOUSE**	54191	26	Bactericidal permeability-increasing protein OS=Mus musculus GN=Bpi PE=2 SV=1

Results List

1. RD23A_MOUSE **Mass:** 39802 **Score:** 92 **Expect:** 9.3e-006 **Matches:** 5

UV excision repair protein RAD23 homolog A OS=Mus musculus GN=Rad23a PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
958.4495	957.4422	957.4416	0.61	186 -	193	0	6	R.ASYNNPHR.A
1145.6043	1144.5971	1144.5989	-1.62	37 -	47	1	---	K.GRDAFPVAGQK.L
1163.5241	1162.5168	1162.5189	-1.84	237 -	245	0	39	R.DQPQFQNMR.Q
1179.5331	1178.5259	1178.5139	10.2	237 -	245	0	---	R.DQPQFQNMR.Q + Oxidation (M)
1217.6272	1216.6199	1216.6122	6.41	17 -	26	1	---	K.IRMEPDETVK.V

No match to: 1111.5682, 1115.5537, 1198.6607, 1913.9460, 2225.0629, 2248.0682

2. WDR38_MOUSE **Mass:** 33715 **Score:** 38 **Expect:** 2.7 **Matches:** 4

WD repeat-containing protein 38 OS=Mus musculus GN=Wdr38 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1163.5241	1162.5168	1162.5263	-8.18	1 -	9	0	---	-.MEWAPMNIR.A + Oxidation (M)
1179.5331	1178.5259	1178.5212	3.93	1 -	9	0	---	-.MEWAPMNIR.A + 2 Oxidation (M)
1913.9460	1912.9387	1912.9683	-15.46	236 -	252	0	---	K.GHTIWVNSLAFSPDELK.L
2225.0629	2224.0556	2224.0648	-4.15	112 -	132	1	---	R.SVETVSFSPDSKQLASGGWDK.R

No match to: 958.4495, 1111.5682, 1115.5537, 1145.6043, 1198.6607, 1217.6272, 2248.0682

3. PP1A_MOUSE **Mass:** 38257 **Score:** 35 **Expect:** 4.9 **Matches:** 3

Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1198.6607	1197.6534	1197.6182	29.4	114 -	122	0	---	R.YPENFFLLR.G
1913.9460	1912.9387	1912.9908	-27.21	306 -	323	0	---	K.YGQFSGLNPGGRPITPPR.N
2248.0682	2247.0610	2247.0235	16.7	169 -	187	0	---	K.IFCCHGGLSPDLQSMEQIR.R

No match to: 958.4495, 1111.5682, 1115.5537, 1145.6043, 1163.5241, 1179.5331, 1217.6272, 2225.0629

4. GLCTK_MOUSE **Mass:** 55543 **Score:** 30 **Expect:** 16 **Matches:** 3

Glycerate kinase OS=Mus musculus GN=Glyctk PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
958.4495	957.4422	957.4702	-29.18	118 -	126	1	---	R.AAMEHAGKK.E + Oxidation (M)
1913.9460	1912.9387	1912.9829	-23.10	40 -	57	0	---	R.QLFDSAVGAVQPGPMLQR.T
2248.0682	2247.0610	2247.1028	-18.60	322 -	342	0	---	R.QAEVLGYHAMVLSTAMQGDVK.R

No match to: 1111.5682, 1115.5537, 1145.6043, 1163.5241, 1179.5331, 1198.6607, 1217.6272, 2225.0629

5. HYEP_MOUSE **Mass:** 52713 **Score:** 28 **Expect:** 26 **Matches:** 3

Epoxide hydrolase 1 OS=Mus musculus GN=Ephx1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
958.4495	957.4422	957.4742	-33.40	289 -	295	0	---	K.VFYNIMR.E + Oxidation (M)
1145.6043	1144.5971	1144.5724	21.6	339 -	348	1	---	R.ELEDGGLERK.F
1217.6272	1216.6199	1216.6241	-3.38	268 -	277	1	---	R.FGRFLGYTEK.D

No match to: 1111.5682, 1115.5537, 1163.5241, 1179.5331, 1198.6607, 1913.9460, 2225.0629, 2248.0682

6. SOS2_MOUSE **Mass:** 154398 **Score:** 27 **Expect:** 32 **Matches:** 4

Son of sevenless homolog 2 OS=Mus musculus GN=Sos2 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1111.5682	1110.5609	1110.5822	-19.17	1314	1322	0	---	R.ELSHPPLYR.L
1179.5331	1178.5259	1178.5568	-26.23	1169	1179	0	---	K.SDDDPPAIPPR.Q
1913.9460	1912.9387	1912.9928	-28.24	552	567	1	---	R.MLDSVLLKEENEQPLR.L
2248.0682	2247.0610	2247.1373	-33.97	341	357	0	---	R.LMLVPVYHCWHYFELLK.Q

No match to: 958.4495, 1115.5537, 1145.6043, 1163.5241, 1198.6607, 1217.6272, 2225.0629

7. HMCS2_MOUSE **Mass:** 57300 **Score:** 27 **Expect:** 32 **Matches:** 3

Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
958.4495	957.4422	957.4450	-2.93	495	501	1	---	R.VDEMHRR.K + Oxidation (M)
1217.6272	1216.6199	1216.6551	-28.87	127	137	0	---	R.LEVGTETIIDK.S
2225.0629	2224.0556	2224.1382	-37.15	16	35	1	---	K.RAMQETSLTPAHLLSAAQQR.F + Oxidation (M)

No match to: 1111.5682, 1115.5537, 1145.6043, 1163.5241, 1179.5331, 1198.6607, 1913.9460, 2248.0682

8. RAB5C_MOUSE **Mass:** 23626 **Score:** 26 **Expect:** 36 **Matches:** 2

Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1913.9460	1912.9387	1912.9690	-15.81	5	23	1	---	R.GGAARPNGPAAGNKICQFK.L
2225.0629	2224.0556	2224.1488	-41.91	93	113	1	---	R.GAQAAIVVYDITNTDTFARAK.N

No match to: 958.4495, 1111.5682, 1115.5537, 1145.6043, 1163.5241, 1179.5331, 1198.6607, 1217.6272, 2248.0682

9. AP4S1_MOUSE **Mass:** 16978 **Score:** 26 **Expect:** 39 **Matches:** 2

AP-4 complex subunit sigma-1 OS=Mus musculus GN=Ap4s1 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1145.6043	1144.5971	1144.6452	-42.02	28	37	1	---	K.RALLETEVSK.S
2225.0629	2224.0556	2224.1344	-35.44	110	128	0	---	K.VHIILDEMVLNGCIVETNR.A

No match to: 958.4495, 1111.5682, 1115.5537, 1163.5241, 1179.5331, 1198.6607, 1217.6272, 1913.9460, 2248.0682

10. BPI_MOUSE **Mass:** 54191 **Score:** 26 **Expect:** 40 **Matches:** 3

Bactericidal permeability-increasing protein OS=Mus musculus GN=Bpi PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
958.4495	957.4422	957.4668	-25.69	2	9	0	---	M.TWAPDNVR.K
1145.6043	1144.5971	1144.6492	-45.53	411	419	1	---	R.WLLELKESK.F
1217.6272	1216.6199	1216.6023	14.5	1	10	1	---	-.MTWAPDNVRK.W

No match to: 1111.5682, 1115.5537, 1163.5241, 1179.5331, 1198.6607, 1913.9460, 2225.0629, 2248.0682

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 (958.4495,1+) : <no title>

Query2 (1111.5682,1+) : <no title>

Query3 (1115.5537,1+) : <no title>

Query4 (1145.6043,1+) : <no title>

Query5 (1163.5241,1+) : <no title>

Query6 (1179.5331,1+) : <no title>

Query7 (1198.6607,1+) : <no title>

Query8 (1217.6272,1+) : <no title>

Query9 (1913.9460,1+) : <no title>

Query10 (2225.0629,1+) : <no title>

Query11 (2248.0682,1+) : <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 : **20 May 2013 at 01:30:16 GMT**

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

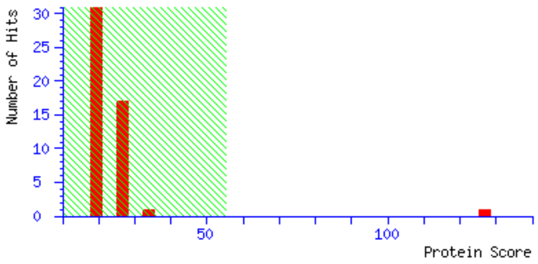
Top Score : **127 for CALU_MOUSE, Calumenin OS=Mus musculus GN=Calu PE=1 SV=1**

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.	**CALU_MOUSE**	37155	127	Calumenin OS=Mus musculus GN=Calu PE=1 SV=1
2.	**CENPX_MOUSE**	8978	37	Centromere protein X OS=Mus musculus GN=Stra13 PE=2 SV=1
3.	**GNPTG_MOUSE**	34546	28	N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Mus musculus GN=Gnptg PE=2 SV=1
4.	**MUC18_MOUSE**	72470	28	Cell surface glycoprotein MUC18 OS=Mus musculus GN=Mcam PE=1 SV=1
5.	**ANO3_MOUSE**	115577	27	Anoctamin-3 OS=Mus musculus GN=Ano3 PE=2 SV=1
6.	**PTPA_MOUSE**	36972	26	Serine/threonine-protein phosphatase 2A regulatory subunit B' OS=Mus musculus GN=Ppp2r4 PE=2 SV=1
7.	**MPPD2_MOUSE**	33524	26	Metallophosphoesterase MPPED2 OS=Mus musculus GN=Mpped2 PE=2 SV=1
8.	**S1PR4_MOUSE**	43034	26	Sphingosine 1-phosphate receptor 4 OS=Mus musculus GN=S1pr4 PE=2 SV=1
9.	**ACYP1_MOUSE**	11234	25	Acylphosphatase-1 OS=Mus musculus GN=Acyp1 PE=2 SV=2
10.	**CBY3_MOUSE**	26731	25	Protein chibby homolog 3 OS=Mus musculus GN=Cby3 PE=2 SV=2

Results List

1. CALU_MOUSE **Mass:** 37155 **Score:** 127 **Expect:** 3.2e-009 **Matches:** 6

Calumenin OS=Mus musculus GN=Calu PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
954.4791	953.4718	953.4607	11.7	235 -	241	0	38	R.EQFVEFR.D
1083.5353	1082.5280	1082.5145	12.5	104 -	111	0	---	R.WIHEDVER.Q
1340.6512	1339.6439	1339.6521	-6.08	232 -	241	1	---	K.TEREQFVEFR.D
1565.7432	1564.7359	1564.7369	-0.61	60 -	72	1	35	K.SFDQLTPEESKER.L
1887.8437	1886.8364	1886.8435	-3.76	256 -	271	0	---	K.DWILPSDYDHAEAEAR.H
2701.3165	2700.3092	2700.3283	-7.07	288 -	311	1	---	K.EEIVDKYDLFVGSQATDFGEALVR.H

No match to: 854.3019, 936.4669, 1338.8235, 1723.5453, 2691.2803, 2749.2675, 3043.5096

2. CENPX_MOUSE **Mass:** 8978 **Score:** 37 **Expect:** 3.3 **Matches:** 3

Centromere protein X OS=Mus musculus GN=Stra13 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
936.4669	935.4596	935.4461	14.4	2 -	9	1	---	M.EGNSGFRK.E + Acetyl (N-term)
1083.5353	1082.5280	1082.4815	43.0	1 -	9	1	---	-.MEGNSGFRK.E + Acetyl (N-term); Oxidation (M)
1565.7432	1564.7359	1564.7919	-35.77	27 -	40	0	---	K.VSGDALQLMAEFLR.I + Oxidation (M)

No match to: 854.3019, 954.4791, 1338.8235, 1340.6512, 1723.5453, 1887.8437, 2691.2803, 2701.3165, 2749.2675, 3043.5096

3. GNPTG_MOUSE **Mass:** 34546 **Score:** 28 **Expect:** 25 **Matches:** 3

N-acetylglucosamine-1-phosphotransferase subunit gamma OS=Mus musculus GN=Gnptg PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1083.5353	1082.5280	1082.5720	-40.67	298 -	307	1	---	R.SDPGLRGNIL.- + Acetyl (N-term)
2691.2803	2690.2730	2690.3281	-20.49	98 -	119	0	---	R.WNAYSGILGIWHEWEIINNTFK.G
2749.2675	2748.2602	2748.3501	-32.71	221 -	246	1	---	K.VPGETHPTQLAGGSKGLGLETLDNCR.K + Acetyl (N-term)

No match to: 854.3019, 936.4669, 954.4791, 1338.8235, 1340.6512, 1565.7432, 1723.5453, 1887.8437, 2701.3165, 3043.5096

4. MUC18_MOUSE **Mass:** 72470 **Score:** 28 **Expect:** 28 **Matches:** 4

Cell surface glycoprotein MUC18 OS=Mus musculus GN=Mcam PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
936.4669	935.4596	935.4964	-39.35	608 -	615	0	---	K.SEFVVEVK.S
1338.8235	1337.8162	1337.7932	17.2	72 -	82	1	---	R.QILIFRVHQGK.G
2691.2803	2690.2730	2690.2871	-5.25	266 -	288	1	---	K.EGDHVTIRCLTDGNPQPHFTINK.K + Acetyl (N-term)
2749.2675	2748.2602	2748.1807	28.9	290 -	314	0	---	K.DPSTGEMEEESTDENGLLSLEPAEK.H + Acetyl (N-term)

No match to: 854.3019, 954.4791, 1083.5353, 1340.6512, 1565.7432, 1723.5453, 1887.8437, 2701.3165, 3043.5096

5. ANO3_MOUSE **Mass:** 115577 **Score:** 27 **Expect:** 36 **Matches:** 5

Anoctamin-3 OS=Mus musculus GN=Ano3 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
954.4791	953.4718	953.5083	-38.22	247 -	253	1	---	R.VQNYFKR.I
1083.5353	1082.5280	1082.5066	19.7	454 -	462	0	---	R.LNDSCIYAK.V
1340.6512	1339.6439	1339.6846	-30.38	573 -	583	0	---	R.LVVMEQFASFK.W + Acetyl (N-term)
1887.8437	1886.8364	1886.9084	-38.16	145 -	161	1	---	K.NDMSYIASSGLLFKDGK.K + Acetyl (N-term)
2701.3165	2700.3092	2700.2312	28.9	863 -	886	1	---	K.GYVNNSLSFFDLSELGMGKSGYCR.Y

No match to: 854.3019, 936.4669, 1338.8235, 1565.7432, 1723.5453, 2691.2803, 2749.2675, 3043.5096

6. PTPA_MOUSE **Mass:** 36972 **Score:** 26 **Expect:** 37 **Matches:** 3

Serine/threonine-protein phosphatase 2A regulatory subunit B' OS=Mus musculus GN=Ppp2r4 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
954.4791	953.4718	953.5004	-29.96	188 -	194	1	---	R.YLEVMRK.L + Oxidation (M)
2691.2803	2690.2730	2690.3915	-44.06	77 -	99	1	---	K.LVALLDTLDRWIDETPPVDQPSR.F + Acetyl (N-term)
2749.2675	2748.2602	2748.2961	-13.07	243 -	264	1	---	K.AVSENHKDYMFLQCILFITEMK.T + 2 Oxidation (M)

No match to: 854.3019, 936.4669, 1083.5353, 1338.8235, 1340.6512, 1565.7432, 1723.5453, 1887.8437, 2701.3165, 3043.5096

7. MPPD2_MOUSE **Mass:** 33524 **Score:** 26 **Expect:** 40 **Matches:** 3

Metallophosphoesterase MPPED2 OS=Mus musculus GN=Mpped2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
936.4669	935.4596	935.4825	-24.46	2 -	10	0	---	M.AHGIPSQGK.V + Acetyl (N-term)
1083.5353	1082.5280	1082.5179	9.34	1 -	10	0	---	-.MAHGIPSQGK.V + Acetyl (N-term); Oxidation (M)
3043.5096	3042.5023	3042.5790	-25.19	200 -	225	1	---	K.WNLIPEGIDILMTHGPPLGFRDWVPK.E + Acetyl (N-term)

No match to: 854.3019, 954.4791, 1338.8235, 1340.6512, 1565.7432, 1723.5453, 1887.8437, 2691.2803, 2701.3165, 2749.2675

8. S1PR4_MOUSE **Mass:** 43034 **Score:** 26 **Expect:** 44 **Matches:** 2

Sphingosine 1-phosphate receptor 4 OS=Mus musculus GN=S1pr4 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
954.4791	953.4718	953.4753	-3.59	368 -	374	1	14	R.SLSFRMR.E + Acetyl (N-term); Oxidation (M)
1887.8437	1886.8364	1886.8945	-30.80	2 -	17	0	---	M.NISTWSTLVTPESCHR.L

No match to: 854.3019, 936.4669, 1083.5353, 1338.8235, 1340.6512, 1565.7432, 1723.5453, 2691.2803, 2701.3165, 2749.2675, 3043.5096

9. ACYP1_MOUSE **Mass:** 11234 **Score:** 25 **Expect:** 49 **Matches:** 2

Acylphosphatase-1 OS=Mus musculus GN=Acyp1 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1340.6512	1339.6439	1339.7096	-49.03	46 -	58	0	---	R.GTVQGQLQGPVSK.V + Acetyl (N-term)
2749.2675	2748.2602	2748.3469	-31.56	1 -	24	1	---	-.MAEGDTLVSVDYEIFGKVQGVFFR.K + Acetyl (N-term)

No match to: 854.3019, 936.4669, 954.4791, 1083.5353, 1338.8235, 1565.7432, 1723.5453, 1887.8437, 2691.2803, 2701.3165, 3043.5096

10. CBY3_MOUSE **Mass:** 26731 **Score:** 25 **Expect:** 55 **Matches:** 3

Protein chibby homolog 3 OS=Mus musculus GN=Cby3 PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1083.5353	1082.5280	1082.5397	-10.79	122 -	130	0	---	R.LSDEAFVFR.G
1340.6512	1339.6439	1339.6884	-33.25	120 -	130	1	---	R.TRLSDEAFVFR.G
2749.2675	2748.2602	2748.3694	-39.72	46 -	69	1	---	R.VAHTTFTLEAFECLAASQAGRLWK.Q + Acetyl (N-term)

No match to: 854.3019, 936.4669, 954.4791, 1338.8235, 1565.7432, 1723.5453, 1887.8437, 2691.2803, 2701.3165, 3043.5096

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (854.3019,1+) : <no title>

Query2 (936.4669,1+) : <no title>

Query3 (954.4791,1+) : <no title>

Query4 (1083.5353,1+) : <no title>

Query5 (1338.8235,1+) : <no title>

Query6 (1340.6512,1+) : <no title>

Query7 (1565.7432,1+) : <no title>

Query8 (1723.5453,1+) : <no title>

Query9 (1887.8437,1+) : <no title>

Query10 (2691.2803,1+) : <no title>

Query11 (2701.3165,1+) : <no title>

Query12 (2749.2675,1+) : <no title>

Query13 (3043.5096,1+) : <no title>

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

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 : 20 Jun 2013 at 07:30:53 GMT

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

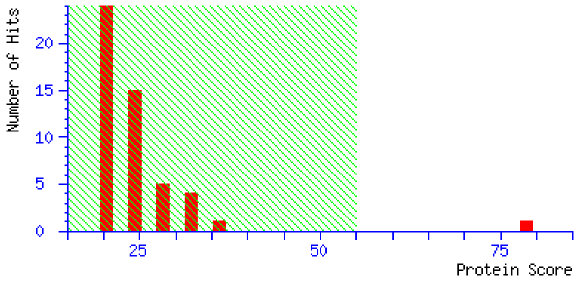
Top Score : 78 for KCRB_MOUSE, Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1

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.	**KCRB_MOUSE**	42971	78	Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1
2.	**ALDOC_MOUSE**	39769	36	Fructose-bisphosphate aldolase C OS=Mus musculus GN=Aldoc PE=1 SV=4
3.	**TBAL3_MOUSE**	50625	34	Tubulin alpha chain-like 3 OS=Mus musculus GN=Tubal3 PE=2 SV=1
4.	**IFI4_MOUSE**	72347	33	Interferon-activable protein 204 OS=Mus musculus GN=Ifi204 PE=1 SV=2
5.	**TF3C4_MOUSE**	92905	32	General transcription factor 3C polypeptide 4 OS=Mus musculus GN=Gtf3c4 PE=1 SV=1
6.	**T11L2_MOUSE**	58423	31	T-complex protein 11-like protein 2 OS=Mus musculus GN=Tcp11l2 PE=2 SV=1
7.	**CPSF3_MOUSE**	78049	30	Cleavage and polyadenylation specificity factor subunit 3 OS=Mus musculus GN=Cpsf3 PE=1 SV=1
8.	**MYO9B_MOUSE**	240225	28	Myosin-IXb OS=Mus musculus GN=Myo9b PE=1 SV=2
9.	**GCH1_MOUSE**	27168	28	GTP cyclohydrolase 1 OS=Mus musculus GN=Gch1 PE=2 SV=1
10.	**P66B_MOUSE**	65712	27	Transcriptional repressor p66-beta OS=Mus musculus GN=Gatad2b PE=1 SV=1

Results List

1. KCRB_MOUSE **Mass:** 42971 **Score:** 78 **Expect:** 0.00023 **Matches:** 7

Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1031.5540	1030.5467	1030.5481	-1.36	359 -	366	0	---	K.LLIEMEQR.L
1230.5507	1229.5434	1229.5434	0.00	139 -	148	0	---	R.GFCLPPHCSR.G
1246.6227	1245.6154	1245.6241	-6.99	87 -	96	0	---	K.DLFDPIIEER.H
1303.7137	1302.7064	1302.7183	-9.15	33 -	43	0	2	K.VLTPELYAELR.A
1602.8152	1601.8079	1601.8260	-11.31	157 -	172	0	---	K.LAVEALSSLDGDLSGR.Y
1671.8329	1670.8257	1670.8416	-9.56	224 -	236	0	---	K.TFLVWINEEDHLR.V
1964.9061	1963.8988	1963.9236	-12.63	321 -	341	0	---	R.GTGGVDTAAVGGVFDVSNADR.L

No match to: 955.4451, 1108.5378, 1198.6730, 1338.8166, 1348.6620, 1474.7198, 1665.9785, 1703.8146, 1755.9081, 1949.8964, 1981.8843, 1997.8835, 2247.0768

2. ALDOC_MOUSE **Mass:** 39769 **Score:** 36 **Expect:** 4.3 **Matches:** 4

Fructose-bisphosphate aldolase C OS=Mus musculus GN=Aldoc PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1348.6620	1347.6548	1347.6704	-11.60	29 -	42	0	---	K.GILAADESVGSMAK.R

1474.7198	1473.7125	1473.6922	13.8	1	13	0	---	-.MPHSYPALSAEQK.K + Oxidation (M)
1602.8152	1601.8079	1601.7871	13.0	1	14	1	---	-.MPHSYPALSAEQKK.E + Oxidation (M)
1671.8329	1670.8257	1670.8702	-26.63	202	215	1	---	R.CQYVTEKVLAAVYK.A

No match to: 955.4451, 1031.5540, 1108.5378, 1198.6730, 1230.5507, 1246.6227, 1303.7137, 1338.8166, 1665.9785, 1703.8146, 1755.9081, 1949.8964, 1964.9061, 1981.8843, 1997.8835, 2247.0768

3. TBAL3_MOUSE **Mass:** 50625 **Score:** 34 **Expect:** 6.8 **Matches:** 4

Tubulin alpha chain-like 3 OS=Mus musculus GN=Tubal3 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1031.5540	1030.5467	1030.5157	30.0	402	409	1	---	K.FDLMYAKK.A + Oxidation (M)
1671.8329	1670.8257	1670.7763	29.5	346	359	0	---	R.TSVQFVDWCPTGFK.V
1703.8146	1702.8074	1702.7985	5.21	147	163	0	---	R.SFGGGTGSGFTSLLMER.L
1949.8964	1948.8892	1948.8738	7.90	49	64	0	---	K.VEHMNASLDTFFHETR.A + Oxidation (M)

No match to: 955.4451, 1108.5378, 1198.6730, 1230.5507, 1246.6227, 1303.7137, 1338.8166, 1348.6620, 1474.7198, 1602.8152, 1665.9785, 1755.9081, 1964.9061, 1981.8843, 1997.8835, 2247.0768

4. IFI4_MOUSE **Mass:** 72347 **Score:** 33 **Expect:** 8.7 **Matches:** 5

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
955.4451	954.4379	954.4593	-22.42	1	7	1	---	-.MVNEYKR.I + Oxidation (M)
1348.6620	1347.6548	1347.6347	14.9	578	589	0	---	K.FIYYGIGDDTGK.M
1474.7198	1473.7125	1473.7504	-25.68	302	313	0	---	K.NFIIISNYFESK.G
1602.8152	1601.8079	1601.8453	-23.33	301	313	1	---	K.KNFIIISNYFESK.G
1755.9081	1754.9008	1754.8814	11.1	13	26	1	---	R.GLECINKHYFSLFK.S

No match to: 1031.5540, 1108.5378, 1198.6730, 1230.5507, 1246.6227, 1303.7137, 1338.8166, 1665.9785, 1671.8329, 1703.8146, 1949.8964, 1964.9061, 1981.8843, 1997.8835, 2247.0768

5. TF3C4_MOUSE **Mass:** 92905 **Score:** 32 **Expect:** 9.1 **Matches:** 5

General transcription factor 3C polypeptide 4 OS=Mus musculus GN=Gtf3c4 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
955.4451	954.4379	954.4705	-34.22	239	246	0	---	R.HSMQTPVR.M
1198.6730	1197.6657	1197.6176	40.2	671	680	0	---	K.IEAVEMHLTR.E
1671.8329	1670.8257	1670.7683	34.4	430	444	1	---	K.QNGTVYTCSSDGKVR.Q
1755.9081	1754.9008	1754.8443	32.2	671	684	1	---	K.IEAVEMHLTREHMK.R + 2 Oxidation (M)
1949.8964	1948.8892	1948.9027	-6.96	222	238	1	---	K.NEAPEGNLGDFAEFQRR.H

No match to: 1031.5540, 1108.5378, 1230.5507, 1246.6227, 1303.7137, 1338.8166, 1348.6620, 1474.7198, 1602.8152, 1665.9785, 1703.8146, 1964.9061, 1981.8843, 1997.8835, 2247.0768

6. T11L2_MOUSE **Mass:** 58423 **Score:** 31 **Expect:** 13 **Matches:** 4

T-complex protein 11-like protein 2 OS=Mus musculus GN=Tcp11l2 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1348.6620	1347.6548	1347.6275	20.2	429	439	1	---	K.DNPVCTLMDKR.I
1474.7198	1473.7125	1473.7405	-18.98	487	498	0	---	K.QVYGPFYANIFR.K

1602.8152	1601.8079	1601.8354	-17.17	487	499	1	---	K.QVYGPFYANIFRK.L
1755.9081	1754.9008	1754.8621	22.1	385	400	0	---	K.EALHSIGVQTCAEVNK.A

No match to: 955.4451, 1031.5540, 1108.5378, 1198.6730, 1230.5507, 1246.6227, 1303.7137, 1338.8166, 1665.9785, 1671.8329, 1703.8146, 1949.8964, 1964.9061, 1981.8843, 1997.8835, 2247.0768

7. CPSF3_MOUSE **Mass:** 78049 **Score:** 30 **Expect:** 18 **Matches:** 5

Cleavage and polyadenylation specificity factor subunit 3 OS=Mus musculus GN=Cpsf3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1031.5540	1030.5467	1030.5407	5.81	643	651	0	---	K.TANINLETR.A
1703.8146	1702.8074	1702.8825	-44.10	466	480	1	---	K.VMGFLADKKPEQGQR.V
1981.8843	1980.8770	1980.9537	-38.68	614	630	0	---	R.LEVMLQDIFGEDCVSVK.D
1997.8835	1996.8762	1996.9486	-36.25	614	630	0	---	R.LEVMLQDIFGEDCVSVK.D + Oxidation (M)
2247.0768	2246.0695	2246.1390	-30.96	631	651	1	---	K.DDSVLSVTVDGKTANINLETR.A

No match to: 955.4451, 1108.5378, 1198.6730, 1230.5507, 1246.6227, 1303.7137, 1338.8166, 1348.6620, 1474.7198, 1602.8152, 1665.9785, 1671.8329, 1755.9081, 1949.8964, 1964.9061

8. MYO9B_MOUSE **Mass:** 240225 **Score:** 28 **Expect:** 26 **Matches:** 7

Myosin-IXb OS=Mus musculus GN=Myo9b PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1031.5540	1030.5467	1030.5910	-43.02	447	455	0	---	R.ETLVEVLTK.R
1198.6730	1197.6657	1197.6540	9.84	801	810	0	---	R.LIISMTLHDR.T
1303.7137	1302.7064	1302.6788	21.2	2018	2028	1	---	R.RTPIMPMANIK.L + 2 Oxidation (M)
1474.7198	1473.7125	1473.7385	-17.63	1234	1247	0	---	R.VSPMLPSSSLESPK.D + Oxidation (M)
1671.8329	1670.8257	1670.8046	12.6	230	245	0	---	K.HVNQCIVISGESGSGK.T
1755.9081	1754.9008	1754.8257	42.8	722	737	1	---	R.SHMEELPRGASTPSEK.L
1964.9061	1963.8988	1963.9673	-34.88	1523	1539	0	---	K.DLMENYQIVVSNLAAER.G

No match to: 955.4451, 1108.5378, 1230.5507, 1246.6227, 1338.8166, 1348.6620, 1602.8152, 1665.9785, 1703.8146, 1949.8964, 1981.8843, 1997.8835, 2247.0768

9. GCH1_MOUSE **Mass:** 27168 **Score:** 28 **Expect:** 28 **Matches:** 3

GTP cyclohydrolase 1 OS=Mus musculus GN=Gch1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1348.6620	1347.6548	1347.7146	-44.42	17	29	0	---	R.ELPRPGASPPAEK.S
1671.8329	1670.8257	1670.8239	1.07	85	98	1	---	K.TPWRAATAMQYFTK.G
1703.8146	1702.8074	1702.8382	-18.14	212	226	1	---	K.MNSKTVTSTMLGVFR.E + 2 Oxidation (M)

No match to: 955.4451, 1031.5540, 1108.5378, 1198.6730, 1230.5507, 1246.6227, 1303.7137, 1338.8166, 1474.7198, 1602.8152, 1665.9785, 1755.9081, 1949.8964, 1964.9061, 1981.8843, 1997.8835, 2247.0768

10. P66B_MOUSE **Mass:** 65712 **Score:** 27 **Expect:** 34 **Matches:** 4

Transcriptional repressor p66-beta OS=Mus musculus GN=Gatad2b PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1108.5378	1107.5305	1107.5746	-39.86	149	158	1	---	K.AANLEMFKGK.G
1246.6227	1245.6154	1245.6427	-21.94	575	584	0	---	R.EYLLDMIPPR.S

1703.8146	1702.8074	1702.8131	-3.35	251 - 265	0	---	R.SATNTTLPHMLMSQR.V + Oxidation (M)
2247.0768	2246.0695	2246.1543	-37.74	53 - 73	1	---	K.DLANLEVPHELPTKQDGSGVK.G

No match to: 955.4451, 1031.5540, 1198.6730, 1230.5507, 1303.7137, 1338.8166, 1348.6620, 1474.7198, 1602.8152, 1665.9785, 1671.8329, 1755.9081, 1949.8964, 1964.9061, 1981.8843, 1997.8835

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 (955.4451,1+) : <no title>
Query2 (1031.5540,1+) : <no title>
Query3 (1108.5378,1+) : <no title>
Query4 (1198.6730,1+) : <no title>
Query5 (1230.5507,1+) : <no title>
Query6 (1246.6227,1+) : <no title>
Query7 (1303.7137,1+) : <no title>
Query8 (1338.8166,1+) : <no title>
Query9 (1348.6620,1+) : <no title>
Query10 (1474.7198,1+) : <no title>
Query11 (1602.8152,1+) : <no title>
Query12 (1665.9785,1+) : <no title>
Query13 (1671.8329,1+) : <no title>
Query14 (1703.8146,1+) : <no title>
Query15 (1755.9081,1+) : <no title>
Query16 (1949.8964,1+) : <no title>
Query17 (1964.9061,1+) : <no title>
Query18 (1981.8843,1+) : <no title>
Query19 (1997.8835,1+) : <no title>
Query20 (2247.0768,1+) : <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 : **20 May 2013 at 02:33:54 GMT**

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

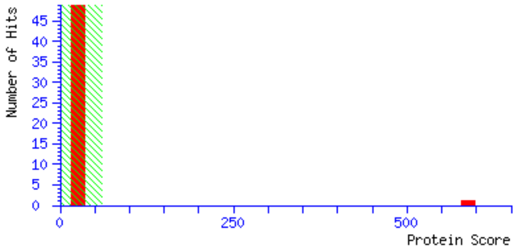
Top Score : **588 for IPI00169998, Tax_Id=10090 Gene_Symbol=Cbr3 carbonyl reductase 3**

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 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.	**IPI00169998**	31333	588	Tax_Id=10090 Gene_Symbol=Cbr3 carbonyl reductase 3
2.	**IPI00458084**	9010	35	Tax_Id=10090 Gene_Symbol=Fkbp1b FK506-binding protein
3.	**IPI00338579**	64341	34	Tax_Id=10090 Gene_Symbol=Cdkl2 Isoform 2 of Cyclin-dependent kinase-like 2
4.	**IPI00131724**	64699	34	Tax_Id=10090 Gene_Symbol=Cdkl2 Isoform 1 of Cyclin-dependent kinase-like 2
5.	**IPI00607992**	70919	33	Tax_Id=10090 Gene_Symbol=Invs Isoform 6 of Inversin
6.	**IPI01007702**	70885	33	Tax_Id=10090 Gene_Symbol=Invs Uncharacterized protein
7.	**IPI00607908**	105463	33	Tax_Id=10090 Gene_Symbol=Invs Isoform 3 of Inversin
8.	**IPI00608108**	105461	33	Tax_Id=10090 Gene_Symbol=Invs Uncharacterized protein
9.	**IPI00338570**	61511	33	Tax_Id=10090 Gene_Symbol=Daam2 Isoform 2 of Disheveled-associated activator of morphogenesis 2
10.	**IPI00137096**	15220	32	Tax_Id=10090 Gene_Symbol=4933414I15Rik Putative uncharacterized protein (Fragment)

Results List

1. IPI00169998 **Mass:** 31333 **Score:** 588 **Expect:** 9.4e-055 **Matches:** 13

Tax_Id=10090 Gene_Symbol=Cbr3 carbonyl reductase 3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4958	833.4886	833.4759	15.1	16 -	23	0	---	K.GIGFAITR.D
1192.7265	1191.7193	1191.6612	48.7	28 -	38	1	---	R.KFSGDVVLTAR.D
1430.7759	1429.7687	1429.7210	33.3	221 -	232	0	---	R.ILLNACCPGWVK.T
1467.8476	1466.8403	1466.7841	38.3	45 -	58	0	107	R.AAVQQLQAEGLSPR.F
1502.7730	1501.7658	1501.7161	33.1	175 -	186	1	---	K.FVEDTKNEVHER.E
1504.7627	1503.7554	1503.6987	37.7	146 -	157	1	---	K.ALENCREDLQEK.F
1583.8329	1582.8256	1582.7740	32.6	59 -	71	0	92	R.FHQLDIDDPQSIR.A
1764.9646	1763.9573	1763.9175	22.6	120 -	134	0	60	R.NVCTELLPIMKPHGR.V
1779.9264	1778.9191	1778.8794	22.3	160 -	174	1	---	R.CDTLTEVDLVDLMKK.F
1806.9929	1805.9856	1805.9424	23.9	80 -	96	0	130	K.EYGGLNVLVNNAGIAFR.M
1935.0814	1934.0741	1934.0374	19.0	79 -	96	1	63	R.KEYGGLNVLVNNAGIAFR.M
1955.0025	1953.9953	1953.9540	21.1	158 -	173	1	---	K.FRCDTLTEVDLVDLMK.K
3002.5446	3001.5373	3001.5397	-0.79	243 -	270	0	---	R.TVEEGAETPVYLALLPPDATEPHGQLVR.D

No match to: 855.3819, 856.5197, 1064.6435, 1332.7919, 1452.7712, 1454.7674, 1630.8647, 1725.9813, 1777.8799, 1788.9702, 1844.9402, 2086.1738, 3016.5633, 3030.5908

2. IPI00458084 **Mass:** 9010 **Score:** 35 **Expect:** 20 **Matches:** 3

Tax_Id=10090 Gene_Symbol=Fkbp1b FK506-binding protein

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1502.7730	1501.7658	1501.7083	38.3	1 -	14	0	---	-.MGVEIETISPGDGR.T + Acetyl (N-term)
1844.9402	1843.9329	1843.9316	0.72	2 -	18	1	---	M.GVEIETISPGDGRTFPK.K + Acetyl (N-term)
3016.5633	3015.5560	3015.4834	24.1	54 -	80	1	---	K.QEVIKGFEEGTAQLGPLSPLPICPHPC.- + Acetyl (N-term)

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1430.7759, 1452.7712, 1454.7674, 1467.8476, 1504.7627, 1583.8329, 1630.8647, 1725.9813, 1764.9646, 1777.8799, 1779.9264, 1788.9702, 1806.9929, 1935.0814, 1955.0025, 2086.1738, 3002.5446, 3030.5908

3. IPI00338579 **Mass:** 64341 **Score:** 34 **Expect:** 23 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Cdkl2 Isoform 2 of Cyclin-dependent kinase-like 2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1430.7759	1429.7687	1429.7817	-9.09	169 -	181	1	---	R.APELLVGDVKYGK.A + Acetyl (N-term)
1467.8476	1466.8403	1466.8245	10.7	232 -	244	1	4	K.NPVFAGVRLPEVK.D + Acetyl (N-term)
1504.7627	1503.7554	1503.7205	23.2	245 -	257	1	---	K.DAEAEPLESRYPK.L
1583.8329	1582.8256	1582.8566	-19.59	336 -	349	1	8	K.TLVVQDTNADPKIK.D + Acetyl (N-term)
1725.9813	1724.9741	1724.9672	3.96	126 -	141	0	---	R.DIKPENILVSQSGVVK.L

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1452.7712, 1454.7674, 1502.7730, 1630.8647, 1764.9646, 1777.8799, 1779.9264, 1788.9702, 1806.9929, 1844.9402, 1935.0814, 1955.0025, 2086.1738, 3002.5446, 3016.5633, 3030.5908

4. IPI00131724 **Mass:** 64699 **Score:** 34 **Expect:** 23 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Cdkl2 Isoform 1 of Cyclin-dependent kinase-like 2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1430.7759	1429.7687	1429.7817	-9.09	169 -	181	1	---	R.APELLVGDVKYGK.A + Acetyl (N-term)
1467.8476	1466.8403	1466.8245	10.7	232 -	244	1	4	K.NPVFAGVRLPEVK.D + Acetyl (N-term)

1504.7627	1503.7554	1503.7205	23.2	245	-	257	1	---	K.DAEAEPLESRYPK.L
1583.8329	1582.8256	1582.8566	-19.59	336	-	349	1	8	K.TLVVQDTNADPKIK.D + Acetyl (N-term)
1725.9813	1724.9741	1724.9672	3.96	126	-	141	0	---	R.DIKPENILVSQSGVVK.L

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1452.7712, 1454.7674, 1502.7730, 1630.8647, 1764.9646, 1777.8799, 1779.9264, 1788.9702, 1806.9929, 1844.9402, 1935.0814, 1955.0025, 2086.1738, 3002.5446, 3016.5633, 3030.5908

5. IPI00607992 **Mass:** 70919 **Score:** 33 **Expect:** 28 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Invs Isoform 6 of Inversin

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Ions**	**Peptide**
1452.7712	1451.7639	1451.7296	23.6	525	-	536	0	---	R.YTPLDYALLGER.H + Acetyl (N-term)
1467.8476	1466.8403	1466.8681	-18.96	28	-	41	1	16	K.GALQRLIVGNSALR.D
1583.8329	1582.8256	1582.7661	37.6	111	-	123	0	---	K.DLEEMTPLHLSTR.H + Acetyl (N-term)
3016.5633	3015.5560	3015.4608	31.6	346	-	374	1	---	K.SDIDINMSDKYGGTALHAAALSGHVSTVK.L + Acetyl (N-term); Oxidation (M)

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1430.7759, 1454.7674, 1502.7730, 1504.7627, 1630.8647, 1725.9813, 1764.9646, 1777.8799, 1779.9264, 1788.9702, 1806.9929, 1844.9402, 1935.0814, 1955.0025, 2086.1738, 3002.5446, 3030.5908

6. IPI01007702 **Mass:** 70885 **Score:** 33 **Expect:** 28 **Matches:** 4

Tax_Id=10090 Gene_Symbol=Invs Uncharacterized protein

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Ions**	**Peptide**
1452.7712	1451.7639	1451.7296	23.6	525	-	536	0	---	R.YTPLDYALLGER.H + Acetyl (N-term)
1467.8476	1466.8403	1466.8681	-18.96	28	-	41	1	16	K.GALQRLIVGNSALR.D
1583.8329	1582.8256	1582.7661	37.6	111	-	123	0	---	K.DLEEMTPLHLSTR.H + Acetyl (N-term)
3016.5633	3015.5560	3015.4608	31.6	346	-	374	1	---	K.SDIDINMSDKYGGTALHAAALSGHVSTVK.L + Acetyl (N-term); Oxidation (M)

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1430.7759, 1454.7674, 1502.7730, 1504.7627, 1630.8647, 1725.9813, 1764.9646, 1777.8799, 1779.9264, 1788.9702, 1806.9929, 1844.9402, 1935.0814, 1955.0025, 2086.1738, 3002.5446, 3030.5908

7. IPI00607908 **Mass:** 105463 **Score:** 33 **Expect:** 28 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Invs Isoform 3 of Inversin

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**		**End**	**Miss**	**Ions**	**Peptide**
1452.7712	1451.7639	1451.7296	23.6	525	-	536	0	---	R.YTPLDYALLGER.H + Acetyl (N-term)
1467.8476	1466.8403	1466.8681	-18.96	28	-	41	1	16	K.GALQRLIVGNSALR.D
1504.7627	1503.7554	1503.7351	13.5	730	-	743	1	---	R.GLPLSTEASRSGCK.Q + Acetyl (N-term)
1583.8329	1582.8256	1582.7661	37.6	111	-	123	0	---	K.DLEEMTPLHLSTR.H + Acetyl (N-term)
3016.5633	3015.5560	3015.4608	31.6	346	-	374	1	---	K.SDIDINMSDKYGGTALHAAALSGHVSTVK.L + Acetyl (N-term); Oxidation (M)

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1430.7759, 1454.7674, 1502.7730, 1630.8647, 1725.9813, 1764.9646, 1777.8799, 1779.9264, 1788.9702, 1806.9929, 1844.9402, 1935.0814, 1955.0025, 2086.1738, 3002.5446, 3030.5908

8. IPI00608108 **Mass:** 105461 **Score:** 33 **Expect:** 28 **Matches:** 5

Tax_Id=10090 Gene_Symbol=Invs Uncharacterized protein

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

1452.7712	1451.7639	1451.7296	23.6	525	-	536	0	---	R.YTPLDYALLGER.H + Acetyl (N-term)
1467.8476	1466.8403	1466.8681	-18.96	28	-	41	1	16	K.GALQRLIVGNSALR.D
1504.7627	1503.7554	1503.7351	13.5	730	-	743	1	---	R.GLPLSTEASRSGCK.Q + Acetyl (N-term)
1583.8329	1582.8256	1582.7661	37.6	111	-	123	0	---	K.DLEEMTPLHLSTR.H + Acetyl (N-term)
3016.5633	3015.5560	3015.4608	31.6	346	-	374	1	---	K.SDIDINMSDKYGGTALHAAALSGHVSTVK.L + Acetyl (N-term); Oxidation (M)

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1430.7759, 1454.7674, 1502.7730, 1630.8647, 1725.9813, 1764.9646, 1777.8799, 1779.9264, 1788.9702, 1806.9929, 1844.9402, 1935.0814, 1955.0025, 2086.1738, 3002.5446, 3030.5908

9. IPI00338570 **Mass:** 61511 **Score:** 33 **Expect:** 29 **Matches:** 6

Tax_Id=10090 Gene_Symbol=Daam2 Isoform 2 of Disheveled-associated activator of morphogenesis 2

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
1504.7627	1503.7554	1503.6810	49.5	454	-	464	1	---	K.EHMELMSRLER.K + Acetyl (N-term); 2 Oxidation (M)
1777.8799	1776.8726	1776.8894	-9.44	52	-	66	1	---	R.FAELVDELDLTDKNR.E
1779.9264	1778.9191	1778.8774	23.5	236	-	250	0	---	K.VLQAMLHYQAYAAER.T + Oxidation (M)
1935.0814	1934.0741	1934.0699	2.17	302	-	317	1	---	R.YEFLMLGIQPVIDKLR.Q
3002.5446	3001.5373	3001.5410	-1.23	391	-	414	1	---	R.NGGYFQQWQLLDRILQQIVLQDER.G + Acetyl (N-term)
3030.5908	3029.5835	3029.5392	14.6	275	-	301	1	---	K.TAIMSFINAVLNAGAGEDNLEFRLHLR.Y + Acetyl (N-term); Oxidation (M)

No match to: 834.4958, 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1430.7759, 1452.7712, 1454.7674, 1467.8476, 1502.7730, 1583.8329, 1630.8647, 1725.9813, 1764.9646, 1788.9702, 1806.9929, 1844.9402, 1955.0025, 2086.1738, 3016.5633

10. IPI00137096 **Mass:** 15220 **Score:** 32 **Expect:** 36 **Matches:** 4

Tax_Id=10090 Gene_Symbol=4933414I15Rik Putative uncharacterized protein (Fragment)

Observed	Mr(expt)	Mr(calc)	ppm	Start		End	Miss	Ions	Peptide
834.4958	833.4886	833.4508	45.3	124	-	129	1	---	R.FSNIRR.L + Acetyl (N-term)
1777.8799	1776.8726	1776.8393	18.8	86	-	101	0	---	R.DSGFSSPKPMSYFLSK.R
1779.9264	1778.9191	1778.8444	42.0	102	-	116	1	---	K.RMVTDCISLPPYGGR.C + Acetyl (N-term); Oxidation (M)
1935.0814	1934.0741	1933.9832	47.0	70	-	85	1	---	K.VMWIITSQPSFPSRNR.D + Oxidation (M)

No match to: 855.3819, 856.5197, 1064.6435, 1192.7265, 1332.7919, 1430.7759, 1452.7712, 1454.7674, 1467.8476, 1502.7730, 1504.7627, 1583.8329, 1630.8647, 1725.9813, 1764.9646, 1788.9702, 1806.9929, 1844.9402, 1955.0025, 2086.1738, 3002.5446, 3016.5633, 3030.5908

Search Parameters

Type of search : MS/MS Ion Search

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (834.4958,1+) : <no title>

Query2 (855.3819,1+) : <no title>

Query3 (856.5197,1+) : <no title>

Query4 (1064.6435,1+) : <no title>

Query5 (1192.7265,1+) : <no title>

Query6 (1332.7919,1+) : <no title>

Query7 (1430.7759,1+) : <no title>

Query8 (1452.7712,1+) : <no title>

Query9 (1454.7674,1+) : <no title>

Query10 (1467.8476,1+) : <no title>

Query11 (1502.7730,1+) : <no title>

Query12 (1504.7627,1+) : <no title>

Query13 (1583.8329,1+) : <no title>

Query14 (1630.8647,1+) : <no title>

Query15 (1725.9813,1+) : <no title>

Query16 (1764.9646,1+) : <no title>

Query17 (1777.8799,1+) : <no title>

Query18 (1779.9264,1+) : <no title>

Query19 (1788.9702,1+) : <no title>

Query20 (1806.9929,1+) : <no title>

Query21 (1844.9402,1+) : <no title>

Query22 (1935.0814,1+) : <no title>

Query23 (1955.0025,1+) : <no title>

Query24 (2086.1738,1+) : <no title>

Query25 (3002.5446,1+) : <no title>

Query26 (3016.5633,1+) : <no title>

Query27 (3030.5908,1+) : <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 : **20 May 2013 at 01:30:40 GMT**

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

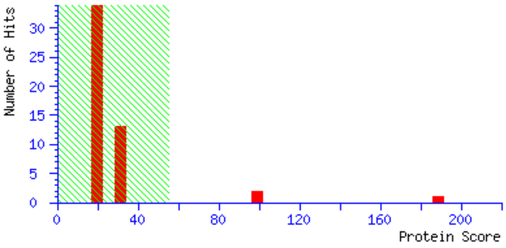
Top Score : **189 for TPM1_MOUSE, Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1**

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.	**TPM1_MOUSE**	32718	189	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1
2.	**TPM3_MOUSE**	32900	104	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2
3.	**TPM2_MOUSE**	32931	101	Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1
4.	**TFB1M_MOUSE**	39222	34	Dimethyladenosine transferase 1, mitochondrial OS=Mus musculus GN=Tfb1m PE=2 SV=1
5.	**DRG2_MOUSE**	41092	34	Developmentally-regulated GTP-binding protein 2 OS=Mus musculus GN=Drg2 PE=1 SV=1
6.	**FAKD5_MOUSE**	87343	33	FAST kinase domain-containing protein 5 OS=Mus musculus GN=Fastkd5 PE=2 SV=1
7.	**TPM4_MOUSE**	28564	32	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3
8.	**AIPL1_MOUSE**	38678	31	Aryl-hydrocarbon-interacting protein-like 1 OS=Mus musculus GN=Aipl1 PE=2 SV=1
9.	**HIBCH_MOUSE**	43295	31	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Mus musculus GN=Hibch PE=1 SV=1
10.	**KAP0_MOUSE**	43443	30	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Results List

1. TPM1_MOUSE **Mass:** 32718 **Score:** 189 **Expect:** 2e-015 **Matches:** 5

Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1186.7231	1185.7159	1185.6605	46.7	169 -	178	0	---	K.LVIIESDLER.A
1243.7037	1242.6964	1242.6456	41.0	92 -	101	0	84	R.IQLVEEELDR.A
1314.8203	1313.8130	1313.7554	43.8	168 -	178	1	86	R.KLVIIESDLER.A
1671.9058	1670.8985	1670.8839	8.75	169 -	182	1	---	K.LVIIESDLERAEER.A
1727.9609	1726.9537	1726.8849	39.8	92 -	105	1	---	R.IQLVEEELDRAQER.L

No match to: 806.4246, 894.5205, 898.4999, 915.5359, 926.4952, 938.4736, 988.5624, 1018.5862, 1045.6290, 1174.6813, 1257.7003, 1271.7403, 1275.7345, 1298.7726, 1328.8479, 1346.7135, 1360.7309, 1374.7492, 1385.7668, 1399.8259, 1413.8658, 1431.8366, 1544.8971, 1701.6466, 1723.5980, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

2. TPM3_MOUSE **Mass:** 32900 **Score:** 104 **Expect:** 6.5e-007 **Matches:** 4

Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
988.5624	987.5551	987.5171	38.5	126 -	133	1	---	R.GMKVIENR.A + Acetyl (N-term)
1243.7037	1242.6964	1242.6456	41.0	92 -	101	0	84	R.IQLVEEELDR.A
1671.9058	1670.8985	1670.8839	8.74	169 -	182	1	---	K.LVIIEGDLERTEER.A
1727.9609	1726.9537	1726.8849	39.8	92 -	105	1	---	R.IQLVEEELDRAQER.L

No match to: 806.4246, 894.5205, 898.4999, 915.5359, 926.4952, 938.4736, 1018.5862, 1045.6290, 1174.6813, 1186.7231, 1257.7003, 1271.7403, 1275.7345, 1298.7726, 1314.8203, 1328.8479, 1346.7135, 1360.7309, 1374.7492, 1385.7668, 1399.8259, 1413.8658, 1431.8366, 1544.8971, 1701.6466, 1723.5980, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

3. TPM2_MOUSE **Mass:** 32931 **Score:** 101 **Expect:** 1.3e-006 **Matches:** 5

Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
988.5624	987.5551	987.5171	38.5	126 -	133	1	---	R.GMKVIENR.A + Acetyl (N-term)
1243.7037	1242.6964	1242.6456	41.0	92 -	101	0	84	R.IQLVEEELDR.A
1298.7726	1297.7653	1297.7605	3.71	168 -	178	1	---	R.KLVILEGELER.S
1671.9058	1670.8985	1670.8839	8.75	169 -	182	1	---	K.LVILEGELERSEER.A
1727.9609	1726.9537	1726.8849	39.8	92 -	105	1	---	R.IQLVEEELDRAQER.L

No match to: 806.4246, 894.5205, 898.4999, 915.5359, 926.4952, 938.4736, 1018.5862, 1045.6290, 1174.6813, 1186.7231, 1257.7003, 1271.7403, 1275.7345, 1314.8203, 1328.8479, 1346.7135, 1360.7309, 1374.7492, 1385.7668, 1399.8259, 1413.8658, 1431.8366, 1544.8971, 1701.6466, 1723.5980, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

4. TFB1M_MOUSE **Mass:** 39222 **Score:** 34 **Expect:** 6.2 **Matches:** 6

Dimethyladenosine transferase 1, mitochondrial OS=Mus musculus GN=Tfb1m PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
926.4952	925.4879	925.4579	32.4	172 -	178	0	---	K.MTLTFQK.E + Acetyl (N-term); Oxidation (M)
988.5624	987.5551	987.5753	-20.41	240 -	247	1	---	K.QPFKLVEK.V
1346.7135	1345.7062	1345.7354	-21.67	32 -	42	0	8	K.QLSQNFLLDLR.L
1360.7309	1359.7236	1359.7358	-8.96	179 -	191	1	---	K.EVAERLVATTGSK.Q
1413.8658	1412.8586	1412.8140	31.6	105 -	116	1	---	K.LRIVHGDVLTYK.I
1431.8366	1430.8293	1430.8860	-39.63	12 -	23	1	---	R.LPPLPTIREIIK.L + Acetyl (N-term)

No match to: 806.4246, 894.5205, 898.4999, 915.5359, 938.4736, 1018.5862, 1045.6290, 1174.6813, 1186.7231, 1243.7037, 1257.7003, 1271.7403, 1275.7345, 1298.7726, 1314.8203, 1328.8479, 1374.7492, 1385.7668, 1399.8259, 1544.8971, 1671.9058, 1701.6466, 1723.5980, 1727.9609, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

5. DRG2_MOUSE **Mass:** 41092 **Score:** 34 **Expect:** 6.6 **Matches:** 7

Developmentally-regulated GTP-binding protein 2 OS=Mus musculus GN=Drg2 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1186.7231	1185.7159	1185.6618	45.6	322 -	331	1	---	R.IHRSLASQFK.Y
1257.7003	1256.6930	1256.7088	-12.60	162 -	172	1	---	K.ELESVGIRLNK.H
1271.7403	1270.7330	1270.7186	11.4	173 -	182	0	---	K.HKPNIYFKPK.K
1385.7668	1384.7595	1384.7714	-8.61	22 -	33	1	---	K.ATEYHLGLLKAK.L + Acetyl (N-term)
1399.8259	1398.8186	1398.8136	3.60	173 -	183	1	---	K.HKPNIYFKPKK.G
1431.8366	1430.8293	1430.7690	42.2	1 -	12	1	---	-.MGILEKISEIEK.E + Acetyl (N-term)
1671.9058	1670.8985	1670.9104	-7.12	298 -	311	1	---	R.GQRPDFTDAIILRK.G + Acetyl (N-term)

No match to: 806.4246, 894.5205, 898.4999, 915.5359, 926.4952, 938.4736, 988.5624, 1018.5862, 1045.6290, 1174.6813, 1243.7037, 1275.7345, 1298.7726, 1314.8203, 1328.8479, 1346.7135, 1360.7309, 1374.7492, 1413.8658, 1544.8971, 1701.6466, 1723.5980, 1727.9609, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

6. FAKD5_MOUSE **Mass:** 87343 **Score:** 33 **Expect:** 7.8 **Matches:** 9

FAST kinase domain-containing protein 5 OS=Mus musculus GN=Fastkd5 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
894.5205	893.5132	893.4858	30.6	505 -	511	1	---	R.SKFELTK.E + Acetyl (N-term)
915.5359	914.5287	914.4861	46.5	750 -	756	0	---	K.LAYLHEK.V + Acetyl (N-term)
1018.5862	1017.5789	1017.5607	17.9	722 -	729	0	---	R.QLVQIGYR.V + Acetyl (N-term)
1045.6290	1044.6217	1044.6219	-0.20	7 -	14	1	---	K.LLEPLKYK.A + Acetyl (N-term)
1174.6813	1173.6740	1173.6618	10.4	721 -	729	1	---	R.RQLVQIGYR.V + Acetyl (N-term)
1243.7037	1242.6964	1242.6972	-0.59	747 -	756	1	---	R.LEKLAYLHEK.V
1820.9320	1819.9247	1819.9217	1.67	67 -	82	1	---	R.RTFTASSAHLGLEFNK.A + Acetyl (N-term)
1864.9909	1863.9836	1863.9560	14.8	409 -	425	1	---	R.VMNAVAASLPPRVAHCR.S + Oxidation (M)
1960.0810	1959.0737	1959.0195	27.6	260 -	273	1	---	R.FFKIFFSYLNLHWR.E + Acetyl (N-term)

No match to: 806.4246, 898.4999, 926.4952, 938.4736, 988.5624, 1186.7231, 1257.7003, 1271.7403, 1275.7345, 1298.7726, 1314.8203, 1328.8479, 1346.7135, 1360.7309, 1374.7492, 1385.7668, 1399.8259, 1413.8658, 1431.8366, 1544.8971, 1671.9058, 1701.6466, 1723.5980, 1727.9609, 1800.0527, 1806.9897

7. TPM4_MOUSE **Mass:** 28564 **Score:** 32 **Expect:** 9.4 **Matches:** 4

Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
988.5624	987.5551	987.5171	38.5	90 -	97	1	---	R.GMKVIENR.A + Acetyl (N-term)
1257.7003	1256.6930	1256.6612	25.3	56 -	65	0	19	R.IQLLEEELDR.A
1346.7135	1345.7062	1345.7023	2.88	1 -	12	1	---	-.MAGLNSLEAVKR.K + Acetyl (N-term); Oxidation (M)
1374.7492	1373.7419	1373.6926	36.0	213 -	223	1	---	K.LEKTIDDLEEK.L + Acetyl (N-term)

No match to: 806.4246, 894.5205, 898.4999, 915.5359, 926.4952, 938.4736, 1018.5862, 1045.6290, 1174.6813, 1186.7231, 1243.7037, 1271.7403, 1275.7345, 1298.7726, 1314.8203, 1328.8479, 1360.7309, 1385.7668, 1399.8259, 1413.8658, 1431.8366, 1544.8971, 1671.9058, 1701.6466, 1723.5980, 1727.9609, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

8. AIPL1_MOUSE **Mass:** 38678 **Score:** 31 **Expect:** 13 **Matches:** 6

Aryl-hydrocarbon-interacting protein-like 1 OS=Mus musculus GN=Aipl1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
806.4246	805.4174	805.4235	-7.64	33 -	38	0	---	R.VTFHFR.T
1243.7037	1242.6964	1242.6642	26.0	290 -	299	1	---	K.VLELEPSMRK.A + Acetyl (N-term)
1385.7668	1384.7595	1384.7027	41.0	215 -	224	0	---	K.EKPWEVEWLK.L + Acetyl (N-term)
1413.8658	1412.8586	1412.8239	24.6	2 -	14	1	---	M.DVSLLLNVEGVKK.T
1544.8971	1543.8899	1543.8643	16.5	1 -	14	1	---	-.MDVSLLLNVEGVKK.T
1671.9058	1670.8985	1670.8549	26.1	285 -	298	1	---	K.ADLEKVLELEPSMR.K + Acetyl (N-term)

No match to: 894.5205, 898.4999, 915.5359, 926.4952, 938.4736, 988.5624, 1018.5862, 1045.6290, 1174.6813, 1186.7231, 1257.7003, 1271.7403, 1275.7345, 1298.7726, 1314.8203, 1328.8479, 1346.7135, 1360.7309, 1374.7492, 1399.8259, 1431.8366, 1701.6466, 1723.5980, 1727.9609, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

9. HIBCH_MOUSE **Mass:** 43295 **Score:** 31 **Expect:** 13 **Matches:** 7

3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Mus musculus GN=Hibch PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
806.4246	805.4174	805.4181	-0.95	377 -	384	0	---	K.SLGSSDLK.F
898.4999	897.4926	897.5072	-16.23	358 -	364	0	---	K.WKPANLK.D + Acetyl (N-term)
938.4736	937.4663	937.4328	35.8	92 -	100	0	---	K.AFCAGGDIK.A
1271.7403	1270.7330	1270.6816	40.5	43 -	54	0	---	R.GCGGVITLNRPK.F
1275.7345	1274.7272	1274.6904	28.9	297 -	307	1	---	K.VINKMSPTSLK.I + Acetyl (N-term); Oxidation (M)
1346.7135	1345.7062	1345.7255	-14.31	2 -	12	1	0	M.GQPYAWRLLSR.V
1820.9320	1819.9247	1819.9138	5.99	285 -	300	1	---	R.QDGSPFAIEQMKVINK.M + Oxidation (M)

No match to: 894.5205, 915.5359, 926.4952, 988.5624, 1018.5862, 1045.6290, 1174.6813, 1186.7231, 1243.7037, 1257.7003, 1298.7726, 1314.8203, 1328.8479, 1360.7309, 1374.7492, 1385.7668, 1399.8259, 1413.8658, 1431.8366, 1544.8971, 1671.9058, 1701.6466, 1723.5980, 1727.9609, 1800.0527, 1806.9897, 1864.9909, 1960.0810

10. KAP0_MOUSE **Mass:** 43443 **Score:** 30 **Expect:** 16 **Matches:** 4

cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1018.5862	1017.5789	1017.6005	-21.19	234 -	242	1	---	R.ILMGSTLRK.R
1045.6290	1044.6217	1044.5703	49.2	253 -	261	0	---	K.VSILESLDK.W + Acetyl (N-term)
1243.7037	1242.6964	1242.6721	19.6	219 -	228	1	8	K.TNVKLWGIDR.D + Acetyl (N-term)
1257.7003	1256.6930	1256.6911	1.51	358 -	368	1	8	R.VLGPCSDILKR.N

No match to: 806.4246, 894.5205, 898.4999, 915.5359, 926.4952, 938.4736, 988.5624, 1174.6813, 1186.7231, 1271.7403, 1275.7345, 1298.7726, 1314.8203, 1328.8479, 1346.7135, 1360.7309, 1374.7492, 1385.7668, 1399.8259, 1413.8658, 1431.8366, 1544.8971, 1671.9058, 1701.6466, 1723.5980, 1727.9609, 1800.0527, 1806.9897, 1820.9320, 1864.9909, 1960.0810

Search Parameters

Type of search : **MS/MS Ion Search**
Enzyme : **Trypsin**

Fixed modifications : Carbamidomethyl (C)
Variable modifications : Acetyl (N-term),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ±50 ppm
Fragment Mass Tolerance: ±0.5 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (806.4246,1+) : <no title>
Query2 (894.5205,1+) : <no title>
Query3 (898.4999,1+) : <no title>
Query4 (915.5359,1+) : <no title>
Query5 (926.4952,1+) : <no title>
Query6 (938.4736,1+) : <no title>
Query7 (988.5624,1+) : <no title>
Query8 (1018.5862,1+) : <no title>
Query9 (1045.6290,1+) : <no title>
Query10 (1174.6813,1+) : <no title>
Query11 (1186.7231,1+) : <no title>
Query12 (1243.7037,1+) : <no title>
Query13 (1257.7003,1+) : <no title>
Query14 (1271.7403,1+) : <no title>
Query15 (1275.7345,1+) : <no title>
Query16 (1298.7726,1+) : <no title>
Query17 (1314.8203,1+) : <no title>
Query18 (1328.8479,1+) : <no title>
Query19 (1346.7135,1+) : <no title>
Query20 (1360.7309,1+) : <no title>
Query21 (1374.7492,1+) : <no title>
Query22 (1385.7668,1+) : <no title>
Query23 (1399.8259,1+) : <no title>
Query24 (1413.8658,1+) : <no title>
Query25 (1431.8366,1+) : <no title>
Query26 (1544.8971,1+) : <no title>
Query27 (1671.9058,1+) : <no title>
Query28 (1701.6466,1+) : <no title>
Query29 (1723.5980,1+) : <no title>
Query30 (1727.9609,1+) : <no title>
Query31 (1800.0527,1+) : <no title>
Query32 (1806.9897,1+) : <no title>
Query33 (1820.9320,1+) : <no title>
Query34 (1864.9909,1+) : <no title>
Query35 (1960.0810,1+) : <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 : **20 Jun 2013 at 07:30:43 GMT**

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

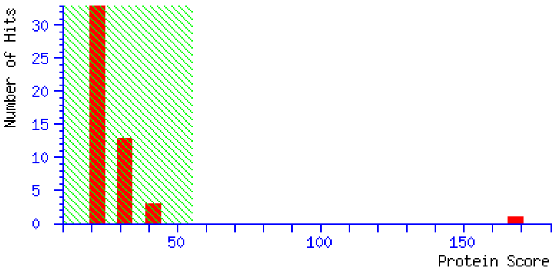
Top Score : **168 for SAMP_MOUSE, Serum amyloid P-component OS=Mus musculus GN=Apcs PE=1 SV=2**

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.	**SAMP_MOUSE**	26401	168	Serum amyloid P-component OS=Mus musculus GN=Apcs PE=1 SV=2
2.	**EPHA2_MOUSE**	110236	44	Ephrin type-A receptor 2 OS=Mus musculus GN=Epha2 PE=1 SV=2
3.	**MTPN_MOUSE**	13024	43	Myotrophin OS=Mus musculus GN=Mtpn PE=2 SV=2
4.	**KLH38_MOUSE**	66577	38	Kelch-like protein 38 OS=Mus musculus GN=Klhl38 PE=2 SV=1
5.	**H12_MOUSE**	21254	35	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2
6.	**TTLL1_MOUSE**	49478	34	Probable tubulin polyglutamylase TTLL1 OS=Mus musculus GN=Ttll1 PE=1 SV=1
7.	**PHB_MOUSE**	29859	31	Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1
8.	**UBE2K_MOUSE**	22507	31	Ubiquitin-conjugating enzyme E2 K OS=Mus musculus GN=Ube2k PE=2 SV=3
9.	**PDIA3_MOUSE**	57099	30	Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2
10.	**BAI1_MOUSE**	176664	30	Brain-specific angiogenesis inhibitor 1 OS=Mus musculus GN=Bai1 PE=1 SV=1

Results List

1. SAMP_MOUSE **Mass:** 26401 **Score:** 168 **Expect:** 2.6e-013 **Matches:** 4

Serum amyloid P-component OS=Mus musculus GN=Apcs PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
892.5088	891.5016	891.5331	-35.34	27 -	33	1	---	R.KVFVFPR.E
1220.6336	1219.6263	1219.6561	-24.37	76 -	85	1	19	K.GRDNELLIYK.E
1343.6510	1342.6437	1342.6769	-24.69	88 -	99	0	---	K.VGEYSLYIGQSK.V
2133.0149	2132.0076	2132.0287	-9.88	147 -	166	0	116	K.APPSIVLGQEQDNYGGGFQR.S

No match to: 856.5027, 917.5335, 924.4977, 982.5669, 995.5929, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1178.5773, 1185.6246, 1198.6361, 1235.6174, 1302.6634, 1338.7552, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1460.6511, 1486.7732, 1494.7413, 1606.8160, 1613.7661, 1682.7602, 1871.8721, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2147.0160, 2170.9748, 2225.0771, 2247.0610

2. EPHA2_MOUSE **Mass:** 110236 **Score:** 44 **Expect:** 0.68 **Matches:** 6

Ephrin type-A receptor 2 OS=Mus musculus GN=Epha2 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
917.5335	916.5262	916.5164	10.7	168 -	175	1	---	R.MVGPLTRK.G + Oxidation (M)
1178.5773	1177.5700	1177.5649	4.37	937 -	946	0	---	K.VVQMSNEDIK.R + Oxidation (M)
1220.6336	1219.6263	1219.5689	47.1	200 -	209	0	20	K.CPEMLQSLAR.F + Oxidation (M)
1235.6174	1234.6101	1234.6631	-42.91	27 -	37	0	---	K.EVVLLDFAAMK.G
1682.7602	1681.7530	1681.7683	-9.10	764 -	779	0	---	R.VLEDDPEATYTTSGGK.I
2147.0160	2146.0088	2146.0148	-2.82	686 -	703	0	---	K.YKPMMIITEYMENGALDK.F

No match to: 856.5027, 892.5088, 924.4977, 982.5669, 995.5929, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1185.6246, 1198.6361, 1302.6634, 1338.7552, 1343.6510, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1460.6511, 1486.7732, 1494.7413, 1606.8160, 1613.7661, 1871.8721, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2170.9748, 2225.0771, 2247.0610

3. MTPN_MOUSE **Mass:** 13024 **Score:** 43 **Expect:** 0.85 **Matches:** 4

Myotrophin OS=Mus musculus GN=Mtpn PE=2 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
924.4977	923.4905	923.4575	35.7	5 -	11	0	---	K.EFMWALK.N
1302.6634	1301.6561	1301.6324	18.2	25 -	36	1	---	K.GEDVNRTLEGGR.K
1343.6510	1342.6437	1342.6050	28.9	2 -	11	1	---	M.CDKEFMWALK.N + Oxidation (M)
2147.0160	2146.0088	2146.0994	-42.21	67 -	85	0	---	K.HHITPLLSAVYEGHVSCVK.L

No match to: 856.5027, 892.5088, 917.5335, 982.5669, 995.5929, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1178.5773, 1185.6246, 1198.6361, 1220.6336, 1235.6174, 1338.7552, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1460.6511, 1486.7732, 1494.7413, 1606.8160, 1613.7661, 1682.7602, 1871.8721, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2170.9748, 2225.0771, 2247.0610

4. KLH38_MOUSE **Mass:** 66577 **Score:** 38 **Expect:** 2.3 **Matches:** 7

Kelch-like protein 38 OS=Mus musculus GN=Klhl38 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
924.4977	923.4905	923.4568	36.4	462 -	468	1	---	K.METRMIK.N + Oxidation (M)
1148.6080	1147.6007	1147.5873	11.7	491 -	500	0	---	R.ILAYDPQSNK.F
1185.6246	1184.6173	1184.6077	8.12	50 -	60	0	---	R.SVLASSSPYFK.A
1427.6598	1426.6525	1426.6234	20.4	61 -	71	1	---	K.AMFCSHFRESR.E
1486.7732	1485.7660	1485.7510	10.0	365 -	377	1	---	R.VGEPMLAARYSHR.S
1613.7661	1612.7589	1612.7555	2.06	258 -	271	0	---	K.QIFSLYGPSAQDCK.L

1871.8721	1870.8648	1870.8189	24.5	174 -	188	1	---	K.ELCAMELRDYLGDDR.L + Oxidation (M)

No match to: 856.5027, 892.5088, 917.5335, 982.5669, 995.5929, 1011.5950, 1147.5963, 1150.5386, 1178.5773, 1198.6361, 1220.6336, 1235.6174, 1302.6634, 1338.7552, 1343.6510, 1365.6472, 1367.6442, 1373.7315, 1460.6511, 1494.7413, 1606.8160, 1682.7602, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2147.0160, 2170.9748, 2225.0771, 2247.0610

5. H12_MOUSE **Mass:** 21254 **Score:** 35 **Expect:** 5.4 **Matches:** 5

Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
856.5027	855.4954	855.5178	-26.17	160 -	168	0	---	K.KPAAAAVTK.K
995.5929	994.5856	994.6287	-43.33	130 -	139	1	---	K.KPAGAAKKPK.K
1185.6246	1184.6173	1184.6513	-28.66	111 -	122	1	---	K.AASGEAKPQAKK.A
1198.6361	1197.6289	1197.6605	-26.42	35 -	46	0	---	K.ASGPPVSELITK.A
1235.6174	1234.6101	1234.6557	-36.91	64 -	75	1	---	K.KALAAAGYDVEK.N

No match to: 892.5088, 917.5335, 924.4977, 982.5669, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1178.5773, 1220.6336, 1302.6634, 1338.7552, 1343.6510, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1460.6511, 1486.7732, 1494.7413, 1606.8160, 1613.7661, 1682.7602, 1871.8721, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2147.0160, 2170.9748, 2225.0771, 2247.0610

6. TTLL1_MOUSE **Mass:** 49478 **Score:** 34 **Expect:** 7.1 **Matches:** 5

Probable tubulin polyglutamylase TTLL1 OS=Mus musculus GN=Ttll1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
856.5027	855.4954	855.4603	41.1	366 -	372	1	---	K.WNKSPPK.E
1494.7413	1493.7340	1493.7007	22.3	130 -	142	0	---	K.SPSSTWIMKPCGK.A + Oxidation (M)
1606.8160	1605.8087	1605.8007	5.01	129 -	142	1	---	R.KSPSSTWIMKPCGK.A
2225.0771	2224.0698	2224.1537	-37.71	199 -	215	1	---	R.LYVLVSTYRPLRCYMYK.L
2247.0610	2246.0537	2246.0729	-8.56	248 -	266	1	---	K.HGEDYNHIHGGKWTVNNLR.L

No match to: 892.5088, 917.5335, 924.4977, 982.5669, 995.5929, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1178.5773, 1185.6246, 1198.6361, 1220.6336, 1235.6174, 1302.6634, 1338.7552, 1343.6510, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1460.6511, 1486.7732, 1613.7661, 1682.7602, 1871.8721, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2147.0160, 2170.9748

7. PHB_MOUSE **Mass:** 29859 **Score:** 31 **Expect:** 13 **Matches:** 4

Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1185.6246	1184.6173	1184.6513	-28.68	84 -	93	0	---	K.DLQNVNITLR.I
1460.6511	1459.6438	1459.6467	-1.98	106 -	117	0	---	R.IYTSIGEDYDER.V
1606.8160	1605.8087	1605.8362	-17.08	240 -	253	1	---	R.KLEAAEDIAYQLSR.S
1998.0530	1997.0458	1997.0793	-16.78	220 -	239	0	---	K.AAELIANSLATAGDGLIELR.K

No match to: 856.5027, 892.5088, 917.5335, 924.4977, 982.5669, 995.5929, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1178.5773, 1198.6361, 1220.6336, 1235.6174, 1302.6634, 1338.7552, 1343.6510, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1486.7732, 1494.7413, 1613.7661, 1682.7602, 1871.8721, 1959.9125, 2117.4501, 2118.4078, 2133.0149, 2147.0160, 2170.9748, 2225.0771, 2247.0610

8. UBE2K_MOUSE **Mass:** 22507 **Score:** 31 **Expect:** 13 **Matches:** 4

Ubiquitin-conjugating enzyme E2 K OS=Mus musculus GN=Ube2k PE=2 SV=3

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

892.5088	891.5016	891.5065	-5.59	12 -	18	1	---	R.EFKEVLK.S
1178.5773	1177.5700	1177.5550	12.8	98 -	107	0	---	K.DQWAAAMTLR.T + Oxidation (M)
1302.6634	1301.6561	1301.6656	-7.27	62 -	72	0	---	K.IPETYPFNPPK.V
1365.6472	1364.6400	1364.6507	-7.85	136 -	146	1	---	K.QNPEMFKQTAR.L + Oxidation (M)

No match to: 856.5027, 917.5335, 924.4977, 982.5669, 995.5929, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1185.6246, 1198.6361, 1220.6336, 1235.6174, 1338.7552, 1343.6510, 1367.6442, 1373.7315, 1427.6598, 1460.6511, 1486.7732, 1494.7413, 1606.8160, 1613.7661, 1682.7602, 1871.8721, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2147.0160, 2170.9748, 2225.0771, 2247.0610

9. PDIA3_MOUSE **Mass:** 57099 **Score:** 30 **Expect:** 15 **Matches:** 3

Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
995.5929	994.5856	994.5560	29.8	131 -	140	0	17	K.QAGPASVPLR.T
1486.7732	1485.7660	1485.6922	49.6	333 -	344	1	---	K.GEKFVMQEEFSR.D
1959.9125	1958.9052	1958.9486	-22.14	467 -	482	1	---	K.YEGGRELNDFISYLQR.E

No match to: 856.5027, 892.5088, 917.5335, 924.4977, 982.5669, 1011.5950, 1147.5963, 1148.6080, 1150.5386, 1178.5773, 1185.6246, 1198.6361, 1220.6336, 1235.6174, 1302.6634, 1338.7552, 1343.6510, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1460.6511, 1494.7413, 1606.8160, 1613.7661, 1682.7602, 1871.8721, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2147.0160, 2170.9748, 2225.0771, 2247.0610

10. BAI1_MOUSE **Mass:** 176664 **Score:** 30 **Expect:** 16 **Matches:** 9

Brain-specific angiogenesis inhibitor 1 OS=Mus musculus GN=Bai1 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
917.5335	916.5262	916.4879	41.8	1527 -	1533	1	---	K.RAWESLR.K
924.4977	923.4905	923.5188	-30.72	1500 -	1507	1	---	R.KLQHAAEK.E
1147.5963	1146.5890	1146.5570	27.9	790 -	799	1	---	K.GWRATGDWAK.V
1148.6080	1147.6007	1147.5444	49.1	192 -	201	0	---	R.WLDACLAGSR.S
1185.6246	1184.6173	1184.5714	38.8	1315 -	1325	0	---	K.SSFIGDGDIFK.K
1220.6336	1219.6263	1219.5728	43.9	276 -	286	1	---	R.DCGGGLQTRTR.T
1343.6510	1342.6437	1342.6914	-35.54	1255 -	1265	1	---	K.RPSLPEEEKMK.L
1460.6511	1459.6438	1459.6119	21.9	180 -	191	0	---	R.NPSHAACQMLCR.W + Oxidation (M)
2225.0771	2224.0698	2224.0146	24.8	616 -	633	0	---	R.CELDEEGIAFWEPPTYIR.C

No match to: 856.5027, 892.5088, 982.5669, 995.5929, 1011.5950, 1150.5386, 1178.5773, 1198.6361, 1235.6174, 1302.6634, 1338.7552, 1365.6472, 1367.6442, 1373.7315, 1427.6598, 1486.7732, 1494.7413, 1606.8160, 1613.7661, 1682.7602, 1871.8721, 1959.9125, 1998.0530, 2117.4501, 2118.4078, 2133.0149, 2147.0160, 2170.9748, 2247.0610

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 (856.5027,1+) : <no title>

Query2 (892.5088,1+) : <no title>

Query3 (917.5335,1+) : <no title>

Query4 (924.4977,1+) : <no title>

Query5 (982.5669,1+) : <no title>

Query6 (995.5929,1+) : <no title>

Query7 (1011.5950,1+) : <no title>

Query8 (1147.5963,1+) : <no title>

Query9 (1148.6080,1+) : <no title>

Query10 (1150.5386,1+) : <no title>

Query11 (1178.5773,1+) : <no title>

Query12 (1185.6246,1+) : <no title>

Query13 (1198.6361,1+) : <no title>

Query14 (1220.6336,1+) : <no title>

Query15 (1235.6174,1+) : <no title>

Query16 (1302.6634,1+) : <no title>

Query17 (1338.7552,1+) : <no title>

Query18 (1343.6510,1+) : <no title>

Query19 (1365.6472,1+) : <no title>

Query20 (1367.6442,1+) : <no title>

Query21 (1373.7315,1+) : <no title>

Query22 (1427.6598,1+) : <no title>

Query23 (1460.6511,1+) : <no title>

Query24 (1486.7732,1+) : <no title>

Query25 (1494.7413,1+) : <no title>

Query26 (1606.8160,1+) : <no title>

Query27 (1613.7661,1+) : <no title>

Query28 (1682.7602,1+) : <no title>

Query29 (1871.8721,1+) : <no title>

Query30 (1959.9125,1+) : <no title>

Query31 (1998.0530,1+) : <no title>

Query32 (2117.4501,1+) : <no title>

Query33 (2118.4078,1+) : <no title>

Query34 (2133.0149,1+) : <no title>

Query35 (2147.0160,1+) : <no title>

Query36 (2170.9748,1+) : <no title>

Query37 (2225.0771,1+) : <no title>

Query38 (2247.0610,1+) : <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 : **20 Jun 2013 at 07:30:34 GMT**

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

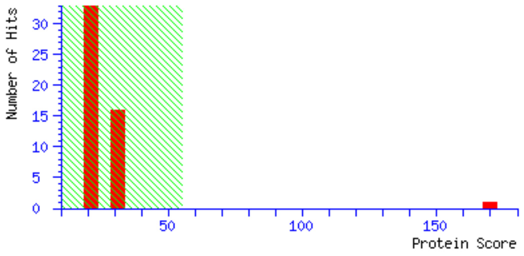
Top Score : **170 for MYL6_MOUSE, Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3**

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.	**MYL6_MOUSE**	17090	170	Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3
2.	**CBLB_MOUSE**	110535	36	E3 ubiquitin-protein ligase CBL-B OS=Mus musculus GN=Cblb PE=1 SV=2
3.	**DNS2B_MOUSE**	41281	34	Deoxyribonuclease-2-beta OS=Mus musculus GN=Dnase2b PE=2 SV=1
4.	**SETX_MOUSE**	301621	33	Probable helicase senataxin OS=Mus musculus GN=Setx PE=2 SV=1
5.	**KCNB1_MOUSE**	96487	32	Potassium voltage-gated channel subfamily B member 1 OS=Mus musculus GN=Kcnb1 PE=1 SV=1
6.	**SOSD1_MOUSE**	23730	32	Sclerostin domain-containing protein 1 OS=Mus musculus GN=Sostdc1 PE=1 SV=1
7.	**CTNB1_MOUSE**	86043	32	Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1
8.	**PTN11_MOUSE**	68988	31	Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2
9.	**RS24_MOUSE**	15413	30	40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1
10.	**DOC2A_MOUSE**	45208	29	Double C2-like domain-containing protein alpha OS=Mus musculus GN=Doc2a PE=2 SV=1

Results List

1. MYL6_MOUSE **Mass:** 17090 **Score:** 170 **Expect:** 1.6e-013 **Matches:** 7

Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
995.6080	994.6007	994.5811	19.7	111 -	119	0	---	R.HVLVTLGEK.M
1025.4902	1024.4829	1024.4978	-14.52	14 -	21	0	22	K.EAFQLFDR.T
1341.6168	1340.6096	1340.6217	-9.05	27 -	37	0	22	K.ILYSQCGDVMR.A
1357.6120	1356.6047	1356.6166	-8.77	27 -	37	0	---	K.ILYSQCGDVMR.A + Oxidation (M)
1446.7364	1445.7291	1445.7184	7.42	51 -	63	1	---	K.VLGNPKSDEMNVK.V + Oxidation (M)
1544.6801	1543.6729	1543.6791	-4.01	82 -	94	0	---	K.DQGTYEDYVEGLR.V
1786.8185	1785.8112	1785.8169	-3.19	80 -	94	1	66	K.NKDQGTYEDYVEGLR.V

No match to: 1007.4783, 1011.6284, 1075.5128, 1137.5381, 1160.5709, 1178.6055, 1206.6118, 1216.5676, 1234.6356, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1376.7063, 1387.6855, 1403.6965, 1455.8826, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1554.6007, 1697.7895, 1721.8494, 1723.8296, 1798.8191, 1836.8735, 1870.9058, 1876.9320, 1898.8765, 1926.9065, 1939.9283, 2539.0777, 3106.3151, 3154.3115

2. CBLB_MOUSE **Mass:** 110535 **Score:** 36 **Expect:** 3.9 **Matches:** 8

E3 ubiquitin-protein ligase CBL-B OS=Mus musculus GN=Cblb PE=1 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1025.4902	1024.4829	1024.4317	50.0	456 -	463	0	2	R.EESLMMNR.L + Oxidation (M)
1178.6055	1177.5982	1177.5947	2.96	631 -	640	1	---	R.MGSEQVLMRK.H
1216.5676	1215.5603	1215.5560	3.54	326 -	335	0	---	R.EGFYLYPDGR.S
1341.6168	1340.6096	1340.6612	-38.51	98 -	108	0	---	K.LAQLSENEYFK.I
1357.6120	1356.6047	1356.5728	23.5	132 -	141	1	---	R.MYEEQSQDRR.N + Oxidation (M)
1446.7364	1445.7291	1445.6867	29.3	628 -	639	1	---	R.HSRMGSEQVLMR.K + Oxidation (M)
1544.6801	1543.6729	1543.7341	-39.63	939 -	951	1	---	K.LMGEGYAFEEVKR.A + Oxidation (M)
1939.9283	1938.9210	1939.0123	-47.09	608 -	627	0	---	R.ILGDGSPKPGVTANSSLNGR.H

No match to: 995.6080, 1007.4783, 1011.6284, 1075.5128, 1137.5381, 1160.5709, 1206.6118, 1234.6356, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1376.7063, 1387.6855, 1403.6965, 1455.8826, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1554.6007, 1697.7895, 1721.8494, 1723.8296, 1786.8185, 1798.8191, 1836.8735, 1870.9058, 1876.9320, 1898.8765, 1926.9065, 2539.0777, 3106.3151, 3154.3115

3. DNS2B_MOUSE **Mass:** 41281 **Score:** 34 **Expect:** 6.3 **Matches:** 5

Deoxyribonuclease-2-beta OS=Mus musculus GN=Dnase2b PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1341.6168	1340.6096	1340.6109	-1.01	290 -	300	1	---	K.SYFSSRQDHSK.W
1387.6855	1386.6782	1386.6714	4.91	296 -	306	1	---	R.QDHSKWCVSIK.G
1723.8296	1722.8223	1722.9053	-48.18	67 -	80	1	---	R.QTWNKSLYLINSTR.S
1786.8185	1785.8112	1785.8575	-25.93	199 -	213	1	---	K.LIYMPRMCANSSSLK.I + Oxidation (M)
1939.9283	1938.9210	1938.9846	-32.82	312 -	327	1	---	R.WTCIGDLNRSLHQALR.G

No match to: 995.6080, 1007.4783, 1011.6284, 1025.4902, 1075.5128, 1137.5381, 1160.5709, 1178.6055, 1206.6118, 1216.5676, 1234.6356, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1357.6120, 1376.7063, 1403.6965, 1446.7364, 1455.8826, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1544.6801, 1554.6007, 1697.7895, 1721.8494, 1798.8191, 1836.8735, 1870.9058, 1876.9320, 1898.8765, 1926.9065, 2539.0777, 3106.3151, 3154.3115

4. SETX_MOUSE **Mass:** 301621 **Score:** 33 **Expect:** 8.1 **Matches:** 13

Probable helicase senataxin OS=Mus musculus GN=Setx PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1338.7690	1337.7617	1337.7092	39.3	1751	1760	1	---	K.ENFYQLQLRK.F
1376.7063	1375.6990	1375.7493	-36.56	1853	1864	0	---	R.CIVISSLVTTQR.K
1446.7364	1445.7291	1445.7772	-33.27	1868	1880	1	---	K.AMSLLSSRNQLAR.A
1455.8826	1454.8753	1454.8456	20.4	1316	1328	1	---	K.LISPQTLSIKNNK.K
1494.7340	1493.7267	1493.7773	-33.83	2048	2059	1	---	K.DLPSHIQEMLRR.K
1510.7327	1509.7254	1509.7722	-30.96	2048	2059	1	---	K.DLPSHIQEMLRR.K + Oxidation (M)
1529.8186	1528.8113	1528.8096	1.08	2060	2072	1	---	R.KEILDAQLDELSR.Q
1697.7895	1696.7822	1696.8342	-30.61	655	668	1	---	R.VLMKVNTTEEENFK.Q + Oxidation (M)
1721.8494	1720.8421	1720.7913	29.5	263	276	0	---	K.QNDFMQSILHTMEK.Q
1798.8191	1797.8118	1797.8389	-15.08	631	645	1	---	K.KNIYCLENCSPVSSK.E
1836.8735	1835.8662	1835.8537	6.78	830	846	0	---	K.EDSIGHNVPSDPVLDDK.H
1926.9065	1925.8992	1925.9193	-10.42	1788	1803	1	---	K.ENDLVFLAPEKSYMDR.H
3154.3115	3153.3042	3153.4423	-43.80	340	365	1	---	K.LEPEPHFDDMVTCSQIVYNFNPEKTK.K + Oxidation (M)

No match to: 995.6080, 1007.4783, 1011.6284, 1025.4902, 1075.5128, 1137.5381, 1160.5709, 1178.6055, 1206.6118, 1216.5676, 1234.6356, 1253.6032, 1293.6295, 1302.7943, 1341.6168, 1357.6120, 1387.6855, 1403.6965, 1532.6220, 1544.6801, 1554.6007, 1723.8296, 1786.8185, 1870.9058, 1876.9320, 1898.8765, 1939.9283, 2539.0777, 3106.3151

5. KCNB1_MOUSE **Mass:** 96487 **Score:** 32 **Expect:** 10 **Matches:** 7

Potassium voltage-gated channel subfamily B member 1 OS=Mus musculus GN=Kcnb1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1025.4902	1024.4829	1024.4978	-14.54	649	657	0	---	R.SGFFVESPR.S
1160.5709	1159.5636	1159.5478	13.7	658	667	1	---	R.SSMKTHNPMK.L
1293.6295	1292.6222	1292.6356	-10.32	457	467	0	---	R.SIEMMDIVVEK.N
1357.6120	1356.6047	1356.6707	-48.65	637	648	0	---	R.LMETNPIPEASR.S
1798.8191	1797.8118	1797.8897	-43.32	791	806	1	---	R.TEKNHFESSPLPTSPK.F
1836.8735	1835.8662	1835.9431	-41.89	88	103	1	---	R.HPGAFTSILNFYRTGR.L
2539.0777	2538.0704	2538.1842	-44.85	517	538	1	---	R.SSSSPQHLNVQQLQDMYSKMAK.T + 2 Oxidation (M)

No match to: 995.6080, 1007.4783, 1011.6284, 1075.5128, 1137.5381, 1178.6055, 1206.6118, 1216.5676, 1234.6356, 1253.6032, 1302.7943, 1338.7690, 1341.6168, 1376.7063, 1387.6855, 1403.6965, 1446.7364, 1455.8826, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1544.6801, 1554.6007, 1697.7895, 1721.8494, 1723.8296, 1786.8185, 1870.9058, 1876.9320, 1898.8765, 1926.9065, 1939.9283, 3106.3151, 3154.3115

6. SOSD1_MOUSE **Mass:** 23730 **Score:** 32 **Expect:** 10 **Matches:** 4

Sclerostin domain-containing protein 1 OS=Mus musculus GN=Sostdc1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1075.5128	1074.5055	1074.5353	-27.67	68	76	1	---	R.NSRVQVGCR.E
1376.7063	1375.6990	1375.6593	28.9	59	70	1	---	R.HFSSTGLDRNSR.V
1403.6965	1402.6892	1402.6702	13.5	55	67	1	---	R.NGGRHFSSTGLDR.N
1697.7895	1696.7822	1696.8203	-22.41	143	156	1	---	R.IQLQCQDGSTRTYK.I

No match to: 995.6080, 1007.4783, 1011.6284, 1025.4902, 1137.5381, 1160.5709, 1178.6055, 1206.6118, 1216.5676, 1234.6356, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1341.6168, 1357.6120, 1387.6855, 1446.7364, 1455.8826, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1544.6801, 1554.6007, 1721.8494, 1723.8296, 1786.8185, 1798.8191, 1836.8735, 1870.9058, 1876.9320, 1898.8765, 1926.9065, 1939.9283, 2539.0777, 3106.3151, 3154.3115

7. CTNB1_MOUSE **Mass:** 86043 **Score:** 32 **Expect:** 11 **Matches:** 6

Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1387.6855	1386.6782	1386.6813	-2.21	458	469	0	---	R.EDITEPAICALR.H
1446.7364	1445.7291	1445.7561	-18.66	516	528	0	---	R.NLALCPANHAPLR.E
1455.8826	1454.8753	1454.8643	7.58	275	288	1	---	R.LAGGLQKMVALLNK.T
1786.8185	1785.8112	1785.8679	-31.74	454	469	1	3	R.AGDREDITEPAICALR.H
1836.8735	1835.8662	1835.9056	-21.46	434	449	1	---	K.NKMMVCQVGGIEALVR.T + 2 Oxidation (M)
1898.8765	1897.8692	1897.9390	-36.74	566	582	0	---	R.MEEIVEGCTGALHILAR.D

No match to: 995.6080, 1007.4783, 1011.6284, 1025.4902, 1075.5128, 1137.5381, 1160.5709, 1178.6055, 1206.6118, 1216.5676, 1234.6356, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1341.6168, 1357.6120, 1376.7063, 1403.6965, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1544.6801, 1554.6007, 1697.7895, 1721.8494, 1723.8296, 1798.8191, 1870.9058, 1876.9320, 1926.9065, 1939.9283, 2539.0777, 3106.3151, 3154.3115

8. PTN11_MOUSE **Mass:** 68988 **Score:** 31 **Expect:** 13 **Matches:** 7

Tyrosine-protein phosphatase non-receptor type 11 OS=Mus musculus GN=Ptpn11 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
995.6080	994.6007	994.5672	33.7	47	55	1	---	R.RNGAVTHIK.I
1025.4902	1024.4829	1024.5124	-28.78	379	386	1	---	K.EYGVMRVR.N + Oxidation (M)
1234.6356	1233.6283	1233.6452	-13.73	232	242	1	---	R.ELSKLAETTDK.V
1403.6965	1402.6892	1402.7357	-33.18	279	289	1	---	R.YKNILPFDHTR.V
1510.7327	1509.7254	1509.6882	24.7	174	186	1	---	R.CQELKYDVGGGER.F
1529.8186	1528.8113	1528.7854	16.9	167	178	1	---	K.VTHVMIRCQELK.Y + Oxidation (M)
1870.9058	1869.8985	1869.9156	-9.10	583	597	1	---	R.VYENVGLMQQQRSFR.- + Oxidation (M)

No match to: 1007.4783, 1011.6284, 1075.5128, 1137.5381, 1160.5709, 1178.6055, 1206.6118, 1216.5676, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1341.6168, 1357.6120, 1376.7063, 1387.6855, 1446.7364, 1455.8826, 1494.7340, 1532.6220, 1544.6801, 1554.6007, 1697.7895, 1721.8494, 1723.8296, 1786.8185, 1798.8191, 1836.8735, 1876.9320, 1898.8765, 1926.9065, 1939.9283, 2539.0777, 3106.3151, 3154.3115

9. RS24_MOUSE **Mass:** 15413 **Score:** 30 **Expect:** 15 **Matches:** 4

40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1178.6055	1177.5982	1177.6390	-34.61	12	20	1	---	K.FMTNRLLQR.K
1206.6118	1205.6045	1205.6187	-11.74	1	10	1	---	-.MNDTVTIRTR.K
1697.7895	1696.7822	1696.7654	9.90	69	83	0	---	K.TTGFGMIYDSLDYAK.K + Oxidation (M)
1836.8735	1835.8662	1835.9281	-33.69	47	61	1	---	K.MYKTTPDVIFVFGFR.T + Oxidation (M)

No match to: 995.6080, 1007.4783, 1011.6284, 1025.4902, 1075.5128, 1137.5381, 1160.5709, 1216.5676, 1234.6356, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1341.6168, 1357.6120, 1376.7063, 1387.6855, 1403.6965, 1446.7364, 1455.8826, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1544.6801, 1554.6007, 1721.8494, 1723.8296, 1786.8185, 1798.8191, 1870.9058, 1876.9320, 1898.8765, 1926.9065, 1939.9283, 2539.0777, 3106.3151, 3154.3115

10. DOC2A_MOUSE **Mass:** 45208 **Score:** 29 **Expect:** 20 **Matches:** 5

Double C2-like domain-containing protein alpha OS=Mus musculus GN=Doc2a PE=2 SV=1

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

1025.4902	1024.4829	1024.4978	-14.52	31 - 38	0	---	R.QISDYFPR.R
1216.5676	1215.5603	1215.6182	-47.64	212 - 220	1	---	K.KHFNICLER.Q
1234.6356	1233.6283	1233.6717	-35.21	298 - 307	1	---	K.TYLRPDVDKK.S
1446.7364	1445.7291	1445.7263	1.96	353 - 367	0	---	K.SNDFIGGVSLGPGAR.G
1697.7895	1696.7822	1696.8268	-26.24	243 - 257	0	---	K.ELEQAEQGPGLLEER.G

No match to: 995.6080, 1007.4783, 1011.6284, 1075.5128, 1137.5381, 1160.5709, 1178.6055, 1206.6118, 1253.6032, 1293.6295, 1302.7943, 1338.7690, 1341.6168, 1357.6120, 1376.7063, 1387.6855, 1403.6965, 1455.8826, 1494.7340, 1510.7327, 1529.8186, 1532.6220, 1544.6801, 1554.6007, 1721.8494, 1723.8296, 1786.8185, 1798.8191, 1836.8735, 1870.9058, 1876.9320, 1898.8765, 1926.9065, 1939.9283, 2539.0777, 3106.3151, 3154.3115

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 (995.6080,1+) : <no title>
Query2 (1007.4783,1+) : <no title>
Query3 (1011.6284,1+) : <no title>
Query4 (1025.4902,1+) : <no title>
Query5 (1075.5128,1+) : <no title>
Query6 (1137.5381,1+) : <no title>
Query7 (1160.5709,1+) : <no title>
Query8 (1178.6055,1+) : <no title>
Query9 (1206.6118,1+) : <no title>
Query10 (1216.5676,1+) : <no title>
Query11 (1234.6356,1+) : <no title>
Query12 (1253.6032,1+) : <no title>
Query13 (1293.6295,1+) : <no title>
Query14 (1302.7943,1+) : <no title>
Query15 (1338.7690,1+) : <no title>
Query16 (1341.6168,1+) : <no title>
Query17 (1357.6120,1+) : <no title>
Query18 (1376.7063,1+) : <no title>
Query19 (1387.6855,1+) : <no title>
Query20 (1403.6965,1+) : <no title>
Query21 (1446.7364,1+) : <no title>
Query22 (1455.8826,1+) : <no title>
Query23 (1494.7340,1+) : <no title>

Query24 (1510.7327,1+) : <no title>

Query25 (1529.8186,1+) : <no title>

Query26 (1532.6220,1+) : <no title>

Query27 (1544.6801,1+) : <no title>

Query28 (1554.6007,1+) : <no title>

Query29 (1697.7895,1+) : <no title>

Query30 (1721.8494,1+) : <no title>

Query31 (1723.8296,1+) : <no title>

Query32 (1786.8185,1+) : <no title>

Query33 (1798.8191,1+) : <no title>

Query34 (1836.8735,1+) : <no title>

Query35 (1870.9058,1+) : <no title>

Query36 (1876.9320,1+) : <no title>

Query37 (1898.8765,1+) : <no title>

Query38 (1926.9065,1+) : <no title>

Query39 (1939.9283,1+) : <no title>

Query40 (2539.0777,1+) : <no title>

Query41 (3106.3151,1+) : <no title>

Query42 (3154.3115,1+) : <no title>

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

Mascot Search Results

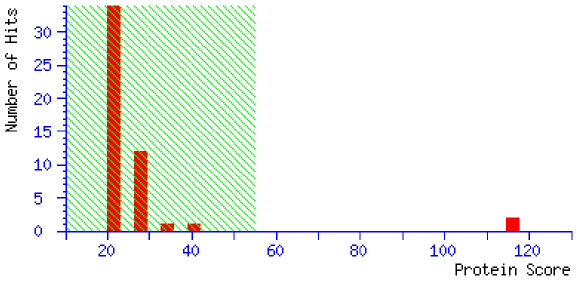
User :
Email :
Search title : **Auto submitted by BioTools**
Database : **SwissProt 57.15 (515203 sequences; 181334896 residues)**
Taxonomy : **Mus. (16281 sequences)**
Timestamp : **20 May 2013 at 01:31:13 GMT**
Warning : **A Peptide summary report will usually give a much clearer picture of MS/MS search results.**
Top Score : **116 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	116	Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3
2.	**TAGL2_MOUSE**	22552	115	Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4
3.	**PPDPF_MOUSE**	12309	38	Pancreatic progenitor cell differentiation and proliferation factor OS=Mus musculus GN=Ppdpf PE=2 SV=1
4.	**PSF2_MOUSE**	21280	35	DNA replication complex GINS protein PSF2 OS=Mus musculus GN=Gins2 PE=1 SV=1
5.	**TRFL_MOUSE**	79698	29	Lactotransferrin OS=Mus musculus GN=Ltf PE=2 SV=3
6.	**YPEL5_MOUSE**	14061	28	Protein yippee-like 5 OS=Mus musculus GN=Ypel5 PE=2 SV=1
7.	**EXOSX_MOUSE**	101593	28	Exosome component 10 OS=Mus musculus GN=Exosc10 PE=1 SV=1
8.	**KATL2_MOUSE**	61514	27	Katanin p60 ATPase-containing subunit A-like 2 OS=Mus musculus GN=Katnal2 PE=2 SV=2
9.	**UD11_MOUSE**	60825	27	UDP-glucuronosyltransferase 1-1 OS=Mus musculus GN=Ugt1a1 PE=2 SV=1
10.	**CIP2A_MOUSE**	103245	27	Protein CIP2A OS=Mus musculus GN=Kiaa1524 PE=2 SV=2

Results List

1. TAGL_MOUSE **Mass:** 22618 **Score:** 116 **Expect:** 4.1e-008 **Matches:** 8

Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
990.5854	989.5781	989.5698	8.35	50 -	57	0	---	R.LGFQVWLK.N
1210.5673	1209.5600	1209.5513	7.20	21 -	29	1	65	K.KYDEELEER.L
1221.6338	1220.6265	1220.6223	3.42	90 -	99	0	---	K.QMEQVAQFLK.A
1244.6205	1243.6132	1243.6271	-11.18	79 -	89	0	---	K.VPENPPSMVFK.Q
1530.8487	1529.8415	1529.8453	-2.52	65 -	78	0	---	K.LVNSLYPEGSKPVK.V
1546.7044	1545.6971	1545.7021	-3.24	109 -	121	0	---	K.TDMFQTVDLYEGK.D
2095.0772	2094.0699	2094.0681	0.89	30 -	47	0	---	R.LVEWIVVQCGPDVGRPDR.G
2318.0894	2317.0821	2317.0719	4.42	109 -	128	1	---	K.TDMFQTVDLYEGKDMAAVQR.T

No match to: 836.4357, 1012.5682, 1028.5487, 1082.5293, 1215.6903, 1224.5719, 1226.6422, 1243.6207, 1266.6168, 1374.7454, 1453.6821, 1552.8336, 1568.7343, 1594.7141, 1616.7077, 1661.7964, 1678.8320, 1694.8296, 1714.7321, 1724.5583, 1730.7547, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2122.0422, 2377.1552, 2394.1848, 2459.1192, 2691.3030, 3337.7248

2. TAGL2_MOUSE **Mass:** 22552 **Score:** 115 **Expect:** 5.1e-008 **Matches:** 8

Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
836.4357	835.4284	835.4188	11.5	5 -	12	0	---	R.GPSYGLSR.E
1082.5293	1081.5220	1081.5152	6.24	40 -	49	0	---	R.EDVGQPQPGR.E
1215.6903	1214.6830	1214.6805	2.09	128 -	139	0	13	R.TLMNLGGLAVAR.D
1244.6205	1243.6132	1243.6343	-16.97	172 -	182	0	---	K.NVIGLQMGTNR.G + Acetyl (N-term)
1594.7141	1593.7068	1593.7100	-2.01	140 -	153	0	---	R.DDGLFSGDPNWFPK.K
1678.8320	1677.8247	1677.8144	6.12	89 -	102	0	56	K.QMEQISQFLQAAER.Y
1694.8296	1693.8223	1693.8093	7.66	89 -	102	0	---	K.QMEQISQFLQAAER.Y + Oxidation (M)
2394.1848	2393.1775	2393.1685	3.77	21 -	39	0	---	K.QYDADLEQILIQWITTQCR.E

No match to: 990.5854, 1012.5682, 1028.5487, 1210.5673, 1221.6338, 1224.5719, 1226.6422, 1243.6207, 1266.6168, 1374.7454, 1453.6821, 1530.8487, 1546.7044, 1552.8336, 1568.7343, 1616.7077, 1661.7964, 1714.7321, 1724.5583, 1730.7547, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2095.0772, 2122.0422, 2318.0894, 2377.1552, 2459.1192, 2691.3030, 3337.7248

3. PPDPF_MOUSE **Mass:** 12309 **Score:** 38 **Expect:** 2.7 **Matches:** 4

Pancreatic progenitor cell differentiation and proliferation factor OS=Mus musculus GN=Ppdpf PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1694.8296	1693.8223	1693.7678	32.2	49 -	62	0	---	K.ADPGHWWASFFFGK.S + Acetyl (N-term)
2095.0772	2094.0699	2094.0316	18.3	1 -	19	1	---	-.MAAIPSSGSLVATHDYYRR.R
2394.1848	2393.1775	2393.1025	31.4	78 -	99	1	---	R.SAESPQVSRSPMTCGLTPETMK.Q
2691.3030	2690.2957	2690.3221	-9.81	63 -	86	1	---	K.STLPFMTTVLESPERSAESPQVSR.S + Acetyl (N-term)

No match to: 836.4357, 990.5854, 1012.5682, 1028.5487, 1082.5293, 1210.5673, 1215.6903, 1221.6338, 1224.5719, 1226.6422, 1243.6207, 1244.6205, 1266.6168, 1374.7454, 1453.6821, 1530.8487, 1546.7044, 1552.8336, 1568.7343, 1594.7141, 1616.7077, 1661.7964, 1678.8320, 1714.7321, 1724.5583, 1730.7547, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2122.0422, 2318.0894, 2377.1552, 2459.1192, 3337.7248

4. PSF2_MOUSE **Mass:** 21280 **Score:** 35 **Expect:** 5.1 **Matches:** 5

DNA replication complex GINS protein PSF2 OS=Mus musculus GN=Gins2 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1221.6338	1220.6265	1220.5925	27.9	2 -	12	0	---	M.DAAEVEFLAEK.E
1530.8487	1529.8415	1529.8341	4.82	13 -	25	0	---	K.ELVTIIPNFSLDK.I + Acetyl (N-term)
1730.7547	1729.7474	1729.8167	-40.08	58 -	70	1	---	K.CRLLPPEWMDVEK.L + Acetyl (N-term); Oxidation (M)
2691.3030	2690.2957	2690.4054	-40.77	2 -	25	1	---	M.DAAEVEFLAEKELVTIIPNFSLDK.I
3337.7248	3336.7176	3336.6700	14.3	81 -	109	1	---	K.EETFTPVPSPHYMEITKLLLNHASDNIPK.A + Oxidation (M)

No match to: 836.4357, 990.5854, 1012.5682, 1028.5487, 1082.5293, 1210.5673, 1215.6903, 1224.5719, 1226.6422, 1243.6207, 1244.6205, 1266.6168, 1374.7454, 1453.6821, 1546.7044, 1552.8336, 1568.7343, 1594.7141, 1616.7077, 1661.7964, 1678.8320, 1694.8296, 1714.7321, 1724.5583, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2095.0772, 2122.0422, 2318.0894, 2377.1552, 2394.1848, 2459.1192

5. TRFL_MOUSE **Mass:** 79698 **Score:** 29 **Expect:** 20 **Matches:** 9

Lactotransferrin OS=Mus musculus GN=Ltf PE=2 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1028.5487	1027.5414	1027.5087	31.8	541 -	549	0	---	R.YQGYTGALR.C
1221.6338	1220.6265	1220.6765	-40.92	682 -	691	1	---	K.EYVIATERLK.Q
1244.6205	1243.6132	1243.6343	-16.97	62 -	71	0	---	R.QCIQAIVTNR.A + Acetyl (N-term)

1453.6821	1452.6749	1452.6997	-17.13	460 -	472	1	---	R.EDAGFTWSSLRGK.K
1552.8336	1551.8263	1551.7682	37.5	300 -	314	0	---	K.QASGFQLFASPSGQK.D
1594.7141	1593.7068	1593.7787	-45.13	300 -	314	0	---	K.QASGFQLFASPSGQK.D + Acetyl (N-term)
1908.9082	1907.9009	1907.8683	17.1	21 -	36	1	---	K.ATTVRWCAVSNSEEEK.C + Acetyl (N-term)
2095.0772	2094.0699	2094.0125	27.4	690 -	707	1	---	R.LKQCSSSPLLEACAFLTQ.- + Acetyl (N-term)
2318.0894	2317.0821	2317.1842	-44.05	332 -	351	0	---	K.VDVGLYLTFSYTTSIQNLNK.K + Acetyl (N-term)

No match to: 836.4357, 990.5854, 1012.5682, 1082.5293, 1210.5673, 1215.6903, 1224.5719, 1226.6422, 1243.6207, 1266.6168, 1374.7454, 1530.8487, 1546.7044, 1568.7343, 1616.7077, 1661.7964, 1678.8320, 1694.8296, 1714.7321, 1724.5583, 1730.7547, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2122.0422, 2377.1552, 2394.1848, 2459.1192, 2691.3030, 3337.7248

6. YPEL5_MOUSE **Mass:** 14061 **Score:** 28 **Expect:** 25 **Matches:** 4

Protein yippee-like 5 OS=Mus musculus GN=Ypel5 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1215.6903	1214.6830	1214.6376	37.4	60 -	69	1	---	R.VMLTGRHMVR.D + Oxidation (M)
1530.8487	1529.8415	1529.7773	42.0	1 -	13	1	---	-.MGRIFLDHIGGTR.L + Acetyl (N-term); Oxidation (M)
1714.7321	1713.7248	1713.7998	-43.79	80 -	93	0	---	K.LGWIYEFATEDSQR.Y
2318.0894	2317.0821	2317.0433	16.7	75 -	93	1	---	K.NCNSKLGWIYEFATEDSQR.Y

No match to: 836.4357, 990.5854, 1012.5682, 1028.5487, 1082.5293, 1210.5673, 1221.6338, 1224.5719, 1226.6422, 1243.6207, 1244.6205, 1266.6168, 1374.7454, 1453.6821, 1546.7044, 1552.8336, 1568.7343, 1594.7141, 1616.7077, 1661.7964, 1678.8320, 1694.8296, 1724.5583, 1730.7547, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2095.0772, 2122.0422, 2377.1552, 2394.1848, 2459.1192, 2691.3030, 3337.7248

7. EXOSX_MOUSE **Mass:** 101593 **Score:** 28 **Expect:** 27 **Matches:** 9

Exosome component 10 OS=Mus musculus GN=Exosc10 PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
990.5854	989.5781	989.5406	37.8	401 -	408	0	---	R.HSLDHLLR.L
1226.6422	1225.6349	1225.5761	48.0	868 -	878	1	---	K.SMSFAVGKSDR.G + Acetyl (N-term)
1243.6207	1242.6134	1242.6568	-34.86	771 -	781	1	---	R.QQAALENATKK.R + Acetyl (N-term)
1374.7454	1373.7381	1373.6861	37.9	124 -	136	0	---	R.VGMLLDEASGVNK.H + Acetyl (N-term)
1530.8487	1529.8415	1529.7871	35.5	578 -	591	1	---	R.EMPLLKSENAAGVR.K + Oxidation (M)
1552.8336	1551.8263	1551.8256	0.44	756 -	770	0	---	K.EEAAAGVLEQAIPVR.Q
1661.7964	1660.7892	1660.8672	-46.99	110 -	123	0	---	K.FDLLVDTNDVILER.V
1908.9082	1907.9009	1907.9550	-28.37	347 -	363	0	---	R.SDMYILNESLTDPAIVK.V
2691.3030	2690.2957	2690.2040	34.1	65 -	86	1	---	R.SFPAFQAFCETQGDRLLQCMSR.V + Acetyl (N-term)

No match to: 836.4357, 1012.5682, 1028.5487, 1082.5293, 1210.5673, 1215.6903, 1221.6338, 1224.5719, 1244.6205, 1266.6168, 1453.6821, 1546.7044, 1568.7343, 1594.7141, 1616.7077, 1678.8320, 1694.8296, 1714.7321, 1724.5583, 1730.7547, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2095.0772, 2122.0422, 2318.0894, 2377.1552, 2394.1848, 2459.1192, 3337.7248

8. KATL2_MOUSE **Mass:** 61514 **Score:** 27 **Expect:** 31 **Matches:** 7

Katanin p60 ATPase-containing subunit A-like 2 OS=Mus musculus GN=Katnal2 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1215.6903	1214.6830	1214.6295	44.1	254 -	264	0	---	K.WNDIIGLDAAK.Q
1226.6422	1225.6349	1225.6455	-8.63	244 -	253	0	---	R.DIYLHNPNIK.W

1546.7044	1545.6971	1545.7358	-25.01	10 -	21	1	---	K.LTHQAREAYEMR.T + Acetyl (N-term)
1616.7077	1615.7005	1615.7447	-27.36	364 -	378	1	---	R.GMVPGGEHEGSLRMK.T + 2 Oxidation (M)
1678.8320	1677.8247	1677.8430	-10.88	377 -	390	1	---	R.MKTELLVQMDGLAR.S + Acetyl (N-term); 2 Oxidation (M)
2377.1552	2376.1479	2376.2399	-38.69	28 -	47	0	---	K.NLLILILHYLTQEGYMDAAK.A + Acetyl (N-term); Oxidation (M)
2691.3030	2690.2957	2690.3084	-4.70	391 -	413	0	---	R.SEDLVFVLAASNLPWELDCAMLR.R + Acetyl (N-term)

No match to: 836.4357, 990.5854, 1012.5682, 1028.5487, 1082.5293, 1210.5673, 1221.6338, 1224.5719, 1243.6207, 1244.6205, 1266.6168, 1374.7454, 1453.6821, 1530.8487, 1552.8336, 1568.7343, 1594.7141, 1661.7964, 1694.8296, 1714.7321, 1724.5583, 1730.7547, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2095.0772, 2122.0422, 2318.0894, 2394.1848, 2459.1192, 3337.7248

9. UD11_MOUSE **Mass:** 60825 **Score:** 27 **Expect:** 31 **Matches:** 8

UDP-glucuronosyltransferase 1-1 OS=Mus musculus GN=Ugt1a1 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
990.5854	989.5781	989.5698	8.35	80 -	87	1	---	R.KFPVPFQK.E
1012.5682	1011.5609	1011.5865	-25.35	331 -	338	0	5	R.IPQTVLWR.Y
1082.5293	1081.5220	1081.5226	-0.55	437 -	444	1	---	K.SYKENIMR.L + Acetyl (N-term)
1552.8336	1551.8263	1551.7538	46.8	214 -	226	0	---	K.NVLLAVSENFMCR.V
1568.7343	1567.7270	1567.7487	-13.84	214 -	226	0	---	K.NVLLAVSENFMCR.V + Oxidation (M)
1594.7141	1593.7068	1593.7643	-36.09	214 -	226	0	---	K.NVLLAVSENFMCR.V + Acetyl (N-term)
1730.7547	1729.7474	1729.8206	-42.30	198 -	211	1	---	K.SLSFNSDRMNFLQR.V + Oxidation (M)
2691.3030	2690.2957	2690.3255	-11.06	406 -	430	1	---	R.METRGAGVTLNVLEMTADDLENALK.T

No match to: 836.4357, 1028.5487, 1210.5673, 1215.6903, 1221.6338, 1224.5719, 1226.6422, 1243.6207, 1244.6205, 1266.6168, 1374.7454, 1453.6821, 1530.8487, 1546.7044, 1616.7077, 1661.7964, 1678.8320, 1694.8296, 1714.7321, 1724.5583, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2095.0772, 2122.0422, 2318.0894, 2377.1552, 2394.1848, 2459.1192, 3337.7248

10. CIP2A_MOUSE **Mass:** 103245 **Score:** 27 **Expect:** 36 **Matches:** 8

Protein CIP2A OS=Mus musculus GN=Kiaa1524 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
836.4357	835.4284	835.4473	-22.66	483 -	489	0	---	K.TLTLMNK.L + Oxidation (M)
1215.6903	1214.6830	1214.6255	47.4	790 -	799	1	---	R.KEVQSQLADR.E + Acetyl (N-term)
1530.8487	1529.8415	1529.7759	42.9	847 -	859	1	---	K.ELSIKASSLEMHK.A + Acetyl (N-term); Oxidation (M)
1694.8296	1693.8223	1693.8536	-18.47	705 -	718	1	---	R.AQNDIEHLFQHSKK.L
2122.0422	2121.0350	2121.1178	-39.05	22 -	40	1	---	K.SEANATQLLRHLEVVSGQK.L + Acetyl (N-term)
2318.0894	2317.0821	2317.0943	-5.28	110 -	128	0	---	R.SSACHNDSVFLQCIQLLQR.L + Acetyl (N-term)
2459.1192	2458.1119	2458.2097	-39.76	316 -	337	0	---	R.HVLSQMMFEQSPSGNILGSRPK.S + Oxidation (M)
2691.3030	2690.2957	2690.3520	-20.91	883 -	907	1	---	K.HSHMIAMIHSLSGGKISPETVNLSI.- + 2 Oxidation (M)

No match to: 990.5854, 1012.5682, 1028.5487, 1082.5293, 1210.5673, 1221.6338, 1224.5719, 1226.6422, 1243.6207, 1244.6205, 1266.6168, 1374.7454, 1453.6821, 1546.7044, 1552.8336, 1568.7343, 1594.7141, 1616.7077, 1661.7964, 1678.8320, 1714.7321, 1724.5583, 1730.7547, 1908.9082, 1946.5789, 2058.8849, 2079.4661, 2081.3996, 2095.0772, 2377.1552, 2394.1848, 3337.7248

Search Parameters

Type of search : **MS/MS Ion Search**

Enzyme : **Trypsin**

Fixed modifications : **Carbamidomethyl (C)**

Variable modifications : Acetyl (N-term),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ±50 ppm

Fragment Mass Tolerance: ±0.5 Da

Max Missed Cleavages : 1

Instrument type : MALDI-TOF-TOF

Query1 (836.4357,1+) : <no title>

Query2 (990.5854,1+) : <no title>

Query3 (1012.5682,1+) : <no title>

Query4 (1028.5487,1+) : <no title>

Query5 (1082.5293,1+) : <no title>

Query6 (1210.5673,1+) : <no title>

Query7 (1215.6903,1+) : <no title>

Query8 (1221.6338,1+) : <no title>

Query9 (1224.5719,1+) : <no title>

Query10 (1226.6422,1+) : <no title>

Query11 (1243.6207,1+) : <no title>

Query12 (1244.6205,1+) : <no title>

Query13 (1266.6168,1+) : <no title>

Query14 (1374.7454,1+) : <no title>

Query15 (1453.6821,1+) : <no title>

Query16 (1530.8487,1+) : <no title>

Query17 (1546.7044,1+) : <no title>

Query18 (1552.8336,1+) : <no title>

Query19 (1568.7343,1+) : <no title>

Query20 (1594.7141,1+) : <no title>

Query21 (1616.7077,1+) : <no title>

Query22 (1661.7964,1+) : <no title>

Query23 (1678.8320,1+) : <no title>

Query24 (1694.8296,1+) : <no title>

Query25 (1714.7321,1+) : <no title>

Query26 (1724.5583,1+) : <no title>

Query27 (1730.7547,1+) : <no title>

Query28 (1908.9082,1+) : <no title>

Query29 (1946.5789,1+) : <no title>

Query30 (2058.8849,1+) : <no title>

Query31 (2079.4661,1+) : <no title>

Query32 (2081.3996,1+) : <no title>

Query33 (2095.0772,1+) : <no title>

Query34 (2122.0422,1+) : <no title>

Query35 (2318.0894,1+) : <no title>

Query36 (2377.1552,1+) : <no title>

Query37 (2394.1848,1+) : <no title>

Query38 (2459.1192,1+) : <no title>

Query39 (2691.3030,1+) : <no title>

Query40 (3337.7248,1+) : <no title>

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

MATRIX SCIENCE Mascot Search Results

User :

Email :

Search title : Auto submitted by BioTools

Database : SwissProt 57.15 (515203 sequences; 181334896 residues)

Taxonomy : Mus. (16281 sequences)

Timestamp : 20 May 2013 at 01:31:22 GMT

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

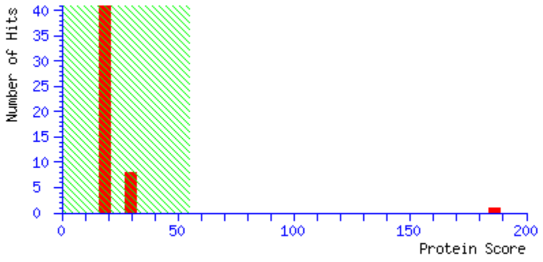
Top Score : 186 for TAGL_MOUSE, Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3

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	186	Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3
2.	**SORCN_MOUSE**	21898	33	Sorcin OS=Mus musculus GN=Sri PE=1 SV=1
3.	**KLRA1_MOUSE**	31276	32	T-cell surface glycoprotein YE1/48 OS=Mus musculus GN=Klra1 PE=1 SV=1
4.	**CO6A1_MOUSE**	109562	32	Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=2 SV=1
5.	**NOP16_MOUSE**	21183	32	Nucleolar protein 16 OS=Mus musculus GN=Nop16 PE=2 SV=1
6.	**PCNT_MOUSE**	220085	29	Pericentrin OS=Mus musculus GN=Pcnt PE=1 SV=1

7. RM38_MOUSE	45287	27	39S ribosomal protein L38, mitochondrial OS=Mus musculus GN=Mrpl38 PE=2 SV=2
8. RT24_MOUSE	19174	26	28S ribosomal protein S24, mitochondrial OS=Mus musculus GN=Mrps24 PE=2 SV=1
9. MBRL_MOUSE	63805	24	Membralin OS=Mus musculus GN=ORF61 PE=1 SV=2
10. KLC4_MOUSE	69084	24	Kinesin light chain 4 OS=Mus musculus GN=Klc4 PE=1 SV=1

Results List

1. TAGL_MOUSE **Mass:** 22618 **Score:** 186 **Expect:** 4.1e-015 **Matches:** 19

Transgelin OS=Mus musculus GN=Tagln PE=1 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
806.3542	805.3470	805.3752	-35.09	122 -	128	0	---	K.DMAAVQR.T + Oxidation (M)
965.4665	964.4592	964.4865	-28.36	100 -	108	0	---	K.AAEDYGVIK.T
990.5630	989.5557	989.5698	-14.29	50 -	57	0	---	R.LGFQVWLK.N
994.4527	993.4454	993.4378	7.63	147 -	154	0	---	R.GDPNWFMK.K
1082.4225	1081.4153	1081.4563	-38.00	22 -	29	0	---	K.YDEELEER.L
1203.6778	1202.6705	1202.6924	-18.24	48 -	57	1	---	R.GRLGFQVWLK.N
1204.6653	1203.6580	1203.6897	-26.33	129 -	140	0	---	R.TLMALGSLAVTK.N
1210.5495	1209.5422	1209.5513	-7.54	21 -	29	1	79	K.KYDEELEER.L
1221.6211	1220.6138	1220.6223	-7.00	90 -	99	0	---	K.QMEQVAQFLK.A
1244.6184	1243.6112	1243.6271	-12.81	79 -	89	0	---	K.VPENPPSMVFK.Q
1260.5941	1259.5868	1259.6220	-27.92	79 -	89	0	---	K.VPENPPSMVFK.Q + Oxidation (M)
1530.8219	1529.8147	1529.8453	-20.05	65 -	78	0	---	K.LVNSLYPEGSKPVK.V
1546.6759	1545.6686	1545.7021	-21.68	109 -	121	0	---	K.TDMFQTVDLYEGK.D
1562.6804	1561.6731	1561.6970	-15.31	109 -	121	0	---	K.TDMFQTVDLYEGK.D + Oxidation (M)
1713.7156	1712.7084	1712.7365	-16.45	141 -	154	1	---	K.NDGNYRGDPNWFMK.K
1729.6720	1728.6647	1728.7314	-38.62	141 -	154	1	---	K.NDGNYRGDPNWFMK.K + Oxidation (M)
2095.0590	2094.0517	2094.0681	-7.82	30 -	47	0	---	R.LVEWIVVQCGPDVGRPDR.G
2318.0530	2317.0457	2317.0719	-11.30	109 -	128	1	---	K.TDMFQTVDLYEGKDMAAVQR.T
2334.0475	2333.0402	2333.0668	-11.39	109 -	128	1	---	K.TDMFQTVDLYEGKDMAAVQR.T + Oxidation (M)

No match to: 834.2970, 896.4857, 1004.5310, 1012.5411, 1022.5492, 1028.5188, 1042.4301, 1044.5361, 1064.4260, 1224.5717, 1226.6667, 1236.5985, 1238.5813, 1243.6046, 1266.5884, 1282.5857, 1532.5496, 1552.8113, 1568.6914, 1584.6583, 1701.5453, 1723.5328, 1761.7026, 1946.5805, 1959.9017, 2037.0076, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2088.0137, 2108.0341, 2110.0611, 2111.0488, 2116.0316, 2127.0376, 2279.0052, 2420.0215, 2459.0992, 2475.0828

2. SORCN_MOUSE **Mass:** 21898 **Score:** 33 **Expect:** 7.6 **Matches:** 6

Sorcin OS=Mus musculus GN=Sri PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
896.4857	895.4784	895.4586	22.2	128 -	135	0	---	K.ALTTMGFR.L
1022.5492	1021.5419	1021.4936	47.3	77 -	84	0	---	R.LMVSMLDR.D + Acetyl (N-term); Oxidation (M)
1243.6046	1242.5973	1242.6092	-9.57	117 -	127	0	---	R.SGTVDPQELQK.A + Acetyl (N-term)
1546.6759	1545.6686	1545.6844	-10.19	154 -	165	0	---	K.ITFDDYIACCVK.L + Acetyl (N-term)
2037.0076	2036.0004	2036.0725	-35.41	128 -	146	1	---	K.ALTTMGFRLSPQTVNSVAK.R + Oxidation (M)
2095.0590	2094.0517	2094.0416	4.83	117 -	135	1	---	R.SGTVDPQELQKALTTMGFR.L + Oxidation (M)

No match to: 806.3542, 834.2970, 965.4665, 990.5630, 994.4527, 1004.5310, 1012.5411, 1028.5188, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1204.6653, 1210.5495, 1221.6211, 1224.5717, 1226.6667, 1236.5985, 1238.5813, 1244.6184, 1260.5941, 1266.5884, 1282.5857, 1530.8219, 1532.5496, 1552.8113, 1562.6804, 1568.6914, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 1959.9017, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2088.0137, 2108.0341, 2110.0611, 2111.0488, 2116.0316, 2127.0376, 2279.0052, 2318.0530, 2334.0475, 2420.0215, 2459.0992, 2475.0828

3. KLRA1_MOUSE **Mass:** 31276 **Score:** 32 **Expect:** 10 **Matches:** 7

T-cell surface glycoprotein YE1/48 OS=Mus musculus GN=Klra1 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1028.5188	1027.5115	1027.5298	-17.82	22 -	29	0	---	K.QVRPEETK.G + Acetyl (N-term)
1226.6667	1225.6595	1225.6415	14.6	127 -	137	0	---	K.TVLDSLQHTGR.G
1568.6914	1567.6841	1567.7487	-41.16	225 -	237	1	---	K.YNIRDGGCMLLSK.T + Acetyl (N-term)
2111.0488	2110.0415	2109.9394	48.4	240 -	256	1	---	R.LDNGNCDQVFICICGKR.L + Acetyl (N-term)
2127.0376	2126.0303	2126.0909	-28.46	207 -	224	1	---	K.DWAWIDNRPSKLALNTGK.Y + Acetyl (N-term)
2279.0052	2277.9980	2278.0998	-44.71	165 -	184	1	---	K.QACQSSSLSLLKIDDEDELK.F
2420.0215	2419.0143	2418.9934	8.61	141 -	157	1	---	K.VYWFCYGMKCYYFVMDR.K + 2 Oxidation (M)

No match to: 806.3542, 834.2970, 896.4857, 965.4665, 990.5630, 994.4527, 1004.5310, 1012.5411, 1022.5492, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1204.6653, 1210.5495, 1221.6211, 1224.5717, 1236.5985, 1238.5813, 1243.6046, 1244.6184, 1260.5941, 1266.5884, 1282.5857, 1530.8219, 1532.5496, 1546.6759, 1552.8113, 1562.6804, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 1959.9017, 2037.0076, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2088.0137, 2095.0590, 2108.0341, 2110.0611, 2116.0316, 2318.0530, 2334.0475, 2459.0992, 2475.0828

4. CO6A1_MOUSE **Mass:** 109562 **Score:** 32 **Expect:** 11 **Matches:** 12

Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
896.4857	895.4784	895.4988	-22.76	433 -	441	1	---	R.GTPGVRGPR.G
990.5630	989.5557	989.5076	48.6	101 -	109	1	---	R.GLTRMPSGR.D + Oxidation (M)
1022.5492	1021.5419	1021.5556	-13.46	1012 -	1020	0	---	R.GVLYQTVSR.K
1028.5188	1027.5115	1027.4644	45.8	125 -	133	0	---	K.GTYTDCAIK.K
1226.6667	1225.6595	1225.6343	20.5	114 -	124	1	---	K.ASVDAVKYFGK.G + Acetyl (N-term)
1568.6914	1567.6841	1567.7406	-36.00	788 -	800	0	---	K.ENYAELLDDGFLK.N + Acetyl (N-term)
2037.0076	2036.0004	2035.9997	0.34	166 -	184	1	---	K.EPCGGLEDAVNEAKHLGIK.V
2088.0137	2087.0064	2086.9782	13.5	693 -	710	0	---	K.LQWMAGGTFTGEALQYTR.D + Acetyl (N-term); Oxidation (M)
2108.0341	2107.0268	2106.9715	26.3	325 -	345	1	---	R.GIDGVDGMKGETGYPGLPGCK.G
2110.0611	2109.0538	2109.0491	2.24	456 -	477	1	---	R.EGPVGIPGDSGEAGPIGPKGYR.G
2116.0316	2115.0243	2114.9691	26.1	280 -	300	0	---	K.GEAGDPGRPGDLGPVGYQGMK.G + Acetyl (N-term); Oxidation (M)
2318.0530	2317.0457	2317.0036	18.2	508 -	530	0	---	R.GEDGPPGNGTEGFPGFPGYPGNR.G + Acetyl (N-term)

No match to: 806.3542, 834.2970, 965.4665, 994.4527, 1004.5310, 1012.5411, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1204.6653, 1210.5495, 1221.6211, 1224.5717, 1236.5985, 1238.5813, 1243.6046, 1244.6184, 1260.5941, 1266.5884, 1282.5857, 1530.8219, 1532.5496, 1546.6759, 1552.8113, 1562.6804, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 1959.9017, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2095.0590, 2111.0488, 2127.0376, 2279.0052, 2334.0475, 2420.0215, 2459.0992, 2475.0828

5. NOP16_MOUSE **Mass:** 21183 **Score:** 32 **Expect:** 11 **Matches:** 6

Nucleolar protein 16 OS=Mus musculus GN=Nop16 PE=2 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1028.5188	1027.5115	1027.4611	49.1	139 -	146	0	---	K.NYYQDTPK.Q
1236.5985	1235.5912	1235.6160	-20.04	41 -	50	1	---	R.HAWDHTKSVR.Q
1959.9017	1958.8945	1958.9414	-23.97	158 -	173	0	---	R.FYPTEWQAFIDSLQSK.K
2088.0137	2087.0064	2087.0364	-14.36	158 -	174	1	---	R.FYPTEWQAFIDSLQSKK.M
2110.0611	2109.0538	2109.0710	-8.16	51 -	69	1	---	R.QNLAEMGLAMDPNKAVPLR.K + Acetyl (N-term)
2116.0316	2115.0243	2115.0425	-8.61	157 -	173	1	---	K.RFYPTEWQAFIDSLQSK.K

No match to: 806.3542, 834.2970, 896.4857, 965.4665, 990.5630, 994.4527, 1004.5310, 1012.5411, 1022.5492, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1204.6653, 1210.5495, 1221.6211, 1224.5717, 1226.6667, 1238.5813, 1243.6046, 1244.6184, 1260.5941, 1266.5884, 1282.5857, 1530.8219, 1532.5496, 1546.6759, 1552.8113, 1562.6804, 1568.6914, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 2037.0076, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2095.0590, 2108.0341, 2111.0488, 2127.0376, 2279.0052, 2318.0530, 2334.0475, 2420.0215, 2459.0992, 2475.0828

6. PCNT_MOUSE **Mass:** 220085 **Score:** 29 **Expect:** 21 **Matches:** 15

Pericentrin OS=Mus musculus GN=Pcnt PE=1 SV=1

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
806.3542	805.3470	805.3640	-21.11	188 -	193	0	---	K.EEMALR.S + Acetyl (N-term); Oxidation (M)
1064.4260	1063.4187	1063.4240	-4.95	1 -	8	0	---	-.MEDEQEQR.R
1203.6778	1202.6705	1202.6547	13.1	1789 -	1798	0	---	K.TTWDVIDIIK.N
1204.6653	1203.6580	1203.6863	-23.52	262 -	271	1	---	K.VELEKIFQAK.H
1210.5495	1209.5422	1209.5084	27.9	1254 -	1263	0	18	R.QFMDDQAAER.D
1226.6667	1225.6595	1225.6778	-15.00	1084 -	1092	1	---	K.QQELLERLR.E + Acetyl (N-term)
1236.5985	1235.5912	1235.5353	45.2	539 -	547	1	---	R.FEHRESSMR.H + Acetyl (N-term); Oxidation (M)
1238.5813	1237.5740	1237.6051	-25.12	771 -	780	0	---	R.QHAEELQSVR.D + Acetyl (N-term)
1244.6184	1243.6112	1243.6482	-29.78	1472 -	1482	0	---	K.LQSELSLMGPK.V + Acetyl (N-term)
1260.5941	1259.5868	1259.6431	-44.67	1472 -	1482	0	---	K.LQSELSLMGPK.V + Acetyl (N-term); Oxidation (M)
1266.5884	1265.5811	1265.6404	-46.88	633 -	642	1	---	K.FAKEQDAFLR.D + Acetyl (N-term)
1546.6759	1545.6686	1545.6664	1.45	1072 -	1083	1	---	R.HRNEEMAQAMQK.Q + Acetyl (N-term); 2 Oxidation (M)
2058.8658	2057.8585	2057.9510	-44.92	754 -	769	1	---	K.ESCHREMLTQELENLK.R + Acetyl (N-term)
2108.0341	2107.0268	2107.0143	5.95	1569 -	1587	0	---	R.EAEVEAMASQIQEFAATLK.A + Acetyl (N-term)
2116.0316	2115.0243	2115.1072	-39.19	272 -	290	1	---	K.HEAEVSLKNLEAQHQAAIK.K

No match to: 834.2970, 896.4857, 965.4665, 990.5630, 994.4527, 1004.5310, 1012.5411, 1022.5492, 1028.5188, 1042.4301, 1044.5361, 1082.4225, 1221.6211, 1224.5717, 1243.6046, 1282.5857, 1530.8219, 1532.5496, 1552.8113, 1562.6804, 1568.6914, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 1959.9017, 2037.0076, 2051.3401, 2078.4905, 2080.4178, 2088.0137, 2095.0590, 2110.0611, 2111.0488, 2127.0376, 2279.0052, 2318.0530, 2334.0475, 2420.0215, 2459.0992, 2475.0828

7. RM38_MOUSE **Mass:** 45287 **Score:** 27 **Expect:** 30 **Matches:** 8

39S ribosomal protein L38, mitochondrial OS=Mus musculus GN=Mrpl38 PE=2 SV=2

Observed	**Mr(expt)**	**Mr(calc)**	**ppm**	**Start**	**End**	**Miss**	**Ions**	**Peptide**
1012.5411	1011.5338	1011.5614	-27.27	108 -	114	1	1	K.HFLRELR.A + Acetyl (N-term)
1221.6211	1220.6138	1220.6414	-22.64	356 -	364	1	---	K.RFPHEQPLR.Y + Acetyl (N-term)
1224.5717	1223.5644	1223.5975	-27.06	297 -	305	1	---	R.TFRTFDFYK.R
1244.6184	1243.6112	1243.6156	-3.60	112 -	121	1	---	R.ELRANVEEER.A
1266.5884	1265.5811	1265.6081	-21.33	297 -	305	1	---	R.TFRTFDFYK.R + Acetyl (N-term)

2058.8658	2057.8585	2057.9265	-33.05	323 -	338	0	---	R.WDDSVTHTFHQLLDMR.E + Acetyl (N-term); Oxidation (M)
2095.0590	2094.0517	2094.1051	-25.49	339 -	355	1	---	R.EPVFEFVRPPPYHPKQK.R
2110.0611	2109.0538	2109.0048	23.2	29 -	47	0	---	R.TPPLGPMPNEDIDVSNLER.L + Oxidation (M)

No match to: 806.3542, 834.2970, 896.4857, 965.4665, 990.5630, 994.4527, 1004.5310, 1022.5492, 1028.5188, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1204.6653, 1210.5495, 1226.6667, 1236.5985, 1238.5813, 1243.6046, 1260.5941, 1282.5857, 1530.8219, 1532.5496, 1546.6759, 1552.8113, 1562.6804, 1568.6914, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 1959.9017, 2037.0076, 2051.3401, 2078.4905, 2080.4178, 2088.0137, 2108.0341, 2111.0488, 2116.0316, 2127.0376, 2279.0052, 2318.0530, 2334.0475, 2420.0215, 2459.0992, 2475.0828

8. RT24_MOUSE **Mass:** 19174 **Score:** 26 **Expect:** 37 **Matches:** 5

28S ribosomal protein S24, mitochondrial OS=Mus musculus GN=Mrps24 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
965.4665	964.4592	964.4436	16.1	1 -	8	0	---	-.MAWSASVR.G + Acetyl (N-term); Oxidation (M)
1022.5492	1021.5419	1021.5920	-49.06	153 -	161	0	---	R.LHLQTVPSK.V
1959.9017	1958.8945	1958.9304	-18.36	95 -	111	0	---	K.FMMGTFPGCLADQIVLK.R + 2 Oxidation (M)
2088.0137	2087.0064	2087.0254	-9.10	94 -	111	1	---	R.KFMMGTFPGCLADQIVLK.R + 2 Oxidation (M)
2116.0316	2115.0243	2115.0315	-3.42	95 -	112	1	---	K.FMMGTFPGCLADQIVLKR.R + 2 Oxidation (M)

No match to: 806.3542, 834.2970, 896.4857, 990.5630, 994.4527, 1004.5310, 1012.5411, 1028.5188, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1204.6653, 1210.5495, 1221.6211, 1224.5717, 1226.6667, 1236.5985, 1238.5813, 1243.6046, 1244.6184, 1260.5941, 1266.5884, 1282.5857, 1530.8219, 1532.5496, 1546.6759, 1552.8113, 1562.6804, 1568.6914, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 2037.0076, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2095.0590, 2108.0341, 2110.0611, 2111.0488, 2127.0376, 2279.0052, 2318.0530, 2334.0475, 2420.0215, 2459.0992, 2475.0828

9. MBRL_MOUSE **Mass:** 63805 **Score:** 24 **Expect:** 59 **Matches:** 9

Membralin OS=Mus musculus GN=ORF61 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
990.5630	989.5557	989.5069	49.3	161 -	168	0	---	K.FELDIEPK.V
1012.5411	1011.5338	1011.5614	-27.28	104 -	111	1	6	R.WPREGVLR.V
1022.5492	1021.5419	1021.5749	-32.32	43 -	50	0	---	R.LFHALFFK.M
1224.5717	1223.5644	1223.6081	-35.68	92 -	101	0	---	R.SPINCLEHVR.D
1266.5884	1265.5811	1265.6186	-29.67	92 -	101	0	---	R.SPINCLEHVR.D + Acetyl (N-term)
2088.0137	2087.0064	2086.9603	22.1	1 -	24	0	---	-.MSEHAAAPGPGPNGGGGGGAAPVR.G + Oxidation (M)
2108.0341	2107.0268	2106.9781	23.1	398 -	412	0	---	R.FFYLYHFAFYAYHYR.F
2111.0488	2110.0415	2109.9877	25.5	276 -	292	1	---	R.NVVSGEHYRFVSMWMAR.T + Acetyl (N-term)
2127.0376	2126.0303	2125.9826	22.5	276 -	292	1	---	R.NVVSGEHYRFVSMWMAR.T + Acetyl (N-term); Oxidation (M)

No match to: 806.3542, 834.2970, 896.4857, 965.4665, 994.4527, 1004.5310, 1028.5188, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1204.6653, 1210.5495, 1221.6211, 1226.6667, 1236.5985, 1238.5813, 1243.6046, 1244.6184, 1260.5941, 1282.5857, 1530.8219, 1532.5496, 1546.6759, 1552.8113, 1562.6804, 1568.6914, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 1959.9017, 2037.0076, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2095.0590, 2110.0611, 2116.0316, 2279.0052, 2318.0530, 2334.0475, 2420.0215, 2459.0992, 2475.0828

10. KLC4_MOUSE **Mass:** 69084 **Score:** 24 **Expect:** 66 **Matches:** 9

Kinesin light chain 4 OS=Mus musculus GN=Klc4 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1004.5310	1003.5237	1003.5563	-32.46	469 -	476	1	---	K.NLGALYRR.Q + Acetyl (N-term)
1204.6653	1203.6580	1203.6347	19.4	17 -	27	0	---	R.LSQEEILGSTK.V
1210.5495	1209.5422	1209.5725	-25.05	607 -	619	0	---	R.GLSASTVDLSSSS.-
1243.6046	1242.5973	1242.6568	-47.88	506 -	517	1	---	K.VAELLGEGDGRK.A
1244.6184	1243.6112	1243.6408	-23.85	495 -	505	1	---	R.KQGTDPISQTK.V + Acetyl (N-term)
1530.8219	1529.8147	1529.7573	37.5	133 -	145	1	---	R.SEQAVAQLEEEKK.H + Acetyl (N-term)
1546.6759	1545.6686	1545.7344	-42.58	480 -	492	0	---	K.LEAAETLEECALR.S + Acetyl (N-term)
1562.6804	1561.6731	1561.7406	-43.20	573 -	586	0	---	K.LQGTEPRPSSSSMK.R + Acetyl (N-term); Oxidation (M)
2108.0341	2107.0268	2107.1021	-35.74	271 -	289	1	---	K.EAAHLLNDALSIRESTLGR.D + Acetyl (N-term)

No match to: 806.3542, 834.2970, 896.4857, 965.4665, 990.5630, 994.4527, 1012.5411, 1022.5492, 1028.5188, 1042.4301, 1044.5361, 1064.4260, 1082.4225, 1203.6778, 1221.6211, 1224.5717, 1226.6667, 1236.5985, 1238.5813, 1260.5941, 1266.5884, 1282.5857, 1532.5496, 1552.8113, 1568.6914, 1584.6583, 1701.5453, 1713.7156, 1723.5328, 1729.6720, 1761.7026, 1946.5805, 1959.9017, 2037.0076, 2051.3401, 2058.8658, 2078.4905, 2080.4178, 2088.0137, 2095.0590, 2110.0611, 2111.0488, 2116.0316, 2127.0376, 2279.0052, 2318.0530, 2334.0475, 2420.0215, 2459.0992, 2475.0828

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Acetyl (N-term),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ±50 ppm
Fragment Mass Tolerance: ±0.5 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (806.3542,1+) : <no title>
Query2 (834.2970,1+) : <no title>
Query3 (896.4857,1+) : <no title>
Query4 (965.4665,1+) : <no title>
Query5 (990.5630,1+) : <no title>
Query6 (994.4527,1+) : <no title>
Query7 (1004.5310,1+) : <no title>
Query8 (1012.5411,1+) : <no title>
Query9 (1022.5492,1+) : <no title>
Query10 (1028.5188,1+) : <no title>
Query11 (1042.4301,1+) : <no title>
Query12 (1044.5361,1+) : <no title>
Query13 (1064.4260,1+) : <no title>
Query14 (1082.4225,1+) : <no title>
Query15 (1203.6778,1+) : <no title>
Query16 (1204.6653,1+) : <no title>
Query17 (1210.5495,1+) : <no title>

Query18 (1221.6211,1+) : <no title>

Query19 (1224.5717,1+) : <no title>

Query20 (1226.6667,1+) : <no title>

Query21 (1236.5985,1+) : <no title>

Query22 (1238.5813,1+) : <no title>

Query23 (1243.6046,1+) : <no title>

Query24 (1244.6184,1+) : <no title>

Query25 (1260.5941,1+) : <no title>

Query26 (1266.5884,1+) : <no title>

Query27 (1282.5857,1+) : <no title>

Query28 (1530.8219,1+) : <no title>

Query29 (1532.5496,1+) : <no title>

Query30 (1546.6759,1+) : <no title>

Query31 (1552.8113,1+) : <no title>

Query32 (1562.6804,1+) : <no title>

Query33 (1568.6914,1+) : <no title>

Query34 (1584.6583,1+) : <no title>

Query35 (1701.5453,1+) : <no title>

Query36 (1713.7156,1+) : <no title>

Query37 (1723.5328,1+) : <no title>

Query38 (1729.6720,1+) : <no title>

Query39 (1761.7026,1+) : <no title>

Query40 (1946.5805,1+) : <no title>

Query41 (1959.9017,1+) : <no title>

Query42 (2037.0076,1+) : <no title>

Query43 (2051.3401,1+) : <no title>

Query44 (2058.8658,1+) : <no title>

Query45 (2078.4905,1+) : <no title>

Query46 (2080.4178,1+) : <no title>

Query47 (2088.0137,1+) : <no title>

Query48 (2095.0590,1+) : <no title>

Query49 (2108.0341,1+) : <no title>

Query50 (2110.0611,1+) : <no title>

Query51 (2111.0488,1+) : <no title>

Query52 (2116.0316,1+) : <no title>

Query53 (2127.0376,1+) : <no title>

Query54 (2279.0052,1+) : <no title>

Query55 (2318.0530,1+) : <no title>

Query56 (2334.0475,1+) : <no title>

Query57 (2420.0215,1+) : <no title>

Query58 (2459.0992,1+) : <no title>

Query59 (2475.0828,1+) : <no title>