


Mascot Search Results

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User           : cclee
Email          : cclee@hkbu.edu.hk
Search title   :
MS data file   : DATA.TXT
Database       : IPI_human_human_3.77 (89422 sequences; 35797929 residues)
Taxonomy       : Homo sapiens (human) (89422 sequences)
Timestamp      :
Warning        : Taxonomy 'Homo sapiens (human)' ignored. No taxonomy indexes for this database
Enzyme         : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values    : Monoisotopic
Protein Mass   : Unrestricted
Peptide Mass Tolerance : ± 0.3 Da (# 13C = 1)
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 12564
Protein hits   : IPI00007752 Tax_Id=9606 Gene_Symbol=TUBB2C Tubulin beta-2C chain
                 IPI00220327 Tax_Id=9606 Gene_Symbol=KRT1 Keratin, type II cytoskeletal 1
                 IPI00023598 Tax_Id=9606 Gene_Symbol=TUBB4 Tubulin beta-4 chain
                 IPI00930130 Tax_Id=9606 Gene_Symbol=TUBB6 cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain
                 IPI00013683 Tax_Id=9606 Gene_Symbol=TUBB3 Tubulin beta-3 chain
                 IPI00410402 Tax_Id=9606 Gene_Symbol=TUBA3E Tubulin alpha-3E chain
                 IPI00179709 Tax_Id=9606 Gene_Symbol=TUBA3D/TUBA3C Isoform 1 of Tubulin alpha-3C/D chain
                 IPI00180675 Tax_Id=9606 Gene_Symbol=TUBA1A Tubulin alpha-1A chain
                 IPI00019359 Tax_Id=9606 Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9
                 IPI00013475 Tax_Id=9606 Gene_Symbol=TUBB2A Tubulin beta-2A chain
                 IPI00908770 Tax_Id=9606 Gene_Symbol=TUBB cDNA FLJ53063, highly similar to Tubulin beta-7 chain
                 IPI00646779 Tax_Id=9606 Gene_Symbol=TUBB6 TUBB6 protein
                 IPI00009865 Tax_Id=9606 Gene_Symbol=KRT10 Keratin, type I cytoskeletal 10
                 IPI00303476 Tax_Id=9606 Gene_Symbol=ATP5B ATP synthase subunit beta, mitochondrial
                 IPI00440493 Tax_Id=9606 Gene_Symbol=ATP5A1 ATP synthase subunit alpha, mitochondrial
                 IPI00745872 Tax_Id=9606 Gene_Symbol=ALB Isoform 1 of Serum albumin
                 IPI00953417 Tax_Id=9606 Gene_Symbol=TUBB cDNA FLJ53012, highly similar to Tubulin beta-7 chain
                 IPI00645452 Tax_Id=9606 Gene_Symbol=TUBB Tubulin, beta
                 IPI00909140 Tax_Id=9606 Gene_Symbol=TUBB cDNA FLJ56903, highly similar to Tubulin beta-7 chain
                 IPI00290854 Tax_Id=9606 Gene_Symbol=AKAP3 A-kinase anchor protein 3
                 IPI00646909 Tax_Id=9606 Gene_Symbol=TUBA8 Tubulin alpha-8 chain
                 IPI00021304 Tax_Id=9606 Gene_Symbol=KRT2 Keratin, type II cytoskeletal 2 epidermal
                 IPI00292496 Tax_Id=9606 Gene_Symbol=TUBB8 Tubulin beta-8 chain
                 IPI00293665 Tax_Id=9606 Gene_Symbol=KRT6B Keratin, type II cytoskeletal 6B
                 IPI00964764 Tax_Id=9606 Gene_Symbol=SDHA cDNA FLJ55072, highly similar to Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial
                 IPI00299145 Tax_Id=9606 Gene_Symbol=KRT6C Keratin, type II cytoskeletal 6C
                 IPI00157860 Tax_Id=9606 Gene_Symbol=AKAP4 Isoform 1 of A-kinase anchor protein 4
                 IPI00018511 Tax_Id=9606 Gene_Symbol=TUBB4Q Putative tubulin beta-4q chain
                 IPI00009867 Tax_Id=9606 Gene_Symbol=KRT5 Keratin, type II cytoskeletal 5
                 IPI00641706 Tax_Id=9606 Gene_Symbol=TUBB6 46 kDa protein
                 IPI00290078 Tax_Id=9606 Gene_Symbol=KRT4 keratin, type II cytoskeletal 4
                 IPI00939892 Tax_Id=9606 Gene_Symbol=KRT75 65 kDa protein
                 IPI00306959 Tax_Id=9606 Gene_Symbol=KRT7 Keratin, type II cytoskeletal 7
                 IPI00787323 Tax_Id=9606 Gene_Symbol=LOC728638 Similar to Keratin, type II cytoskeletal 8
                 IPI00554648 Tax_Id=9606 Gene_Symbol=KRT8 Keratin, type II cytoskeletal 8
                 IPI00886833 Tax_Id=9606 Gene_Symbol=LOC100129958 similar to HCG1643231
                 IPI00383815 Tax_Id=9606 Gene_Symbol=GFAP Isoform 2 of Glial fibrillary acidic protein
                 IPI00031169 Tax_Id=9606 Gene_Symbol=RAB2A Ras-related protein Rab-2A
                 IPI00465028 Tax_Id=9606 Gene_Symbol=TPPI1/TPPI1P1 triosephosphate isomerase isoform 2

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[IPI00909560](#) Tax_Id=9606 Gene_Symbol=PKM2 Pyruvate kinase
[IPI00550533](#) Tax_Id=9606 Gene_Symbol=Clorf56 Isoform 1 of Uncharacterized protein Clorf56
[IPI00152561](#) Tax_Id=9606 Gene_Symbol=SPACA4 Sperm acrosome membrane-associated protein 4
[IPI00291262](#) Tax_Id=9606 Gene_Symbol=CLU Isoform 1 of Clusterin
[IPI00643152](#) Tax_Id=9606 Gene_Symbol=HSPA1L cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L
[IPI00013006](#) Tax_Id=9606 Gene_Symbol=ZBPB Zona pellucida-binding protein 1
[IPI00007702](#) Tax_Id=9606 Gene_Symbol=HSPA2 Heat shock-related 70 kDa protein 2
[IPI00945532](#) Tax_Id=9606 Gene_Symbol=TUBB8 tubulin beta-8 chain isoform 2
[IPI00376239](#) Tax_Id=9606 Gene_Symbol=H1FNT Testis-specific H1 histone
[IPI00465363](#) Tax_Id=9606 Gene_Symbol=HIST1H2BA Histone H2B type 1-A
[IPI00003362](#) Tax_Id=9606 Gene_Symbol=HSPA5 HSPA5 protein
[IPI00008910](#) Tax_Id=9606 Gene_Symbol=SPACA1 Sperm acrosome membrane-associated protein 1
[IPI00304925](#) Tax_Id=9606 Gene_Symbol=HSPA1B;HSPA1A Heat shock 70 kDa protein 1A/1B
[IPI00909073](#) Tax_Id=9606 Gene_Symbol=- cDNA FLJ53752, highly similar to Heat shock 70 kDa protein 1
[IPI00554498](#) Tax_Id=9606 Gene_Symbol=LDHC L-lactate dehydrogenase C chain
[IPI00376379](#) Tax_Id=9606 Gene_Symbol=KRT77 Keratin, type II cytoskeletal 1b
[IPI00003925](#) Tax_Id=9606 Gene_Symbol=PDHB Isoform 1 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial
[IPI00339269](#) Tax_Id=9606 Gene_Symbol=HSPA6 Heat shock 70 kDa protein 6
[IPI00023020](#) Tax_Id=9606 Gene_Symbol=SEMGL Isoform 1 of Semenogelin-1
[IPI00022430](#) Tax_Id=9606 Gene_Symbol=GAPDHS Glycerinaldehyde-3-phosphate dehydrogenase, testis-specific
[IPI00784154](#) Tax_Id=9606 Gene_Symbol=HSPD1 60 kDa heat shock protein, mitochondrial
[IPI00289614](#) Tax_Id=9606 Gene_Symbol=ACR Acrosin
[IPI00006510](#) Tax_Id=9606 Gene_Symbol=TUBB1 Tubulin beta-1 chain
[IPI00641681](#) Tax_Id=9606 Gene_Symbol=SCCPDH Saccharopine dehydrogenase
[IPI00329600](#) Tax_Id=9606 Gene_Symbol=SCCPDH Probable saccharopine dehydrogenase
[IPI00453473](#) Tax_Id=9606 Gene_Symbol=HIST1H4E;HIST1H4L;HIST1H4D;HIST1H4J;HIST1H4F;HIST2H4B;HIST1H4K;HIST1H4I;HIST1H4H;HIST1H4B;HIST1H4C;HIST2H4A;HIST1H4A;HIST4H4 Histone H4
[IPI00171611](#) Tax_Id=9606 Gene_Symbol=HIST2H3C;HIST2H3A;HIST2H3D Histone H3.2
[IPI00798360](#) Tax_Id=9606 Gene_Symbol=SARNP 18 kDa protein
[IPI00217966](#) Tax_Id=9606 Gene_Symbol=LDHA Isoform 1 of L-lactate dehydrogenase A chain
[IPI00877807](#) Tax_Id=9606 Gene_Symbol=- 21 kDa protein
[IPI00018246](#) Tax_Id=9606 Gene_Symbol=HK1 Isoform 1 of Hexokinase-1
[IPI00005721](#) Tax_Id=9606 Gene_Symbol=DEFA1;DEFA1B Neutrophil defensin 1
[IPI00010420](#) Tax_Id=9606 Gene_Symbol=SLC25A31 ADP/ATP translocase 4
[IPI00902754](#) Tax_Id=9606 Gene_Symbol=SDHA cDNA FLJ16373 fis, clone THYMU3000269, highly similar to Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial
[IPI00395769](#) Tax_Id=9606 Gene_Symbol=ATP5C1 Isoform Heart of ATP synthase subunit gamma, mitochondrial
[IPI00300567](#) Tax_Id=9606 Gene_Symbol=DCI Isoform 1 of 3,2-trans-enoyl-CoA isomerase, mitochondrial
[IPI00019329](#) Tax_Id=9606 Gene_Symbol=DYNLL1 Dynein light chain 1, cytoplasmic

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Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

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1. [IPI00007752](#) Mass: 50255 Score: 956 Queries matched: 81 emPAI: 2.14
 Tax_Id=9606 Gene_Symbol=TUBB2C Tubulin beta-2C chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3487	520.3000	1038.5854	1038.5862	-0.0008	0	45	0.011	1	R.YLTVAAVFR.G 3486 3495
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREYYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVFPFR.L 4339

2243	418.2000	1251.5782	1251.7088	-0.1306	1	8	1.3e+002	1	R.YLTVAAVFRGR.M
6513	660.8000	1319.5854	1318.6955	0.8899	0	68	5.3e-005	1	R.IMNTFVVPVSPK.V 6506 6507 6508 6510
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPRGLK.M
6594	664.8000	1327.5854	1327.6408	-0.0554	0	85	1e-006	1	R.INVYYNEATGGK.Y 6593 6595 6596 6597 6598 6611
7639	723.8000	1445.5854	1445.6820	-0.0966	0	(16)	7.7	1	K.EVDEQMLNVQNK.N
7739	731.8000	1461.5854	1461.6769	-0.0915	0	38	0.05	1	K.EVDEQMLNVQNK.N
8658	801.3000	1600.5854	1600.8131	-0.2276	0	77	4.9e-006	1	R.AVLVDLEPGTMDSVR.S 8662 8663 8672 8677
8748	809.3000	1616.5854	1616.8080	-0.2225	0	(45)	0.007	1	R.AVLVDLEPGTMDSVR.S 8749
9127	846.4000	1690.7854	1690.8600	-0.0746	0	92	1.7e-007	1	R.ALTVPPELTQQMFDAK.N 9117 9118 9120 9124 9125 9126 9128 9129 9135
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVWIPNNVK.T 9154 9156 9157 9158
9218	854.4000	1706.7854	1706.8549	-0.0695	0	(40)	0.026	1	R.ALTVPPELTQQMFDAK.N
9735	608.3000	1821.8782	1821.9156	-0.0374	0	33	0.12	1	R.EIVHLQAGQCGNQIGAK.F 9738
10277	652.6000	1954.7782	1954.8798	-0.1016	1	(0)	1.7e+002	5	R.MSMKEVDEQMLNVQNK.N
10278	652.7000	1955.0782	1954.8798	0.1984	1	6	47	5	R.MSMKEVDEQMLNVQNK.N
10288	653.6000	1957.7782	1957.9745	-0.1964	0	21	1.6	1	K.GHYTEGAELVDSVLDVVR.K 10290
6767	672.1000	2013.2782	2013.0353	0.2428	1	1	93	1	K.MSATFIGNSTAIQELFKR.I
10695	522.5000	2085.9709	2086.0695	-0.0986	1	14	7.7	1	K.GHYTEGAELVDSVLDVVR.K 10697 10701
7320	704.0000	2108.9782	2109.0571	-0.0790	1	75	1.3e-005	1	-.MREIVHLQAGQCGNQIGAK.F 10782 10783 10784 7321 10788 10789 10791 10792 10795 10796 10797 10800
10856	709.3000	2124.8782	2125.0521	-0.1739	1	(44)	0.0069	1	-.MREIVHLQAGQCGNQIGAK.F 10855 10857 10858
11920	913.7000	2738.0782	2737.2696	0.8086	1	5	29	2	R.ALTVPPELTQQMFDAKNMAACDPR.H

2. [IPI00220327](#) Mass: 66170 Score: 860 Queries matched: 58 emPAI: 1.90

Tax_Id=9606 Gene_Symbol=KRT1 Keratin, type II cytoskeletal 1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2227	416.7000	831.3854	831.4814	-0.0960	0	7	93	1	K.SISISVAR.G
2493	437.7000	873.3854	873.4920	-0.1065	0	11	38	1	R.SLVNLTGGSK.S
3053	487.3000	972.5854	972.5240	0.0615	0	37	0.13	1	K.IEISELNR.V 3052
3211	500.2000	998.3854	998.4379	-0.0524	0	22	2.1	1	K.DVDGAYMTK.V 3210
3422	517.3000	1032.5854	1032.5087	0.0767	0	34	0.17	1	R.TLLEGEESR.M 3424
4310	571.2000	1140.3854	1140.5121	-0.1267	0	26	1.2	1	R.DYQELMNTK.L 4329
4461	579.3000	1156.5854	1156.5070	0.0784	0	(4)	1.3e+002	5	R.DYQELMNTK.L
4658	590.3000	1178.5854	1178.5931	-0.0077	0	67	6.4e-005	1	K.YEELQITAGR.H
5490	633.3000	1264.5854	1264.6299	-0.0445	0	9	69	1	R.TNAENEFVTTIK.K
5633	639.4000	1276.7854	1276.7027	0.0828	0	89	4.1e-007	1	K.LALDLETATYR.T 5634 5635
6279	650.8000	1299.5854	1299.5224	0.0631	0	28	0.56	1	K.NMQDMVEDYR.N 6280
6305	651.8000	1301.5854	1301.7078	-0.1224	0	81	2.2e-006	1	R.SLDLDSIIAEVK.A 6326
6465	658.8000	1315.5854	1315.5173	0.0682	0	(17)	7.3	1	K.NMQDMVEDYR.N
6728	670.8000	1339.5854	1339.6619	-0.0765	1	66	7.7e-005	1	K.SKAEAESLYQSK.Y 6727 2617
6884	679.3000	1356.5854	1356.6885	-0.1030	0	30	0.35	1	K.LNDLEDALQAK.E 6897
7146	692.3000	1382.5854	1382.6830	-0.0976	0	67	6.4e-005	1	K.SLNQFASFDIK.V 7147 7149
7221	697.4000	1392.7854	1392.7249	0.0606	1	44	0.011	1	R.TNAENEFVTTIK.D 7214 7215 7217 7224
7838	738.3000	1474.5854	1474.7416	-0.1562	0	71	3.6e-005	1	K.WELLQQVDTSTR.T 7839
7843	738.4000	1474.7854	1474.7780	0.0075	0	38	0.05	1	R.FLEQQQVLQTK.W 7837
8640	800.3000	1598.5854	1598.8264	-0.2409	1	6	83	1	K.NKLNLEDALQAK.E
8941	829.4000	1656.7854	1656.7856	-0.0002	0	62	0.00023	1	R.SGGFSSGSAGIINYQR.R 8939
9460	883.3000	1764.5854	1764.7275	-0.1420	0	92	8.5e-008	1	R.FSSCGGGGSGAGGGFGR.S 9459 9461 9463 9464
4975	605.6000	1813.7782	1812.8867	0.8915	1	4	82	1	R.SGGFSSGSAGIINYQR.T
11227	762.7000	2285.0782	2285.1175	-0.0393	1	32	0.1	1	K.AEAEESLYQSKYEELQITAGR.H 11228
11436	795.3000	2382.8782	2382.9447	-0.0665	0	67	1.6e-005	1	R.GGGGGYSGSGSSYSGSGSGGGGGGR.G 11437
11724	856.0000	2564.9782	2564.1595	0.8186	0	38	0.012	1	R.MSGECAPNVSVSVTSHHTISGGGR.G 11722 11725 11726
11743	861.0000	2579.9782	2580.1545	-0.1763	0	(24)	0.27	1	R.MSGECAPNVSVSVTSHHTISGGGR.G 11744
12384	895.9000	3579.5709	3578.6577	0.9132	1	27	0.14	1	R.TLLEGEESRMSGECAPNVSVSVTSHHTISGGGR.G

3. [IPI00023598](#) Mass: 50010 Score: 814 Queries matched: 65 emPAI: 1.60

Tax_Id=9606 Gene_Symbol=TUBB4 Tubulin beta-4 chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
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3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3487	520.3000	1038.5854	1038.5862	-0.0008	0	45	0.011	1	R.YLTVAAVFR.G 3486 3495
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVFPFR.L 4339
2243	418.2000	1251.5782	1251.7088	-0.1306	1	8	1.3e+002	1	R.YLTVAAVFRGR.M
6513	660.8000	1319.5854	1318.6955	0.8899	0	68	5.3e-005	1	R.IMNTFVVVPSPK.V 6506 6507 6508 6510
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
8658	801.3000	1600.5854	1600.8131	-0.2276	0	77	4.9e-006	1	R.AVLVDLEPGTMDSVR.S 8662 8663 8672 8677
8748	809.3000	1616.5854	1616.8080	-0.2225	0	(45)	0.007	1	R.AVLVDLEPGTMDSVR.S 8749
9127	846.4000	1690.7854	1690.8600	-0.0746	0	92	1.7e-007	1	R.ALTVPQLTQMFDAK.N 9117 9118 9120 9124 9125 9126 9128 9129 9135
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVVEWIPNNVK.T 9154 9156 9157 9158
9218	854.4000	1706.7854	1706.8549	-0.0695	0	(40)	0.026	1	R.ALTVPQLTQMFDAK.N
9735	608.3000	1821.8782	1821.9156	-0.0374	0	33	0.12	1	R.EIVHLQAGQCGNQIGAK.F 9738
6767	672.1000	2013.2782	2013.0353	0.2428	1	1	93	1	K.MAATFIGNSTAIQELFKR.I
7129	691.0000	2069.9782	2070.0746	-0.0964	1	1	2.7e+002	3	K.GHYTEGAEVLDAVLVVRK.E
7320	704.0000	2108.9782	2109.0571	-0.0790	1	75	1.3e-005	1	-.MREIVHLQAGQCGNQIGAK.F 10782 10783 10784 7321 10788 10789 10791 10792 10795 10796 10797 10800
10856	709.3000	2124.8782	2125.0521	-0.1739	1	(44)	0.0069	1	-.MREIVHLQAGQCGNQIGAK.F 10855 10857 10858
11920	913.7000	2738.0782	2737.2696	0.8086	1	5	29	2	R.ALTVPQLTQMFDAKNMMAACDPR.H

4. [IPI00930130](#) Mass: 44916 Score: 736 Queries matched: 62 emPAI: 1.70
 Tax_Id=9606 Gene_Symbol=TUBB6 cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3487	520.3000	1038.5854	1038.5862	-0.0008	0	45	0.011	1	R.YLTVAAVFR.G 3486 3495
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREYYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVFPFR.L 4339
2243	418.2000	1251.5782	1251.7088	-0.1306	1	8	1.3e+002	1	R.YLTVAAVFRGR.M
6513	660.8000	1319.5854	1318.6955	0.8899	0	68	5.3e-005	1	R.IMNTFVVVPSPK.V 6506 6507 6508 6510
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
6594	664.8000	1327.5854	1327.6408	-0.0554	0	85	1e-006	1	R.INVYNEATGGK.Y 6593 6595 6596 6597 6598 6611
7639	723.8000	1445.5854	1445.6820	-0.0966	0	(16)	7.7	1	K.EVDEQMLNVQNK.N
7739	731.8000	1461.5854	1461.6769	-0.0915	0	38	0.05	1	K.EVDEQMLNVQNK.N
8658	801.3000	1600.5854	1600.8131	-0.2276	0	77	4.9e-006	1	R.AVLVDLEPGTMDSVR.S 8662 8663 8672 8677
8748	809.3000	1616.5854	1616.8080	-0.2225	0	(45)	0.007	1	R.AVLVDLEPGTMDSVR.S 8749
9127	846.4000	1690.7854	1690.8600	-0.0746	0	92	1.7e-007	1	R.ALTVPQLTQMFDAK.N 9117 9118 9120 9124 9125 9126 9128 9129 9135
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVVEWIPNNVK.T 9154 9156 9157 9158
9218	854.4000	1706.7854	1706.8549	-0.0695	0	(40)	0.026	1	R.ALTVPQLTQMFDAK.N
10277	652.6000	1954.7782	1954.8798	-0.1016	1	(0)	1.7e+002	5	R.MSMKEVDEQMLNVQNK.N
10278	652.7000	1955.0782	1954.8798	0.1984	1	6	47	5	R.MSMKEVDEQMLNVQNK.N
6767	672.1000	2013.2782	2013.0353	0.2428	1	1	93	1	K.MSATFIGNSTAIQELFKR.I
10804	704.7000	2111.0782	2110.0160	1.0622	1	26	0.48	1	-.MRENVHLQAGQCGNQIGAK.F 10800 10802
10857	532.5000	2125.9709	2126.0109	-0.0400	1	(20)	2	3	-.MRENVHLQAGQCGNQIGAK.F 10860
11920	913.7000	2738.0782	2737.2696	0.8086	1	5	29	2	R.ALTVPQLTQMFDAKNMMAACDPR.H

5. [IPI00013683](#) Mass: 50856 Score: 696 Queries matched: 59 emPAI: 1.26

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3386	514.3000	1026.5854	1025.5328	1.0526	0	11	44	1	K.VAVCDIPPR.G 3383
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214

4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVPPFR.L 4339
5990	641.8000	1281.5854	1281.7194	-0.1339	1	8	43	1	R.YLTVATVFRGR.M 6097
6513	660.8000	1319.5854	1318.6955	0.8899	0	68	5.3e-005	1	R.IMNTFSSVVPSPK.V 6506 6507 6508 6510
9127	846.4000	1690.7854	1690.8600	-0.0746	0	92	1.7e-007	1	R.ALTVPPELTQQMFDK.N 9117 9118 9120 9124 9125 9126 9128 9129 9135
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVWIPNNVK.V 9154 9156 9157 9158
9218	854.4000	1706.7854	1706.8549	-0.0695	0	(40)	0.026	1	R.ALTVPPELTQQMFDK.N
9735	608.3000	1821.8782	1821.9156	-0.0374	0	33	0.12	1	R.EIVHIIQAGQCGNQIGAK.F 9738
10288	653.6000	1957.7782	1957.9745	-0.1964	0	21	1.6	1	K.GHYTEGAELVDSVLDVVR.K 10290
10695	522.5000	2085.9709	2086.0695	-0.0986	1	14	7.7	1	K.GHYTEGAELVDSVLDVVRK.E 10697 10701
7320	704.0000	2108.9782	2109.0571	-0.0790	1	75	1.3e-005	1	- .MREIVHIQAGQCGNQIGAK.F 10782 10783 10784 7321 10788 10789 10791 10792 10795 10796 10797 10800
10856	709.3000	2124.8782	2125.0521	-0.1739	1	(44)	0.0069	1	- .MREIVHIQAGQCGNQIGAK.F 10855 10857 10858
11920	913.7000	2738.0782	2737.2696	0.8086	1	5	29	2	R.ALTVPPELTQQMFDKNNMAACDPR.H

6. [IPI00410402](#) Mass: 50568 Score: 595 Queries matched: 47 emPAI: 1.13

Tax_Id=9606 Gene_Symbol=TUBA3E Tubulin alpha-3E chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2561	444.2000	886.3854	886.4259	-0.0404	0	34	0.16	1	K.FDLMYAK.W 2559 2563
2566	444.7000	887.3854	887.4600	-0.0745	0	24	1.7	1	R.EDLALEK.D 2567 2581 2590
3306	508.2000	1014.3854	1014.5709	-0.1855	0	82	2.6e-006	1	K.DVNAAIATIK.T 3307 3308 3309 3311 3312
5506	634.2000	1266.3854	1266.5018	-0.1163	0	37	0.05	1	K.YMACCMYLR.G 5505
7357	705.9000	1409.7854	1409.7667	0.0188	0	1	2.5e+002	7	R.QLFHPEQLITGK.E
8637	799.9000	1597.7854	1597.7599	0.0255	0	68	4.1e-005	1	R.TIQFVDCPTGFK.V 8635 8638
9102	844.4000	1686.7854	1686.8829	-0.0974	0	82	1.4e-006	1	R.AVFVDELTVPVDEVR.T 9099 9100 9101 9103 9107
4582	586.4000	1756.1782	1755.9559	0.2222	0	41	0.039	1	R.IHFPLATYAPVISAEK.A 9413 9414 9415 9416 9417 9420 4591
9749	913.4000	1824.7854	1823.9782	0.8073	0	46	0.0053	1	K.VGINYPPTVPPGDLAK.V 9742 9748
9884	621.6000	1861.7782	1861.8347	-0.0566	1	13	11	1	K.YMACCMYLRGDDVVPK.D 9885
9895	933.4000	1864.7854	1863.8971	0.8883	0	63	0.00011	1	R.AVCMLSNNTAIAEAWAR.L 9889
6714	669.9000	2006.6782	2006.8858	-0.2076	0	7	80	1	K.TIGGGDDSFNTFFSETGAGK.H
11153	563.0000	2247.9709	2247.1252	0.8457	1	2	1.2e+002	2	K.VQRAVCMLSNNTAIAEAWAR.L
11189	756.4000	2266.1782	2265.1641	1.0140	1	15	5.2	1	R.AVFVDELTVPVDEVRTGTYSR.Q 11188
9784	917.7000	2750.0782	2749.2840	0.7942	0	(5)	30	1	K.AYHEQLSVAEITNACFEPANQMVK.C
11957	922.7000	2765.0782	2765.2789	-0.2007	0	53	0.00037	1	K.AYHEQLSVAEITNACFEPANQMVK.C 11956

7. [IPI00179709](#) Mass: 50612 Score: 595 Queries matched: 48 emPAI: 1.13

Tax_Id=9606 Gene_Symbol=TUBA3D;TUBA3C Isoform 1 of Tubulin alpha-3C/D chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2561	444.2000	886.3854	886.4259	-0.0404	0	34	0.16	1	K.FDLMYAK.R 2559 2563
2566	444.7000	887.3854	887.4600	-0.0745	0	24	1.7	1	R.EDLALEK.D 2567 2581 2590
3306	508.2000	1014.3854	1014.5709	-0.1855	0	82	2.6e-006	1	K.DVNAAIATIK.T 3307 3308 3309 3311 3312
5506	634.2000	1266.3854	1266.5018	-0.1163	0	37	0.05	1	K.YMACCMYLR.G 5505
7357	705.9000	1409.7854	1409.7667	0.0188	0	1	2.5e+002	7	R.QLFHPEQLITGK.E
8637	799.9000	1597.7854	1597.7599	0.0255	0	68	4.1e-005	1	R.TIQFVDCPTGFK.V 8635 8638
9102	844.4000	1686.7854	1686.8829	-0.0974	0	82	1.4e-006	1	R.AVFVDELTVPVDEVR.T 9099 9100 9101 9103 9107
4582	586.4000	1756.1782	1755.9559	0.2222	0	41	0.039	1	R.IHFPLATYAPVISAEK.A 9413 9414 9415 9416 9417 9420 4591
9749	913.4000	1824.7854	1823.9782	0.8073	0	46	0.0053	1	K.VGINYPPTVPPGDLAK.V 9742 9748
9884	621.6000	1861.7782	1861.8347	-0.0566	1	13	11	1	K.YMACCMYLRGDDVVPK.D 9885
9895	933.4000	1864.7854	1863.8971	0.8883	0	63	0.00011	1	R.AVCMLSNNTAIAEAWAR.L 9889
6714	669.9000	2006.6782	2006.8858	-0.2076	0	7	80	1	K.TIGGGDDSFNTFFSETGAGK.H
11147	750.0000	2246.9782	2246.8862	0.0919	0	1	1.4e+002	8	K.DYEEVGVDSVEAEAEEGEY.-
11153	563.0000	2247.9709	2247.1252	0.8457	1	2	1.2e+002	2	K.VQRAVCMLSNNTAIAEAWAR.L
11189	756.4000	2266.1782	2265.1641	1.0140	1	15	5.2	1	R.AVFVDELTVPVDEVRTGTYSR.Q 11188
9784	917.7000	2750.0782	2749.2840	0.7942	0	(5)	30	1	K.AYHEQLSVAEITNACFEPANQMVK.C
11957	922.7000	2765.0782	2765.2789	-0.2007	0	53	0.00037	1	K.AYHEQLSVAEITNACFEPANQMVK.C 11956

Proteins matching the same set of peptides:

[IPI00915791](#) Mass: 46605 Score: 595 Queries matched: 48
Tax_Id=9606 Gene_Symbol=TUBA3D;TUBA3C 46 kDa protein

8. [IPI00180675](#) Mass: 50788 Score: 487 Queries matched: 35 emPAI: 0.87

Tax_Id=9606 Gene_Symbol=TUBA1A Tubulin alpha-1A chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2561	444.2000	886.3854	886.4259	-0.0404	0	34	0.16	1	K.FDLMYAK.R 2559 2563
3306	508.2000	1014.3854	1014.5709	-0.1855	0	82	2.6e-006	1	K.DVNAAIATIK.T 3307 3308 3309 3311 3312
7357	705.9000	1409.7854	1409.7667	0.0188	0	1	2.5e+002	7	R.QLFHPEQLITGK.E
8637	799.9000	1597.7854	1597.7599	0.0255	0	68	4.1e-005	1	R.TIQFVDWCPTGFK.V 8635 8638
9188	851.4000	1700.7854	1700.8985	-0.1131	0	83	1.4e-006	1	R.AVFVDLEPTVIDEVR.T 9187 9189 9190
4582	586.4000	1756.1782	1755.9559	0.2222	0	41	0.039	1	R.IHFPLATYAPVISAEK.A 9413 9414 9415 9416 9417 9420 4591
9749	913.4000	1824.7854	1823.9782	0.8073	0	46	0.0053	1	K.VGINYPPTVPPGGDLAK.V 9742 9748
9895	933.4000	1864.7854	1863.8971	0.8883	0	63	0.00011	1	R.AVCMLSNTTAIAEAWAR.L 9889
6714	669.9000	2006.6782	2006.8858	-0.2076	0	7	80	1	K.TIGGGDDSPNTFFSETGAGK.H
11153	563.0000	2247.9709	2247.1252	0.8457	1	2	1.2e+002	2	K.VQRAVCMLSNTTAIAEAWAR.L
9784	917.7000	2750.0782	2749.2840	0.7942	0	(5)	30	1	K.AYHEQLSVAEITNACFEPANQMK.C
11957	922.7000	2765.0782	2765.2789	-0.2007	0	53	0.00037	1	K.AYHEQLSVAEITNACFEPANQMK.C 11956

9. [IPI00019359](#) Mass: 62255 Score: 378 Queries matched: 39 emPAI: 1.28

Tax_Id=9606 Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2121	405.2000	808.3854	808.4330	-0.0476	0	9	42	1	R.LASYLDK.V
2640	449.2000	896.3854	896.4062	-0.0208	0	35	0.1	1	R.MTLDDFR.I 2638
2711	457.2000	912.3854	912.4011	-0.0157	0	(29)	0.38	1	R.MTLDDFR.I 2713
3658	530.8000	1059.5854	1059.5560	0.0294	0	33	0.18	1	K.TLLDIDNTR.M 3659
3686	533.2000	1064.3854	1064.4920	-0.1066	0	49	0.0044	1	K.STMQELNSR.L 3689
3749	537.7000	1073.3854	1073.5142	-0.1287	0	28	0.69	1	R.QFSSSYLSR.S
4125	561.3000	1120.5854	1120.5764	0.0090	0	24	1.5	1	R.QEYBQLIAK.N 4124
5173	616.8000	1231.5854	1231.5906	-0.0051	0	61	0.00026	1	R.SGGGGGGGLSGGSIR.S 5174
5195	618.2000	1234.3854	1234.5215	-0.1360	0	61	0.00025	1	R.FSSSSGYGGSSR.V 5194
6379	436.6000	1306.7782	1306.6703	0.1079	1	42	0.02	1	R.IKFEMEQLNR.Q 6374 6376
6545	662.3000	1322.5854	1322.6652	-0.0798	1	(6)	65	1	R.IKFEMEQLNR.Q
8576	793.8000	1585.5854	1585.7583	-0.1729	0	43	0.013	1	K.VQALEEANNLENK.I 8577
9216	854.3000	1706.5854	1706.7431	-0.1577	1	10	22	3	R.FSSSSGYGGSSRVCGR.G
9602	896.3000	1790.5854	1790.7205	-0.1350	0	76	3.1e-006	1	R.GSGSGSYGGSGGGYGGSGSR.G
9795	613.3000	1836.8782	1836.9581	-0.0799	0	40	0.027	1	R.HGVQELEIELQSLSK.K
9856	618.0000	1850.9782	1850.9196	0.0586	1	10	23	1	K.TLNDMRQEYQLIAK.N 9863 9864
10307	656.0000	1964.9782	1965.0531	-0.0749	1	6	46	1	R.HGVQELEIELQSLSK.K
10728	699.0000	2093.9782	2094.0303	-0.0521	0	9	25	1	R.QEIECQEQEYSLLSIK.M
11025	733.6000	2197.7782	2197.9373	-0.1592	1	45	0.0025	1	R.FSSSGGGGGGRFSSSSGYGGSSR.V 11031
11419	793.0000	2375.9782	2376.1808	-0.2026	1	23	0.73	1	R.LASYLDKQVQALEEANNLENK.I 8560 11418
11631	837.3000	2508.8782	2509.1245	-0.2463	0	54	0.00018	1	K.EIETYHNLLEGGQEDFESSGAGK.I 11632
11901	902.3000	2703.8782	2704.1539	-0.2757	0	39	0.0015	1	R.GGGSGFGYSYGGSGGGFSASSLGGGFGGSR.G 11902

10. [IPI00013475](#) Mass: 50274 Score: 374 Queries matched: 47 emPAI: 0.89

Tax_Id=9606 Gene_Symbol=TUBB2A Tubulin beta-2A chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREEYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVPPPR.L 4339
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
7639	723.8000	1445.5854	1445.6820	-0.0966	0	(16)	7.7	1	K.EVDEQMLNVQNK.N

7739	731.8000	1461.5854	1461.6769	-0.0915	0	38	0.05	1	K.EVDEQMLNVQNK.N
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVVEWIPNNVK.T 9154 9156 9157 9158
9218	854.4000	1706.7854	1706.8549	-0.0695	0	17	5.1	2	R.ALTVPELTQQMPFDSK.N
9735	608.3000	1821.8782	1821.9156	-0.0374	0	33	0.12	1	R.EIVHIQAGQCGNQIGAK.F 9738
10277	652.6000	1954.7782	1954.8798	-0.1016	1	(0)	1.7e+002	5	R.MSMKEVDEQMLNVQNK.N
10278	652.7000	1955.0782	1954.8798	0.1984	1	6	47	5	R.MSMKEVDEQMLNVQNK.N
10288	653.6000	1957.7782	1957.9745	-0.1964	0	21	1.6	1	K.GHYTEGAEVLVDSVLDVVR.K 10290
6767	672.1000	2013.2782	2013.0353	0.2428	1	1	93	1	K.MSATFIGNSTAIQELFKR.I
10695	522.5000	2085.9709	2086.0695	-0.0986	1	14	7.7	1	K.GHYTEGAEVLVDSVLDVVRK.E 10697 10701
7320	704.0000	2108.9782	2109.0571	-0.0790	1	75	1.3e-005	1	-.MREIVHIQAGQCGNQIGAK.F 10782 10783 10784 7321 10788 10789 10791 10792 10795 10796 10797 10800
10856	709.3000	2124.8782	2125.0521	-0.1739	1	(44)	0.0069	1	-.MREIVHIQAGQCGNQIGAK.F 10855 10857 10858

Proteins matching the same set of peptides:

[IPI00031370](#) Mass: 50377 Score: 374 Queries matched: 47

Tax_Id=9606 Gene_Symbol=TUBB2B Tubulin beta-2B chain

11. [IPI00908770](#) Mass: 36239 Score: 366 Queries matched: 39 emPAI: 1.20
Tax_Id=9606 Gene_Symbol=TUBB cDNA FLJ53063, highly similar to Tubulin beta-7 chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3487	520.3000	1038.5854	1038.5862	-0.0008	0	45	0.011	1	R.YLTVAAVFR.G 3486 3495
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPQQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVPPFR.L 4339
2243	418.2000	1251.5782	1251.7088	-0.1306	1	8	1.3e+002	1	R.YLTVAAVFRGR.M
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
7639	723.8000	1445.5854	1445.6820	-0.0966	0	(16)	7.7	1	K.EVDEQMLNVQNK.S
7739	731.8000	1461.5854	1461.6769	-0.0915	0	38	0.05	1	K.EVDEQMLNVQNK.S
9735	608.3000	1821.8782	1821.9156	-0.0374	0	33	0.12	1	R.EIVHIQAGQCGNQIGAK.F 9738
10277	652.6000	1954.7782	1954.8798	-0.1016	1	(0)	1.7e+002	5	R.MSMKEVDEQMLNVQNK.S
10278	652.7000	1955.0782	1954.8798	0.1984	1	6	47	5	R.MSMKEVDEQMLNVQNK.S
7320	704.0000	2108.9782	2109.0571	-0.0790	1	75	1.3e-005	1	-.MREIVHIQAGQCGNQIGAK.F 10782 10783 10784 7321 10788 10789 10791 10792 10795 10796 10797 10800
10856	709.3000	2124.8782	2125.0521	-0.1739	1	(44)	0.0069	1	-.MREIVHIQAGQCGNQIGAK.F 10855 10857 10858
11920	913.7000	2738.0782	2737.2874	0.7908	1	10	8.5	1	R.ALTVPELTQQVFDKNNMMAACDPR.H

12. [IPI00646779](#) Mass: 50514 Score: 358 Queries matched: 35 emPAI: 0.66
Tax_Id=9606 Gene_Symbol=TUBB6 TUBB6 protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3386	514.3000	1026.5854	1025.5328	1.0526	0	11	44	1	K.VAVCDIPPR.G 3383
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREYYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPQQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVPPFR.L 4339
9127	846.4000	1690.7854	1690.8600	-0.0746	0	92	1.7e-007	1	R.ALTVPELTQQMPDAK.N 9117 9118 9120 9124 9125 9126 9128 9129 9135
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVVEWIPNNVK.V 9154 9156 9157 9158
9218	854.4000	1706.7854	1706.8549	-0.0695	0	(40)	0.026	1	R.ALTVPELTQQMPDAK.N
10288	653.6000	1957.7782	1957.9745	-0.1964	0	21	1.6	1	K.GHYTEGAEVLVDSVLDVVR.K 10290
6767	672.1000	2013.2782	2013.0353	0.2428	1	1	93	1	K.MASTFIGNSTAIQELFKR.I
10695	522.5000	2085.9709	2086.0695	-0.0986	1	14	7.7	1	K.GHYTEGAEVLVDSVLDVVRK.E 10697 10701
11920	913.7000	2738.0782	2737.2696	0.8086	1	5	29	2	R.ALTVPELTQQMPDAKNNMMAACDPR.H

13. [IPI00009865](#) Mass: 59020 Score: 354 Queries matched: 41 emPAI: 0.92
Tax_Id=9606 Gene_Symbol=KRT10 Keratin, type I cytoskeletal 10

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2102	404.2000	806.3854	806.3923	-0.0068	0	35	0.13	1	R.LAADDFR.L 2101
2121	405.2000	808.3854	808.4330	-0.0476	0	9		42	R.LASYLDK.V
3175	497.2000	992.3854	992.4927	-0.1072	0	17	7.8	1	K.YENEVALR.Q 3178
3417	516.8000	1031.5854	1030.5910	0.9944	0	58	0.00057	1	R.VLDELTLTK.A 3411
4018	555.2000	1108.3854	1108.4825	-0.0971	0	34	0.13	1	K.DAEAWFNEK.S 4019 4027
4529	583.3000	1164.5854	1164.5775	0.0080	0	38	0.057	1	R.LENEIQTYR.S
5189	617.9000	1233.7854	1233.6717	0.1138	1	22	1.9	1	R.LKYENEVALR.Q 5190 5204
6281	650.8000	1299.5854	1299.5877	-0.0023	1	27	0.57	1	K.NHEEMKDLR.N 6277 6278 6283
6488	659.3000	1316.5854	1315.5826	1.0028	1	(1)	2.9e+002	2	K.NHEEMKDLR.N
6970	683.3000	1364.5854	1364.6320	-0.0466	0	57	0.00069	1	R.SQYEQLAEQNR.K
7132	691.3000	1380.5854	1380.6408	-0.0554	0	73	1.6e-005	1	R.ALEESNYELEGK.I 7133
7194	695.8000	1389.5854	1389.6736	-0.0881	0	23	1.7	1	K.QSLEASLAETEGR.Y
2967	478.9000	1433.6782	1433.7626	-0.0845	1	8	74	2	K.IRLENEIQTYR.S
7988	747.3000	1492.5854	1492.7270	-0.1415	1	18	5	1	R.SQYEQLAEQNRK.D 7987 7992
9215	854.3000	1706.5854	1706.7649	-0.1795	0	109	2.3e-009	1	K.GSLGGGFSGGFSGGSFGR.G 9216
9645	899.4000	1796.7854	1796.0043	0.7811	0	47	0.0043	1	R.NVQALEIQLQSQALK.Q 9641
11048	737.3000	2208.8782	2209.0400	-0.1618	1	0	1.5e+002	2	R.ISSKSLGGGFSGGFSGGSFGR.G
11337	781.6000	2341.7782	2341.9771	-0.1990	0	41	0.0029	1	R.GSSGGCFGGSSGGYGLGGFSGGSFGR.G 11338 11339 11343
12029	958.4000	2872.1782	2871.3855	0.7927	0	28	0.14	1	R.NVSTGDNVEMNAAPGVDLTQLLNMR.S 10148 12030
10186	963.8000	2888.3782	2887.3804	0.9978	0	(0)	1.5e+002	2	R.NVSTGDNVEMNAAPGVDLTQLLNMR.S
12051	968.7000	2903.0782	2903.3753	-0.2971	0	(22)	0.27	1	R.NVSTGDNVEMNAAPGVDLTQLLNMR.S

14. [IPI00303476](#) Mass: 56525 Score: 330 Queries matched: 34 emPAI: 0.57

Tax_Id=9606 Gene_Symbol=ATP5B ATP synthase subunit beta, mitochondrial

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3836	544.2000	1086.3854	1085.4989	0.8866	1	2	2.5e+002	7	K.ADKLAEHSS.-
3856	545.2000	1088.3854	1087.6277	0.7577	0	40	0.038	1	K.VVDLLAPYAK.G
5444	631.8000	1261.5854	1261.6336	-0.0482	0	56	0.0008	1	R.TIAMDGTGLVLR.G 5443 5445
5649	639.8000	1277.5854	1277.6286	-0.0431	0	(20)	3.3	1	R.TIAMDGTGLVLR.G 5681
8668	801.4000	1600.7854	1600.8031	-0.0177	0	49	0.0029	1	K.VALVYQMNPPGAR.A 8658 8662 8665 8666
8749	809.4000	1616.7854	1616.7981	-0.0126	0	(11)	21	2	K.VALVYQMNPPGAR.A 8748
8899	551.0000	1649.9782	1649.9101	0.0681	0	(39)	0.034	1	R.LVLEVAQHLGESTVR.T 8900 8901 8902
9718	606.0000	1814.9782	1814.8621	0.1161	0	11	18	2	R.IMDPNIVGSEHYDVAR.G 9716 9719 9720
5680	640.3000	1917.8782	1918.0888	-0.2106	1	38	0.095	1	K.VLDSGAPIKIPVGPETLGR.I 10159 10160
10369	994.4000	1986.7854	1987.0262	-0.2408	0	75	5.6e-006	1	R.AIAELGIYPAVDPLDSTSR.I 10370 10371 10372 10373 10374
10671	693.0000	2075.9782	2075.9833	-0.0052	0	1	1.7e+002	3	R.EGNDLYHEMIESGVINLK.D
8731	808.0000	2420.9782	2420.2733	0.7048	1	3	2.2e+002	5	K.IPVGPETLGRIMNVIGEPIDER.G
12020	573.1000	2860.4636	2860.4905	-0.0269	1	0	1.2e+002	1	K.TVLIMELINNVAKAHGGYSVFAVGGER.T

15. [IPI00440493](#) Mass: 59828 Score: 317 Queries matched: 26 emPAI: 0.53

Tax_Id=9606 Gene_Symbol=ATP5A1 ATP synthase subunit alpha, mitochondrial

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2138	408.3000	814.5854	814.4548	0.1306	0	8	72	1	R.ELIIGDR.Q 2139
3215	500.8000	999.5854	999.5713	0.0142	0	41	0.03	1	R.VLSIGDGIAR.V 3220
3375	513.8000	1025.5854	1025.5869	-0.0015	0	41	0.024	1	K.AVDSLVIPIGR.G 3374
1600	369.9000	1106.6782	1105.5880	1.0902	0	2	2.6e+002	4	R.NALGSSFIAAR.N
6463	658.8000	1315.5854	1315.7347	-0.1493	0	36	0.086	1	K.TSIAIDTIINQK.R 6464
7585	480.3000	1437.8782	1437.8416	0.0366	0	42	0.019	1	K.GIRPAINVGLSVSR.V 7586
7698	729.0000	1455.9854	1454.7955	1.1899	1	0	3.6e+002	4	K.KLYCIYVAIGQK.R
7814	491.6000	1471.7782	1471.8358	-0.0576	1	15	8.5	1	K.TSIAIDTIINQK.R.F
7918	742.9000	1483.7854	1482.8017	0.9838	1	1	2.2e+002	7	K.LYCIYVAIGQK.R.S
8364	518.6000	1552.7782	1552.7310	0.0471	0	12	19	1	R.EAYPGDVVFLHSR.L 8363 3462
8503	788.3000	1574.5854	1574.7788	-0.1933	0	115	8.9e-010	1	R.ILGADTSVDLEETGR.V 8502 8508
8780	812.9000	1623.7854	1623.8832	-0.0977	0	18	4.1	1	R.TGAIVDVPVGEELLGR.V
8994	834.4000	1666.7854	1666.7872	-0.0018	0	83	1.2e-006	1	R.NVQAEEMVEFSSGLK.G 8993 8998

[8836](#) 820.4000 2458.1782 2457.2937 0.8844 1 1 3.4e+002 5 K.GMSLNLEPDPNVGVVFGNDKLIK.E
[11704](#) 853.4000 2557.1782 2556.3395 0.8387 1 26 0.42 1 R.ILGADTSVDLEETGRVLSIGDGIAR.V

16. [IPI00745872](#) Mass: 71317 Score: 290 Queries matched: 28 emPAI: 0.25

Tax_Id=9606 Gene_Symbol=ALB Isoform 1 of Serum albumin

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2806	464.2000	926.3854	926.4861	-0.1007	0	20	3.2	1	K.YLYEIR.R
3290	507.3000	1012.5854	1012.5917	-0.0062	0	64	0.00014	1	K.LVAASQAALGL.-
4282	569.7000	1137.3854	1137.4907	-0.1052	0	28	0.47	1	K.CCTESLVNR.R 4283
7611	722.3000	1442.5854	1442.6347	-0.0493	0	44	0.011	1	K.YICENQDSISSK.L 7610 7612
8095	756.4000	1510.7854	1510.8355	-0.0501	0	35	0.13	1	K.VPQVSTPTLVEVSR.N 8094
8840	547.3000	1638.8782	1638.9305	-0.0523	1	55	0.0007	1	K.KVPQVSTPTLVEVSR.N 3896 3897 3898 8838 8839 8841 8842 8843 8844 8845 8846 8847 8848 8849 8850 8851 3905
8518	789.3000	2364.8782	2364.0218	0.8564	1	1	2.8e+002	3	K.LCTVATLRETYGEMADCCAK.Q

17. [IPI00953417](#) Mass: 27533 Score: 288 Queries matched: 33 emPAI: 0.99

Tax_Id=9606 Gene_Symbol=TUBB cDNA FLJ53012, highly similar to Tubulin beta-7 chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVWIPNNVK.T 9154 9156 9157 9158
4272	569.0000	1703.9782	1702.8196	1.1586	1	3	1.3e+002	2	R.KEEVDEQMLNVQNK.N 4274
9735	608.3000	1821.8782	1821.9156	-0.0374	0	33	0.12	1	R.EIVHIQAGQCGNQIGAK.F 9738
10288	653.6000	1957.7782	1957.9745	-0.1964	0	21	1.6	1	K.GHYTEGAELVDSVLDVVR.K 10290
10695	522.5000	2085.9709	2086.0695	-0.0986	1	14	7.7	1	K.GHYTEGAELVDSVLDVVRK.E 10697 10701
7320	704.0000	2108.9782	2109.0571	-0.0790	1	75	1.3e-005	1	-.MREIVHIQAGQCGNQIGAK.F 10782 10783 10784 7321 10788 10789 10791 10792 10795 10796 10797 10800
10856	709.3000	2124.8782	2125.0521	-0.1739	1	(44)	0.0069	1	-.MREIVHIQAGQCGNQIGAK.F 10855 10857 10858

18. [IPI00645452](#) Mass: 48135 Score: 284 Queries matched: 36 emPAI: 0.70

Tax_Id=9606 Gene_Symbol=TUBB Tubulin, beta

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3487	520.3000	1038.5854	1038.5862	-0.0008	0	45	0.011	1	R.YLTVAAVFR.G 3486 3495
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREYYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVFPFR.L 4339
2243	418.2000	1251.5782	1251.7088	-0.1306	1	8	1.3e+002	1	R.YLTVAAVFRGR.M
6513	660.8000	1319.5854	1318.6955	0.8899	0	68	5.3e-005	1	R.IMNTFSVVPSPK.V 6506 6507 6508 6510
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
7639	723.8000	1445.5854	1445.6820	-0.0966	0	(16)	7.7	1	K.EVDEQMLNVQNK.N
7739	731.8000	1461.5854	1461.6769	-0.0915	0	38	0.05	1	K.EVDEQMLNVQNK.N
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVWIPNNVK.T 9154 9156 9157 9158
10277	652.6000	1954.7782	1954.8798	-0.1016	1	(0)	1.7e+002	5	R.MSMKEVDEQMLNVQNK.N
10278	652.7000	1955.0782	1954.8798	0.1984	1	6	47	5	R.MSMKEVDEQMLNVQNK.N
10288	653.6000	1957.7782	1957.9745	-0.1964	0	21	1.6	1	K.GHYTEGAELVDSVLDVVR.K 10290
10695	522.5000	2085.9709	2086.0695	-0.0986	1	14	7.7	1	K.GHYTEGAELVDSVLDVVRK.E 10697 10701
11920	913.7000	2738.0782	2737.2874	0.7908	1	10	8.5	1	R.ALTVPELTQQVFDKNNMMAACDPR.H

Proteins matching the same set of peptides:

[IPI00647896](#) Mass: 42114 Score: 284 Queries matched: 36

Tax_Id=9606 Gene_Symbol=TUBB Tubulin, beta

19. [IPI00909140](#) Mass: 52414 Score: 282 Queries matched: 32 emPAI: 0.53

Tax_Id=9606 Gene_Symbol=TUBB cDNA FLJ56903, highly similar to Tubulin beta-7 chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3487	520.3000	1038.5854	1038.5862	-0.0008	0	45	0.011	1	R.YLTVAAVFR.G 3486 3495
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREEYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVFPFR.L 4339
2243	418.2000	1251.5782	1251.7088	-0.1306	1	8	1.3e+002	1	R.YLTVAAVFRGR.M
6513	660.8000	1319.5854	1318.6955	0.8899	0	68	5.3e-005	1	R.IMNTFSVVPSPK.V 6506 6507 6508 6510
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
7639	723.8000	1445.5854	1445.6820	-0.0966	0	(16)	7.7	1	K.EVDEQMLNVQNK.N
7739	731.8000	1461.5854	1461.6769	-0.0915	0	38	0.05	1	K.EVDEQMLNVQNK.N
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVWIPNNVK.T 9154 9156 9157 9158
10277	652.6000	1954.7782	1954.8798	-0.1016	1	(0)	1.7e+002	5	R.MSMKEVDEQMLNVQNK.N
10278	652.7000	1955.0782	1954.8798	0.1984	1	6	47	5	R.MSMKEVDEQMLNVQNK.N
8130	759.1000	2274.2782	2274.1757	0.1025	1	2	1.2e+002	1	R.DHPGQSETLPHATFLQKIK.F
11920	913.7000	2738.0782	2737.2874	0.7908	1	10	8.5	1	R.ALTVPPELTQQVFDKNNMMAACDPR.H

20. [IPI00290854](#) Mass: 95433 Score: 269 Queries matched: 15 emPAI: 0.14

Tax_Id=9606 Gene_Symbol=AKAP3 A-kinase anchor protein 3

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3951	551.3000	1100.5854	1100.6376	-0.0521	0	69	4.3e-005	1	R.LTNLVIAMAR.K 3952 3954
4874	600.8000	1199.5854	1199.6146	-0.0292	0	26	0.82	1	R.VSGSSQSPPNLK.Y
8086	504.3000	1509.8782	1509.8085	0.0696	1	9	32	1	R.KLCERPLASSPPR.L
8809	818.3000	1634.5854	1634.7934	-0.2079	0	52	0.0014	1	K.IASELVNETVSACSR.N 3868 8813
9224	854.9000	1707.7854	1707.8203	-0.0348	0	77	5e-006	1	R.LYEDDETPGALSGLTK.M 9230
9244	429.2000	1712.7709	1712.8113	-0.0404	1	4	86	3	K.AESYSLISMKGMDPK.N
9500	591.9000	1772.6782	1772.8594	-0.1812	0	20	2.4	1	K.SLGFQHAAPFAPNTQR.K 4705
10265	651.9000	1952.6782	1952.8382	-0.1600	1	13	5.9	1	K.SCDASLAEELGDDKSGDASR.L
9781	917.1000	2748.2782	2747.2749	1.0033	0	1	2.1e+002	1	R.SFVEAAGTTNFPANEPVPADESCLK.S

21. [IPI00646909](#) Mass: 50746 Score: 218 Queries matched: 22 emPAI: 0.46

Tax_Id=9606 Gene_Symbol=TUBA8 Tubulin alpha-8 chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2561	444.2000	886.3854	886.4259	-0.0404	0	34	0.16	1	K.FDLMYAK.R 2559 2563
2566	444.7000	887.3854	887.4600	-0.0745	0	24	1.7	1	R.EDLAALEK.D 2567 2581 2590
5506	634.2000	1266.3854	1266.5018	-0.1163	0	37	0.05	1	K.YMACCMLYR.G 5505
7357	705.9000	1409.7854	1409.7667	0.0188	0	1	2.5e+002	7	R.QLFHPQLITGK.E
8637	799.9000	1597.7854	1597.7599	0.0255	0	68	4.1e-005	1	R.TIQFVWCPGTPK.V 8635 8638
9188	851.4000	1700.7854	1700.8655	-0.0800	0	6	62	7	R.AVMIDLEPTVVDEV.R.A
9749	913.4000	1824.7854	1823.9782	0.8073	0	46	0.0053	1	K.VGINYQPPTVPPGGDLAK.V 9742 9748
9884	621.6000	1861.7782	1861.8347	-0.0566	1	13	11	1	K.YMACCMLYR.GDVPVK.D 9885
9895	933.4000	1864.7854	1863.8971	0.8883	0	63	0.00011	1	R.AVCMLSNTTAAIAEAWAR.L 9889
11153	563.0000	2247.9709	2247.1252	0.8457	1	2	1.2e+002	2	K.VQRAVCMLSNTTAAIAEAWAR.L

Proteins matching the same set of peptides:

[IPI00791613](#) Mass: 52750 Score: 218 Queries matched: 22

Tax_Id=9606 Gene_Symbol=TUBA8 Uncharacterized protein

[IPI00952875](#) Mass: 54619 Score: 218 Queries matched: 22

Tax_Id=9606 Gene_Symbol=TUBA8 Putative uncharacterized protein DKFZp686L04275 (Fragment)

22. [IPI00021304](#) Mass: 66110 Score: 200 Queries matched: 23 emPAI: 0.62

Tax_Id=9606 Gene_Symbol=KRT2 Keratin, type II cytoskeletal 2 epidermal

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2223	416.3000	830.5854	830.4862	0.0993	0	33	0.23	1	R.SLVGLGGTK.S 2224

3053	487.3000	972.5854	972.5240	0.0615	0	37	0.13	1	K.IEISELNR.V 3052
3243	503.3000	1004.5854	1004.4597	0.1258	0	29	0.46	1	K.LLEGEECR.M 3242
4002	554.3000	1106.5854	1106.5356	0.0498	0	46	0.0089	1	K.AQYEEIAQR.S 4000
4228	566.2000	1130.3854	1130.5026	-0.1172	0	38	0.049	1	R.STSSFSCLSR.H 4229 4231
6155	429.8000	1286.3782	1286.6037	-0.2256	1	18	2.9	1	R.RSTSSFSCLSR.H
6516	660.8000	1319.5854	1319.5756	0.0098	0	1	2.8e+002	3	R.HGGGGGGFSGGFGSR.S
6610	665.3000	1328.5854	1328.7187	-0.1333	0	88	5.4e-007	1	R.NLDLDSIIAEVK.A 6609
7723	730.9000	1459.7854	1459.7922	-0.0068	0	30	0.32	1	K.VDLLNQETIEFLK.V 7734
7843	738.4000	1474.7854	1474.7780	0.0075	0	38	0.05	1	R.FLEQQNQVLQTK.W 7837
4548	584.9000	1751.6782	1751.8764	-0.1982	1	2	3.2e+002	2	K.DVDNAYMIKVELQSK.V
9800	919.9000	1837.7854	1837.9072	-0.1217	0	35	0.066	1	K.SISISVAGGGGFGAAGGFGR.G 9801
8828	820.0000	2456.9782	2457.1905	-0.2123	0	22	2.2	1	R.MSGDLSNVTVSVTSTTSSNVASK.A

23. [IPI00292496](#) Mass: 50257 Score: 187 Queries matched: 21 emPAI: 0.37

Tax_Id=9606 Gene_Symbol=TUBB8 Tubulin beta-8 chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREEYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPQQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVPPPR.L 4339
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
8658	801.3000	1600.5854	1600.8131	-0.2276	0	77	4.9e-006	1	R.AVLVDLEPGTMDSVR.S 8662 8663 8672 8677
8748	809.3000	1616.5854	1616.8080	-0.2225	0	(45)	0.007	1	R.AVLVDLEPGTMDSVR.S 8749
5396	629.0000	1883.9782	1883.9451	0.0331	0	3	1.4e+002	3	K.MSATFIGNNTAIQELFK.R
10829	530.6000	2118.3709	2118.0997	0.2712	1	0	75	4	R.EEYPDRIINTFISILPSPK.V

24. [IPI00293665](#) Mass: 60315 Score: 173 Queries matched: 12 emPAI: 0.30

Tax_Id=9606 Gene_Symbol=KRT6B Keratin, type II cytoskeletal 6B

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3243	503.3000	1004.5854	1004.4597	0.1258	0	29	0.46	1	K.LLEGEECR.L 3242
4002	554.3000	1106.5854	1106.5356	0.0498	0	46	0.0089	1	K.AQYEEIAQR.S 4000
4658	590.3000	1178.5854	1178.5931	-0.0077	0	67	6.4e-005	1	K.YEELQITAGR.H
6610	665.3000	1328.5854	1328.7187	-0.1333	0	88	5.4e-007	1	R.NLDLDSIIAEVK.A 6609
7330	704.3000	1406.5854	1406.7041	-0.1187	0	43	0.021	1	K.ADTLTDEINFLR.A 7331
7462	712.8000	1423.5854	1423.6263	-0.0408	0	23	1.8	1	R.GSGGLGACGAGFGR.S 7460 7461

25. [IPI00964764](#) Mass: 68283 Score: 148 Queries matched: 5 emPAI: 0.10

Tax_Id=9606 Gene_Symbol=SDHA cDNA FLJ55072, highly similar to Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
9356	872.4000	1742.7854	1742.8298	-0.0443	0	80	2.5e-006	1	R.AAFGLSEAGNTACVTK.L 9355 9365
9698	604.6000	1810.7782	1810.8737	-0.0955	0	38	0.038	1	R.IDEYDYSKPIQQQK.K
11181	755.6000	2263.7782	2263.9838	-0.2056	0	9	7.8	1	R.TYFCTSHTSTGDTAMITR.A

Proteins matching the same set of peptides:

[IPI00965327](#) Mass: 64439 Score: 148 Queries matched: 5

Tax_Id=9606 Gene_Symbol=SDHA Uncharacterized protein

26. [IPI00299145](#) Mass: 60273 Score: 146 Queries matched: 14 emPAI: 0.30

Tax_Id=9606 Gene_Symbol=KRT6C Keratin, type II cytoskeletal 6C

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3243	503.3000	1004.5854	1004.4597	0.1258	0	29	0.46	1	K.LLEGEECR.L 3242
4002	554.3000	1106.5854	1106.5356	0.0498	0	46	0.0089	1	K.AQYEEIAQR.S 4000
6610	665.3000	1328.5854	1328.7187	-0.1333	0	88	5.4e-007	1	R.NLDLDSIIAEVK.A 6609

[7330](#) 704.3000 1406.5854 1406.7041 -0.1187 0 43 0.021 1 K.ADTLTDEINFLR.A [7331](#)
[7462](#) 712.8000 1423.5854 1423.6263 -0.0408 0 23 1.8 1 R.GSGGLGGACGAGFGR.S [7460](#) [7461](#)
[7656](#) 724.3000 1446.5854 1446.7678 -0.1824 0 24 1.3 1 R.AIGGGLSSVGGGSSTIK.Y [7657](#) [7658](#)

Proteins matching the same set of peptides:

[IPI00300725](#) Mass: 60293 Score: 146 Queries matched: 14
 Tax_Id=9606 Gene_Symbol=KRT6A Keratin, type II cytoskeletal 6A
[IPI00909059](#) Mass: 58088 Score: 146 Queries matched: 14
 Tax_Id=9606 Gene_Symbol=KRT6A cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A
[IPI00930073](#) Mass: 60275 Score: 146 Queries matched: 14
 Tax_Id=9606 Gene_Symbol=KRT6C cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA
[IPI00942257](#) Mass: 58599 Score: 146 Queries matched: 14
 Tax_Id=9606 Gene_Symbol=KRT6A 58 kDa protein
[IPI00956313](#) Mass: 58579 Score: 146 Queries matched: 14
 Tax_Id=9606 Gene_Symbol=KRT6C 58 kDa protein

27. [IPI00157860](#) Mass: 95842 Score: 146 Queries matched: 25 emPAI: 0.27

Tax_Id=9606 Gene_Symbol=AKAP4 Isoform 1 of A-kinase anchor protein 4

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3492	520.7000	1039.3854	1039.5008	-0.1154	0	33	0.15	1	K.TEGSVCLFK.Q 3493
3820	542.3000	1082.5854	1082.5608	0.0247	0	32	0.2	1	K.SQSLSYASLK.A 3818
4761	594.9000	1187.7854	1186.5870	1.1985	0	47	0.0069	1	K.SFLYSLSNKK.S 4750 4752 4753
5237	620.8000	1239.5854	1239.5983	-0.0128	1	14	13	1	R.ESKEFADSISK.G
7342	705.3000	1408.5854	1408.6578	-0.0723	0	15	9.3	1	K.EIVSDLDLSDCMK.N
8029	500.3000	1497.8782	1497.7133	0.1648	1	2	1.7e+002	4	K.DQSKTEGSLVCLFK.Q
9679	602.3000	1803.8782	1803.8387	0.0394	1	4	96	1	K.VDLYNPEGGQDQDRK.V
10129	954.9000	1907.7854	1906.8755	0.9099	0	1	2.3e+002	2	K.DAASSSSEGNLNLGSLSEK.E
10355	992.9000	1983.7854	1983.9281	-0.1427	0	50	0.0018	1	K.IASEMAYEAVELTAAEMR.G 10356 10361
10765	702.6000	2104.7782	2105.0250	-0.2468	0	24	0.49	1	K.NTNNNQSPSAPPKPPSTQR.A 10764 10775 10776
10834	708.0000	2120.9782	2119.9593	1.0189	1	30	0.19	1	R.GVCKVDLYNPEGGQDQDR.K
8057	753.0000	2255.9782	2256.0369	-0.0587	0	8	58	1	R.AVISPDGECISIDDLDFVYVNR.L 11171
11629	628.2000	2508.7709	2509.0155	-0.2446	1	16	0.26	1	R.SDKAEQCQEHQELDCTSGMK.Q
11723	856.0000	2564.9782	2565.2095	-0.2313	0	20	0.74	1	K.YSNDGAALAELEEQAASANKPNFR.G

Proteins matching the same set of peptides:

[IPI00333264](#) Mass: 94811 Score: 146 Queries matched: 25
 Tax_Id=9606 Gene_Symbol=AKAP4 Isoform 2 of A-kinase anchor protein 4

28. [IPI00018511](#) Mass: 48917 Score: 144 Queries matched: 19 emPAI: 0.30

Tax_Id=9606 Gene_Symbol=TUBB4Q Putative tubulin beta-4q chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREYYPDR.I
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPGQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVFPFR.L 4339
8658	801.3000	1600.5854	1600.8131	-0.2276	0	77	4.9e-006	1	R.AVLVDLEPGTMDSVR.S 8662 8663 8672 8677
8748	809.3000	1616.5854	1616.8080	-0.2225	0	(45)	0.007	1	R.AVLVDLEPGTMDSVR.S 8749
10001	948.9000	1895.7854	1894.9571	0.8284	1	4	1e+002	3	K.MSVTFTGNNTAVQELKR.V 10000 10031 10039
10829	530.6000	2118.3709	2118.0997	0.2712	1	0	75	4	R.EEYVDRILINTFSLPSPK.V

29. [IPI00009867](#) Mass: 62568 Score: 133 Queries matched: 10 emPAI: 0.23

Tax_Id=9606 Gene_Symbol=KRT5 Keratin, type II cytoskeletal 5

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3243	503.3000	1004.5854	1004.4597	0.1258	0	29	0.46	1	K.LLEGECCR.L 3242
3890	547.2000	1092.3854	1092.5199	-0.1345	0	36	0.088	1	K.AQYERIANR.S 3889
4040	556.3000	1110.5854	1110.5669	0.0185	0	16	8	1	R.ISISTSGGSFR.N

[6610](#) 665.3000 1328.5854 1328.7187 -0.1333 0 88 5.4e-007 1 R.NLDLDSIIAEVK.A [6609](#)
[7349](#) 705.8000 1409.5854 1409.7151 -0.1296 0 23 1.9 1 R.SFSTASAITPSVSR.T [7348](#)
[7487](#) 476.5000 1426.4782 1425.7173 0.7608 1 2 1.6e+002 2 R.TTAENEVMLKK.D

30. [IPI00641706](#) Mass: 46248 Score: 132 Queries matched: 18 emPAI: 0.32

Tax_Id=9606 Gene_Symbol=TUBB6 46 kDa protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3386	514.3000	1026.5854	1025.5328	1.0526	0	11	44	1	K.VAVCDIPPR.G 3383
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	R.NMMAACDPR.H 3688
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	R.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPQQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVPPR.L 4339
9155	848.9000	1695.7854	1695.8257	-0.0402	0	38	0.04	1	K.NSSYFVEWIPNNVK.V 9154 9156 9157 9158
6767	672.1000	2013.2782	2013.0353	0.2428	1	1	93	1	K.MASTFIGNSTAIQELFKR.I
7129	691.0000	2069.9782	2070.0746	-0.0964	1	1	2.7e+002	3	K.GHYTEGAELVDAVLDDVVRK.E

Proteins matching the same set of peptides:

[IPI00643158](#) Mass: 42963 Score: 132 Queries matched: 18

Tax_Id=9606 Gene_Symbol=TUBB6 43 kDa protein

31. [IPI00290078](#) Mass: 64442 Score: 128 Queries matched: 11 emPAI: 0.10

Tax_Id=9606 Gene_Symbol=KRT4 keratin, type II cytoskeletal 4

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4002	554.3000	1106.5854	1106.5356	0.0498	0	46	0.0089	1	R.AQYEEIAQR.S 4000
4328	381.5000	1141.4782	1141.5325	-0.0543	0	4	1.4e+002	8	R.EYQELMSVK.L
1898	390.9000	1169.6782	1168.5836	1.0946	1	5	1e+002	5	R.GENALKDAHSK.R
5633	639.4000	1276.7854	1276.7027	0.0828	0	89	4.1e-007	1	K.LALDIEIATYR.K 5634 5635
6884	679.3000	1356.5854	1356.7249	-0.1394	0	10	35	2	R.NLDLDSIIAEVR.A 6897
7845	738.5000	1474.9854	1474.7562	0.2293	1	1	2.1e+002	2	K.SEIAELNRMVQR.L
7808	736.3000	2205.8782	2205.1641	0.7141	1	0	4.1e+002	4	K.VLETKWNLLQQQTTTSSK.N

Proteins matching the same set of peptides:

[IPI00797452](#) Mass: 52069 Score: 128 Queries matched: 11

Tax_Id=9606 Gene_Symbol=KRT4 cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4

32. [IPI00939892](#) Mass: 65720 Score: 126 Queries matched: 6 emPAI: 0.10

Tax_Id=9606 Gene_Symbol=KRT75 65 kDa protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3243	503.3000	1004.5854	1004.4597	0.1258	0	29	0.46	1	K.LLEGEECR.L 3242
4805	597.2000	1192.3854	1191.6135	0.7719	0	2	2.8e+002	6	R.TAAENEFVALK.K
6610	665.3000	1328.5854	1328.7187	-0.1333	0	88	5.4e-007	1	R.NLDLDSIIAEVK.A 6609
7717	730.4000	2188.1782	2188.0331	0.1451	1	2	3.4e+002	5	R.ECHQKALSTSSAPPPQDAHK.S

33. [IPI00306959](#) Mass: 51430 Score: 120 Queries matched: 6 emPAI: 0.06

Tax_Id=9606 Gene_Symbol=KRT7 Keratin, type II cytoskeletal 7

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3210	500.2000	998.3854	998.4379	-0.0524	0	6	86	4	K.DVDAAYMSK.V 3211
4328	381.5000	1141.4782	1141.5325	-0.0543	0	4	1.4e+002	8	R.EYQELMSVK.L
5633	639.4000	1276.7854	1276.7027	0.0828	0	89	4.1e-007	1	K.LALDIEIATYR.K 5634 5635

Proteins matching the same set of peptides:

[IPI00792841](#) Mass: 49062 Score: 120 Queries matched: 6

Tax_Id=9606 Gene_Symbol=KRT7 cDNA FLJ46620 fis, clone TLUNG2000654, highly similar to Keratin, type II cytoskeletal 7

34. [IPI00787323](#) Mass: 49532 Score: 120 Queries matched: 6 emPAI: 0.07
 Tax_Id=9606 Gene_Symbol=LOC728638 Similar to Keratin, type II cytoskeletal 8

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
258	518.0000	516.9927	517.2496	-0.2569	0	4	1.8e+002	2	K.DANAK.L
5633	639.4000	1276.7854	1276.7027	0.0828	0	89	4.1e-007	1	K.LALDIEIATYR.K 5634 5635
2795	463.9000	1388.6782	1387.7394	0.9388	1	2	2.7e+002	3	K.WSLLQQQKMAR.S
9706	907.4000	1812.7854	1812.8200	-0.0345	1	3	1.1e+002	2	K.DVDEAYMKNVELES.R.L

35. [IPI00554648](#) Mass: 53671 Score: 120 Queries matched: 6 emPAI: 0.06
 Tax_Id=9606 Gene_Symbol=KRT8 Keratin, type II cytoskeletal 8

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
258	518.0000	516.9927	517.2496	-0.2569	0	4	1.8e+002	2	K.DANAK.L
5633	639.4000	1276.7854	1276.7027	0.0828	0	89	4.1e-007	1	K.LALDIEIATYR.K 5634 5635
7837	738.3000	1474.5854	1474.6908	-0.1054	0	3	1.5e+002	6	R.LESGMQNSIHTK.T
9706	907.4000	1812.7854	1812.8200	-0.0345	1	3	1.1e+002	2	K.DVDEAYMKNVELES.R.L

36. [IPI00886833](#) Mass: 35706 Score: 120 Queries matched: 5 emPAI: 0.09
 Tax_Id=9606 Gene_Symbol=LOC100129958 similar to hCG1643231

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5633	639.4000	1276.7854	1276.7027	0.0828	0	89	4.1e-007	1	K.LALDIEIATYR.K 5634 5635
6659	445.1000	1332.2782	1331.5461	0.7321	0	3	10	1	K.MAWSNMGNMFK.S
8438	782.0000	2342.9782	2343.0962	-0.1181	1	1	3.1e+002	2	K.WSLLQQQKMAWSNMGNMFK.S

Proteins matching the same set of peptides:

[IPI00888053](#) Mass: 35448 Score: 120 Queries matched: 5
 Tax_Id=9606 Gene_Symbol=LOC100129958 similar to hCG1643231

37. [IPI00383815](#) Mass: 50372 Score: 120 Queries matched: 4 emPAI: 0.07
 Tax_Id=9606 Gene_Symbol=GFAP Isoform 2 of Glial fibrillary acidic protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4316	571.3000	1140.5854	1139.6775	0.9080	1	1	2.7e+002	5	R.LGPGTRLSLAR.M
5633	639.4000	1276.7854	1276.7027	0.0828	0	89	4.1e-007	1	K.LALDIEIATYR.K 5634 5635

Proteins matching the same set of peptides:

[IPI00443478](#) Mass: 49533 Score: 120 Queries matched: 4
 Tax_Id=9606 Gene_Symbol=GFAP Isoform 3 of Glial fibrillary acidic protein
[IPI00025363](#) Mass: 49907 Score: 120 Queries matched: 4
 Tax_Id=9606 Gene_Symbol=GFAP Isoform 1 of Glial fibrillary acidic protein

38. [IPI00031169](#) Mass: 23702 Score: 116 Queries matched: 8 emPAI: 0.30
 Tax_Id=9606 Gene_Symbol=RAB2A Ras-related protein Rab-2A

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2705	454.8000	1361.3782	1361.6649	-0.2867	0	19	6.7	1	R.EHGLIFMETSAR.T 6957
7123	461.0000	1379.9782	1379.7231	0.2551	1	4	83	6	K.SCLLLQFTDKR.F
8003	747.9000	1493.7854	1493.7362	0.0493	0	27	0.52	1	K.TASNVEEAFINTAK.E 7998
8343	775.8000	1549.5854	1549.7525	-0.1671	0	59	0.00029	1	K.LQIWDTAGQESFR.S 8342 8344

39. [IPI00465028](#) Mass: 31057 Score: 116 Queries matched: 12 emPAI: 0.84
 Tax_Id=9606 Gene_Symbol=TP11;TP11P1 triosephosphate isomerase isoform 2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3835	544.2000	1086.3854	1086.5782	-0.1927	1	34	0.17	1	R.LRADTDLQR.L 3837
4277	569.3000	1136.5854	1136.5648	0.0206	0	50	0.0038	1	K.IAVAAQNCYK.V 4278
5188	617.8000	1233.5854	1233.5949	-0.0095	0	39	0.042	1	K.SNVSDAVAQSTR.I
6570	663.8000	1325.5854	1325.6649	-0.0795	0	52	0.0018	1	R.IIYGGSVTGATCK.E 6572

[8670](#) 801.8000 1601.5854 1601.8817 -0.2963 0 22 1.3 1 K.VVLAYEPVWAIQTGK.T
[8766](#) 811.3000 1620.5854 1620.8181 -0.2327 0 24 0.81 1 K.VTNGAFTGEISPGMIK.D [8771](#)
[11007](#) 731.7000 2192.0782 2191.0620 1.0162 0 20 2.1 1 K.VPADTEVVCAPTAYIDFAR.Q [11006](#)

40. [IPI00909560](#) Mass: 56404 Score: 115 Queries matched: 15 emPAI: 0.12
 Tax_Id=9606 Gene_Symbol=PKM2 Pyruvate kinase

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
691	607.3000	606.2927	606.2982	-0.0054	0	5	1.5e+002	2	K.MMIGR.C
4859	599.8000	1197.5854	1196.6401	0.9454	0	6		90	R.LDIDSPPITAR.N
6923	680.8000	1359.5854	1358.6976	0.8878	0	37	0.068	1	R.NTGIICTIGPASR.S 6906 6910 6922
7740	731.9000	1461.7854	1461.8079	-0.0224	0	69	4e-005	1	K.IYVDDGLISLQVK.Q 7741
9177	567.2000	1698.5782	1698.8498	-0.2716	1	4		56	K.GSTLKITLDNAYMEK.C
9549	890.9000	1779.7854	1778.8687	0.9168	0	12		13	K.GADFLVTEVNGGSLGSK.K 9548
9731	608.0000	1820.9782	1820.9091	0.0691	1	16		6.1	R.RFDEILEASDGIMVAR.G 5007
10372	663.3000	1986.8782	1986.9874	-0.1092	1	2	1.4e+002	4	K.FGVEQDVMVFASFIRK.A
11610	832.0000	2492.9782	2493.1363	-0.1581	0	6		30	R.AEGSDVANAVLDGADCIMLSGETAK.G

41. [IPI00550533](#) Mass: 37259 Score: 115 Queries matched: 7 emPAI: 0.29
 Tax_Id=9606 Gene_Symbol=Clorf56 Isoform 1 of Uncharacterized protein Clorf56

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2317	422.9000	843.7854	842.4974	1.2881	0	7		24	R.VGALSQLR.T
6328	652.3000	1302.5854	1302.6568	-0.0713	0	60	0.00029	1	R.FIANSQPEIR.L 6341
8504	788.3000	1574.5854	1574.7536	-0.1682	0	42	0.018	1	R.ELPSATPNTAGSSSTR.F 8505
11828	880.0000	2636.9782	2637.2002	-0.2220	1	53	0.00034	1	R.SSAINEDGSSEGGVINAGKDSTR.E 11829

42. [IPI00152561](#) Mass: 13622 Score: 114 Queries matched: 4 emPAI: 0.56
 Tax_Id=9606 Gene_Symbol=SPACA4 Sperm acrosome membrane-associated protein 4

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
7790	734.8000	1467.5854	1467.6664	-0.0809	0	51	0.0022	1	R.ATSCGLEEPVSYR.G 7800
8594	795.3000	1588.5854	1588.6974	-0.1120	0	54	0.001	1	R.GVTYSLTNCCTGR.L 8595

43. [IPI00291262](#) Mass: 53031 Score: 113 Queries matched: 7 emPAI: 0.13
 Tax_Id=9606 Gene_Symbol=CLU Isoform 1 of Clusterin

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5175	616.8000	1231.5854	1231.6408	-0.0553	1	21		2.5	K.TLEKTNEER.K
9444	881.9000	1761.7854	1761.8203	-0.0349	0	56	0.00071	1	R.EILSVDCTNNPSQAK.I 9447
5313	625.0000	1871.9782	1871.8407	0.1375	0	2	1.8e+002	3	R.QQTHMLDVMQDHFSR.A
9920	937.4000	1872.7854	1872.9833	-0.1979	0	51	0.0017	1	K.LFDSDPITVTPVEVSR.K 9921 9924

Proteins matching the same set of peptides:

[IPI00400826](#) Mass: 58537 Score: 113 Queries matched: 7
 Tax_Id=9606 Gene_Symbol=CLU Isoform 2 of Clusterin
[IPI00795633](#) Mass: 52902 Score: 113 Queries matched: 7
 Tax_Id=9606 Gene_Symbol=CLU CLU
[IPI00954954](#) Mass: 54236 Score: 113 Queries matched: 7
 Tax_Id=9606 Gene_Symbol=CLU clusterin isoform 3

44. [IPI00643152](#) Mass: 77912 Score: 111 Queries matched: 9 emPAI: 0.18
 Tax_Id=9606 Gene_Symbol=HSPALL cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5112	614.8000	1227.5854	1227.6207	-0.0353	0	32	0.23	1	K.VEILANDQGNR.T 5113
6160	644.3000	1286.5854	1286.5965	-0.0110	0	32	0.21	1	K.NALESYAFNMK.S
7937	744.3000	1486.5854	1486.6940	-0.1086	0	44	0.012	1	R.TTPSYVAFDTER.L 7938 7939
8952	830.4000	1658.7854	1658.8879	-0.1024	0	45	0.0082	1	R.IINEPTAAALAYGLDK.G

[9026](#) 559.2000 1674.5782 1674.7234 -0.1452 0 5 65 2 [K.ATAGDTHLGGEDFDNR.L](#) [9025](#)

Proteins matching the same set of peptides:

[IPI00893099](#) Mass: 70760 Score: 111 Queries matched: 9
 Tax_Id=9606 Gene_Symbol=HSPALL Heat shock 70kDa protein 1-like variant
[IPI00939442](#) Mass: 70730 Score: 111 Queries matched: 9
 Tax_Id=9606 Gene_Symbol=HSPALL Heat shock 70 kDa protein 1-like
[IPI00939753](#) Mass: 64434 Score: 111 Queries matched: 9
 Tax_Id=9606 Gene_Symbol=- 64 kDa protein
[IPI00940023](#) Mass: 64464 Score: 111 Queries matched: 9
 Tax_Id=9606 Gene_Symbol=- 64 kDa protein
[IPI00942823](#) Mass: 64463 Score: 111 Queries matched: 9
 Tax_Id=9606 Gene_Symbol=HSPALL 64 kDa protein

45. [IPI00013006](#) Mass: 40971 Score: 104 Queries matched: 11 emPAI: 0.36

Tax_Id=9606 Gene_Symbol=ZBPB Zona pellucida-binding protein 1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3426	517.8000	1033.5854	1033.5808	0.0046	0	19	5.1	1	K.IVGSTSPFPVK.A
6828	675.8000	1349.5854	1349.7092	-0.1237	0	32	0.23	1	R.FFNQVVEILGR.R 6827
7582	480.3000	1437.8782	1436.7558	1.1223	0	24	1.1	1	K.SPHVLCVTQQLR.N 7566
9466	883.4000	1764.7854	1763.8519	0.9336	0	30	0.25	1	R.NAELIDPSFQWYGP.K 9465
10272	978.3000	1954.5854	1954.7794	-0.1940	0	37	0.0088	1	K.CPECCVICSPGYSNPR.D 10273 10274 10279

Proteins matching the same set of peptides:

[IPI00926275](#) Mass: 40872 Score: 104 Queries matched: 11
 Tax_Id=9606 Gene_Symbol=ZBPB zona pellucida-binding protein 1 isoform 2

46. [IPI00007702](#) Mass: 70263 Score: 103 Queries matched: 12 emPAI: 0.20

Tax_Id=9606 Gene_Symbol=HSPA2 Heat shock-related 70 kDa protein 2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2827	465.8000	929.5854	929.5004	0.0850	0	19	5.3	1	R.VCNPIISK.L
5112	614.8000	1227.5854	1227.6207	-0.0353	0	32	0.23	1	K.VEILANDQGNR.T 5113
5365	627.8000	1253.5854	1252.6088	0.9767	0	1	2.7e+002	2	R.FEELNADLFR.G
6452	658.3000	1314.5854	1314.6455	-0.0601	0	21	2.3	1	K.NALESYTYNIK.Q
7937	744.3000	1486.5854	1486.6940	-0.1086	0	44	0.012	1	R.TTPSYVAFTDTER.L 7938 7939
8952	830.4000	1658.7854	1658.8879	-0.1024	0	45	0.0082	1	R.IINEPTAAAIAYGLDK.K
9116	846.3000	1690.5854	1690.7183	-0.1329	0	15	5.5	1	K.STAGDTHLGGEDFDNR.M 9114
10775	703.0000	2105.9782	2106.0633	-0.0851	1	1	1.9e+002	7	R.FEELNADLFRGTLPEVEK.A

47. [IPI00945532](#) Mass: 46180 Score: 97 Queries matched: 15 emPAI: 0.23

Tax_Id=9606 Gene_Symbol=TUBB8 tubulin beta-8 chain isoform 2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3390	514.8000	1027.5854	1027.5121	0.0734	0	17	7.1	1	K.TAVCDIPPR.G
3690	533.2000	1064.3854	1064.4201	-0.0347	0	49	0.0041	1	K.NMMAACDPR.H 3688
3783	539.2000	1076.3854	1076.5250	-0.1396	1	25	1.2	1	K.IREEYPDR.I
3801	541.1000	1080.1854	1080.4151	-0.2296	0	(3)	23	1	K.NMMAACDPR.H
4212	565.8000	1129.5854	1129.5880	-0.0025	0	23	1.5	1	R.FPQQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416	0	45	0.011	1	K.LAVNMVFPFR.L 4339
6576	442.9000	1325.6782	1325.7126	-0.0344	1	14	12	1	K.TAVCDIPPRGLK.M
5396	629.0000	1883.9782	1883.9451	0.0331	0	3	1.4e+002	3	K.MSATFIGNNTAIQELFK.R
10829	530.6000	2118.3709	2118.0997	0.2712	1	0	75	4	R.EEYDRIINTFSLPSPK.V
7868	739.6000	2215.7782	2214.9752	0.8029	0	1	72	2	R.INVYYNEASGCGAGNNWAK.G

48. [IPI00376239](#) Mass: 28213 Score: 92 Queries matched: 3 emPAI: 0.12

Tax_Id=9606 Gene_Symbol=H1FNT Testis-specific H1 histone

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3177	497.3000	992.5854	992.5152	0.0703	1	6	91	1	R.HEAPRGQAK.A
4199	565.2000	1128.3854	1128.5200	-0.1345	0	73	1.6e-005	1	R.VSGSDAAGYFR.V 4201

49. [IPI00465363](#) Mass: 14159 Score: 90 Queries matched: 23 emPAI: 2.63

Tax_Id=9606 Gene_Symbol=HIST1H2BA Histone H2B type 1-A

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2951	477.3000	952.5854	952.5957	-0.0102	0	22	2	1	R.LLLPGELAK.H 2945 2946 2947 2949
4531	583.3000	1164.5854	1164.5703	0.0152	0	17	7	1	K.ESYSIYIK.V 4533
4915	602.3000	1202.5854	1202.6507	-0.0652	1	62	0.00023	1	M.PEVSSKGATISK.K 4916 4918
7653	483.2000	1446.5782	1446.7790	-0.2009	1	17	5.6	1	R.STISSREIQTAVR.L 7655 7660
8072	754.9000	1507.7854	1507.8358	-0.0504	1	16	6.8	1	K.VLKQVHPDTGISSEK.A 8075
9393	584.4000	1750.1782	1750.0352	0.1429	1	9	15	2	R.EIQTAVRLLLPGELAK.H 9392
9432	880.8000	1759.5854	1759.8273	-0.2419	0	(22)	1.8	1	K.AMSIMNSFVTDIFER.I 9438
9522	889.3000	1776.5854	1775.8222	0.7632	0	29	0.14	1	K.AMSIMNSFVTDIFER.I 9514
9609	896.8000	1791.5854	1791.8172	-0.2317	0	(26)	0.64	1	K.AMSIMNSFVTDIFER.I 9615

50. [IPI00003362](#) Mass: 72492 Score: 89 Queries matched: 10 emPAI: 0.25

Tax_Id=9606 Gene_Symbol=HSPA5 HSPA5 protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3767	538.4000	1074.7854	1073.5465	1.2389	0	5	1e+002	2	K.ITITNDQNR.L
5037	609.7000	1217.3854	1216.6234	0.7621	0	11	26	1	K.DAGTIAGLNVMR.I
5112	614.8000	1227.5854	1227.6207	-0.0353	0	32	0.23	1	R.VEIIANDQGNR.I 5113
7518	716.3000	1430.5854	1429.6838	0.9017	0	34	0.12	1	R.TWNDPVQQDIK.F
8457	784.4000	1566.7854	1565.7726	1.0129	0	29	0.32	1	R.ITPSYVAFTPEGER.L 8460
8952	830.4000	1658.7854	1658.8879	-0.1024	0	45	0.0082	1	R.IINEPTAAAIAYGLDK.R
9791	918.9000	1835.7854	1835.9265	-0.1411	0	32	0.16	1	K.SQIFSTASDNQPTVTIK.V 9792

51. [IPI00008910](#) Mass: 32693 Score: 88 Queries matched: 9 emPAI: 0.21

Tax_Id=9606 Gene_Symbol=SPACA1 Sperm acrosome membrane-associated protein 1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
7729	731.3000	1460.5854	1460.6970	-0.1115	0	68	4.2e-005	1	K.FTVYTSSELQMR.R 7730
7733	731.3000	1460.5854	1459.6977	0.8878	0	17	6.2	1	R.EVILTINGCPGESK.C 7731 7732
8055	752.8000	1503.5854	1503.7165	-0.1311	0	17	4.8	1	K.ASTPEVQSEQSSVR.Y
10664	692.3000	2073.8782	2073.9790	-0.1008	0	14	8.4	1	R.GPTDCGWGKPISESLESVR.L 10663
11839	661.8000	2643.1709	2643.2850	-0.1141	1	8	22	1	R.KESHPLAFECDFLDNNEIVATIK.F

52. [IPI00304925](#) Mass: 70294 Score: 84 Queries matched: 9 emPAI: 0.15

Tax_Id=9606 Gene_Symbol=HSPA1B;HSPA1A Heat shock 70 kDa protein 1A/1B

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5112	614.8000	1227.5854	1227.6207	-0.0353	0	32	0.23	1	K.VEIIANDQGNR.T 5113
5438	631.4000	1260.7854	1260.6503	0.1352	0	2	1.9e+002	6	R.LVNHVVEEFK.R
6160	644.3000	1286.5854	1286.5965	-0.0110	0	32	0.21	1	K.NALESYAFNMK.S
7937	744.3000	1486.5854	1486.6940	-0.1086	0	44	0.012	1	R.TTPSYVAFTDTER.L 7938 7939
9026	559.2000	1674.5782	1674.7234	-0.1452	0	5	65	2	K.ATAGDTHLGGEDFDNR.L 9025

Proteins matching the same set of peptides:

IPI00845339	Mass: 70280	Score: 84	Queries matched: 9
Tax_Id=9606 Gene_Symbol=HSPA1B;HSPA1A cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1			
IPI00911039	Mass: 64170	Score: 84	Queries matched: 9
Tax_Id=9606 Gene_Symbol=HSPA1B;HSPA1A cDNA FLJ54408, highly similar to Heat shock 70 kDa protein 1			

53. [IPI00909073](#) Mass: 45270 Score: 84 Queries matched: 7 emPAI: 0.24

Tax_Id=9606 Gene_Symbol=- cDNA FLJ53752, highly similar to Heat shock 70 kDa protein 1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5112	614.8000	1227.5854	1227.6207	-0.0353	0	32	0.23	1	K.VEILANDQGNR.T 5113
6097	642.3000	1282.5854	1281.6578	0.9276	1	1	2.5e+002	8	R.RGPGFGGFGAQQPK.G
6160	644.3000	1286.5854	1286.5965	-0.0110	0	32	0.21	1	K.NALESYAFNMK.S
7937	744.3000	1486.5854	1486.6940	-0.1086	0	44	0.012	1	R.TTPSYVAFTDTER.L 7938 7939

54. [IPI00554498](#) Mass: 36630 Score: 77 Queries matched: 7 emPAI: 0.19

Tax_Id=9606 Gene_Symbol=LHDC L-lactate dehydrogenase C chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2654	450.2000	898.3854	898.5600	-0.1746	0	53	0.0017	1	R.IVIVTAGAR.Q 2656
5299	624.8000	1247.5854	1247.5928	-0.0074	0	44	0.012	1	R.VIGSGCNLDSAR.F 5296
7918	742.9000	1483.7854	1483.7267	0.0588	1	1	2.3e+002	10	K.ITSGKDYSVSANSR.I
8249	512.2000	1533.5782	1533.8038	-0.2256	1	13		15	1 K.INLNSEEEALFKK.S 8252

55. [IPI00376379](#) Mass: 62149 Score: 77 Queries matched: 5 emPAI: 0.11

Tax_Id=9606 Gene_Symbol=KRT77 Keratin, type II cytoskeletal 1b

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4658	590.3000	1178.5854	1177.6091	0.9763	0	51	0.0028	2	K.YQELQITAGR.H 4640
7843	738.4000	1474.7854	1474.7780	0.0075	0	38	0.05	1	R.FLEQQNQVLQTK.W 7837
5154	615.9000	1844.6782	1844.8224	-0.1442	1	0	5e+002	8	M.SHQFSSQSASFSSMSRR.V

56. [IPI00003925](#) Mass: 39550 Score: 75 Queries matched: 12 emPAI: 0.17

Tax_Id=9606 Gene_Symbol=PDHB Isoform 1 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5297	624.8000	1247.5854	1247.6220	-0.0366	0	28	0.49	1	R.VTGADVMPYAK.I 5298
5512	634.3000	1266.5854	1266.7772	-0.1917	1	3	1.4e+002	4	R.RPLREVSGLLK.R 5513
9378	874.4000	1746.7854	1746.8763	-0.0909	0	60	0.00025	1	R.IMEGPAFNFLDAPAVR.V 9377 9382
9759	610.3000	1827.8782	1826.9389	0.9392	0	1	1.9e+002	1	K.TYYMSGGLQPVPIVFR.G
9854	618.0000	1850.9782	1850.8940	0.0842	0	19	2.8	1	R.TIRPMDMETIEASVMK.T 9853 9863
5389	628.7000	1883.0782	1882.8838	0.1943	0	(0)	4.5e+002	7	R.TIRPMDMETIEASVMK.T

57. [IPI00339269](#) Mass: 71440 Score: 70 Queries matched: 8 emPAI: 0.09

Tax_Id=9606 Gene_Symbol=HSPA6 Heat shock 70 kDa protein 6

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
5112	614.8000	1227.5854	1227.6207	-0.0353	0	32	0.23	1	R.VEILANDQGNR.T 5113
7558	719.0000	1435.9854	1435.7823	0.2031	1	1	1.7e+002	7	K.VQKLLQDFNKG.E
7937	744.3000	1486.5854	1486.6940	-0.1086	0	44	0.012	1	R.TTPSYVAFTDTER.L 7938 7939
9026	559.2000	1674.5782	1674.7234	-0.1452	0	5		65	2 K.ATAGDTHLGGEDFDNR.L 9025

58. [IPI00023020](#) Mass: 52157 Score: 68 Queries matched: 8 emPAI: 0.13

Tax_Id=9606 Gene_Symbol=SEMG1 Isoform 1 of Semenogelin-1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2960	478.3000	954.5854	954.4658	0.1196	0	8	46	1	R.SIYSQTEK.L
3098	491.8000	981.5854	981.5243	0.0611	0	38	0.049	1	K.SQIQAPNPK.Q
7016	685.8000	1369.5854	1369.6110	-0.0255	0	48	0.0051	1	K.GISSQYSNTEER.L 7015
9089	562.6000	1684.7782	1683.8356	0.9426	0	14	11	1	K.DIFSTQDELLVYNK.N 9092
10944	722.7000	2165.0782	2165.0964	-0.0182	1	1	1.5e+002	1	R.KQGSQSSYVLQTELVANK.Q
11545	817.7000	2450.0782	2449.2197	0.8585	1	1	1.5e+002	8	K.QGSQSSYVLQTELVANKQQR.E

Proteins matching the same set of peptides:

[IPI00414684](#) Mass: 45352 Score: 68 Queries matched: 8

Tax_Id=9606 Gene_Symbol=SEMG1 Isoform 2 of Semenogelin-1

59.	IPI00022430	Mass: 44815	Score: 67	Queries matched: 13	emPAI: 0.24	
Tax_Id=9606 Gene_Symbol=GAPDH5 Glyceraldehyde-3-phosphate dehydrogenase, testis-specific						
Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
3119	493.3000	984.5854	984.5029	0.0826 1 9	47 1	R.YKGSVEFR.N 3116
4471	579.8000	1157.5854	1157.6444	-0.0590 0 26	0.8 1	R.LAQAPYSAIK.E 4469
4513	582.3000	1162.5854	1161.6142	0.9712 0 13	17 1	R.ELTVGINGFGR.I
7548	718.3000	1434.5854	1434.7579	-0.1725 0 25	0.85 1	R.GAHQNIIPASTGAAK.A 7546 7547 7552
8395	779.3000	1556.5854	1556.7869	-0.2014 0 48	0.0043 1	R.VPTPDVSVVDLTCR.L
8573	529.3000	1584.8782	1584.8875	-0.0093 1 2	1.6e+002 3	R.LAQAPYSAIKEAVK.A
9019	837.4000	1672.7854	1672.8420	-0.0566 0 26	0.56 1	K.AEVEFPQPEPTPVR.E
11318	779.0000	2333.9782	2333.1872	0.7910 1 30	0.16 1	K.LTGMAFRVTPPDVSVVDLTCR.L
60.	IPI00784154	Mass: 61187	Score: 54	Queries matched: 5	emPAI: 0.11	
Tax_Id=9606 Gene_Symbol=HSPD1 60 kDa heat shock protein, mitochondrial						
Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
5012	608.3000	1214.5854	1214.6507	-0.0652 0 15	12 1	K.NAGVEGSLIVEK.I
3841	544.3000	1629.8782	1629.9011	-0.0230 1 3	3.8e+002 3	K.VGEVIVTKDDAMLLK.G
9080	842.9000	1683.7854	1683.8978	-0.1123 0 54	0.00096 1	R.AAEVEEIVLGGGCALLR.C
4376	574.8000	1721.3782	1721.5977	-0.2195 0 0	3.2e+002 1	K.DPGMGAMGGMGGMGGMF.-
11708	854.0000	2558.9782	2559.2413	-0.2631 0 25	0.31 1	K.LVQDVANNTNEAGDGTITATVLAR.S
61.	IPI00289614	Mass: 46502	Score: 53	Queries matched: 5	emPAI: 0.15	
Tax_Id=9606 Gene_Symbol=ACR Acrosin						
Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
6592	443.5000	1327.4782	1326.7078	0.7704 0 19	3.8 1	K.APRPSSILMEAR.V
2795	463.9000	1388.6782	1387.7071	0.9711 0 2	2.7e+002 3	R.WVLTAHCFVVGK.N
8823	819.8000	1637.5854	1637.6848	-0.0993 0 40	0.019 1	K.IDTCQGGSGGPLMCK.D 8822
11599	826.4000	2476.1782	2476.1904	-0.0122 0 23	0.73 1	K.YNSATEGNDIALVEITPPI SCGR.F
62.	IPI00006510	Mass: 50865	Score: 53	Queries matched: 13	emPAI: 0.13	
Tax_Id=9606 Gene_Symbol=TUBB1 Tubulin beta-1 chain						
Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
3386	514.3000	1026.5854	1025.5328	1.0526 0 11	44 1	K.VAVCDIPPR.G 3383
3783	539.2000	1076.3854	1076.5250	-0.1396 1 25	1.2 1	K.IREYYPDR.I
4212	565.8000	1129.5854	1129.5880	-0.0025 0 23	1.5 1	R.FPQQLNADLR.K 4209 4211 4214
4338	572.3000	1142.5854	1142.6270	-0.0416 0 45	0.011 1	K.LAVNMVFPFR.L 4339
6707	446.6000	1336.7782	1336.6519	0.1263 0 5	1e+002 3	R.IMNSFSVMPSPK.V
9887	932.4000	1862.7854	1861.9568	0.8287 1 1	1.7e+002 5	K.MSTKEVDQQLLSVQTR.N
10893	715.3000	2142.8782	2141.9762	0.9020 1 0	1.6e+002 3	R.EEYPDRIMNSFSVMPSPK.V
11926	687.1000	2744.3709	2743.2728	1.0981 1 1	1.2e+002 8	R.ALSVAELTQQMFARNTMAACDLR.R
63.	IPI00641681	Mass: 26466	Score: 51	Queries matched: 4	emPAI: 0.13	
Tax_Id=9606 Gene_Symbol=SCCPDH Saccharopine dehydrogenase						
Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
7488	714.3000	1426.5854	1426.6841	-0.0986 0 51	0.0042 1	K.SAIYGFQDSNLR.K 7491
7855	493.0000	1475.9782	1474.8871	1.0910 0 9	35 1	R.NVSNLKPVLIGPK.L
12101	595.1000	2970.4636	2970.4831	-0.0194 0 0	1.2e+002 8	K.GPEAGYVATPIAMVQAAMTLLSDASHLPK.A
64.	IPI00329600	Mass: 47464	Score: 51	Queries matched: 6	emPAI: 0.07	
Tax_Id=9606 Gene_Symbol=SCCPDH Probable saccharopine dehydrogenase						
Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
2948	477.3000	952.5854	951.5066	1.0789 0 0	6e+002 2	R.FYGEFVIK.A
4873	600.8000	1199.5854	1198.6571	0.9284 1 1	2.9e+002 4	R.SSRLPWAVAGR.S

7488	714.3000	1426.5854	1426.6841	-0.0986	0	51	0.0042	1	K.SAIYGFQDSNLR.K 7491
7855	493.0000	1475.9782	1474.8871	1.0910	0	9		35	R.NVSNLKPVPPLIGPK.L
12101	595.1000	2970.4636	2970.4831	-0.0194	0	0	1.2e+002	8	K.GPEAGYVATPIAMVQAAMTLSDASHLPK.A

65. [IPI00453473](#) Mass: 11360 Score: 50 Queries matched: 12 emPAI: 0.30
Tax_Id=9606 Gene_Symbol=HIST1H4E;HIST1H4L;HIST1H4D;HIST1H4J;HIST1H4F;HIST2H4B;HIST1H4K;HIST1H4I;HIST1H4H;HIST1H4B;HIST1H4C;HIST2H4A;HIST1H4A;HIST4H4 Histone H4

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3142	495.3000	988.5854	988.5706	0.0149	0	15		14	2 K.VFLENVIR.D
4667	590.8000	1179.5854	1179.6135	-0.0281	0	20		3.5	1 R.ISGLIYEETR.G
6405	655.8000	1309.5854	1309.6952	-0.1097	0	45	0.0093	1	K.TVTAMDVVYALK.R 6406
6574	442.9000	1325.6782	1324.7463	0.9319	0	28	0.42	1	R.DNIQGITKPAIR.R 6567 6568 6575
7771	489.6000	1465.7782	1465.7963	-0.0181	1	13		13	1 K.TVTAMDVVYALKR.Q 7768 7770
7898	494.6000	1480.7782	1480.8474	-0.0692	1	8		46	1 R.DNIQGITKPAIRR.L

66. [IPI00171611](#) Score: 48 Queries matched: 3
Tax_Id=9606 Gene_Symbol=HIST2H3C;HIST2H3A;HIST2H3D Histone H3.2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1437	358.2000	714.3854	714.4024	-0.0170	0	9		47	2 K.DIQLAR.R
2222	416.3000	830.5854	830.4861	0.0993	0	48	0.0072	1	K.STELLIR.K
2315	422.8000	843.5854	843.5000	0.0854	1	8		71	9 K.RVTIMPK.D

Proteins matching the same set of peptides:

IPI00216402	Score: 48	Queries matched: 3
IPI00219038	Score: 48	Queries matched: 3
IPI00419884	Score: 48	Queries matched: 3
IPI00465070	Score: 48	Queries matched: 3
IPI00909530	Score: 48	Queries matched: 3

67. [IPI00798360](#) Mass: 18352 Score: 48 Queries matched: 1 emPAI: 0.18
Tax_Id=9606 Gene_Symbol=SARNP 18 kDa protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2222	416.3000	830.5854	830.4861	0.0993	0	48	0.0072	1	K.STEILLR.K

68. [IPI00217966](#) Mass: 36950 Score: 46 Queries matched: 4 emPAI: 0.19
Tax_Id=9606 Gene_Symbol=LDHA Isoform 1 of L-lactate dehydrogenase A chain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2715	457.3000	912.5854	912.5756	0.0098	0	24		1.3	1 K.LVIITAGAR.Q
4256	567.7000	1133.3854	1133.5564	-0.1710	0	7	1.1e+002	3	K.VTLTSEEAR.L
5299	624.8000	1247.5854	1247.5928	-0.0074	0	44	0.012	1	R.VIGSGCNLDSAR.F 5296

Proteins matching the same set of peptides:

IPI00607708	Mass: 37084	Score: 46	Queries matched: 4
Tax_Id=9606 Gene_Symbol=LDHA Isoform 2 of L-lactate dehydrogenase A chain			
IPI00908791	Mass: 33970	Score: 46	Queries matched: 4
Tax_Id=9606 Gene_Symbol=LDHA L-lactate dehydrogenase			
IPI00939286	Mass: 37172	Score: 46	Queries matched: 4
Tax_Id=9606 Gene_Symbol=LDHA L-lactate dehydrogenase			
IPI00947127	Mass: 40097	Score: 46	Queries matched: 4
Tax_Id=9606 Gene_Symbol=LDHA L-lactate dehydrogenase A chain isoform 3			

69. [IPI00877807](#) Mass: 20849 Score: 45 Queries matched: 2 emPAI: 0.16

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
8952	830.4000	1658.7854	1658.8879	-0.1024	0	45	0.0082	1	R.IINEPTAAAIAYGLDK.K

[10101](#) 950.5000 1898.9854 1897.8013 1.1841 1 3 1.6e+002 9 K.SRAGDTHLCGEDFDYR.M

70. [IPI00018246](#) Mass: 103561 Score: 44 Queries matched: 12 emPAI: 0.10
 Tax_Id=9606 Gene_Symbol=HK1 Isoform 1 of Hexokinase-1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2227	416.7000	831.3854	831.3974	-0.0120	0	4	1.9e+002	6	R.SIPDGSEK.G
2429	433.2000	864.3854	864.4528	-0.0673	0	2	2.5e+002	6	K.MLPSFVR.R
2864	471.8000	941.5854	941.5546	0.0309	0	0	3.1e+002	6	R.ITPELLTR.G
4289	570.3000	1138.5854	1138.5870	-0.0016	0	18	4.6	1	R.TTVGVDGSLYK.T
4963	604.8000	1207.5854	1207.6084	-0.0230	0	23	1.7	1	R.LVDEYSLNAGK.Q
7684	727.9000	1453.7854	1453.7202	0.0653	0	35	0.1	1	K.GDFIALDLGGSSFR.I
5097	613.4000	1837.1782	1835.9604	1.2178	1	1	4.1e+002	4	R.DFNPTATVKMLPTFVR.S
10228	646.8000	1937.3782	1936.0889	1.2892	1	2	10	1	K.MVSGMYLGELVRLILVK.M
6785	673.1000	2016.2782	2015.0220	1.2562	1	3	61	4	K.QLFEKMYVSGMYLGELVR.L
8098	756.8000	2267.3782	2267.1070	0.2712	1	13	18	1	R.SIPDGSEKGDFFIALDLGGSSFR.I 11190
11655	631.4000	2521.5709	2520.3006	1.2703	1	0	54	1	K.CNVSFLLSEDSGKGAALITAVGVR.L

Proteins matching the same set of peptides:

[IPI00220663](#) Mass: 103390 Score: 44 Queries matched: 12
 Tax_Id=9606 Gene_Symbol=HK1 Isoform 2 of Hexokinase-1
[IPI00220665](#) Mass: 103870 Score: 44 Queries matched: 12
 Tax_Id=9606 Gene_Symbol=HK1 Isoform 3 of Hexokinase-1
[IPI00220667](#) Mass: 102180 Score: 44 Queries matched: 12
 Tax_Id=9606 Gene_Symbol=HK1 Isoform 4 of Hexokinase-1

71. [IPI00005721](#) Mass: 10536 Score: 39 Queries matched: 4 emPAI: 0.33
 Tax_Id=9606 Gene_Symbol=DEFA1;DEFA1B Neutrophil defensin 1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3125	493.8000	985.5854	985.5015	0.0840	0	39	0.041	1	R.IPACIAGER.R 3121
4326	381.5000	1141.4782	1141.6026	-0.1244	1	11	26	2	R.IPACIAGERR.Y 4328

Proteins matching the same set of peptides:

[IPI00021827](#) Mass: 10580 Score: 39 Queries matched: 4
 Tax_Id=9606 Gene_Symbol=DEFA3 Neutrophil defensin 3

72. [IPI00010420](#) Mass: 35285 Score: 38 Queries matched: 2 emPAI: 0.09
 Tax_Id=9606 Gene_Symbol=SLC25A31 ADP/ATP translocase 4

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3360	512.7000	1023.3854	1022.5219	0.8636	0	6	88	1	K.QLFMSGVGNK.E
3831	543.9000	1085.7854	1085.6444	0.1410	0	38	0.096	1	K.LLLQVQASSK.Q

73. [IPI00902754](#) Mass: 29035 Score: 38 Queries matched: 2 emPAI: 0.11
 Tax_Id=9606 Gene_Symbol=SDHA cDNA FLJ16373 fis, clone THYMU3000269, highly similar to Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
9698	604.6000	1810.7782	1810.8737	-0.0955	0	38	0.038	1	R.IDEYDYSKPIQGQQK.K
12390	719.9000	3594.4636	3594.7116	-0.2480	1	1	31	6	R.ACAPSIEESCRPGDKVPPPIKPNAGEESVMNLDK.L

74. [IPI00395769](#) Mass: 32917 Score: 37 Queries matched: 2 emPAI: 0.10
 Tax_Id=9606 Gene_Symbol=ATP5C1 Isoform Heart of ATP synthase subunit gamma, mitochondrial

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
6569	663.8000	1325.5854	1325.7231	-0.1376	0	37	0.058	1	R.IYGLGSLALYK.A
5310	625.0000	1871.9782	1871.8063	0.1719	1	6	73	1	R.MTAMDNASKNASEMIDK.L

Proteins matching the same set of peptides:

[IPI00478410](#) Mass: 33032 Score: 37 Queries matched: 2
 Tax_Id=9606 Gene_Symbol=ATP5C1 Isoform Liver of ATP synthase subunit gamma, mitochondrial

75. [IPI00300567](#) Mass: 33080 Score: 37 Queries matched: 2 emPAI: 0.10
 Tax_Id=9606 Gene_Symbol=DCI Isoform 1 of 3,2-trans-enoyl-CoA isomerase, mitochondrial

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2568	444.7000	887.3854	886.4369	0.9485	1	10	52	2	R.AAGGGDGARR.F
7695	728.9000	1455.7854	1454.7803	1.0051	0	37	0.056	1	R.VLVEPDAGAGVAVMK.F

Proteins matching the same set of peptides:

[IPI00398758](#) Mass: 31104 Score: 37 Queries matched: 2
 Tax_Id=9606 Gene_Symbol=DCI Isoform 2 of 3,2-trans-enoyl-CoA isomerase, mitochondrial

76. [IPI00019329](#) Mass: 10530 Score: 36 Queries matched: 1 emPAI: 0.33
 Tax_Id=9606 Gene_Symbol=DYNLL1 Dynein light chain 1, cytoplasmic

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
11639	838.6000	2512.7782	2513.0356	-0.2574	0	36	0.003	1	K.NADMSEEMQQDSVECATQALEK.Y

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