

# Mascot Search Results

User : Kari  
 Email : kleinholtz.1@osu.edu  
 Search title : Trypsin Swiss Prot  
 MS data file : \\filesrv\Mass\_Spec\Data\_New\31456 HammerDiakonova\31456\_1\_Control.mgf  
 Database : SwissProt ID ID\_2015\_10 (549646 sequences; 195983064 residues)  
 Taxonomy : Homo sapiens (human) (20197 sequences)  
 Timestamp : 19 Jan 2016 at 19:30:26 GMT  
 Enzyme : Trypsin  
 Variable modifications : [Carboxymethyl \(C\)](#), [Deamidated \(NQ\)](#), [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance :  $\pm 20$  ppm ( $^{13}\text{C} = 1$ )  
 Fragment Mass Tolerance :  $\pm 0.5$  Da  
 Max Missed Cleavages : 2  
 Instrument type : ESI-TRAP  
 Number of queries : 5013

**Protein hits** : [HS90A HUMAN](#) Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5  
[HS90B HUMAN](#) Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4  
[GRP78 HUMAN](#) 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2  
[EF2 HUMAN](#) Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4  
[EZRI HUMAN](#) Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4  
[FETA HUMAN](#) Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1  
[ALBU HUMAN](#) Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
[H90B2 HUMAN](#) Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2  
[ACTN1 HUMAN](#) Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2  
[GELS HUMAN](#) Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1  
[LUM HUMAN](#) Lumican OS=Homo sapiens GN=LUM PE=1 SV=2  
[TERA HUMAN](#) Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4  
[IMB1 HUMAN](#) Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[A2MG HUMAN](#) Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3  
[K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[ENPL HUMAN](#) Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1  
[HBA HUMAN](#) Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2  
[ITIH2 HUMAN](#) Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2  
[VPS35 HUMAN](#) Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2  
[K1C10 HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
[K2C1B HUMAN](#) Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3  
[PDC6I HUMAN](#) Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1  
[TRAP1 HUMAN](#) Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3  
[RADI HUMAN](#) Radixin OS=Homo sapiens GN=RDY PE=1 SV=1  
[HEP2 HUMAN](#) Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3  
[VTNC HUMAN](#) Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1  
[NUCL HUMAN](#) Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3  
[PSMD2 HUMAN](#) 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3  
[K2C6B HUMAN](#) Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5  
[SYG HUMAN](#) Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3  
[PDIA4 HUMAN](#) Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2  
[MX1 HUMAN](#) Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=4  
[QS0X1 HUMAN](#) Sulfhydryl oxidase 1 OS=Homo sapiens GN=QS0X1 PE=1 SV=3  
[H2A1B HUMAN](#) Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2  
[VASN HUMAN](#) Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1  
[COPG1 HUMAN](#) Coatamer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1  
[FUBP2 HUMAN](#) Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4  
[H4 HUMAN](#) Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2  
[CAND1 HUMAN](#) Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2  
[SEC23B HUMAN](#) Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[PYGL HUMAN](#) Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4  
[GFPT1 HUMAN](#) Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3  
[K2C8 HUMAN](#) Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7  
[CADH1 HUMAN](#) Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3  
[XPP3 HUMAN](#) Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1  
[KATL2 HUMAN](#) Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens GN=KATNAL2 PE=2 SV=3  
[TRFL HUMAN](#) Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6  
[ACPH HUMAN](#) Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4  
[ITIH3 HUMAN](#) Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2  
[HGFA HUMAN](#) Hepatocyte growth factor activator OS=Homo sapiens GN=HGFA PE=1 SV=1  
[HBB HUMAN](#) Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2  
[HNRPR HUMAN](#) Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNP R PE=1 SV=1  
[COPB HUMAN](#) Coatamer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3  
[HSPB1 HUMAN](#) Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2  
[G3PT HUMAN](#) Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDH PE=1 SV=2  
[FBLN1 HUMAN](#) Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4  
[XRCC5 HUMAN](#) X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3  
[HS71L HUMAN](#) Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2  
[CROCC HUMAN](#) Rootletin OS=Homo sapiens GN=CROCC PE=1 SV=1  
[RS27A HUMAN](#) Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2  
[XPOT HUMAN](#) Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2  
[NIBL1 HUMAN](#) Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3  
[STAT1 HUMAN](#) Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2

<a href="#">GOGB1_HUMAN</a>	Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2
<a href="#">PYGB_HUMAN</a>	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5
<a href="#">TFR1_HUMAN</a>	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2
<a href="#">GNS_HUMAN</a>	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3
<a href="#">C04A_HUMAN</a>	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2
<a href="#">COPB2_HUMAN</a>	Coatamer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2
<a href="#">CTNA1_HUMAN</a>	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1
<a href="#">AFAM_HUMAN</a>	Afamin OS=Homo sapiens GN=AFM PE=1 SV=1
<a href="#">EXOC3_HUMAN</a>	Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2
<a href="#">S31E1_HUMAN</a>	Spermatogenesis-associated protein 31E1 OS=Homo sapiens GN=SPATA31E1 PE=2 SV=2
<a href="#">CLCF1_HUMAN</a>	Cardiotrophin-like cytokine factor 1 OS=Homo sapiens GN=CLCF1 PE=1 SV=1
<a href="#">SKI_HUMAN</a>	Ski oncogene OS=Homo sapiens GN=SKI PE=1 SV=1
<a href="#">PLCE1_HUMAN</a>	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 OS=Homo sapiens GN=PLCE1 PE=1 SV=3
<a href="#">IRPL1_HUMAN</a>	Interleukin-1 receptor accessory protein-like 1 OS=Homo sapiens GN=IL1RAPL1 PE=1 SV=2
<a href="#">MRO2A_HUMAN</a>	Maestro heat-like repeat-containing protein family member 2A OS=Homo sapiens GN=MROH2A PE=4 SV=4
<a href="#">OR4A5_HUMAN</a>	Olfactory receptor 4A5 OS=Homo sapiens GN=OR4A5 PE=3 SV=4
<a href="#">MSL1_HUMAN</a>	Male-specific lethal 1 homolog OS=Homo sapiens GN=MSL1 PE=1 SV=3
<a href="#">PYR1_HUMAN</a>	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3
<a href="#">C06A1_HUMAN</a>	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3
<a href="#">ACTBM_HUMAN</a>	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1
<a href="#">UBA1_HUMAN</a>	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3
<a href="#">STIM2_HUMAN</a>	Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=2
<a href="#">SYTC_HUMAN</a>	Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3
<a href="#">RENT2_HUMAN</a>	Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 PE=1 SV=1
<a href="#">ABLM1_HUMAN</a>	Actin-binding LIM protein 1 OS=Homo sapiens GN=ABLM1 PE=1 SV=3
<a href="#">PSA_HUMAN</a>	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2
<a href="#">FAK2_HUMAN</a>	Protein-tyrosine kinase 2-beta OS=Homo sapiens GN=PTK2B PE=1 SV=2
<a href="#">GOGA4_HUMAN</a>	Golgin subfamily A member 4 OS=Homo sapiens GN=GOLGA4 PE=1 SV=1
<a href="#">PLAK_HUMAN</a>	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3
<a href="#">KCC2D_HUMAN</a>	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=1 SV=3
<a href="#">XYLB_HUMAN</a>	Xylulose kinase OS=Homo sapiens GN=XYLB PE=1 SV=3
<a href="#">DNJB8_HUMAN</a>	DnaJ homolog subfamily B member 8 OS=Homo sapiens GN=DNAJB8 PE=1 SV=1
<a href="#">NEK10_HUMAN</a>	Serine/threonine-protein kinase Nek10 OS=Homo sapiens GN=NEK10 PE=2 SV=3
<a href="#">5HT6R_HUMAN</a>	5-hydroxytryptamine receptor 6 OS=Homo sapiens GN=HTR6 PE=1 SV=1
<a href="#">HS12B_HUMAN</a>	Heat shock 70 kDa protein 12B OS=Homo sapiens GN=HSPA12B PE=1 SV=2
<a href="#">ZN594_HUMAN</a>	Zinc finger protein 594 OS=Homo sapiens GN=ZNF594 PE=2 SV=3
<a href="#">DMD_HUMAN</a>	Dystrophin OS=Homo sapiens GN=DMD PE=1 SV=3
<a href="#">DYM_HUMAN</a>	Dymeclin OS=Homo sapiens GN=DYM PE=1 SV=1
<a href="#">POSTN_HUMAN</a>	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2
<a href="#">MOS_HUMAN</a>	Proto-oncogene serine/threonine-protein kinase mos OS=Homo sapiens GN=MOS PE=1 SV=1
<a href="#">H2B1A_HUMAN</a>	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3
<a href="#">HES2_HUMAN</a>	Transcription factor HES-2 OS=Homo sapiens GN=HES2 PE=2 SV=1

SwissProt\_ID [Decoy](#) False discovery rate

Peptide matches above identity threshold	380	36	9.47 %
Peptide matches above homology or identity threshold	465	56	12.04 %

## Select Summary Report

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Significance threshold p< 
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 Show Percolator scores ☐

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off 
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 Require bold red ☐

Preferred taxonomy

☒ All queries
 ☐ Unassigned
 ☐ Below homology threshold
 ☐ Below identity threshold

1. [HS90A\\_HUMAN](#) Mass: 84607 Score: 2216 Matches: 64(64) Sequences: 32(32) emPAI: 2.73

Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">133</a>	365.7270	729.4394	729.4385	1.24	0	40	0.0057	1		K.LSELLR.Y
<a href="#">278</a>	408.2595	814.5044	814.5065	-2.54	0	50	0.00033	1	U	R.ALLFVPR.R <a href="#">279</a>
<a href="#">372</a>	429.7731	857.5317	857.5334	-2.06	1	36	0.011	1	U	K.KLSELLR.Y <a href="#">374</a>
<a href="#">519</a>	474.7268	947.4391	947.4389	0.26	0	51	0.00051	1	U	K.FYEQFSK.N <a href="#">518</a>
<a href="#">597</a>	329.5499	985.6280	985.6284	-0.43	2	26	0.04	1	U	R.KKSELLR.Y
<a href="#">931</a>	554.7729	1107.5313	1107.5349	-3.21	0	56	0.00022	1	U	R.APFDLFENR.K <a href="#">932</a>
<a href="#">1069</a>	576.2847	1150.5548	1150.5506	3.65	0	47	0.0015	1		K.YIDQEELNK.T
<a href="#">1317</a>	612.8174	1223.6203	1223.6186	1.40	0	50	0.00089	1	U	K.HIYYITGETK.D <a href="#">1316</a>
<a href="#">1357</a>	618.3049	1234.5953	1234.5942	0.89	0	85	3e-007	1	U	K.DQVANSFVER.L <a href="#">1356</a>
<a href="#">1374</a>	621.8557	1241.6969	1241.6979	-0.84	0	80	5.4e-007	1		K.ADLINNLGTIAK.S <a href="#">1375</a>
<a href="#">1436</a>	632.8252	1263.6358	1263.6360	-0.13	1	55	0.0003	1	U	R.RAPFDLFENR.K <a href="#">1434</a> <a href="#">1440</a>
<a href="#">1515</a>	646.3229	1290.6313	1290.6303	0.80	0	70	9.6e-006	1	U	R.ELISNSDALDK.I <a href="#">1516</a>
<a href="#">1575</a>	436.8994	1307.6762	1307.6721	3.16	1	36	0.022	1		K.IRYESLTPSK.L
<a href="#">1578</a>	656.2864	1310.5583	1310.5626	-3.27	0	45	0.0013	1		K.EDQTEYLEER.R
<a href="#">1679</a>	450.2270	1347.6592	1347.6572	1.54	0	42	0.0065	1		K.HFSVEGQLEFR.A
<a href="#">1743</a>	683.3696	1364.7247	1364.7221	1.88	0	104	2.8e-009	1	U	R.TLTIVDTGIGMTK.A <a href="#">1739</a> <a href="#">1742</a> <a href="#">1744</a>

<a href="#">1853</a>	470.2359	1407.6859	1407.6881	-1.60	1	37	0.019	1		K.EKYIDQEELNK.T
<a href="#">1854</a>	704.8520	1407.6894	1407.6881	0.92	1	(36)	0.025	1		K.EKYIDQEELNK.T
<a href="#">1871</a>	708.8221	1415.6297	1415.6303	-0.43	0	53	0.00023	1		K.EGLELPEDEEEK.K
<a href="#">2165</a>	505.2659	1512.7760	1512.7784	-1.60	0	(46)	0.0024	1		R.GVVDSEDLPLNISR.E
<a href="#">2166</a>	757.3958	1512.7771	1512.7784	-0.86	0	108	1.4e-009	1		R.GVVDSEDLPLNISR.E <a href="#">2168</a>
<a href="#">2197</a>	509.9178	1526.7317	1526.7365	-3.14	0	(43)	0.0039	1		K.SLTNDWEDHLAVK.H
<a href="#">2199</a>	764.3779	1526.7413	1526.7365	3.14	0	76	2.5e-006	1		K.SLTNDWEDHLAVK.H
<a href="#">2236</a>	513.9229	1538.7467	1538.7464	0.21	1	(34)	0.036	1		R.YESLTDPSKLDGK.E
<a href="#">2238</a>	770.3824	1538.7503	1538.7464	2.56	1	57	0.00018	1		R.YESLTDPSKLDGK.E
<a href="#">2309</a>	520.9458	1559.8156	1559.8155	0.07	1	(34)	0.043	1	U	R.ELISNSSDALDKIR.Y
<a href="#">2310</a>	780.9163	1559.8180	1559.8155	1.61	1	96	2.7e-008	1	U	R.ELISNSSDALDKIR.Y
<a href="#">2322</a>	783.8549	1565.6953	1565.6919	2.15	0	92	4.4e-008	1	U	R.YYTSASGDEMVSILK.D <a href="#">2323</a>
<a href="#">2933</a>	593.6555	1777.9447	1777.9403	2.48	0	62	5.4e-005	1	U	K.HSQFIGYPITLFVEK.E <a href="#">2930</a> <a href="#">2931</a> <a href="#">2932</a> <a href="#">2935</a>
<a href="#">2936</a>	889.9812	1777.9479	1777.9403	4.24	0	(58)	0.00011	1	U	K.HSQFIGYPITLFVEK.E <a href="#">2937</a>
<a href="#">2962</a>	596.3207	1785.9404	1785.9373	1.72	0	(42)	0.0059	1	U	K.HLEINPDHSIETLR.Q <a href="#">2959</a>
<a href="#">2963</a>	893.9780	1785.9414	1785.9373	2.27	0	77	1.7e-006	1	U	K.HLEINPDHSIETLR.Q
<a href="#">3076</a>	917.3964	1832.7782	1832.7741	2.24	0	99	6.4e-009	1	U	R.NPDDITNEEYGEFYK.S <a href="#">3077</a>
<a href="#">3259</a>	479.5150	1914.0307	1914.0323	-0.82	1	36	0.018	1	U	K.KHLEINPDHSIETLR.Q
<a href="#">3568</a>	672.3538	2014.0395	2014.0371	1.18	1	52	0.00073	1		K.VILHLKEDQTEYLEER.R
<a href="#">3651</a>	688.7009	2063.0808	2063.0840	-1.56	1	93	5.1e-008	1	U	K.HSQFIGYPITLFVEKER.D <a href="#">3650</a> <a href="#">3653</a> <a href="#">3655</a>
<a href="#">4112</a>	611.0590	2440.2070	2440.2023	1.93	1	44	0.0054	1	U	K.HIYITGETKQVANSFAVER.L
<a href="#">4516</a>	751.3943	3001.5483	3001.5396	2.88	0	91	8.4e-008	1	U	K.DLVILLYETALLSSGFSLEDPTQTHANR.I
<a href="#">4606</a>	1106.2064	3315.5974	3315.5832	4.30	0	42	0.0097	1		K.AFMEALQAGADISMIQGVGFYSAYLVAEK.V

2. [HS90B\\_HUMAN](#) Mass: 83212 Score: 1626 Matches: 49(49) Sequences: 30(30) emPAI: 2.44

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">133</a>	365.7270	729.4394	729.4385	1.24	0	40	0.0057	1		R.LSELLR.Y
<a href="#">326</a>	415.2684	828.5222	828.5221	0.06	0	40	0.0039	1	U	R.ALLFIPR.R <a href="#">327</a>
<a href="#">416</a>	443.7763	885.5380	885.5396	-1.77	1	39	0.0054	1	U	R.RSELLR.Y <a href="#">417</a>
<a href="#">422</a>	446.2166	890.4186	890.4174	1.29	0	38	0.0091	1	U	K.FYEAFSK.N
<a href="#">858</a>	540.7722	1079.5299	1079.5287	1.05	0	41	0.006	1	U	R.APFDLFENK.K
<a href="#">1069</a>	576.2847	1150.5548	1150.5506	3.65	0	47	0.0015	1		K.YIDQEELNK.T
<a href="#">1112</a>	580.7964	1159.5782	1159.5761	1.85	0	64	3.4e-005	1		K.SIYYITGESK.E
<a href="#">1233</a>	597.8266	1193.6386	1193.6404	-1.48	0	58	8.7e-005	1	U	K.IDIIPNPQER.T <a href="#">1236</a>
<a href="#">1363</a>	618.8226	1235.6307	1235.6299	0.70	1	42	0.0054	1	U	R.RAPFDLFENK.K <a href="#">1364</a>
<a href="#">1374</a>	621.8557	1241.6969	1241.6979	-0.84	0	80	5.4e-007	1		K.ADLINNLGTIAK.S <a href="#">1375</a>
<a href="#">1392</a>	625.3105	1248.6064	1248.6098	-2.75	0	60	9e-005	1	U	K.EQVANSFAVER.V
<a href="#">1480</a>	638.3262	1274.6379	1274.6354	1.99	0	86	2.7e-007	1		R.ELISNASDALDK.I <a href="#">1479</a>
<a href="#">1575</a>	436.8994	1307.6762	1307.6721	3.16	1	36	0.022	1		K.IRYESLTDPSK.L
<a href="#">1578</a>	656.2864	1310.5583	1310.5626	-3.27	0	45	0.0013	1		K.EDQTEYLEER.R
<a href="#">1679</a>	450.2270	1347.6592	1347.6572	1.54	0	42	0.0065	1		K.HFSVEGQLEFR.A
<a href="#">1743</a>	683.3696	1364.7247	1364.7221	1.88	0	104	2.8e-009	1	U	R.TLTLVDTGIGMTK.A <a href="#">1739</a> <a href="#">1742</a> <a href="#">1744</a>
<a href="#">1853</a>	470.2359	1407.6859	1407.6881	-1.60	1	37	0.019	1		K.EKYIDQEELNK.T
<a href="#">1854</a>	704.8520	1407.6894	1407.6881	0.92	1	(36)	0.025	1		K.EKYIDQEELNK.T
<a href="#">1871</a>	708.8221	1415.6297	1415.6303	-0.43	0	53	0.00023	1		K.EGLELPEDEEEK.K
<a href="#">2165</a>	505.2659	1512.7760	1512.7784	-1.60	0	(46)	0.0024	1		R.GVVDSEDLPLNISR.E
<a href="#">2166</a>	757.3958	1512.7771	1512.7784	-0.86	0	108	1.4e-009	1		R.GVVDSEDLPLNISR.E <a href="#">2168</a>
<a href="#">2197</a>	509.9178	1526.7317	1526.7365	-3.14	0	(43)	0.0039	1		K.SLTNDWEDHLAVK.H
<a href="#">2199</a>	764.3779	1526.7413	1526.7365	3.14	0	76	2.5e-006	1		K.SLTNDWEDHLAVK.H
<a href="#">2236</a>	513.9229	1538.7467	1538.7464	0.21	1	(34)	0.036	1		R.YESLTDPSKLDGK.E
<a href="#">2238</a>	770.3824	1538.7503	1538.7464	2.56	1	57	0.00018	1		R.YESLTDPSKLDGK.E
<a href="#">2262</a>	515.6126	1543.8160	1543.8205	-2.94	1	(43)	0.0049	1		R.ELISNASDALDKIR.Y
<a href="#">2263</a>	772.9161	1543.8177	1543.8205	-1.82	1	99	1.3e-008	1		R.ELISNASDALDKIR.Y
<a href="#">2942</a>	594.9855	1781.9346	1781.9424	-4.39	0	49	0.00093	1	U	K.HLEINPDHPIVETLR.Q <a href="#">2944</a>
<a href="#">3025</a>	603.6592	1807.9557	1807.9509	2.69	0	77	1.7e-006	1	U	K.HSQFIGYPITLYLEK.E <a href="#">3024</a>
<a href="#">3113</a>	924.3993	1846.7840	1846.7897	-3.08	0	89	5.6e-008	1	U	R.NPDDITQEEYGEFYK.S <a href="#">3115</a>
<a href="#">3114</a>	616.6051	1846.7935	1846.7897	2.04	0	(47)	0.00098	1	U	R.NPDDITQEEYGEFYK.S
<a href="#">3568</a>	672.3538	2014.0395	2014.0371	1.18	1	52	0.00073	1		K.VILHLKEDQTEYLEER.R
<a href="#">3708</a>	698.7075	2093.1005	2093.0945	2.87	1	73	4.7e-006	1	U	K.HSQFIGYPITLYLEKER.E
<a href="#">3819</a>	731.6500	2191.9282	2191.9328	-2.07	0	48	0.00076	1	U	R.YHTSQSGDEMISLSEYVSR.M
<a href="#">4606</a>	1106.2064	3315.5974	3315.5832	4.30	0	42	0.0097	1		K.AFMEALQAGADISMIQGVGFYSAYLVAEK.V
<a href="#">4766</a>	1384.6331	4150.8773	4150.8536	5.73	1	60	0.0001	1	U	K.LGLGIDEDEVAEEPNAAVPDEIPPLEGDEASRMEEVD.-

3. [GRP78\\_HUMAN](#) Mass: 72288 Score: 628 Matches: 15(15) Sequences: 14(14) emPAI: 0.74

78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1338</a>	617.3156	1232.6167	1232.6183	-1.33	0	74	4.4e-006	1	U	K.DAGTIAGLNVMR.I
<a href="#">1596</a>	658.8202	1315.6258	1315.6295	-2.83	0	54	0.00029	1	U	R.NELESYAYSLK.N
<a href="#">1815</a>	699.3955	1396.7765	1396.7813	-3.47	0	55	0.00015	1	U	K.ELEEIVQPIISK.L
<a href="#">1905</a>	715.8485	1429.6825	1429.6838	-0.90	0	91	6.6e-008	1	U	R.TWNPSPVQDIK.F

<a href="#">2282</a>	776.9019	1551.7893	1551.7854	2.48	0	97	2e-008	1	U	K.TFAPEEISAMVLTK.M <a href="#">2283</a>
<a href="#">2294</a>	519.2709	1554.7910	1554.7862	3.05	1	53	0.00044	1	U	K.NGRVEIANDQGNR.I
<a href="#">2328</a>	783.8976	1565.7807	1565.7726	5.22	0	59	0.00012	1	U	R.ITPSYVAFTPEGER.L
<a href="#">2445</a>	535.6274	1603.8603	1603.8570	2.08	0	33	0.04	1	U	K.TKPYIQVDIGGGQTK.T
<a href="#">2599</a>	551.9963	1652.9670	1652.9712	-2.55	2	30	0.018	1	U	K.KKELEEIVQPIISK.L
<a href="#">2672</a>	839.4100	1676.8055	1676.8006	2.95	0	99	1.3e-008	1	U	K.NQLTSNPENTVFDK.R
<a href="#">3003</a>	601.3047	1800.8924	1800.8893	1.71	1	58	0.00018	1	U	R.IDTRNELESYAYSLLK.N
<a href="#">3042</a>	606.0045	1814.9917	1814.9890	1.50	1	48	0.001	1	U	R.IINEPTAAAIAYGLDKR.E
<a href="#">3785</a>	1083.0009	2163.9872	2163.9848	1.09	0	89	1.3e-007	1	U	R.IEIESFYEGEDFSETLTR.A
<a href="#">3803</a>	1088.5044	2174.9942	2174.9855	4.01	1	85	3.1e-007	1	U	K.LYGAGPPPTGEEDTAEKDEL.-

4. [EF2\\_HUMAN](#) Mass: 95277 Score: 570 Matches: 16(16) Sequences: 12(12) emPAI: 0.52

Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">420</a>	445.7592	889.5039	889.5022	2.00	0	31	0.046	1	U	K.FSVSPVVR.V
<a href="#">883</a>	546.2961	1090.5777	1090.5771	0.56	0	67	1.9e-005	1	U	M.VNFTVDQIR.A
<a href="#">912</a>	550.7773	1099.5400	1099.5372	2.54	0	31	0.041	1	U	K.VFDAIMNFK.K
<a href="#">916</a>	551.7638	1101.5130	1101.5165	-3.11	0	32	0.033	1	U	K.QFAEMYVAK.F
<a href="#">928</a>	554.3250	1106.6354	1106.6336	1.60	0	80	3.3e-007	1	U	R.VFSGVLSTGLK.V
<a href="#">1841</a>	351.4570	1401.7988	1401.7980	0.58	1	30	0.048	1	U	K.KEDLYLKPIQR.T
<a href="#">1970</a>	722.8901	1443.7657	1443.7609	3.32	1	78	1.4e-006	1	U	K.EGIPALDNFLDKL.- <a href="#">1971</a> <a href="#">1972</a>
<a href="#">2844</a>	581.6625	1741.9656	1741.9614	2.40	2	36	0.013	1	U	K.GLKEGIPALDNFLDKL.-
<a href="#">2998</a>	900.4567	1798.8989	1798.8890	5.51	0	106	2.3e-009	1	U	K.AYLPVNESFGFTADLR.S
<a href="#">3829</a>	735.3750	2203.1032	2203.1048	-0.75	0	(86)	3.4e-007	1	U	K.STAISLFYELSENDLNFIK.Q
<a href="#">3831</a>	1102.5604	2203.1063	2203.1048	0.67	0	91	9.8e-008	1	U	K.STAISLFYELSENDLNFIK.Q
<a href="#">3852</a>	740.7251	2219.1535	2219.1474	2.75	0	(56)	0.00025	1	U	R.ALLELQLEPEELYQTFQR.I
<a href="#">3853</a>	1110.5859	2219.1573	2219.1474	4.49	0	91	7.4e-008	1	U	R.ALLELQLEPEELYQTFQR.I
<a href="#">4342</a>	872.8152	2615.4237	2615.4145	3.52	0	35	0.014	1	U	R.WLPAGDALLQMITIHLSPVTAQK.Y

5. [EZRI\\_HUMAN](#) Mass: 69370 Score: 534 Matches: 14(14) Sequences: 11(11) emPAI: 0.64

Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">425</a>	447.7754	893.5363	893.5375	-1.33	0	47	0.00029	1		K.LFFLQVK.E <a href="#">426</a>
<a href="#">463</a>	457.7703	913.5260	913.5232	3.06	0	50	0.00044	1	U	K.IALLEEAR.R
<a href="#">565</a>	488.7773	975.5400	975.5389	1.10	0	45	0.0026	1		K.QLFDQVVK.T
<a href="#">840</a>	357.5490	1069.6252	1069.6243	0.80	1	33	0.015	1	U	K.IALLEEAR.R
<a href="#">925</a>	552.7944	1103.5743	1103.5764	-1.86	0	63	5.2e-005	1		K.IGFPWSEIR.N
<a href="#">967</a>	560.7839	1119.5533	1119.5560	-2.41	1	40	0.0095	1	U	K.QRIDEFEAL.-
<a href="#">1190</a>	591.7996	1181.5847	1181.5869	-1.91	0	71	6e-006	1		K.APDFVFYAPR.L
<a href="#">1975</a>	723.4037	1444.7928	1444.7885	2.97	0	117	1.4e-010	1	U	R.QLTLSSSELSQAR.D
<a href="#">2593</a>	826.4152	1650.8159	1650.8100	3.55	0	124	4.2e-011	1	U	K.SQEQLAAELAEYAK.I
<a href="#">3404</a>	981.9842	1961.9538	1961.9444	4.79	0	67	2.6e-005	1	U	K.IAQDLEMYGINYFEIK.N
<a href="#">3618</a>	680.0073	2037.0000	2036.9942	2.81	0	(61)	9.4e-005	1	U	K.FYPEDVAEELIQDITQK.L <a href="#">3617</a>
<a href="#">3619</a>	1019.5117	2037.0088	2036.9942	7.13	0	62	7.6e-005	1	U	K.FYPEDVAEELIQDITQK.L

6. [FETA\\_HUMAN](#) Mass: 68633 Score: 512 Matches: 15(15) Sequences: 3(3) emPAI: 0.18

Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">572</a>	490.2584	978.5022	978.5022	0.05	0	50	0.00082	1	U	K.GYQELLEK.C <a href="#">573</a>
<a href="#">1067</a>	575.8114	1149.6083	1149.6030	4.61	0	50	0.00075	1	U	K.YIQESQALAK.R
<a href="#">3202</a>	631.6644	1891.9713	1891.9720	-0.37	0	(57)	0.00025	1	U	K.LGEYYLQNAFLVAYTK.K <a href="#">3201</a> <a href="#">3203</a> <a href="#">3210</a> <a href="#">3213</a>
<a href="#">3208</a>	946.9937	1891.9729	1891.9720	0.48	0	80	1e-006	1	U	K.LGEYYLQNAFLVAYTK.K <a href="#">3200</a> <a href="#">3205</a> <a href="#">3206</a> <a href="#">3215</a> <a href="#">3216</a> <a href="#">3218</a>

7. [ALBU\\_HUMAN](#) Mass: 69321 Score: 407 Matches: 11(11) Sequences: 3(3) emPAI: 0.18

Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">492</a>	464.2503	926.4861	926.4861	-0.01	0	48	0.00061	1	U	K.YLYEIAR.R <a href="#">489</a> <a href="#">490</a> <a href="#">491</a> <a href="#">493</a>
<a href="#">2160</a>	756.4263	1510.8380	1510.8355	1.63	0	82	2.7e-007	1	U	K.VPQVSTPTLVEVSR.N
<a href="#">2547</a>	547.3177	1638.9312	1638.9305	0.46	1	(82)	2e-007	1	U	K.KVPQVSTPTLVEVSR.N <a href="#">2546</a> <a href="#">2548</a>
<a href="#">2550</a>	820.4749	1638.9352	1638.9305	2.85	1	107	5.5e-010	1	U	K.KVPQVSTPTLVEVSR.N <a href="#">2549</a>

8. [H90B2\\_HUMAN](#) Mass: 44321 Score: 381 Matches: 12(12) Sequences: 8(8) emPAI: 0.89

Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1069</a>	576.2847	1150.5548	1150.5506	3.65	0	47	0.0015	1		K.YIDQEELNK.T
<a href="#">1112</a>	580.7964	1159.5782	1159.5761	1.85	0	64	3.4e-005	1		K.SIYYITGESK.E
<a href="#">1374</a>	621.8557	1241.6969	1241.6979	-0.84	0	80	5.4e-007	1		K.ADLINNLGTIAK.F <a href="#">1375</a>
<a href="#">1575</a>	436.8994	1307.6762	1307.6721	3.16	1	36	0.022	1		K.IRYESLTPSK.L
<a href="#">1853</a>	470.2359	1407.6859	1407.6881	-1.60	1	37	0.019	1		K.EKYIDQEELNK.T

<a href="#">1854</a>	704.8520	1407.6894	1407.6881	0.92	1	(36)	0.025	1		K.EKYIDQEELNK.T
<a href="#">2236</a>	513.9229	1538.7467	1538.7464	0.21	1	(34)	0.036	1		R.YESLTDPSKLDGK.E
<a href="#">2238</a>	770.3824	1538.7503	1538.7464	2.56	1	57	0.00018	1		R.YESLTDPSKLDGK.E
<a href="#">3025</a>	603.6592	1807.9557	1807.9509	2.69	0	77	1.7e-006	1	U	K.HSQFLGPITLYLEK.E <a href="#">3024</a>
<a href="#">3708</a>	698.7075	2093.1005	2093.0945	2.87	1	73	4.7e-006	1	U	K.HSQFLGPITLYLEKER.E

9. [ACTN1\\_HUMAN](#) Mass: 102993 Score: 378 Matches: 8(8) Sequences: 7(7) emPAI: 0.21

Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1281</a>	608.3417	1214.6688	1214.6659	2.39	0	75	2.7e-006	1	U	K.LASDLLEWIR.R
<a href="#">1797</a>	693.8928	1385.7710	1385.7667	3.09	0	85	2.3e-007	1	U	R.VGWEQLLTTIAR.T <a href="#">1798</a>
<a href="#">1801</a>	694.8962	1387.7779	1387.7745	2.50	0	60	5.3e-005	1	U	K.LMLLLEVISGER.L
<a href="#">1904</a>	715.3835	1428.7524	1428.7572	-3.37	0	70	9.6e-006	1	U	R.TINEVENQILTR.D
<a href="#">2231</a>	769.3931	1536.7717	1536.7671	2.97	0	72	6.1e-006	1	U	R.FAIQDISVEETSAK.E
<a href="#">2748</a>	856.4615	1710.9085	1710.9080	0.34	0	66	1.8e-005	1	U	K.LLETIDQLYLEYAK.R
<a href="#">4015</a>	780.4029	2338.1869	2338.1805	2.73	0	63	5.4e-005	1	U	K.IDQLEGDHQLIQEALIFDNK.H

10. [GELS\\_HUMAN](#) Mass: 85644 Score: 354 Matches: 11(11) Sequences: 7(7) emPAI: 0.31

Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">120</a>	346.7101	691.4056	691.4057	-0.26	0	30	0.03	1	U	K.IFVWK.G
<a href="#">1481</a>	425.9104	1274.7093	1274.7095	-0.20	0	44	0.0022	1	U	K.HVVPNEVVVQR.L <a href="#">1483</a>
<a href="#">1482</a>	638.3622	1274.7099	1274.7095	0.32	0	(37)	0.012	1	U	K.HVVPNEVVVQR.L
<a href="#">1604</a>	660.3525	1318.6905	1318.6881	1.84	0	85	2.8e-007	1	U	K.AGALNSNDAFVLK.T
<a href="#">2782</a>	861.9231	1721.8316	1721.8301	0.90	0	98	1.7e-008	1	U	R.EVQGFSATFLGYFK.S <a href="#">2783</a>
<a href="#">3064</a>	915.4894	1828.9643	1828.9571	3.96	0	69	1.2e-005	1	U	K.QTQVSVLPEGGETPLFK.Q <a href="#">3065</a>
<a href="#">4403</a>	924.4512	2770.3319	2770.3279	1.44	0	39	0.018	1	U	K.VPVPATYQGFGGDSYIILYNR.H
<a href="#">4693</a>	1134.2203	3399.6392	3399.6299	2.73	1	36	0.039	1	U	R.IEGSNKVPVPATYQGFGGDSYIILYNR.H

11. [LUM\\_HUMAN](#) Mass: 38405 Score: 319 Matches: 8(8) Sequences: 1(1) emPAI: 0.16

Lumican OS=Homo sapiens GN=LUM PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3384</a>	653.0404	1956.0994	1956.0932	3.19	0	(54)	0.00012	1	U	R.LPSGLPVSLLTLYLDNNK.I <a href="#">3383</a> <a href="#">3386</a>
<a href="#">3387</a>	979.0587	1956.1029	1956.0932	4.97	0	82	2e-007	1	U	R.LPSGLPVSLLTLYLDNNK.I <a href="#">3385</a> <a href="#">3388</a> <a href="#">3389</a> <a href="#">3390</a>

12. [TERA\\_HUMAN](#) Mass: 89266 Score: 315 Matches: 11(11) Sequences: 7(7) emPAI: 0.29

Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">726</a>	516.7833	1031.5520	1031.5499	2.03	0	42	0.0059	1	U	K.GDDLSTAILK.Q
<a href="#">789</a>	525.2777	1048.5409	1048.5441	-3.05	0	59	0.00011	1	U	K.DVDLEFLAK.M
<a href="#">1149</a>	586.8365	1171.6585	1171.6601	-1.34	0	68	1e-005	1	U	R.GILLYGPPGTGK.T
<a href="#">1297</a>	778.9359	1555.8573	1555.8497	4.85	0	57	0.00012	1	U	R.LDQLIYIPLPDEK.S
<a href="#">2567</a>	549.2741	1644.8005	1644.7930	4.58	1	48	0.0018	1	U	R.KYEMFAQTLQQSR.G
<a href="#">3030</a>	604.3400	1809.9981	1809.9876	5.78	0	(51)	0.00035	1	U	K.NAPAIIFIDELDAIAPK.R <a href="#">3028</a>
<a href="#">3032</a>	906.0093	1810.0041	1809.9876	9.12	0	71	3.3e-006	1	U	K.NAPAIIFIDELDAIAPK.R <a href="#">3031</a> <a href="#">3033</a>
<a href="#">3938</a>	758.0520	2271.1342	2271.1245	4.24	0	43	0.0062	1	U	R.AVANETGAFFFLINGPEIMSK.L

13. [IMB1\\_HUMAN](#) Mass: 97108 Score: 303 Matches: 10(10) Sequences: 5(5) emPAI: 0.23

Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">715</a>	515.2781	1028.5416	1028.5403	1.27	0	43	0.0029	1	U	R.WLAIDANAR.R
<a href="#">2449</a>	803.4484	1604.8823	1604.8773	3.09	0	63	2.8e-005	1	U	K.LAATNALLNSLEFTK.A
<a href="#">2618</a>	553.6432	1657.9077	1657.9039	2.31	0	(46)	0.0016	1	U	R.AAVENLPTFLVLSR.V
<a href="#">2620</a>	829.9628	1657.9110	1657.9039	4.27	0	82	4e-007	1	U	R.AAVENLPTFLVLSR.V <a href="#">2621</a>
<a href="#">2884</a>	880.0214	1758.0282	1758.0291	-0.54	0	(38)	0.0022	1	U	K.GALQYLVPILTQTLTK.Q
<a href="#">2886</a>	587.0198	1758.0375	1758.0291	4.77	0	47	0.00022	1	U	K.GALQYLVPILTQTLTK.Q <a href="#">2885</a> <a href="#">2887</a>
<a href="#">3576</a>	672.6641	2014.9705	2014.9742	-1.81	0	46	0.0032	1	U	R.LQQVLQMESHQSTSDR.I

14. [K2C1\\_HUMAN](#) Mass: 65999 Score: 301 Matches: 6(6) Sequences: 5(5) emPAI: 0.24

Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">559</a>	487.2681	972.5216	972.5240	-2.46	0	58	0.00013	1		K.IEISELNR.V
<a href="#">1179</a>	590.3026	1178.5905	1178.5931	-2.18	0	64	3.7e-005	1		K.YEELQITAGR.H
<a href="#">1541</a>	651.8630	1301.7115	1301.7078	2.84	0	115	2.3e-010	1	U	R.SLDLDSIIAEVK.A
<a href="#">2055</a>	738.3959	1474.7772	1474.7780	-0.53	0	103	4.5e-009	1		R.FLEQQNQVLQTK.W <a href="#">2056</a>
<a href="#">4063</a>	1192.4880	2382.9615	2382.9447	7.08	0	37	0.0045	1	U	R.GGGGGGYSGGSSYSGGGGSGGGGGGGR.G



15. [A2MG\\_HUMAN](#) Mass: 163188 Score: 295 Matches: 8(8) Sequences: 3(3) emPAI: 0.05

Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">673</a>	509.8008	1017.5871	1017.5859	1.19	0	61	3.6e-005	1	U	K.ATVLNLYPK.C <a href="#">671</a> <a href="#">672</a>
<a href="#">962</a>	558.8050	1115.5954	1115.5975	-1.87	0	69	1.1e-005	1	U	R.QTVSWAVTPK.S
<a href="#">1263</a>	605.8229	1209.6313	1209.6353	-3.31	0	75	1.9e-006	1	U	K.LPPNVVEESAR.A <a href="#">1264</a> <a href="#">1265</a> <a href="#">1266</a>

16. [K22E\\_HUMAN](#) Mass: 65393 Score: 269 Matches: 5(5) Sequences: 4(4) emPAI: 0.19

Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">559</a>	487.2681	972.5216	972.5240	-2.46	0	58	0.00013	1		K.IEISELNR.V
<a href="#">1630</a>	665.3682	1328.7219	1328.7187	2.39	0	83	3.8e-007	1		R.NLDLDSIAEVK.A
<a href="#">2011</a>	730.9057	1459.7968	1459.7922	3.17	0	83	3.5e-007	1	U	K.VDLLNQIEFLK.V
<a href="#">2055</a>	738.3959	1474.7772	1474.7780	-0.53	0	103	4.5e-009	1		R.FLEQQNQVLQTK.W <a href="#">2056</a>

17. [ENPL\\_HUMAN](#) Mass: 92411 Score: 256 Matches: 6(6) Sequences: 4(4) emPAI: 0.17

Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">546</a>	482.2965	962.5784	962.5800	-1.69	0	32	0.011	1	U	K.LIINSLYK.N
<a href="#">1480</a>	638.3262	1274.6379	1274.6354	1.99	0	86	2.7e-007	1		R.ELISNASDALDK.I <a href="#">1479</a>
<a href="#">2089</a>	743.3826	1484.7506	1484.7471	2.35	0	61	7.1e-005	1	U	K.GVVDSDDLPLNVS.R
<a href="#">2262</a>	515.6126	1543.8160	1543.8205	-2.94	1	(43)	0.0049	1		R.ELISNASDALDKIR.L
<a href="#">2263</a>	772.9161	1543.8177	1543.8205	-1.82	1	99	1.3e-008	1		R.ELISNASDALDKIR.L

18. [HBA\\_HUMAN](#) Mass: 15248 Score: 248 Matches: 8(8) Sequences: 3(3) emPAI: 1.04

Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">879</a>	363.2132	1086.6177	1086.6186	-0.84	1	34	0.026	1	U	K.LRVDPVNFK.L
<a href="#">1419</a>	626.8597	1251.7048	1251.7075	-2.12	0	104	1.6e-009	1	U	K.FLASVSTVLSK.Y <a href="#">1420</a>
<a href="#">2207</a>	510.5816	1528.7231	1528.7270	-2.56	0	(55)	0.00024	1	U	K.VGAHAGEYGAEALER.M <a href="#">2209</a> <a href="#">2210</a>
<a href="#">2211</a>	765.3726	1528.7307	1528.7270	2.42	0	74	3.5e-006	1	U	K.VGAHAGEYGAEALER.M <a href="#">2208</a>

19. [ITIH2\\_HUMAN](#) Mass: 106397 Score: 225 Matches: 6(6) Sequences: 3(3) emPAI: 0.11

Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1651</a>	669.3624	1336.7102	1336.7139	-2.80	0	57	0.00013	1	U	K.FYNQVSTPLLR.N <a href="#">1652</a>
<a href="#">2379</a>	791.9331	1581.8517	1581.8474	2.66	0	101	4.4e-009	1	U	K.IQPSGGTINIEALLR.A <a href="#">2378</a>
<a href="#">2728</a>	568.6532	1702.9378	1702.9406	-1.66	0	(41)	0.0047	1	U	K.LWAYLTINQLLAER.S
<a href="#">2729</a>	852.4778	1702.9411	1702.9406	0.32	0	79	7.5e-007	1	U	K.LWAYLTINQLLAER.S

20. [VPS35\\_HUMAN](#) Mass: 91649 Score: 223 Matches: 9(9) Sequences: 8(8) emPAI: 0.32

Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">592</a>	492.8138	983.6130	983.6128	0.25	0	70	1.8e-006	1	U	R.ILVGTNLVR.L
<a href="#">661</a>	506.2961	1010.5777	1010.5760	1.71	0	45	0.00087	1	U	K.AELAEPLR.L
<a href="#">749</a>	520.8276	1039.6406	1039.6389	1.59	0	35	0.0039	1	U	K.NIIIALIDR.L
<a href="#">1377</a>	622.3354	1242.6562	1242.6568	-0.46	0	61	5.7e-005	1	U	R.LSQLEGVNVVER.Y
<a href="#">2431</a>	801.9567	1601.8988	1601.9028	-2.54	0	71	3.7e-006	1	U	K.IPVDTYNNILTVLK.L
<a href="#">2480</a>	539.6499	1615.9279	1615.9297	-1.14	0	30	0.028	1	U	K.AQLAATLIIGTFER.M
<a href="#">3129</a>	618.0048	1850.9926	1850.9891	1.93	0	57	0.00013	1	U	K.LFDIFSQQVATVIQSR.Q
<a href="#">3131</a>	926.5076	1851.0007	1850.9891	6.29	0	(39)	0.008	1	U	K.LFDIFSQQVATVIQSR.Q
<a href="#">3302</a>	645.3517	1933.0334	1933.0309	1.31	0	32	0.043	1	U	K.VADLYELVQYAGNIIPR.L

21. [K1C10\\_HUMAN](#) Mass: 58792 Score: 215 Matches: 6(6) Sequences: 5(5) emPAI: 0.34

Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">721</a>	516.3013	1030.5880	1030.5910	-2.94	0	70	6e-006	1	U	R.VLDELTLTK.A
<a href="#">831</a>	355.5414	1063.6024	1063.6026	-0.15	1	39	0.0054	1	U	R.LASYLDKVR.A
<a href="#">938</a>	555.2493	1108.4840	1108.4825	1.33	0	53	0.00024	1	U	K.DAEAWFNEK.S
<a href="#">1783</a>	691.3289	1380.6433	1380.6408	1.77	0	84	3.4e-007	1	U	R.ALEESNYELEGK.I
<a href="#">4539</a>	1018.2182	3051.6328	3051.6200	4.19	1	60	5.2e-005	1	U	K.TIDDLKNQILNLTNDANILLQIDNAR.L
<a href="#">4540</a>	763.9167	3051.6379	3051.6200	5.86	1	(37)	0.011	1	U	K.TIDDLKNQILNLTNDANILLQIDNAR.L

22. [K2C1B\\_HUMAN](#) Mass: 61864 Score: 171 Matches: 3(3) Sequences: 2(2) emPAI: 0.10

Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1179</a>	590.3026	1178.5905	1178.5931	-2.18	0	64	3.7e-005	1	U	K.YQELQITAGR.H

[2055](#) 738.3959 1474.7772 1474.7780 -0.53 0 103 4.5e-009 1 R.FLEQQNQVLQTK.W [2056](#)

23. [PDC6I\\_HUMAN](#) Mass: 95963 Score: 170 Matches: 8(8) Sequences: 6(6) emPAI: 0.23

Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">563</a>	488.2758	974.5370	974.5396	-2.69	0	34	0.031	1	U	K.ETVLSALSR.E
<a href="#">621</a>	499.2860	996.5573	996.5604	-3.03	0	29	0.045	1	U	K.ELPELLQR.N
<a href="#">699</a>	341.5388	1021.5947	1021.5920	2.67	0	34	0.0091	1	U	R.LQHAELIK.T
<a href="#">1608</a>	660.8467	1319.6789	1319.6755	2.59	0	50	0.0011	1	U	K.TMQGSEVNVLK.S
<a href="#">2806</a>	864.4811	1726.9476	1726.9465	0.63	0	33	0.025	1	U	R.SVIEQGGIQTVDQLIK.E
<a href="#">3222</a>	632.3365	1893.9876	1893.9836	2.13	0	(50)	0.00087	1	U	K.NLATAYDNFVELVANLK.E <a href="#">3223</a>
<a href="#">3224</a>	948.0029	1893.9912	1893.9836	4.01	0	68	1.5e-005	1	U	K.NLATAYDNFVELVANLK.E

24. [TRAP1\\_HUMAN](#) Mass: 80060 Score: 170 Matches: 3(3) Sequences: 1(1) emPAI: 0.07

Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2165</a>	505.2659	1512.7760	1512.7784	-1.60	0	(46)	0.0024	1	U	R.GVVDSEDIPLNLSR.E
<a href="#">2166</a>	757.3958	1512.7771	1512.7784	-0.86	0	108	1.4e-009	1	U	R.GVVDSEDIPLNLSR.E <a href="#">2168</a>

25. [RADI\\_HUMAN](#) Mass: 68521 Score: 165 Matches: 7(7) Sequences: 6(6) emPAI: 0.28

Radixin OS=Homo sapiens GN=RDY PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">425</a>	447.7754	893.5363	893.5375	-1.33	0	47	0.00029	1		R.LFFLQVK.E <a href="#">426</a>
<a href="#">565</a>	488.7773	975.5400	975.5389	1.10	0	45	0.0026	1		K.QLFDQVVK.T
<a href="#">666</a>	338.8787	1013.6142	1013.6120	2.08	1	29	0.044	1	U	K.IALLEEAKK.K
<a href="#">925</a>	552.7944	1103.5743	1103.5764	-1.86	0	63	5.2e-005	1		K.IGFPWSEIR.N
<a href="#">1076</a>	577.7612	1153.5079	1153.5074	0.48	1	32	0.027	1	U	K.QRIDEFEAM.-
<a href="#">1190</a>	591.7996	1181.5847	1181.5869	-1.91	0	71	6e-006	1		K.APDFVFYAPR.L

26. [HEP2\\_HUMAN](#) Mass: 57034 Score: 141 Matches: 3(3) Sequences: 2(2) emPAI: 0.16

Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">383</a>	435.7258	869.4370	869.4395	-2.87	0	31	0.029	1	U	R.NFGYTLR.S
<a href="#">2718</a>	566.6398	1696.8977	1696.9300	-19.07	1	(68)	1.1e-005	1	U	R.LNILNAKFAFNLYR.V
<a href="#">2719</a>	849.4586	1696.9026	1696.9300	-16.18	1	94	2.8e-008	1	U	R.LNILNAKFAFNLYR.V

27. [VTNC\\_HUMAN](#) Mass: 54271 Score: 135 Matches: 3(3) Sequences: 1(1) emPAI: 0.11

Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2573</a>	549.6115	1645.8127	1645.8100	1.63	0	(55)	0.00035	1	U	R.DVWGIEGPIDAAFR.I
<a href="#">2575</a>	823.9154	1645.8163	1645.8100	3.79	0	67	2.2e-005	1	U	R.DVWGIEGPIDAAFR.I <a href="#">2570</a>

28. [NUCL\\_HUMAN](#) Mass: 76568 Score: 119 Matches: 5(5) Sequences: 5(5) emPAI: 0.20

Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">343</a>	422.7604	843.5062	843.5065	-0.41	0	36	0.016	1	U	K.ALELTGLK.V
<a href="#">508</a>	470.7598	939.5050	939.5065	-1.60	0	34	0.016	1	U	K.GIAYIEFK.T
<a href="#">639</a>	500.7754	999.5363	999.5349	1.38	0	68	7.5e-006	1	U	K.NDLAVVDVR.I
<a href="#">3462</a>	664.6706	1990.9900	1990.9847	2.62	1	38	0.019	1	U	K.VTQDELKEVFEDAAEIR.L
<a href="#">3995</a>	771.3907	2311.1504	2311.1485	0.84	0	50	0.0012	1	U	K.VEGTEPTAFNLFVGNLNFNK.S

29. [PSMD2\\_HUMAN](#) Mass: 100136 Score: 117 Matches: 5(5) Sequences: 5(5) emPAI: 0.15

26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">670</a>	508.8050	1015.5954	1015.5913	3.97	0	33	0.025	1	U	R.LNILDTLISK.F
<a href="#">744</a>	346.5416	1036.6029	1036.6029	-0.05	0	32	0.013	1	U	R.LAQGLTHLGK.G
<a href="#">1990</a>	484.9436	1451.8089	1451.8096	-0.52	0	39	0.0049	1	U	R.VGQAVDVVGQAGKPK.T
<a href="#">3758</a>	711.6727	2131.9964	2131.9997	-1.56	0	57	0.00022	1	U	R.MNLASSFVNGFVNAAFQDK.L
<a href="#">4130</a>	819.7987	2456.3743	2456.3566	7.18	0	35	0.0082	1	U	R.AELATEEFLPVTPILEGFVILR.K

30. [K2C6B\\_HUMAN](#) Mass: 60030 Score: 115 Matches: 2(2) Sequences: 2(2) emPAI: 0.10

Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1179</a>	590.3026	1178.5905	1178.5931	-2.18	0	64	3.7e-005	1		K.YEELQITAGR.H
<a href="#">1630</a>	665.3682	1328.7219	1328.7187	2.39	0	83	3.8e-007	1		R.NLDLDSIIAEVK.A

31. [SYG\\_HUMAN](#) Mass: 83113 Score: 112 Matches: 2(2) Sequences: 2(2) emPAI: 0.07

Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1997</a>	729.3972	1456.7799	1456.7755	3.01	0	45	0.0027	1	U	R.TFFSFPVAVAPFK.C
<a href="#">3875</a>	1118.0989	2234.1832	2234.1695	6.12	0	87	1.6e-007	1	U	R.LGDAVEQGVINNTVLGYFGR.I

32. [PDIA4\\_HUMAN](#) Mass: 72887 Score: 106 Matches: 2(2) Sequences: 2(2) emPAI: 0.08

Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1223</a>	595.8229	1189.6313	1189.6302	0.90	0	90	8.1e-008	1	U	K.IDATSASVLASR.F
<a href="#">2002</a>	729.8858	1457.7571	1457.7548	1.53	0	45	0.0029	1	U	K.VSQGQLVVMQPEK.F

33. [MX1\\_HUMAN](#) Mass: 75473 Score: 103 Matches: 4(4) Sequences: 2(2) emPAI: 0.08

Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2542</a>	819.4625	1636.9104	1636.9036	4.14	0	53	0.00022	1	U	R.DVPDLTLIDLPGTR.V <a href="#">2539</a> <a href="#">2543</a>
<a href="#">3899</a>	751.4130	2251.2171	2251.2060	4.93	0	40	0.0048	1	U	R.ALGVEQDLALPAIAVIGDQSSGK.S

34. [QSOX1\\_HUMAN](#) Mass: 82526 Score: 102 Matches: 4(4) Sequences: 4(4) emPAI: 0.15

Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1713</a>	678.8443	1355.6740	1355.6721	1.42	0	40	0.007	1	U	R.LAGAPSEDPQFPK.V
<a href="#">2080</a>	741.8793	1481.7441	1481.7402	2.67	0	36	0.023	1	U	R.NNEEYLALIFEK.G
<a href="#">3055</a>	608.6521	1822.9345	1822.9287	3.16	0	35	0.033	1	U	K.IYMDLESALHYILR.I
<a href="#">3140</a>	620.3405	1857.9997	1857.9877	6.49	0	52	0.0005	1	U	R.LDVPVWDVEATLNFLK.A

35. [H2A1B\\_HUMAN](#) Mass: 14127 Score: 100 Matches: 3(3) Sequences: 2(2) emPAI: 0.78

Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">511</a>	472.7683	943.5220	943.5240	-2.06	0	65	2.2e-005	1	U	R.AGLQFPVGR.V
<a href="#">3294</a>	644.3961	1930.1665	1930.1615	2.59	0	(30)	0.0036	1	U	R.VTIAQGGVLPNIQAVLLPK.K
<a href="#">3295</a>	966.0922	1930.1698	1930.1615	4.27	0	50	3.6e-005	1	U	R.VTIAQGGVLPNIQAVLLPK.K

Proteins matching the same set of peptides:

[H2A1C\\_HUMAN](#) Mass: 14097 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3

[H2A1D\\_HUMAN](#) Mass: 14099 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2

[H2A1H\\_HUMAN](#) Mass: 13898 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3

[H2A1J\\_HUMAN](#) Mass: 13928 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3

[H2A1\\_HUMAN](#) Mass: 14083 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2

[H2A2A\\_HUMAN](#) Mass: 14087 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3

[H2A2C\\_HUMAN](#) Mass: 13980 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4

[H2A3\\_HUMAN](#) Mass: 14113 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3

[H2A7\\_HUMAN](#) Mass: 14011 Score: 100 Matches: 3(3) Sequences: 2(2)

Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1 SV=1

36. [VASN\\_HUMAN](#) Mass: 71668 Score: 97 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2768</a>	858.9660	1715.9175	1715.9206	-1.85	0	97	1.6e-008	1	U	R.LAGLGLQLDEGLFSR.L

37. [COPG1\\_HUMAN](#) Mass: 97655 Score: 96 Matches: 2(2) Sequences: 2(2) emPAI: 0.06

Coatomeer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1384</a>	622.8970	1243.7795	1243.7751	3.54	0	61	4.2e-006	1	U	R.SIATLAITLLK.T
<a href="#">1795</a>	693.8548	1385.6950	1385.6973	-1.62	0	56	0.0002	1	U	K.SVPLATAPMAEQR.T

38. [FUBP2\\_HUMAN](#) Mass: 73070 Score: 96 Matches: 2(2) Sequences: 2(2) emPAI: 0.08

Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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[1203](#) 592.8543 1183.6941 1183.6924 1.37 0 75 1.1e-006 1 U R.IINDLLQSLR.S  
[1540](#) 651.8483 1301.6820 1301.6827 -0.55 0 49 0.0012 1 U R.SVSLTGAPESVQK.A

39. [H4\\_HUMAN](#) Mass: 11360 Score: 88 Matches: 4(4) Sequences: 2(2) emPAI: 1.02

Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">605</a>	495.2917	988.5689	988.5706	-1.63	0	46	0.0015	1	U	K.VFLENVIR.D <a href="#">606</a>
<a href="#">1619</a>	442.5897	1324.7473	1324.7463	0.80	0	45	0.0012	1	U	R.DNIQGITKPAIR.R
<a href="#">1620</a>	663.3812	1324.7479	1324.7463	1.23	0	(44)	0.0014	1	U	R.DNIQGITKPAIR.R

40. [CAND1\\_HUMAN](#) Mass: 136289 Score: 85 Matches: 2(2) Sequences: 2(2) emPAI: 0.04

Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2083</a>	742.4489	1482.8832	1482.8770	4.18	0	82	9.1e-008	1	U	K.ISGSILNELIGLVR.S
<a href="#">3661</a>	689.0837	2064.2294	2064.2095	9.62	0	23	0.019	1	U	K.IDLRPVLGEGVPILASFRL.R

41. [SEC23B\\_HUMAN](#) Mass: 86424 Score: 85 Matches: 2(2) Sequences: 1(1) emPAI: 0.03

Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3867</a>	744.4094	2230.2064	2230.1958	4.79	0	52	0.00034	1	U	R.STGVALSIAVGLLEGTFPNTGAR.I <a href="#">3868</a>

42. [K1C9\\_HUMAN](#) Mass: 62027 Score: 77 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1100</a>	579.2986	1156.5826	1156.5836	-0.89	0	77	1e-006	1	U	R.QGVDADINGLR.Q

43. [PYGL\\_HUMAN](#) Mass: 97087 Score: 76 Matches: 3(3) Sequences: 3(3) emPAI: 0.09

Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2047</a>	492.2809	1473.8209	1473.8231	-1.51	1	32	0.042	1	U	R.IFVDIEKLPSWK.A
<a href="#">2403</a>	797.4164	1592.8182	1591.8246	624	0	36	0.028	1	U	K.LVIDQIDNGFFSPK.Q
<a href="#">2502</a>	542.2717	1623.7934	1623.7893	2.51	0	49	0.0013	1	U	R.DFNVDYIQAVALDR.N

44. [GFPT1\\_HUMAN](#) Mass: 78756 Score: 75 Matches: 2(2) Sequences: 1(1) emPAI: 0.08

Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2316</a>	521.6373	1561.8902	1561.8868	2.14	0	(44)	0.0012	1	U	R.VIQQLEGAFALVFK.S
<a href="#">2317</a>	781.9531	1561.8916	1561.8868	3.05	0	49	0.00034	1	U	R.VIQQLEGAFALVFK.S

Proteins matching the same set of peptides:

[GFPT2\\_HUMAN](#) Mass: 76882 Score: 75 Matches: 2(2) Sequences: 1(1)

Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 OS=Homo sapiens GN=GFPT2 PE=1 SV=3

45. [K2C8\\_HUMAN](#) Mass: 53671 Score: 75 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1883</a>	710.3797	1418.7448	1418.7405	3.05	0	75	3.4e-006	1	U	R.LEGLTDEINFLR.Q

46. [CADH1\\_HUMAN](#) Mass: 97396 Score: 71 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">4044</a>	1183.6233	2365.2320	2365.2318	0.09	0	71	7.1e-006	1	U	K.VFYISITGQADTPPVGVFIIR.E

47. [XPP3\\_HUMAN](#) Score: 68 Matches: 2(2) Sequences: 1(1) emPAI: 0.05

Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPPEP3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">278</a>	408.2595	814.5044	814.5065	-2.54	0	50	0.00033	1	U	K.AILFVPR.R <a href="#">279</a>

48. [KATL2\\_HUMAN](#) Mass: 61214 Score: 68 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens GN=KATNAL2 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1149</a>	586.8365	1171.6585	1171.6601	-1.34	0	68	1e-005	1	U	K.GLLLYGPPGTGK.T

49. [TRFL\\_HUMAN](#) Mass: 78132 Score: 67 Matches: 3(3) Sequences: 2(2) emPAI: 0.08

Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">58</a>	318.1914	634.3683	634.3690	-1.07	0	34	0.011	2		K.DLLFK.D <a href="#">59</a>
<a href="#">903</a>	549.2562	1096.4978	1096.4978	-0.01	0	54	0.0002	1	U	R.YYGYTGAFR.C

50. [ACPH\\_HUMAN](#) Mass: 81173 Score: 67 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1720</a>	681.3316	1360.6487	1360.6470	1.20	0	67	1.5e-005	1	U	K.ALDVSASDDEIAR.L

51. [ITIH3\\_HUMAN](#) Mass: 99787 Score: 64 Matches: 2(2) Sequences: 2(2) emPAI: 0.06

Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1122</a>	581.8019	1161.5893	1161.5918	-2.08	0	50	0.0011	1	U	K.EVSFDVELPK.T
<a href="#">2557</a>	547.6351	1639.8836	1639.8821	0.90	1	40	0.006	1	U	K.VTFELTYEELLKR.H

52. [HGFA\\_HUMAN](#) Mass: 70636 Score: 63 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Hepatocyte growth factor activator OS=Homo sapiens GN=HGFA PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1655</a>	670.3419	1338.6693	1338.6667	1.91	0	63	3.7e-005	1	U	R.TTDVTQTFGIEK.Y

53. [HBB\\_HUMAN](#) Mass: 15988 Score: 61 Matches: 2(2) Sequences: 1(1) emPAI: 0.19

Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1476</a>	637.8669	1273.7193	1273.7183	0.82	0	46	0.0015	1	U	R.LLVVYPWQR.F <a href="#">1478</a>

Proteins matching the same set of peptides:

[HBD\\_HUMAN](#) Mass: 16045 Score: 61 Matches: 2(2) Sequences: 1(1)

Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2

[HBE\\_HUMAN](#) Mass: 16192 Score: 61 Matches: 2(2) Sequences: 1(1)

Hemoglobin subunit epsilon OS=Homo sapiens GN=HBE1 PE=1 SV=2

[HBG1\\_HUMAN](#) Mass: 16130 Score: 61 Matches: 2(2) Sequences: 1(1)

Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2

[HBG2\\_HUMAN](#) Mass: 16116 Score: 61 Matches: 2(2) Sequences: 1(1)

Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2

54. [HNRNP\\_HUMAN](#) Mass: 70899 Score: 60 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2010</a>	730.8969	1459.7791	1459.7770	1.50	0	60	9.9e-005	1	U	R.NLATTVEIELEK.S

55. [COPB\\_HUMAN](#) Mass: 107074 Score: 59 Matches: 2(2) Sequences: 1(1) emPAI: 0.03

Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1634</a>	665.8750	1329.7354	1329.7326	2.13	0	48	0.0012	1	U	R.VLQDLVMDILR.V <a href="#">1633</a>

56. [HSPB1\\_HUMAN](#) Mass: 22768 Score: 59 Matches: 1(1) Sequences: 1(1) emPAI: 0.13

Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1129</a>	582.3124	1162.6102	1162.6135	-2.83	0	59	0.00011	1	U	R.LFDQAFGLPR.L

57. [G3PT\\_HUMAN](#) Mass: 44473 Score: 59 Matches: 2(2) Sequences: 1(1) emPAI: 0.07

Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDH PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1120</a>	581.3177	1160.6208	1160.6190	1.61	0	48	0.0015	1	U	K.AGIALNDNFVK.L <a href="#">1119</a>

58. [FBLN1\\_HUMAN](#) Mass: 77162 Score: 58 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2362</a>	525.9374	1574.7903	1574.7875	1.77	0	58	0.00017	1	U	K.LEMNYVVGVSISR.N

59. [XRCC5\\_HUMAN](#) Mass: 82652 Score: 58 Matches: 3(3) Sequences: 3(3) emPAI: 0.11

X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">180</a>	391.7137	781.4128	781.4123	0.71	0	30	0.039	1	U	R.FNNFLK.A
<a href="#">723</a>	516.3108	1030.6070	1030.6063	0.75	0	39	0.0049	1	U	K.TLFPLIEAK.K
<a href="#">4229</a>	1263.0718	2524.1290	2524.1163	5.03	0	37	0.022	1	U	K.DKPSGDTAAVFEEGGVDVLLDMLI.-

60. [HS71L\\_HUMAN](#) Mass: 70331 Score: 57 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2672</a>	839.4100	1676.8055	1676.7828	13.5	0	57	0.00021	2	U	K.NQVAMNPQNTVFDAK.R

61. [CROCC\\_HUMAN](#) Mass: 228388 Score: 55 Matches: 2(2) Sequences: 2(2) emPAI: 0.03

Rootletin OS=Homo sapiens GN=CROCC PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">463</a>	457.7703	913.5260	913.5232	3.06	0	50	0.00044	1	U	K.LALLEEAR.T
<a href="#">1706</a>	677.8035	1353.5924	1353.5904	1.46	1	34	0.021	1	U	R.QMKMLDSENTR.L

62. [RS27A\\_HUMAN](#) Mass: 17953 Score: 55 Matches: 1(1) Sequences: 1(1) emPAI: 0.16

Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2965</a>	894.4718	1786.9291	1786.9200	5.06	0	55	0.00034	1	U	K.TITLEVEPSDTIENVK.A

Proteins matching the same set of peptides:

[RL40\\_HUMAN](#) Mass: 14719 Score: 55 Matches: 1(1) Sequences: 1(1)

Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2

[UBB\\_HUMAN](#) Mass: 25746 Score: 55 Matches: 1(1) Sequences: 1(1)

Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1

[UBC\\_HUMAN](#) Mass: 76992 Score: 55 Matches: 1(1) Sequences: 1(1)

Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3

63. [XPOT\\_HUMAN](#) Mass: 109893 Score: 55 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2117</a>	748.4425	1494.8705	1494.8770	-4.34	0	55	7.1e-005	1	U	R.LAQVSPPELLLSVR.R

64. [NIBL1\\_HUMAN](#) Mass: 84085 Score: 48 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1864</a>	707.8563	1413.6980	1413.6929	3.62	0	48	0.0014	1	U	R.FQELIFEDFAR.F

65. [STAT1\\_HUMAN](#) Mass: 87280 Score: 47 Matches: 2(2) Sequences: 1(1) emPAI: 0.07

Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3605</a>	677.0333	2028.0781	2028.0680	4.98	0	(34)	0.034	1	U	R.TFSLFQQLIQSSFVVER.Q
<a href="#">3606</a>	1015.0480	2028.0814	2028.0680	6.59	0	39	0.011	1	U	R.TFSLFQQLIQSSFVVER.Q

66. [GOGB1\\_HUMAN](#) Mass: 375790 Score: 47 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2827</a>	867.9000	1733.7854	1733.8141	-16.58	0	47	0.0017	1	U	K.MNLLNQIQEELSR.V

67. [PYGB\\_HUMAN](#) Mass: 96635 Score: 46 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2491</a>	540.9668	1619.8786	1619.8770	0.96	1	46	0.0016	1	U	K.IGEEFLDLSQLKK.L

68. [TFR1\\_HUMAN](#) Mass: 84818 Score: 44 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1916</a>	717.4125	1432.8104	1432.8177	-5.10	0	44	0.0016	1	U	K.VSASPLLYTLIEK.T

69. [GNS\\_HUMAN](#) Mass: 62042 Score: 43 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2266</a>	773.4129	1544.8113	1544.8086	1.70	0	43	0.0048	1	U	R.WQTLLSVDDLVEK.L

70.	<a href="#">C04A_HUMAN</a>	Mass: 192664	Score: 41	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.02
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">1748</a>	684.3659	1366.7173	1366.7133	2.92	0	41 0.0061 1 U R.DSSTWLTAFLVK.V
71.	<a href="#">COPB2_HUMAN</a>	Mass: 102422	Score: 40	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.03
Coatamer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">3659</a>	1033.0123	2064.0101	2064.0051	2.42	0	40 0.012 1 U K.AAESLADPTEYENLFPLK.E
72.	<a href="#">CTNA1_HUMAN</a>	Mass: 100009	Score: 39	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.03
Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">4570</a>	1067.5347	3199.5822	3199.5772	1.54	0	39 0.018 1 U R.VLTDAVDDITSIDDFLAVSENHILEDVVK.C
73.	<a href="#">AFAM_HUMAN</a>	Score: 38	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04	
Afinin OS=Homo sapiens GN=AFM PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">336</a>	416.7683	831.5221	831.5218	0.37	0	38 0.0018 1 U R.FLVNLVK.L
74.	<a href="#">EXOC3_HUMAN</a>	Mass: 86790	Score: 38	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.03
Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">1012</a>	567.3068	1132.5990	1132.5975	1.27	0	38 0.014 1 U R.QSINTIESLK.D
75.	<a href="#">S31E1_HUMAN</a>	Mass: 157037	Score: 38	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.02
Spermatogenesis-associated protein 31E1 OS=Homo sapiens GN=SPATA31E1 PE=2 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">737</a>	518.7679	1035.5213	1035.5236	-2.22	0	38 0.014 1 U K.YNQLQLEK.G
76.	<a href="#">CLCF1_HUMAN</a>	Mass: 25160	Score: 37	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12
Cardiotrophin-like cytokine factor 1 OS=Homo sapiens GN=CLCF1 PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">361</a>	428.7511	855.4876	855.4814	7.30	0	37 0.0064 1 U R.LGAETLPR.A
77.	<a href="#">SKI_HUMAN</a>	Mass: 79955	Score: 36	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04
Ski oncogene OS=Homo sapiens GN=SKI PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">2194</a>	509.6153	1525.8240	1524.8300	652	1	36 0.016 1 U K.VVKELQEQWLWPR.A
78.	<a href="#">PLCE1_HUMAN</a>	Mass: 258551	Score: 36	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.01
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 OS=Homo sapiens GN=PLCE1 PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">1910</a>	716.8639	1431.7132	1431.7205	-5.07	2	36 0.029 1 U K.LKEQVQASREDK.K
79.	<a href="#">IRPL1_HUMAN</a>	Score: 35	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04	
Interleukin-1 receptor accessory protein-like 1 OS=Homo sapiens GN=IL1RAPL1 PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">417</a>	443.7776	885.5407	885.5396	1.32	1	35 0.011 2 U K.RDTLLIR.E
80.	<a href="#">MRO2A_HUMAN</a>	Score: 35	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.02	
Maestro heat-like repeat-containing protein family member 2A OS=Homo sapiens GN=MROH2A PE=4 SV=4						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">417</a>	443.7776	885.5407	885.5284	14.0	0	35 0.011 2 U R.VGTLNLIR.A
81.	<a href="#">OR4A5_HUMAN</a>	Mass: 34891	Score: 35	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
Olfactory receptor 4A5 OS=Homo sapiens GN=OR4A5 PE=3 SV=4						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
<a href="#">596</a>	493.7963	985.5781	985.5807	-2.69	1	35 0.016 1 U R.NAIEKLLGK.K
82.	<a href="#">MSL1_HUMAN</a>	Mass: 67087	Score: 35	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04

Male-specific lethal 1 homolog OS=Homo sapiens GN=MSL1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1398</a>	625.3154	1248.6163	1248.6384	-17.65	2	35	0.031	1	U	R.MQLVKKDNEK.E

83. [PYR1\\_HUMAN](#) Mass: 242829 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1837</a>	701.3721	1400.7296	1400.7499	-14.52	2	35	0.032	1	U	R.IDRWFLHRMK.R

84. [CO6A1\\_HUMAN](#) Mass: 108462 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2924</a>	592.3135	1773.9188	1773.9122	3.71	0	34	0.044	1	U	R.VAVVQYSGTGQQRPER.A

85. [ACTBM\\_HUMAN](#) Mass: 41989 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.07

Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2172</a>	506.2377	1515.6914	1515.6954	-2.64	0	34	0.029	1	U	K.QEYDESGPSIVHR.K

Proteins matching the same set of peptides:

[ACTB\\_HUMAN](#) Mass: 41710 Score: 34 Matches: 1(1) Sequences: 1(1)

Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1

[ACTG\\_HUMAN](#) Mass: 41766 Score: 34 Matches: 1(1) Sequences: 1(1)

Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1

[POTEE\\_HUMAN](#) Mass: 121286 Score: 34 Matches: 1(1) Sequences: 1(1)

POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3

[POTEF\\_HUMAN](#) Mass: 121367 Score: 34 Matches: 1(1) Sequences: 1(1)

POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2

[POTEI\\_HUMAN](#) Mass: 121205 Score: 34 Matches: 1(1) Sequences: 1(1)

POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1

[POTEJ\\_HUMAN](#) Mass: 117315 Score: 34 Matches: 1(1) Sequences: 1(1)

POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1

86. [UBA1\\_HUMAN](#) Mass: 117774 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">4344</a>	873.8037	2618.3893	2618.3778	4.40	0	33	0.031	1	U	K.LAYVAAGDLAPINAFIGGLAAQEVMK.A

87. [STIM2\\_HUMAN](#) Mass: 83918 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Stromal interaction molecule 2 OS=Homo sapiens GN=STIM2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1082</a>	577.8134	1153.6123	1153.6131	-0.75	0	33	0.028	1	U	K.HITIEDLWK.R

88. [SYTC\\_HUMAN](#) Mass: 83382 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1493</a>	641.3293	1280.6441	1280.6442	-0.01	0	33	0.044	1	U	R.TVYSVFGFSFK.L

89. [RENT2\\_HUMAN](#) Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">278</a>	408.2595	814.5044	814.5065	-2.54	0	33	0.018	3	U	R.ALFIIVPR.Q

90. [ABLM1\\_HUMAN](#) Mass: 87631 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Actin-binding LIM protein 1 OS=Homo sapiens GN=ABLM1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1096</a>	578.8408	1155.6670	1155.6863	-16.73	0	33	0.021	1	U	K.LNSGLGQLILK.E

91. [PSA\\_HUMAN](#) Mass: 103211 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1782</a>	690.9256	1379.8366	1379.8388	-1.56	0	33	0.0041	1	U	R.VLGATLLPDLIQK.V

92. [FAK2\\_HUMAN](#) Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.03



Protein-tyrosine kinase 2-beta OS=Homo sapiens GN=PTK2B PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">573</a>	490.2585	978.5025	978.5022	0.30	0	33	0.042	2	U	K.SNFELLEK.E

93. [GOGA4\\_HUMAN](#) Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Golgin subfamily A member 4 OS=Homo sapiens GN=GOLGA4 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">446</a>	450.7658	899.5171	899.5188	-1.96	1	32	0.029	1	U	R.QENLLKR.C

94. [PLAK\\_HUMAN](#) Mass: 81693 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">421</a>	445.7715	889.5284	889.5273	1.27	0	32	0.019	1	U	R.EGLLAIFK.S

Proteins matching the same set of peptides:

[CTNB1\\_HUMAN](#) Mass: 85442 Score: 32 Matches: 1(1) Sequences: 1(1)

Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1

95. [KCC2D\\_HUMAN](#) Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2297</a>	778.9359	1555.8573	1555.8821	-15.93	1	31	0.045	2	U	R.DLKPEQLLLASKSK.G

96. [XYLB\\_HUMAN](#) Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Xylulose kinase OS=Homo sapiens GN=XYLB PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1619</a>	442.5897	1324.7473	1324.7211	19.8	1	31	0.026	2	U	K.TKILATGGASHNR.E

97. [DNJB8\\_HUMAN](#) Mass: 25670 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.11

DnaJ homolog subfamily B member 8 OS=Homo sapiens GN=DNJB8 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1544</a>	652.3040	1302.5935	1302.5939	-0.30	2	31	0.042	1	U	K.NPDNKEAEKK.F

98. [NEK10\\_HUMAN](#) Mass: 133176 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

Serine/threonine-protein kinase Nek10 OS=Homo sapiens GN=NEK10 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">531</a>	477.3063	952.5980	952.6069	-9.37	1	30	0.0079	1	U	K.LILPNKQK.N

99. [5HT6R\\_HUMAN](#) Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.06

5-hydroxytryptamine receptor 6 OS=Homo sapiens GN=HTR6 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">416</a>	443.7763	885.5380	885.5218	18.3	1	30	0.046	2	U	K.LRMTPLR.A

100. [HS12B\\_HUMAN](#) Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Heat shock 70 kDa protein 12B OS=Homo sapiens GN=HSPA12B PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">592</a>	492.8138	983.6130	983.5988	14.4	2	29	0.022	2	U	K.LLVDRGRR.W

101. [ZN594\\_HUMAN](#) Mass: 93847 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Zinc finger protein 594 OS=Homo sapiens GN=ZNF594 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">701</a>	341.5409	1021.6009	1021.6145	-13.24	1	29	0.024	1	U	R.SLLIQHRR.I

102. [DMD\\_HUMAN](#) Mass: 426484 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Dystrophin OS=Homo sapiens GN=DMD PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">723</a>	516.3108	1030.6070	1030.6022	4.65	1	29	0.046	2	U	K.ITETQLAK.D

103. [DYM\\_HUMAN](#) Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Dymeclin OS=Homo sapiens GN=DYM PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1782</a>	690.9256	1379.8366	1379.8176	13.8	1	29	0.011	2	U	K.LVKTLLYNFIR.Q

104. [POSTN\\_HUMAN](#) Mass: 93255 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">4036</a>	589.3369	2353.3183	2353.3158	1.07	1	27	0.048	1	U	R.DKNALQNIILYHLTPGVFIGK.G

105. [MOS\\_HUMAN](#) Score: 24 Matches: 1(1) Sequences: 1(1) emPAI: 0.08

Proto-oncogene serine/threonine-protein kinase mos OS=Homo sapiens GN=MOS PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">531</a>	477.3063	952.5980	952.6069	-9.38	0	24	0.03	2	U	K.LLLGATLPR.A

106. [H2B1A\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.21

Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">531</a>	477.3063	952.5980	952.5957	2.42	0	23	0.042	3	U	R.LLLPGELAK.H

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

[H2B1B\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2

[H2B1C\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4

[H2B1D\\_HUMAN](#) Mass: 13928 Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2

[H2B1H\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3

[H2B1J\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3

[H2B1K\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3

[H2B1L\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3

[H2B1M\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3

[H2B1N\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3

[H2B1O\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3

[H2B2E\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3

[H2B2F\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3

[H2B3B\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3

[H2BFS\\_HUMAN](#) Score: 23 Matches: 1(1) Sequences: 1(1)

Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2

107. [HES2\\_HUMAN](#) Mass: 18459 Score: 22 Matches: 2(2) Sequences: 1(1) emPAI: 0.16

Transcription factor HES-2 OS=Homo sapiens GN=HES2 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">528</a>	476.3198	950.6250	950.6277	-2.84	0	21	0.01	1	U	K.GLILPLLGR.E <a href="#">529</a>

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