

# Mascot Search Results

User : Kari  
 Email : kleinholz.1@osu.edu  
 Search title : Trypsin Swiss Prot  
 MS data file : \\filesrv\Mass\_Spec\Data\_New\31456 HammerDiakonova\31456\_2\_PRL.mgf  
 Database : SwissProt ID ID\_2015\_10 (549646 sequences; 195983064 residues)  
 Taxonomy : Homo sapiens (human) (20197 sequences)  
 Timestamp : 19 Jan 2016 at 19:33:46 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 : 4933

**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  
[ACTN1 HUMAN](#) Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2  
[FETA HUMAN](#) Alpha-fetoprotein OS=Homo sapiens GN=AFP PE=1 SV=1  
[ACTN4 HUMAN](#) Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2  
[EF2 HUMAN](#) Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4  
[ALBU HUMAN](#) Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[EZRI HUMAN](#) Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4  
[GRP78 HUMAN](#) 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2  
[K1C10 HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
[ENPL HUMAN](#) Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1  
[LG3BP HUMAN](#) Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1  
[TERA HUMAN](#) Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4  
[MX1 HUMAN](#) Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=4  
[K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[QSOX1 HUMAN](#) Sulphydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3  
[IMB1 HUMAN](#) Importin subunit beta-1 OS=Homo sapiens GN=KPMB1 PE=1 SV=2  
[CADH1 HUMAN](#) Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3  
[GELS HUMAN](#) Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1  
[A2MG HUMAN](#) Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3  
[CFAB HUMAN](#) Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2  
[LUM HUMAN](#) Lumican OS=Homo sapiens GN=LUM PE=1 SV=2  
[HBA HUMAN](#) Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2  
[H90B2 HUMAN](#) Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2  
[VPS35 HUMAN](#) Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2  
[VTNC HUMAN](#) Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1  
[ITIH2 HUMAN](#) Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2  
[CD166 HUMAN](#) CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2  
[NUCL HUMAN](#) Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3  
[VASN HUMAN](#) Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1  
[K2C1B HUMAN](#) Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3  
[K2C6B HUMAN](#) Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5  
[PSA HUMAN](#) Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2  
[PDIA4 HUMAN](#) Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2  
[C3 HUMAN](#) Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[HEP2 HUMAN](#) Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3  
[IQGAP1 HUMAN](#) Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1  
[COPG1 HUMAN](#) Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1  
[TRAP1 HUMAN](#) Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3  
[GOLM1 HUMAN](#) Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 PE=1 SV=1  
[PSMD2 HUMAN](#) 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3  
[HGFA HUMAN](#) Hepatocyte growth factor activator OS=Homo sapiens GN=HGFA PE=1 SV=1  
[TRFL HUMAN](#) Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6  
[G3PT HUMAN](#) Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2  
[SLIK4 HUMAN](#) SLIT and NTRK-like protein 4 OS=Homo sapiens GN=SLITRK4 PE=2 SV=1  
[H2A1B HUMAN](#) Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2  
[PDC61 HUMAN](#) Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDC61 PE=1 SV=1  
[BCAM HUMAN](#) Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2  
[S10A9 HUMAN](#) Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1  
[COPB HUMAN](#) Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3  
[GFPT1 HUMAN](#) Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3  
[XPP3 HUMAN](#) Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPPEP3 PE=1 SV=1  
[FBLN1 HUMAN](#) Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4  
[TSP1 HUMAN](#) Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2  
[XPOT HUMAN](#) Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2  
[H7FL HUMAN](#) Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2  
[CAND1 HUMAN](#) Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2  
[DPP3 HUMAN](#) Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 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  
[TFR1 HUMAN](#) Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2  
[C04A HUMAN](#) Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2  
[CLCF1 HUMAN](#) Cardiotrophin-like cytokine factor 1 OS=Homo sapiens GN=CLCF1 PE=1 SV=1

<a href="#">G0GB1_HUMAN</a>	Golgin subfamily B member 1 OS=Homo sapiens GN=G0GLB1 PE=1 SV=2
<a href="#">KATL2_HUMAN</a>	Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens GN=KATNAL2 PE=2 SV=3
<a href="#">AFAM_HUMAN</a>	Afamin OS=Homo sapiens GN=AFM PE=1 SV=1
<a href="#">ITIH3_HUMAN</a>	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2
<a href="#">AGRIN_HUMAN</a>	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5
<a href="#">POSTN_HUMAN</a>	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2
<a href="#">SYG_HUMAN</a>	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3
<a href="#">PIP_HUMAN</a>	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1
<a href="#">S100A7_HUMAN</a>	Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4
<a href="#">MCF2_HUMAN</a>	Proto-oncogene DBL OS=Homo sapiens GN=MCF2 PE=1 SV=3
<a href="#">HBB_HUMAN</a>	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2
<a href="#">DR4L1_HUMAN</a>	Putative dehydrogenase/reductase SDR family member 4-like 1 OS=Homo sapiens GN=DHRS4L1 PE=5 SV=1
<a href="#">EXOC3_HUMAN</a>	Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2
<a href="#">CAPSL_HUMAN</a>	Calcyphosin-like protein OS=Homo sapiens GN=CAPSL PE=2 SV=4
<a href="#">H4_HUMAN</a>	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2
<a href="#">PLCE1_HUMAN</a>	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase epsilon-1 OS=Homo sapiens GN=PLCE1 PE=1 SV=3
<a href="#">MO4L1_HUMAN</a>	Mortality factor 4-like protein 1 OS=Homo sapiens GN=MORF4L1 PE=1 SV=2
<a href="#">RGPA2_HUMAN</a>	Ral GTPase-activating protein subunit alpha-2 OS=Homo sapiens GN=RALGAP2 PE=1 SV=2
<a href="#">DSG2_HUMAN</a>	Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2
<a href="#">S31E1_HUMAN</a>	Spermatogenesis-associated protein 31E1 OS=Homo sapiens GN=SPATA31E1 PE=2 SV=2
<a href="#">PPIA_HUMAN</a>	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2
<a href="#">CUL4A_HUMAN</a>	Cullin-4A OS=Homo sapiens GN=CUL4A PE=1 SV=3
<a href="#">LIPA3_HUMAN</a>	Liprin-alpha-3 OS=Homo sapiens GN=PPFIA3 PE=1 SV=3
<a href="#">XPO2_HUMAN</a>	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3
<a href="#">SKI_HUMAN</a>	Ski oncogene OS=Homo sapiens GN=SKI PE=1 SV=1
<a href="#">PYGB_HUMAN</a>	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5
<a href="#">VNN1_HUMAN</a>	Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2
<a href="#">ZN101_HUMAN</a>	Zinc finger protein 101 OS=Homo sapiens GN=ZNF101 PE=1 SV=1
<a href="#">DYM_HUMAN</a>	Dymeclin OS=Homo sapiens GN=DYM PE=1 SV=1
<a href="#">TNIK_HUMAN</a>	TRAF2 and NCK-interacting protein kinase OS=Homo sapiens GN=TNIK PE=1 SV=1
<a href="#">PAR6G_HUMAN</a>	Partitioning defective 6 homolog gamma OS=Homo sapiens GN=PAR6G PE=1 SV=1
<a href="#">CAH2_HUMAN</a>	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2
<a href="#">MDHM_HUMAN</a>	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3
<a href="#">MELT_HUMAN</a>	Ventricular zone-expressed PH domain-containing protein homolog 1 OS=Homo sapiens GN=VEPH1 PE=2 SV=1
<a href="#">TTBK1_HUMAN</a>	Tau-tubulin kinase 1 OS=Homo sapiens GN=TTBK1 PE=1 SV=2
<a href="#">CENPH_HUMAN</a>	Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1
<a href="#">ANM3_HUMAN</a>	Protein arginine N-methyltransferase 3 OS=Homo sapiens GN=PRMT3 PE=1 SV=3
<a href="#">HES2_HUMAN</a>	Transcription factor HES-2 OS=Homo sapiens GN=HES2 PE=2 SV=1
<a href="#">TAAR2_HUMAN</a>	Trace amine-associated receptor 2 OS=Homo sapiens GN=TAAR2 PE=2 SV=2
<a href="#">CBPC1_HUMAN</a>	Cytosolic carboxypeptidase 1 OS=Homo sapiens GN=AGTPBP1 PE=1 SV=3
<a href="#">THMS2_HUMAN</a>	Protein THEMIS2 OS=Homo sapiens GN=THEMIS2 PE=1 SV=1

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

Peptide matches above identity threshold	363	26	7.16 %
Peptide matches above homology or identity threshold	445	44	9.89 %

## Select Summary Report

Format As  Select Summary (protein hits)  [Help](#)

Significance threshold p<  Max. number of hits  Show Percolator scores ☐

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

Show pop-ups ☒ Suppress pop-ups ☐ Require bold red ☐

Preferred taxonomy

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

1. [HS90A\\_HUMAN](#) Mass: 84607 Score: 1289 Matches: 34(34) Sequences: 18(18) emPAI: 0.96

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="#">295</a>	<a href="#">408.2594</a>	<a href="#">814.5043</a>	<a href="#">814.5065</a>	<a href="#">-2.69</a>	<a href="#">0</a>	<a href="#">44</a>	<a href="#">0.0014</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.ALLFVPR.R</a> <a href="#">294</a>
<a href="#">575</a>	<a href="#">474.7253</a>	<a href="#">947.4359</a>	<a href="#">947.4389</a>	<a href="#">-3.09</a>	<a href="#">0</a>	<a href="#">43</a>	<a href="#">0.0028</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">K.FYEQFSK.N</a> <a href="#">576</a>
<a href="#">1013</a>	<a href="#">554.7728</a>	<a href="#">1107.5311</a>	<a href="#">1107.5349</a>	<a href="#">-3.43</a>	<a href="#">0</a>	<a href="#">64</a>	<a href="#">3.4e-005</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.APFDLFENR.K</a> <a href="#">1014</a>
<a href="#">1432</a>	<a href="#">612.8168</a>	<a href="#">1223.6191</a>	<a href="#">1223.6186</a>	<a href="#">0.40</a>	<a href="#">0</a>	<a href="#">51</a>	<a href="#">0.00065</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">K.HIYYITGETK.D</a> <a href="#">1433</a>
<a href="#">1471</a>	<a href="#">618.3023</a>	<a href="#">1234.5901</a>	<a href="#">1234.5942</a>	<a href="#">-3.36</a>	<a href="#">0</a>	<a href="#">89</a>	<a href="#">1.1e-007</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">K.DQVANSFVER.L</a> <a href="#">1472</a>
<a href="#">1483</a>	<a href="#">621.8545</a>	<a href="#">1241.6944</a>	<a href="#">1241.6979</a>	<a href="#">-2.81</a>	<a href="#">0</a>	<a href="#">81</a>	<a href="#">4.1e-007</a>	<a href="#">1</a>		<a href="#">K.ADLINNLGTIAK.S</a> <a href="#">1486</a>
<a href="#">1653</a>	<a href="#">646.3230</a>	<a href="#">1290.6314</a>	<a href="#">1290.6303</a>	<a href="#">0.89</a>	<a href="#">0</a>	<a href="#">72</a>	<a href="#">7.2e-006</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.ELISNSSDALDK.I</a>
<a href="#">1718</a>	<a href="#">656.2904</a>	<a href="#">1310.5663</a>	<a href="#">1310.5626</a>	<a href="#">2.79</a>	<a href="#">0</a>	<a href="#">35</a>	<a href="#">0.012</a>	<a href="#">1</a>		<a href="#">K.EDQTEYLEER.R</a>
<a href="#">1893</a>	<a href="#">683.3683</a>	<a href="#">1364.7221</a>	<a href="#">1364.7221</a>	<a href="#">0.00</a>	<a href="#">0</a>	<a href="#">107</a>	<a href="#">1.6e-009</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.TLTIVDTGIGMTK.A</a> <a href="#">1892</a> <a href="#">1894</a> <a href="#">1895</a>
<a href="#">2039</a>	<a href="#">708.8245</a>	<a href="#">1415.6345</a>	<a href="#">1415.6303</a>	<a href="#">2.94</a>	<a href="#">0</a>	<a href="#">48</a>	<a href="#">0.00084</a>	<a href="#">1</a>		<a href="#">K.EGLELPEDEEEK.K</a> <a href="#">2038</a>
<a href="#">2338</a>	<a href="#">505.2651</a>	<a href="#">1512.7734</a>	<a href="#">1512.7784</a>	<a href="#">-3.29</a>	<a href="#">0</a>	<a href="#">(39)</a>	<a href="#">0.011</a>	<a href="#">1</a>		<a href="#">R.GVDSDELPLNISR.E</a>
<a href="#">2339</a>	<a href="#">757.3942</a>	<a href="#">1512.7738</a>	<a href="#">1512.7784</a>	<a href="#">-3.04</a>	<a href="#">0</a>	<a href="#">93</a>	<a href="#">4.1e-008</a>	<a href="#">1</a>		<a href="#">R.GVDSDELPLNISR.E</a>
<a href="#">2416</a>	<a href="#">770.3829</a>	<a href="#">1538.7513</a>	<a href="#">1538.7464</a>	<a href="#">3.20</a>	<a href="#">1</a>	<a href="#">43</a>	<a href="#">0.0055</a>	<a href="#">1</a>		<a href="#">R.YESLTDPSKLDGK.E</a>
<a href="#">2481</a>	<a href="#">780.9163</a>	<a href="#">1559.8180</a>	<a href="#">1559.8155</a>	<a href="#">1.61</a>	<a href="#">1</a>	<a href="#">102</a>	<a href="#">6.6e-009</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.ELISNSSDALDKIR.Y</a>
<a href="#">2491</a>	<a href="#">783.8524</a>	<a href="#">1565.6903</a>	<a href="#">1565.6919</a>	<a href="#">-1.05</a>	<a href="#">0</a>	<a href="#">81</a>	<a href="#">4.8e-007</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.YYTSASGDEMVSLEK.D</a>
<a href="#">3096</a>	<a href="#">593.6554</a>	<a href="#">1777.9444</a>	<a href="#">1777.9403</a>	<a href="#">2.28</a>	<a href="#">0</a>	<a href="#">60</a>	<a href="#">8.1e-005</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">K.HSQFIGYPITLFVEK.E</a> <a href="#">3092</a> <a href="#">3094</a> <a href="#">3095</a>
<a href="#">3118</a>	<a href="#">596.3190</a>	<a href="#">1785.9351</a>	<a href="#">1785.9373</a>	<a href="#">-1.25</a>	<a href="#">0</a>	<a href="#">43</a>	<a href="#">0.0049</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">K.HLEINPDHSIIETLR.Q</a>

[3229](#) 917.3975 1832.7804 1832.7741 3.44 0 91 3.8e-008 1 U R.NPDDITNEEYGEFYK.S [3228](#)  
[4635](#) 751.3961 3001.5551 3001.5396 5.16 0 87 1.9e-007 1 U K.DLVILLYETALLSSGFSLEDPQTHANR.I  
[4636](#) 1001.5258 3001.5554 3001.5396 5.26 0 (64) 3.9e-005 1 U K.DLVILLYETALLSSGFSLEDPQTHANR.I

2. [HS90B\\_HUMAN](#) Mass: 83212 Score: 961 Matches: 26(26) Sequences: 17(17) emPAI: 0.85

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="#">349</a>	415.2679	828.5213	828.5221	-1.04	0	47	0.00069	1	U	R.ALLFIPR.R <a href="#">350</a>
<a href="#">458</a>	443.7769	885.5392	885.5396	-0.46	1	34	0.019	1	U	R.RLSSELLR.Y
<a href="#">463</a>	446.2162	890.4178	890.4174	0.40	0	49	0.00064	1	U	K.FYEAFSK.N
<a href="#">1353</a>	597.8282	1193.6418	1193.6404	1.18	0	64	2.3e-005	1	U	K.IDIIPNPQER.T <a href="#">1351</a>
<a href="#">1483</a>	621.8545	1241.6944	1241.6979	-2.81	0	81	4.1e-007	1		K.ADLINNLTIAK.S <a href="#">1486</a>
<a href="#">1505</a>	625.3127	1248.6109	1248.6098	0.87	0	72	6.8e-006	1	U	K.EQVANSFVER.V
<a href="#">1604</a>	638.3254	1274.6362	1274.6354	0.65	0	90	9.7e-008	1		R.ELISNASDALDK.I
<a href="#">1718</a>	656.2904	1310.5663	1310.5626	2.79	0	35	0.012	1		K.EDQTEYLEER.R
<a href="#">1893</a>	683.3683	1364.7221	1364.7221	0.00	0	107	1.6e-009	1	U	R.TLTLDVTGIGMTK.A <a href="#">1892</a> <a href="#">1894</a> <a href="#">1895</a>
<a href="#">2039</a>	708.8245	1415.6345	1415.6303	2.94	0	48	0.00084	1		K.EGLELPEDEEEK.K <a href="#">2038</a>
<a href="#">2338</a>	505.2651	1512.7734	1512.7784	-3.29	0	(39)	0.011	1		R.GVVDSEDLPLNISR.E
<a href="#">2339</a>	757.3942	1512.7738	1512.7784	-3.04	0	93	4.1e-008	1		R.GVVDSEDLPLNISR.E
<a href="#">2416</a>	770.3829	1538.7513	1538.7464	3.20	1	43	0.0055	1		R.YESLTDPSKLDGSK.E
<a href="#">2440</a>	772.9152	1543.8158	1543.8205	-3.09	1	91	7e-008	1		R.ELISNASDALDKIR.Y
<a href="#">3102</a>	594.9883	1781.9432	1781.9424	0.44	0	39	0.0094	1	U	K.HLEINPDHPIVETLR.Q
<a href="#">3180</a>	603.6584	1807.9533	1807.9509	1.37	0	52	0.00058	1	U	K.HSQFIGYPITLYLEK.E <a href="#">3179</a>
<a href="#">3267</a>	924.4046	1846.7947	1846.7897	2.67	0	104	2.3e-009	1	U	R.NPDDITQEEYGEFYK.S
<a href="#">4002</a>	731.6523	2191.9352	2191.9328	1.10	0	45	0.002	1	U	R.YHTSQSGDEMTSLSEYVSR.M

3. [ACTN1\\_HUMAN](#) Mass: 102993 Score: 758 Matches: 22(22) Sequences: 19(19) emPAI: 0.74

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="#">160</a>	374.7155	747.4165	747.4167	-0.18	0	33	0.031	1		K.YLDIPK.M
<a href="#">408</a>	432.7439	863.4732	863.4752	-2.33	0	54	0.00022	1		K.ALDFIASK.G
<a href="#">1400</a>	608.3412	1214.6679	1214.6659	1.69	0	75	2.7e-006	1		K.LASDLLEWIR.R
<a href="#">1441</a>	409.8882	1226.6428	1226.6407	1.69	0	33	0.029	1	U	R.HRPELIDYGK.L
<a href="#">1654</a>	431.9216	1292.7431	1292.7452	-1.66	0	30	0.027	1	U	R.LAILGIHNEVSK.I
<a href="#">1955</a>	693.8919	1385.7693	1385.7667	1.85	0	91	5.9e-008	1		R.VGWEQLTTIAR.T <a href="#">1956</a>
<a href="#">1960</a>	694.8959	1387.7772	1387.7745	1.97	0	77	1e-006	1		K.LMLLLEVISGER.L
<a href="#">2079</a>	715.3856	1428.7566	1428.7572	-0.47	0	83	5.2e-007	1		R.TINEVENQILTR.D
<a href="#">2221</a>	493.2433	1476.7080	1476.7143	-4.26	0	36	0.025	1	U	R.LSNRPAPMPSEGR.M
<a href="#">2237</a>	740.4096	1478.8047	1478.7989	3.88	0	64	2.6e-005	1		K.MTLGMIWTIILR.F <a href="#">2233</a>
<a href="#">2410</a>	769.3923	1536.7701	1536.7671	1.94	0	83	4.9e-007	1		R.FAIQDISVEETSAK.E
<a href="#">2434</a>	772.4150	1542.8155	1541.8301	639	0	67	1.8e-005	1	U	K.LVSI GAEEIVDGNVK.M
<a href="#">2905</a>	571.3108	1710.9105	1710.9080	1.51	0	(43)	0.0037	1	U	K.LLETIDQLYLEYAK.R
<a href="#">2906</a>	856.4644	1710.9142	1710.9080	3.62	0	76	1.8e-006	1	U	K.LLETIDQLYLEYAK.R
<a href="#">3007</a>	873.3790	1744.7434	1744.7462	-1.60	0	109	5.9e-010	1	U	R.ETADTDTADQVMASFK.I
<a href="#">3017</a>	439.2101	1752.8114	1752.8179	-3.75	1	37	0.018	1		K.KHEAFESDLAAHQDR.V
<a href="#">3036</a>	879.4714	1756.9282	1756.9261	1.22	0	33	0.043	1	U	K.QFGA QANVIGPWITK.M
<a href="#">3056</a>	881.9309	1761.8473	1761.8421	2.93	0	60	0.00011	1	U	K.DDPLTNLNTAFDVAEK.Y
<a href="#">3090</a>	592.6218	1774.8435	1774.8407	1.55	0	48	0.0016	1	U	K.MLDAEDIVGTARPDEK.A
<a href="#">4191</a>	780.4030	2338.1872	2338.1805	2.89	0	49	0.0015	1	U	K.IDQLEGDHLIQEALIFDNK.H

4. [FETA\\_HUMAN](#) Mass: 68633 Score: 549 Matches: 13(13) 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="#">631</a>	490.2576	978.5006	978.5022	-1.63	0	52	0.00047	1	U	K.GYQELLEK.C <a href="#">632</a>
<a href="#">1166</a>	575.8101	1149.6057	1149.6030	2.38	0	45	0.0022	1	U	K.YIQESQALAK.R
<a href="#">3370</a>	631.6636	1891.9691	1891.9720	-1.53	0	(62)	7.8e-005	1	U	K.LGEYYLQNAFLVAYTK.K <a href="#">3369</a> <a href="#">3376</a>
<a href="#">3373</a>	946.9948	1891.9751	1891.9720	1.64	0	87	2.3e-007	1	U	K.LGEYYLQNAFLVAYTK.K <a href="#">3367</a> <a href="#">3368</a> <a href="#">3372</a> <a href="#">3374</a> <a href="#">3378</a> <a href="#">3380</a>

5. [ACTN4\\_HUMAN](#) Mass: 104788 Score: 538 Matches: 14(14) Sequences: 12(12) emPAI: 0.39

Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">160</a>	374.7155	747.4165	747.4167	-0.18	0	33	0.031	1		K.YLDIPK.M
<a href="#">408</a>	432.7439	863.4732	863.4752	-2.33	0	54	0.00022	1		K.ALDFIASK.G
<a href="#">1400</a>	608.3412	1214.6679	1214.6659	1.69	0	75	2.7e-006	1		K.LASDLLEWIR.R
<a href="#">1955</a>	693.8919	1385.7693	1385.7667	1.85	0	91	5.9e-008	1		R.VGWEQLTTIAR.T <a href="#">1956</a>
<a href="#">1960</a>	694.8959	1387.7772	1387.7745	1.97	0	77	1e-006	1		K.LMLLLEVISGER.L
<a href="#">2079</a>	715.3856	1428.7566	1428.7572	-0.47	0	83	5.2e-007	1		R.TINEVENQILTR.D
<a href="#">2237</a>	740.4096	1478.8047	1478.7989	3.88	0	64	2.6e-005	1		K.MTLGMIWTIILR.F <a href="#">2233</a>
<a href="#">2344</a>	757.9053	1513.7961	1513.7988	-1.75	0	99	9.9e-009	1	U	K.LVSI GAEEIVDGNK.M
<a href="#">2410</a>	769.3923	1536.7701	1536.7671	1.94	0	83	4.9e-007	1		R.FAIQDISVEETSAK.E

[2998](#) 871.4127 1740.8109 1740.8054 3.15 0 34 0.035 1 U R.ETD<sup>TD</sup>ADQVIASFK.V  
[3017](#) 439.2101 1752.8114 1752.8179 -3.75 1 37 0.018 1 R.KHEAFESDLAAHQDR.V  
[3226](#) 611.6284 1831.8632 1831.8622 0.59 0 38 0.019 1 U K.MLDAEDIVNTARPDEK.A

6. [EF2\\_HUMAN](#) Mass: 95277 Score: 500 Matches: 12(12) Sequences: 8(8) emPAI: 0.35

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="#">460</a>	445.7571	889.4997	889.5022	-2.74	0	38	0.01	1	U	K.FSVSPVVR.V
<a href="#">956</a>	546.2957	1090.5769	1090.5771	-0.22	0	73	4.7e-006	1	U	M.VNFTVDQIR.A
<a href="#">994</a>	551.7654	1101.5163	1101.5165	-0.12	0	49	0.00059	1	U	K.QFAEM <sup>Y</sup> VAK.F <a href="#">995</a>
<a href="#">1009</a>	554.3248	1106.6350	1106.6336	1.27	0	90	3e-008	1	U	R.VFSGLVSTGLK.V
<a href="#">2136</a>	722.8871	1443.7596	1443.7609	-0.91	1	68	1.5e-005	1	U	K.EGIPALDNFLDKL.- <a href="#">2137</a>
<a href="#">3003</a>	581.6627	1741.9661	1741.9614	2.72	2	58	9e-005	1	U	K.GLKEGIPALDNFLDKL.-
<a href="#">3157</a>	600.6377	1798.8913	1798.8890	1.26	0	(57)	0.00021	1	U	K.AYLPVNESFGFTADLR.S
<a href="#">3158</a>	900.4544	1798.8943	1798.8890	2.93	0	97	1.9e-008	1	U	K.AYLPVNESFGFTADLR.S
<a href="#">4027</a>	740.7258	2219.1557	2219.1474	3.74	0	(69)	1.2e-005	1	U	R.ALLELQLEPEELYQTFQR.I
<a href="#">4028</a>	1110.5874	2219.1603	2219.1474	5.81	0	82	5.5e-007	1	U	R.ALLELQLEPEELYQTFQR.I

7. [ALBU\\_HUMAN](#) Mass: 69321 Score: 429 Matches: 12(12) 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="#">542</a>	464.2491	926.4836	926.4861	-2.71	0	45	0.0012	1	U	K.YLYE <sup>IAR</sup> .R <a href="#">541</a> <a href="#">543</a> <a href="#">544</a> <a href="#">545</a>
<a href="#">2333</a>	756.4261	1510.8376	1510.8355	1.39	0	85	1.5e-007	1	U	K.VPQVSTPTLVEVSR.N <a href="#">2332</a>
<a href="#">2711</a>	547.3173	1638.9300	1638.9305	-0.32	1	(76)	7.9e-007	1	U	K.KVPQVSTPTLVEVSR.N <a href="#">2710</a> <a href="#">2712</a>
<a href="#">2713</a>	820.4737	1638.9328	1638.9305	1.44	1	99	3.9e-009	1	U	K.KVPQVSTPTLVEVSR.N <a href="#">2714</a>

8. [K2C1\\_HUMAN](#) Mass: 65999 Score: 396 Matches: 11(11) Sequences: 8(8) emPAI: 0.47

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="#">1297</a>	590.3041	1178.5937	1178.5931	0.51	0	68	1.3e-005	1		K.YEELQITAGR.H
<a href="#">1672</a>	651.8625	1301.7104	1301.7078	2.00	0	101	6.8e-009	1	U	R.SLDLDSIAEVK.A <a href="#">1673</a>
<a href="#">1947</a>	692.3484	1382.6822	1382.6830	-0.57	0	42	0.0053	1	U	K.SLNQFAS <sup>F</sup> IDK.V
<a href="#">2216</a>	738.3787	1474.7428	1474.7416	0.79	0	67	2.3e-005	1	U	K.WELLQQVDTSTR.T
<a href="#">2218</a>	738.3970	1474.7794	1474.7780	0.96	0	81	8.5e-007	1		R.FLEQQNQVLQTK.W <a href="#">2219</a>
<a href="#">2709</a>	546.9586	1637.8540	1637.8525	0.91	1	38	0.014	1	U	K.SLNQFAS <sup>F</sup> IDKVR.F
<a href="#">3651</a>	665.3288	1992.9646	1992.9693	-2.40	0	34	0.049	1	U	R.THNLEPYFESFINNLR.R
<a href="#">4234</a>	1192.4822	2382.9498	2382.9447	2.16	0	(39)	0.0027	1	U	R.GGGGGGSGSGSSYGSGGGSGSGGGGGGR.G
<a href="#">4235</a>	795.3246	2382.9519	2382.9447	3.05	0	46	0.00054	1	U	R.GGGGGGSGSGSSYGSGGGSGSGGGGGGR.G

9. [EZRI\\_HUMAN](#) Mass: 69370 Score: 392 Matches: 11(11) Sequences: 10(10) emPAI: 0.51

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="#">467</a>	447.7748	893.5350	893.5375	-2.76	0	47	0.00029	1	U	K.LFFLQVK.E
<a href="#">513</a>	457.7692	913.5239	913.5232	0.72	0	44	0.0017	1	U	K.IALLEEAR.R
<a href="#">621</a>	488.7760	975.5375	975.5389	-1.53	0	49	0.00091	1	U	K.QLFDQVVK.T
<a href="#">912</a>	357.5488	1069.6245	1069.6243	0.12	1	33	0.015	1	U	K.IALLEEAR.R
<a href="#">1006</a>	552.7953	1103.5761	1103.5764	-0.20	0	59	0.00014	1	U	K.IGFPWSEIR.N <a href="#">1005</a>
<a href="#">1309</a>	591.8016	1181.5887	1181.5869	1.50	0	70	6.6e-006	1	U	K.APDFVFYAPR.L
<a href="#">2140</a>	723.4036	1444.7926	1444.7885	2.80	0	117	1.4e-010	1	U	R.QLLTLSSELSQAR.D
<a href="#">2756</a>	826.4109	1650.8072	1650.8100	-1.70	0	86	3.2e-007	1	U	K.SQEQLAAELAEY <sup>TAK</sup> .I
<a href="#">3577</a>	981.9822	1961.9499	1961.9444	2.80	0	68	2.3e-005	1	U	K.IAQDLEMYGINYFEIK.N
<a href="#">3796</a>	680.0082	2037.0029	2036.9942	4.25	0	35	0.038	1	U	K.FYPEDVAELIQDITQK.L

10. [GRP78\\_HUMAN](#) Mass: 72288 Score: 313 Matches: 9(9) Sequences: 8(8) emPAI: 0.37

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="#">1452</a>	617.3144	1232.6142	1232.6183	-3.31	0	83	5.5e-007	1	U	K.DAGTIAGLNVMR.I
<a href="#">2081</a>	715.8485	1429.6825	1429.6838	-0.90	0	39	0.01	1	U	R.TWNDPSVQQDIK.F
<a href="#">2457</a>	776.9016	1551.7885	1551.7854	2.01	0	59	0.00012	1	U	K.TFAPEEISAMVLTK.M <a href="#">2456</a>
<a href="#">2467</a>	519.2692	1554.7857	1554.7862	-0.37	1	40	0.0089	1	U	K.NGRVEIANDQGNR.I
<a href="#">2494</a>	783.8945	1565.7745	1565.7726	1.24	0	33	0.048	1	U	R.ITPSYVAFTPEGER.L
<a href="#">2828</a>	839.4099	1676.8052	1676.8006	2.73	0	85	3.1e-007	1	U	K.NQLTSNPENTVFDAK.R
<a href="#">3199</a>	606.0045	1814.9917	1814.9890	1.50	1	47	0.0011	1	U	R.IINEPTAAAIAYGLDKR.E
<a href="#">3972</a>	1082.9957	2163.9769	2163.9848	-3.64	0	105	3.4e-009	1	U	R.IEIESFYEGEDFSETL <sup>TR</sup> .A

11. [K1C10\\_HUMAN](#) Mass: 58792 Score: 308 Matches: 7(7) Sequences: 6(6) emPAI: 0.40

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
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<a href="#">779</a>	516.3028	1030.5910	1030.5910	0.02	0	58	9.4e-005	1	U	R.VLDELTLTK.A
<a href="#">903</a>	532.8089	1063.6032	1063.6026	0.64	1	51	0.00034	1	U	R.LASYLDKVR.A
<a href="#">904</a>	355.5420	1063.6041	1063.6026	1.48	1	(37)	0.008	1	U	R.LASYLDKVR.A
<a href="#">1018</a>	555.2487	1108.4828	1108.4825	0.22	0	40	0.0047	1	U	K.DAEAWFNEK.S
<a href="#">1940</a>	691.3284	1380.6422	1380.6408	0.98	0	83	3.5e-007	1	U	R.ALEESNYELEGK.I
<a href="#">2895</a>	854.3881	1706.7617	1706.7649	-1.88	0	129	1.2e-011	1	U	K.GSLGGGFSSGGFSGGSFSR.G
<a href="#">4653</a>	1018.2171	3051.6295	3051.6200	3.11	1	61	4.2e-005	1	U	K.TIDDLKNQILNLTDDNANILLQIDNAR.L

12. [ENPL\\_HUMAN](#) Mass: 92411 Score: 286 Matches: 6(6) Sequences: 6(6) emPAI: 0.20

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">603</a>	482.2975	962.5804	962.5800	0.40	0	40	0.0016	1	U	K.LIINSLYK.N
<a href="#">674</a>	497.2668	992.5191	992.5179	1.23	0	49	0.001	1	U	R.SGYLLPDTK.A
<a href="#">1604</a>	638.3254	1274.6362	1274.6354	0.65	0	90	9.7e-008	1		R.ELISNASDALDK.I
<a href="#">2255</a>	743.3824	1484.7503	1484.7471	2.18	0	95	2.8e-008	1	U	K.GVVDSDDLPLNVS.R
<a href="#">2440</a>	772.9152	1543.8158	1543.8205	-3.09	1	91	7e-008	1		R.ELISNASDALDKIR.L
<a href="#">3336</a>	939.9811	1877.9476	1877.9352	6.60	0	56	0.00027	1	U	K.YSQFINFPIYVWSSK.T

13. [LG3BP\\_HUMAN](#) Mass: 65289 Score: 273 Matches: 9(9) Sequences: 6(6) emPAI: 0.36

Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">128</a>	352.2106	702.4067	702.4064	0.29	0	36	0.019	1	U	K.SLGWLK.S
<a href="#">620</a>	488.2894	974.5642	974.5648	-0.57	0	52	0.00033	1	U	R.IDITLSSVK.C
<a href="#">1771</a>	442.8895	1325.6467	1325.6463	0.28	0	(41)	0.007	1	U	R.ASHEEVEGLVEK.I
<a href="#">1772</a>	663.8310	1325.6474	1325.6463	0.87	0	65	2.5e-005	1	U	R.ASHEEVEGLVEK.I
<a href="#">1854</a>	678.3912	1354.7678	1354.7708	-2.18	0	60	3.7e-005	1	U	R.SDLAVPSELALLK.A
<a href="#">2563</a>	796.9009	1591.7873	1591.7842	1.98	0	87	2.1e-007	1	U	R.ELSEALGQIFDSQR.G <a href="#">2564</a>
<a href="#">3625</a>	662.0374	1983.0904	1983.0942	-1.90	0	42	0.0032	1	U	K.TLQALEFHTVPFQLLAR.Y <a href="#">3626</a>

14. [TERA\\_HUMAN](#) Mass: 89266 Score: 262 Matches: 11(11) Sequences: 8(8) emPAI: 0.38

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="#">781</a>	516.7822	1031.5498	1031.5499	-0.10	0	37	0.023	1	U	K.GDDLSTAILK.Q
<a href="#">850</a>	525.2791	1048.5436	1048.5441	-0.49	0	51	0.00062	1	U	K.DVDLEFLAK.M
<a href="#">909</a>	534.2601	1066.5057	1066.5117	-5.63	0	44	0.0028	1	U	K.MDELQLFR.G
<a href="#">1262</a>	586.8376	1171.6607	1171.6601	0.54	0	48	0.0011	1	U	R.GILLYGPPGTGK.T
<a href="#">2470</a>	778.9358	1555.8570	1555.8497	4.69	0	55	0.00019	1	U	R.LDQLIYIPLPEK.S
<a href="#">2731</a>	549.2696	1644.7869	1644.7930	-3.66	1	45	0.0028	1	U	R.KYEMFAQTLQSSR.G
<a href="#">3182</a>	906.0032	1809.9918	1809.9876	2.31	0	52	0.00035	1	U	K.NAPAIIFIDELDAIPK.R
<a href="#">3183</a>	604.3387	1809.9942	1809.9876	3.65	0	(38)	0.0078	1	U	K.NAPAIIFIDELDAIPK.R <a href="#">3185</a>
<a href="#">4118</a>	758.0477	2271.1212	2271.1245	-1.48	0	(51)	0.0011	1	U	R.AVANETGAFFFLINGPEIMSK.L
<a href="#">4119</a>	1136.5693	2271.1241	2271.1245	-0.19	0	78	1.9e-006	1	U	R.AVANETGAFFFLINGPEIMSK.L

15. [MX1\\_HUMAN](#) Mass: 75473 Score: 246 Matches: 8(8) Sequences: 4(4) emPAI: 0.21

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="#">1794</a>	666.3521	1330.6896	1330.6881	1.08	0	73	5.3e-006	1	U	R.VAVGNQPADIGYK.I <a href="#">1795</a>
<a href="#">1981</a>	699.9032	1397.7918	1397.7878	2.89	0	31	0.035	1	U	K.SSVLEALSGVALPR.G
<a href="#">2706</a>	819.4614	1636.9083	1636.9036	2.87	0	62	2.8e-005	1	U	R.DVPDLTLIDLPGITR.V <a href="#">2702</a> <a href="#">2703</a>
<a href="#">4067</a>	751.4106	2251.2101	2251.2060	1.84	0	(58)	9.8e-005	1	U	R.ALGVEQDLALPAIAVIGDQSSGK.S
<a href="#">4068</a>	1126.6156	2251.2166	2251.2060	4.75	0	60	5.4e-005	1	U	R.ALGVEQDLALPAIAVIGDQSSGK.S

16. [K22E\\_HUMAN](#) Mass: 65393 Score: 243 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="#">796</a>	519.2678	1036.5210	1036.5189	1.99	0	32	0.046	1	U	R.YLDGLTAER.T
<a href="#">1785</a>	665.3680	1328.7214	1328.7187	2.03	0	97	1.4e-008	1		R.NLDLDSIAEVK.A
<a href="#">2174</a>	730.9056	1459.7966	1459.7922	3.00	0	88	1.1e-007	1	U	K.VDLLNQIEFLK.V
<a href="#">2218</a>	738.3970	1474.7794	1474.7780	0.96	0	81	8.5e-007	1		R.FLEQQNQVLQTK.W <a href="#">2219</a>

17. [QSOX1\\_HUMAN](#) Mass: 82526 Score: 242 Matches: 7(7) Sequences: 5(5) emPAI: 0.27

Sulphydryl 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="#">1155</a>	574.7887	1147.5628	1147.5662	-2.92	0	33	0.048	1	U	R.SFYTAYLQR.L
<a href="#">1857</a>	678.8452	1355.6759	1355.6721	2.77	0	35	0.026	1	U	R.LAGAPSEDQPFK.V
<a href="#">2243</a>	741.8790	1481.7434	1481.7402	2.18	0	91	8e-008	1	U	R.NNEEYLALIFEK.G
<a href="#">3297</a>	620.3402	1857.9988	1857.9877	6.00	0	55	0.00025	1	U	R.LDVPVWDVEATLNFLK.A
<a href="#">3298</a>	930.0076	1858.0007	1857.9877	7.02	0	(34)	0.026	1	U	R.LDVPVWDVEATLNFLK.A



[3799](#) 683.0297 2046.0673 2046.0633 1.96 0 (44) 0.0042 1 U R.SALYSPSDPLTLQADTVR.G  
[3800](#) 1024.0433 2046.0721 2046.0633 4.30 0 98 1.5e-008 1 U R.SALYSPSDPLTLQADTVR.G

18. [IMB1\\_HUMAN](#) Mass: 97108 Score: 232 Matches: 8(8) Sequences: 4(4) emPAI: 0.19

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="#">2611</a>	803.4491	1604.8836	1604.8773	3.93	0	56	0.00015	1	U	K.LAATNALLNSLEFTK.A
<a href="#">2769</a>	553.6406	1657.8999	1657.9039	-2.43	0	(45)	0.0021	1	U	R.AAVENLPTFLVELSR.V
<a href="#">2771</a>	829.9634	1657.9123	1657.9039	5.08	0	84	2.2e-007	1	U	R.AAVENLPTFLVELSR.V <a href="#">2770</a>
<a href="#">3040</a>	880.0242	1758.0338	1758.0291	2.66	0	(28)	0.018	1	U	K.GALQYLVPILTQTLTK.Q
<a href="#">3041</a>	587.0189	1758.0348	1758.0291	3.21	0	37	0.0024	1	U	K.GALQYLVPILTQTLTK.Q <a href="#">3039</a>
<a href="#">3756</a>	672.6671	2014.9793	2014.9742	2.55	0	42	0.0075	1	U	R.LQQVLQMESHIQSTSDR.I

19. [CADH1\\_HUMAN](#) Mass: 97396 Score: 230 Matches: 5(5) Sequences: 4(4) emPAI: 0.16

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="#">803</a>	521.2499	1040.4853	1040.4848	0.47	0	49	0.00065	1	U	K.MALEVG DYK.I
<a href="#">2084</a>	716.3954	1430.7762	1430.7729	2.30	0	57	0.00015	1	U	R.NTGVISVVTGLDR.E
<a href="#">2908</a>	856.4672	1710.9198	1710.9152	2.67	0	82	3.9e-007	1	U	K.GQVPNEANVVITTLK.V
<a href="#">4214</a>	789.4172	2365.2297	2365.2318	-0.90	0	(35)	0.027	1	U	K.VFYSITGQGADTPPVGVFIER.E
<a href="#">4216</a>	1183.6276	2365.2406	2365.2318	3.70	0	100	9.5e-009	1	U	K.VFYSITGQGADTPPVGVFIER.E

20. [GELS\\_HUMAN](#) Mass: 85644 Score: 211 Matches: 6(6) Sequences: 5(5) emPAI: 0.18

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="#">1609</a>	425.9115	1274.7128	1274.7095	2.53	0	40	0.0058	1	U	K.HVVPNEVVQR.L <a href="#">1608</a>
<a href="#">1746</a>	660.3519	1318.6893	1318.6881	0.92	0	58	0.00015	1	U	K.AGALNSNDAFLVK.T
<a href="#">2939</a>	861.9204	1721.8263	1721.8301	-2.22	0	96	3.6e-008	1	U	R.EVQGFESATFLGYFK.S
<a href="#">3216</a>	915.4883	1828.9620	1828.9571	2.69	0	67	1.9e-005	1	U	K.QTQVSVLPEGGETPLFK.Q
<a href="#">4549</a>	924.4493	2770.3262	2770.3279	-0.61	0	40	0.015	1	U	K.VPVPATYGYQFYGGDSYIILNYR.H

21. [A2MG\\_HUMAN](#) Mass: 163188 Score: 211 Matches: 7(7) 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="#">732</a>	509.7979	1017.5813	1017.5859	-4.51	0	53	0.00028	1	U	K.ATVLNLYPK.C <a href="#">733</a> <a href="#">735</a>
<a href="#">1047</a>	558.8069	1115.5992	1115.5975	1.52	0	47	0.0019	1	U	R.QTWSWAVTPK.S
<a href="#">1382</a>	605.8259	1209.6372	1209.6353	1.53	0	72	4e-006	1	U	K.LPPNVVEESAR.A <a href="#">1380</a> <a href="#">1381</a>

22. [CFAB\\_HUMAN](#) Mass: 85479 Score: 205 Matches: 5(5) Sequences: 4(4) emPAI: 0.14

Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">726</a>	508.2752	1014.5358	1014.5346	1.21	0	31	0.046	1	U	K.DISEVVTPT.F
<a href="#">1605</a>	638.3333	1274.6520	1274.6547	-2.14	0	69	1.4e-005	1	U	R.YGLVTYATPK.I <a href="#">1606</a>
<a href="#">2314</a>	754.8447	1507.6749	1507.6791	-2.76	0	102	4.3e-009	1	U	K.VSEADSNADWVTK.Q
<a href="#">3257</a>	921.9645	1841.9145	1841.9087	3.16	0	58	0.00016	1	U	K.EAGIPEFYDYDVALIK.L

23. [LUM\\_HUMAN](#) Mass: 38405 Score: 198 Matches: 7(7) 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="#">3555</a>	653.0400	1956.0981	1956.0932	2.53	0	(45)	0.0011	1	U	R.LPSGLPVSLTLTYLDNNK.I <a href="#">3553</a> <a href="#">3554</a>
<a href="#">3558</a>	979.0584	1956.1023	1956.0932	4.66	0	66	8.8e-006	1	U	R.LPSGLPVSLTLTYLDNNK.I <a href="#">3556</a> <a href="#">3559</a> <a href="#">3560</a>

24. [HBA\\_HUMAN](#) Mass: 15248 Score: 198 Matches: 6(6) 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="#">951</a>	363.2134	1086.6184	1086.6186	-0.16	1	36	0.018	1	U	K.LRVDVNF.K.L
<a href="#">1529</a>	626.8604	1251.7063	1251.7075	-0.95	0	88	5.1e-008	1	U	K.FLASVSTVLT.SK.Y <a href="#">1530</a>
<a href="#">2383</a>	510.5819	1528.7240	1528.7270	-1.96	0	(49)	0.00094	1	U	K.VGAHAGEYGAEALER.M <a href="#">2384</a>
<a href="#">2385</a>	765.3712	1528.7278	1528.7270	0.50	0	57	0.00015	1	U	K.VGAHAGEYGAEALER.M

25. [H90B2\\_HUMAN](#) Mass: 44321 Score: 191 Matches: 5(5) Sequences: 3(3) emPAI: 0.21

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="#">1483</a>	621.8545	1241.6944	1241.6979	-2.81	0	81	4.1e-007	1		K.ADLINNLGTIAK.F <a href="#">1486</a>
<a href="#">2416</a>	770.3829	1538.7513	1538.7464	3.20	1	43	0.0055	1		R.YESLTDPSKLD.SGK.E
<a href="#">3180</a>	603.6584	1807.9533	1807.9509	1.37	0	52	0.00058	1	U	K.HSQFLGYPTILYLEK.E <a href="#">3179</a>

26.	VPS35_HUMAN	Mass: 91649	Score: 187	Matches: 6(6)	Sequences: 5(5)	emPAI: 0.21				
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
719	506.2952	1010.5758	1010.5760	-0.22	0	37	0.0059	1	U	K.AELAEPLR.L
1489	622.3358	1242.6571	1242.6568	0.22	0	59	9.4e-005	1	U	R.LSQLEGVNVVER.Y
2597	801.9572	1601.8998	1601.9028	-1.93	0	75	1.6e-006	1	U	K.IPVDTYNNILTVLK.L
2686	816.9054	1631.7962	1631.7930	1.99	0	63	6.1e-005	1	U	R.ESPESEGPIYEGIL.L
3281	618.0033	1850.9881	1850.9891	-0.54	0	52	0.00047	1	U	K.LFDIFSQQVATVIQSR.Q
3282	926.5067	1850.9989	1850.9891	5.30	0	(35)	0.021	1	U	K.LFDIFSQQVATVIQSR.Q

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27.	VTNC_HUMAN	Mass: 54271	Score: 180	Matches: 4(4)	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
2736	549.6089	1645.8050	1645.8100	-3.05	0	(41)	0.0094	1	U	R.DVWGIEGPIDAAFR.I
2737	823.9099	1645.8052	1645.8100	-2.96	0	83	5.8e-007	1	U	R.DVWGIEGPIDAAFR.I 2740 2741

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28.	ITIH2_HUMAN	Mass: 106397	Score: 165	Matches: 3(3)	Sequences: 3(3)	emPAI: 0.08				
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
1815	669.3652	1336.7158	1336.7139	1.40	0	49	0.00072	1	U	K.FYNQVSTPLLR.N
2539	791.9322	1581.8498	1581.8474	1.51	0	107	1.2e-009	1	U	K.IQPSGGTININEALLR.A
2888	852.4814	1702.9482	1702.9406	4.47	0	65	1.3e-005	1	U	K.LWAYLTINQLLAER.S

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29.	CD166_HUMAN	Mass: 65061	Score: 161	Matches: 6(6)	Sequences: 6(6)	emPAI: 0.30				
CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1541	628.8086	1255.6026	1255.6044	-1.44	0	33	0.031	1	U	R.SSNTYTLTDVR.R
1615	639.3322	1276.6499	1276.6486	1.03	0	65	3.1e-005	1	U	R.LDVPQNLNMFQK.W
2027	471.5759	1411.7058	1411.7056	0.16	1	50	0.00084	1	U	R.SSNTYTLTDVRR.N
2630	538.5840	1612.7303	1612.7369	-4.09	1	35	0.023	1	U	K.SVQYDDVPVEYKDR.L
2786	416.5123	1662.0202	1662.0232	-1.82	1	56	7.4e-006	1	U	K.VLHPLEGAVVIFKK.E
4520	897.7905	2690.3496	2690.3585	-3.33	0	46	0.0031	1	U	K.SMIATAITVHYLDLSLNPSGEVTR.Q

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30.	NUCL_HUMAN	Mass: 76568	Score: 157	Matches: 6(6)	Sequences: 4(4)	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
372	422.7612	843.5079	843.5065	1.61	0	31	0.04	1	U	K.ALELTGLK.V
698	500.7749	999.5353	999.5349	0.34	0	56	0.00013	1	U	K.NDLAVVDVR.I
3646	664.6699	1990.9879	1990.9847	1.61	1	36	0.031	1	U	K.VTQDELKEVFEDAAEIR.L
4171	771.3906	2311.1499	2311.1485	0.60	0	(52)	0.00073	1	U	K.VEGTEPTAFNLFVGNLNFNK.S 4170
4172	1156.5830	2311.1515	2311.1485	1.30	0	61	9.6e-005	1	U	K.VEGTEPTAFNLFVGNLNFNK.S

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31.	VASN_HUMAN	Mass: 71668	Score: 154	Matches: 3(3)	Sequences: 3(3)	emPAI: 0.13				
Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1167	575.8141	1149.6136	1149.6142	-0.51	0	45	0.0021	1	U	R.YLQGSVQLR.S
2510	785.4459	1568.8772	1568.8774	-0.12	0	47	0.00082	1	U	R.SLTGLIEPVSPSLR.V
2925	858.9714	1715.9282	1715.9206	4.41	0	118	1.3e-010	1	U	R.LAGLGLQQLDEGLFSR.L

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32.	K2C1B_HUMAN	Mass: 61864	Score: 152	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
1297	590.3041	1178.5937	1178.5931	0.51	0	68	1.3e-005	1	U	K.YQELQITAGR.H
2218	738.3970	1474.7794	1474.7780	0.96	0	81	8.5e-007	1		R.FLEQQNQLVTK.W 2219

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33.	K2C6B_HUMAN	Mass: 60030	Score: 134	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
1297	590.3041	1178.5937	1178.5931	0.51	0	68	1.3e-005	1		K.YEELQITAGR.H
1785	665.3680	1328.7214	1328.7187	2.03	0	97	1.4e-008	1		R.NLDLDSIIAEVK.A

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34.	PSA_HUMAN	Mass: 103211	Score: 129	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.06				
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

[1831](#) 673.8758 1345.7370 1345.7354 1.23 0 93 4.2e-008 1 U R.LGLQNDLFSLAR.A  
[1939](#) 690.9279 1379.8413 1379.8388 1.81 0 62 3.9e-006 1 U R.VLGATLLPDLIQK.V

35. [PDIA4\\_HUMAN](#) Mass: 72887 Score: 123 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="#">1339</a>	595.8202	1189.6258	1189.6302	-3.72	0	110	8.5e-010	1	U	K.IDATSASVLASR.F
<a href="#">2167</a>	729.8860	1457.7574	1457.7548	1.78	0	40	0.0092	1	U	K.VSQGQLVVMQPEK.F

36. [C3\\_HUMAN](#) Mass: 187030 Score: 123 Matches: 4(4) Sequences: 4(4) emPAI: 0.06

Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">593</a>	480.2802	958.5459	958.5447	1.25	0	35	0.026	1	U	K.GLEVITAR.F
<a href="#">3339</a>	939.9952	1877.9758	1877.9662	5.10	0	54	0.0004	1	U	K.EYVLPSFEVIVEPEK.F
<a href="#">4006</a>	733.3802	2197.1189	2197.1227	-1.71	0	44	0.0039	1	U	R.VPVAVQGEDTVQSLTQGDGVAK.L
<a href="#">4289</a>	1222.6670	2443.3194	2443.2999	8.00	0	55	0.00021	1	U	R.EPGDLVVLPLSITDFIPSR.L

37. [K1C9\\_HUMAN](#) Mass: 62027 Score: 117 Matches: 2(2) Sequences: 2(2) emPAI: 0.10

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="#">1192</a>	579.2999	1156.5852	1156.5836	1.32	0	88	9.4e-008	1	U	R.QGVDADINGLR.Q
<a href="#">4697</a>	1088.8463	3263.5171	3263.5066	3.23	0	54	0.00051	1	U	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E

38. [HEP2\\_HUMAN](#) Mass: 57034 Score: 114 Matches: 2(2) Sequences: 1(1) emPAI: 0.05

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="#">2875</a>	849.4581	1696.9016	1696.9300	-16.76	1	73	3.3e-006	1	U	R.LNILNAKFAFNLYR.V <a href="#">2874</a>

39. [IQGA1\\_HUMAN](#) Mass: 189134 Score: 113 Matches: 3(3) Sequences: 2(2) emPAI: 0.05

Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3350</a>	942.0138	1882.0130	1882.0047	4.42	0	60	7e-005	1	U	R.ILAIGLINEALDEGDAQK.T
<a href="#">3351</a>	628.3458	1882.0155	1882.0047	5.71	0	(50)	0.00059	1	U	R.ILAIGLINEALDEGDAQK.T
<a href="#">3479</a>	969.0080	1936.0014	1935.9942	3.75	0	36	0.029	1	U	K.FALGIFAINAVESGDVGK.T

40. [COPG1\\_HUMAN](#) Mass: 97655 Score: 112 Matches: 2(2) Sequences: 2(2) emPAI: 0.06

Coatomer 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="#">1261</a>	586.8307	1171.6469	1171.6448	1.80	0	58	0.00011	1	U	K.TLEEAVGNIVK.F
<a href="#">1496</a>	622.8937	1243.7729	1243.7751	-1.76	0	79	9.6e-008	1	U	R.SIATLAITTLK.T

41. [TRAP1\\_HUMAN](#) Mass: 80060 Score: 107 Matches: 2(2) 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="#">2338</a>	505.2651	1512.7734	1512.7784	-3.29	0	(39)	0.011	1	U	R.GVVDSEDIPLNLSR.E
<a href="#">2339</a>	757.3942	1512.7738	1512.7784	-3.04	0	93	4.1e-008	1	U	R.GVVDSEDIPLNLSR.E

42. [GOLM1\\_HUMAN](#) Mass: 45306 Score: 106 Matches: 3(3) Sequences: 3(3) emPAI: 0.21

Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">950</a>	544.2892	1086.5638	1086.5669	-2.86	0	55	0.00024	1	U	R.DTINLLDQR.E
<a href="#">1972</a>	697.8745	1393.7343	1393.7314	2.15	0	71	5.3e-006	1	U	R.QQLQALSEPQPR.L
<a href="#">2220</a>	492.9196	1475.7371	1475.7368	0.18	1	34	0.048	1	U	R.NIDVFNVEDQKR.D

43. [PSMD2\\_HUMAN](#) Mass: 100136 Score: 83 Matches: 4(4) Sequences: 4(4) emPAI: 0.12

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="#">730</a>	508.8054	1015.5962	1015.5913	4.81	0	41	0.0044	1	U	R.LNILDTLISK.F
<a href="#">1057</a>	561.7797	1121.5448	1120.5335	902	0	48	0.0015	1	U	K.DPNNLFMVR.L
<a href="#">2155</a>	484.9430	1451.8071	1451.8096	-1.78	0	41	0.0031	1	U	R.VGQAVDVVGQAGPK.T
<a href="#">4301</a>	819.7990	2456.3752	2456.3566	7.56	0	28	0.039	1	U	R.AELATEEFLPVTPILEGFVILR.K

44. [HGFA\\_HUMAN](#) Mass: 70636 Score: 80 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="#">1816</a>	670.3429	1338.6712	1338.6667	3.37	0	80	8.3e-007	1	U	R.TTDVTQTFGIEK.Y

45. [TRFL\\_HUMAN](#) Mass: 78132 Score: 77 Matches: 2(2) Sequences: 1(1) emPAI: 0.04  
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="#">972</a>	549.2541	1096.4936	1096.4978	-3.79	0	52	0.0003	1	U	R.YYGYTGAFR.C <a href="#">973</a>

46. [G3PT\\_HUMAN](#) Mass: 44473 Score: 72 Matches: 2(2) Sequences: 1(1) emPAI: 0.07  
Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1227</a>	581.3167	1160.6189	1160.6190	-0.08	0	49	0.0011	1	U	K.AGIALNDNFVK.L <a href="#">1226</a>

47. [SLIK4\\_HUMAN](#) Mass: 94271 Score: 71 Matches: 2(2) Sequences: 2(2) emPAI: 0.06  
SLIT and NTRK-like protein 4 OS=Homo sapiens GN=SLITRK4 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2270</a>	745.9227	1489.8309	1489.8293	1.09	0	59	6.6e-005	1	U	K.SLPVYIFSGAPLAR.L
<a href="#">2677</a>	815.9620	1629.9094	1629.9090	0.26	0	30	0.048	1	U	K.LQNIEGGAFLGLSALK.Q

48. [H2A1B\\_HUMAN](#) Mass: 14127 Score: 70 Matches: 3(3) Sequences: 1(1) emPAI: 0.47  
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="#">3461</a>	644.3918	1930.1535	1930.1615	-4.15	0	(38)	0.00077	1	U	R.VTIAQGGVLPNIQAVLLPK.K <a href="#">3463</a>
<a href="#">3462</a>	966.0842	1930.1538	1930.1615	-4.01	0	46	0.00014	1	U	R.VTIAQGGVLPNIQAVLLPK.K

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

[H2A1C\\_HUMAN](#) Mass: 14097 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A1D\\_HUMAN](#) Mass: 14099 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A1H\\_HUMAN](#) Mass: 13898 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A1J\\_HUMAN](#) Mass: 13928 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A1\\_HUMAN](#) Mass: 14083 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A2A\\_HUMAN](#) Mass: 14087 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A2C\\_HUMAN](#) Mass: 13980 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A3\\_HUMAN](#) Mass: 14113 Score: 70 Matches: 3(3) Sequences: 1(1)

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

[H2A7\\_HUMAN](#) Mass: 14011 Score: 70 Matches: 3(3) Sequences: 1(1)

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

49. [PDC6I\\_HUMAN](#) Mass: 95963 Score: 69 Matches: 4(4) Sequences: 3(3) emPAI: 0.09  
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="#">682</a>	499.2862	996.5578	996.5604	-2.60	0	32	0.02	1	U	K.ELPELLQR.N
<a href="#">761</a>	341.5375	1021.5908	1021.5920	-1.19	0	36	0.0055	1	U	R.LQHAAELIK.T <a href="#">760</a>
<a href="#">1752</a>	660.8442	1319.6739	1319.6755	-1.20	0	46	0.0026	1	U	K.TMQGSEVVNLK.S

50. [BCAM\\_HUMAN](#) Mass: 67363 Score: 67 Matches: 2(2) Sequences: 2(2) emPAI: 0.09  
Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2094</a>	717.3806	1432.7467	1432.7449	1.22	0	43	0.0057	1	U	R.VAYLDPLELSEK.V
<a href="#">3941</a>	712.6620	2134.9643	2134.9623	0.94	0	49	0.0011	1	U	R.LASAEQSGELQVTMHDTR.G

51. [S10A9\\_HUMAN](#) Mass: 13234 Score: 67 Matches: 1(1) Sequences: 1(1) emPAI: 0.23  
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3170</a>	903.9763	1805.9380	1805.9312	3.75	0	67	2e-005	1	U	R.NIETIINTFHQYSVK.L

52. [COPB\\_HUMAN](#) Mass: 107074 Score: 66 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
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[1790](#) 665.8755 1329.7365 1329.7326 2.95 0 54 0.00032 1 U R.VLQDLVMDILR.V [1789](#)

53. [GFPT1\\_HUMAN](#) Mass: 78756 Score: 63 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  
[2486](#) 781.9475 1561.8805 1561.8868 -4.06 0 (38) 0.0059 1 U R.VIQQLGAFALVFK.S  
[2487](#) 521.6344 1561.8814 1561.8868 -3.48 0 42 0.0021 1 U R.VIQQLGAFALVFK.S

Proteins matching the same set of peptides:

[GFPT2\\_HUMAN](#) Mass: 76882 Score: 63 Matches: 2(2) Sequences: 1(1)  
 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 OS=Homo sapiens GN=GFPT2 PE=1 SV=3

54. [XPP3\\_HUMAN](#) Score: 60 Matches: 2(2) Sequences: 1(1) emPAI: 0.05  
 Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1  
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
[295](#) 408.2594 814.5043 814.5065 -2.69 0 44 0.0014 1 U K.AILFVPR.R [294](#)

55. [FBLN1\\_HUMAN](#) Mass: 77162 Score: 59 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  
[2521](#) 525.9379 1574.7920 1574.7875 2.81 0 59 0.00015 1 U K.LEMNVVGGVVSHR.N

56. [TSP1\\_HUMAN](#) Mass: 129300 Score: 59 Matches: 1(1) Sequences: 1(1) emPAI: 0.02  
 Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2  
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
[660](#) 495.3094 988.6043 988.6069 -2.62 0 59 2.5e-005 1 U K.GFLLASLR.Q

57. [XPOT\\_HUMAN](#) Mass: 109893 Score: 57 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  
[2282](#) 748.4436 1494.8727 1494.8770 -2.87 0 57 3.6e-005 1 U R.LAQVSPPELLLASVR.R

58. [HS71L\\_HUMAN](#) 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  
[2828](#) 839.4099 1676.8051 1676.7828 13.3 0 57 0.00024 2 U K.NQVAMNPQNTVFDK.R

59. [CAND1\\_HUMAN](#) Mass: 136289 Score: 55 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  
[1544](#) 628.8959 1255.7773 1255.7751 1.75 0 48 0.0002 1 U K.LGTLASLDILIK.N  
[3829](#) 689.0786 2064.2140 2064.2095 2.17 0 26 0.015 1 U K.IDLRPVLGEGVPILASFLR.K

60. [DPP3\\_HUMAN](#) Mass: 82538 Score: 54 Matches: 1(1) Sequences: 1(1) emPAI: 0.04  
 Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=1 SV=2  
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Unique Peptide  
[3938](#) 712.0370 2133.0893 2133.0953 -2.82 0 54 0.00045 1 U R.LEGSDVQLLEYEASAAGLIR.S

61. [CROCC\\_HUMAN](#) Mass: 228388 Score: 54 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  
[513](#) 457.7692 913.5239 913.5232 0.72 0 44 0.0017 1 U K.LALLEEAR.T  
[1848](#) 677.8066 1353.5987 1353.5904 6.15 1 39 0.0067 1 U R.QMKMLDSENTR.L

62. [RS27A\\_HUMAN](#) Mass: 17953 Score: 52 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  
[3120](#) 894.4691 1786.9237 1786.9200 2.05 0 52 0.00072 1 U K.TITLEVEPSDTIENVK.A

Proteins matching the same set of peptides:

[RL40\\_HUMAN](#) Mass: 14719 Score: 52 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: 52 Matches: 1(1) Sequences: 1(1)

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

[UBC\\_HUMAN](#) Mass: 76992 Score: 52 Matches: 1(1) Sequences: 1(1)

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

63. [TFR1\\_HUMAN](#) Mass: 84818 Score: 50 Matches: 2(2) Sequences: 2(2) emPAI: 0.07

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="#">731</a>	508.8297	1015.6448	1015.6430	1.79	0	33	0.0031	1	U	K.ILNIFGVIK.G
<a href="#">2096</a>	717.4162	1432.8178	1432.8177	0.10	0	41	0.0029	1	U	K.VSASPLLYTLEK.T

64. [C04A\\_HUMAN](#) Mass: 192664 Score: 49 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="#">1900</a>	684.3660	1366.7175	1366.7133	3.10	0	49	0.00088	1	U	R.DSSTWLTAFLVK.V

65. [CLCF1\\_HUMAN](#) Mass: 25160 Score: 48 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="#">394</a>	428.7488	855.4831	855.4814	1.95	0	48	0.00042	1	U	R.LGAETLPR.A

66. [GOGB1\\_HUMAN](#) Mass: 375790 Score: 48 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="#">2976</a>	867.8979	1733.7813	1733.8141	-18.90	0	48	0.0012	1	U	K.MNLLNQIQEELSR.V

67. [KATL2\\_HUMAN](#) Mass: 61214 Score: 48 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="#">1262</a>	586.8376	1171.6607	1171.6601	0.54	0	48	0.0011	1	U	K.GLLLYGPPGTGK.T

68. [AFAM\\_HUMAN](#) Score: 47 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Aminafin OS=Homo sapiens GN=AFM PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">363</a>	416.7666	831.5187	831.5218	-3.74	0	47	0.00023	1	U	R.FLVNLVK.L

69. [ITIH3\\_HUMAN](#) Mass: 99787 Score: 46 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

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="#">2720</a>	547.6351	1639.8834	1639.8821	0.79	1	46	0.0016	1	U	K.VTFELTYEELLKR.H

70. [AGRIN\\_HUMAN](#) Mass: 217092 Score: 44 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">857</a>	526.3002	1050.5858	1050.5862	-0.40	0	44	0.0015	1	U	R.SFLAFPTLR.A

71. [POSTN\\_HUMAN](#) Mass: 93255 Score: 44 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="#">4039</a>	742.7416	2225.2031	2225.1943	3.94	0	44	0.0021	1	U	K.LLYPADTPVGNDQLLEILNK.L

72. [SYG\\_HUMAN](#) Mass: 83113 Score: 43 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

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="#">2161</a>	729.3935	1456.7724	1456.7755	-2.10	0	43	0.0039	1	U	R.TFFSFPVAVPFK.C

73. [PIP\\_HUMAN](#) Mass: 16562 Score: 42 Matches: 1(1) Sequences: 1(1) emPAI: 0.18

Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1536</a>	627.8531	1253.6917	1253.6907	0.82	1	42	0.0025	1	U	R.FYTIEILKVE.-

74. [S10A7\\_HUMAN](#) Mass: 11464 Score: 42 Matches: 1(1) Sequences: 1(1) emPAI: 0.26

Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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[1952](#) [462.2423](#) [1383.7052](#) [1383.7034](#) [1.28](#) [1](#) [42](#) [0.0052](#) [1](#) [U](#) [K.GTNYLADVFEKK.D](#)

75. [MCF2\\_HUMAN](#) Mass: 107605 Score: 42 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Proto-oncogene DBL OS=Homo sapiens GN=MCF2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1427</a>	<a href="#">407.8877</a>	<a href="#">1220.6412</a>	<a href="#">1220.6288</a>	<a href="#">10.1</a>	<a href="#">0</a>	<a href="#">42</a>	<a href="#">0.0052</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.NAIENFALTVK.E</a>

76. [HBB\\_HUMAN](#) Mass: 15988 Score: 41 Matches: 1(1) 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="#">1602</a>	<a href="#">637.8649</a>	<a href="#">1273.7153</a>	<a href="#">1273.7183</a>	<a href="#">-2.34</a>	<a href="#">0</a>	<a href="#">41</a>	<a href="#">0.0043</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.LLVVYPWTQR.F</a>

Proteins matching the same set of peptides:

[HBD\\_HUMAN](#) Mass: 16045 Score: 41 Matches: 1(1) Sequences: 1(1)

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

[HBE\\_HUMAN](#) Mass: 16192 Score: 41 Matches: 1(1) Sequences: 1(1)

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

[HBG1\\_HUMAN](#) Mass: 16130 Score: 41 Matches: 1(1) Sequences: 1(1)

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

[HBG2\\_HUMAN](#) Mass: 16116 Score: 41 Matches: 1(1) Sequences: 1(1)

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

77. [DR4L1\\_HUMAN](#) Mass: 30588 Score: 41 Matches: 1(1) Sequences: 1(1) emPAI: 0.10

Putative dehydrogenase/reductase SDR family member 4-like 1 OS=Homo sapiens GN=DHRS4L1 PE=5 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">357</a>	<a href="#">415.7529</a>	<a href="#">829.4913</a>	<a href="#">829.4909</a>	<a href="#">0.50</a>	<a href="#">0</a>	<a href="#">41</a>	<a href="#">0.0055</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">K.TALLGLNK.T</a>

78. [EXOC3\\_HUMAN](#) Mass: 86790 Score: 41 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="#">1099</a>	<a href="#">567.3050</a>	<a href="#">1132.5954</a>	<a href="#">1132.5975</a>	<a href="#">-1.85</a>	<a href="#">0</a>	<a href="#">41</a>	<a href="#">0.0081</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.QSINTIESLK.D</a>

79. [CAPSL\\_HUMAN](#) Mass: 24213 Score: 39 Matches: 1(1) Sequences: 1(1) emPAI: 0.12

Calcyphosin-like protein OS=Homo sapiens GN=CAPSL PE=2 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">820</a>	<a href="#">523.8141</a>	<a href="#">1045.6137</a>	<a href="#">1045.5954</a>	<a href="#">17.6</a>	<a href="#">2</a>	<a href="#">39</a>	<a href="#">0.0049</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.EMAIQAKKK.L</a>

80. [H4\\_HUMAN](#) Mass: 11360 Score: 36 Matches: 1(1) Sequences: 1(1) emPAI: 0.26

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="#">1769</a>	<a href="#">442.5885</a>	<a href="#">1324.7438</a>	<a href="#">1324.7463</a>	<a href="#">-1.90</a>	<a href="#">0</a>	<a href="#">36</a>	<a href="#">0.0096</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.DNIQGITKPAIR.R</a>

81. [PLCE1\\_HUMAN](#) 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="#">2089</a>	<a href="#">716.8635</a>	<a href="#">1431.7125</a>	<a href="#">1431.7205</a>	<a href="#">-5.58</a>	<a href="#">2</a>	<a href="#">36</a>	<a href="#">0.029</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">K.LKEQVQASREDK.K</a>

82. [MO4L1\\_HUMAN](#) Mass: 41448 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.07

Mortality factor 4-like protein 1 OS=Homo sapiens GN=MORF4L1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2615</a>	<a href="#">804.4290</a>	<a href="#">1606.8435</a>	<a href="#">1606.8566</a>	<a href="#">-8.16</a>	<a href="#">2</a>	<a href="#">35</a>	<a href="#">0.031</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.VLKVYDTNLQKQR.E</a>

83. [RGPA2\\_HUMAN](#) Mass: 210636 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Ral GTPase-activating protein subunit alpha-2 OS=Homo sapiens GN=RALGAPA2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">819</a>	<a href="#">523.2532</a>	<a href="#">1044.4919</a>	<a href="#">1044.5103</a>	<a href="#">-17.57</a>	<a href="#">0</a>	<a href="#">34</a>	<a href="#">0.018</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.MFASWLFK.A</a>

84. [DSG2\\_HUMAN](#) Mass: 122218 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3272</a>	<a href="#">925.5126</a>	<a href="#">1849.0106</a>	<a href="#">1849.0025</a>	<a href="#">4.35</a>	<a href="#">0</a>	<a href="#">34</a>	<a href="#">0.02</a>	<a href="#">1</a>	<a href="#">U</a>	<a href="#">R.IVSLEPAYPPFYLNK.D</a>

85. [S31E1\\_HUMAN](#) Mass: 157037 Score: 34 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="#">790</a>	518.7673	1035.5200	1035.5236	-3.52	0	34	0.034	1	U	K.YNQLQLEK.G

86. [PPIA\\_HUMAN](#) Mass: 18001 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.16

Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1937</a>	460.5890	1378.7450	1378.7496	-3.34	1	33	0.031	1	U	R.VSFELFADKVPK.T

87. [CUL4A\\_HUMAN](#) Mass: 87624 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Cullin-4A OS=Homo sapiens GN=CUL4A PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1540</a>	628.3876	1254.7606	1254.7547	4.69	0	33	0.0097	1	U	K.TIDGILLIER.E

Proteins matching the same set of peptides:

[CUL4B\\_HUMAN](#) Mass: 103916 Score: 33 Matches: 1(1) Sequences: 1(1)

Cullin-4B OS=Homo sapiens GN=CUL4B PE=1 SV=4

88. [LIPA3\\_HUMAN](#) Mass: 133414 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

Liprin-alpha-3 OS=Homo sapiens GN=PPFIA3 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1721</a>	656.3285	1310.6424	1310.6579	-11.77	1	33	0.039	1	U	R.ELGHEKDSLQR.Q

89. [XPO2\\_HUMAN](#) Mass: 110346 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">659</a>	495.2930	988.5714	988.5705	0.85	0	32	0.029	1	U	R.LLQAFLEK.G

90. [SKI\\_HUMAN](#) Mass: 79955 Score: 32 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="#">2374</a>	509.6150	1525.8231	1524.8300	651	1	32	0.038	1	U	K.VVKELQEQLWPR.A

91. [PYGB\\_HUMAN](#) Mass: 96635 Score: 32 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="#">1992</a>	700.9123	1399.8100	1399.8075	1.81	0	32	0.022	1	U	K.LLPLVSDEVFIR.D

92. [VNN1\\_HUMAN](#) Mass: 56975 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3789</a>	678.4007	2032.1803	2032.1721	4.01	0	32	0.0073	1	U	R.LFSLKPTSGPVLTVTLFGR.L

93. [ZN101\\_HUMAN](#) Mass: 50307 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.06

Zinc finger protein 101 OS=Homo sapiens GN=ZNF101 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">681</a>	499.2769	996.5393	996.5392	0.10	0	31	0.036	1	U	K.AFISAGYLR.T

94. [DYM\\_HUMAN](#) Score: 30 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="#">1939</a>	690.9279	1379.8413	1379.8176	17.1	1	30	0.0058	2	U	K.LVKTLTYNFIR.Q

95. [TNIK\\_HUMAN](#) Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

TRAF2 and NCK-interacting protein kinase OS=Homo sapiens GN=TNIK PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">349</a>	415.2679	828.5213	828.5221	-1.04	0	30	0.041	2	U	R.ALFLIPR.N

Proteins matching the same set of peptides:

[MINK1\\_HUMAN](#) Mass: 149729 Score: 30 Matches: 1(1) Sequences: 1(1)

Misshapen-like kinase 1 OS=Homo sapiens GN=MINK1 PE=1 SV=2

[M4K4\\_HUMAN](#) Mass: 142013 Score: 30 Matches: 1(1) Sequences: 1(1)

Mitogen-activated protein kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2



96.	<a href="#">PAR6G_HUMAN</a>	Mass: 40858	Score: 29	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07
Partitioning defective 6 homolog gamma OS=Homo sapiens GN=PAR6G PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">769</a>	514.2987	1026.5829	1026.5822	0.67	0 29	0.038 1 U K.AVSSANPLLR.V
97.	<a href="#">CAH2_HUMAN</a>	Mass: 29228	Score: 29	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10
Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">2807</a>	834.9873	1667.9601	1667.9610	-0.59	0 29	0.034 1 U K.AVQQPDGLAVLGIFLK.V
98.	<a href="#">MDHM_HUMAN</a>	Mass: 35481	Score: 29	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">1460</a>	617.3652	1232.7158	1232.7129	2.35	0 29	0.039 1 U K.IFGVTTLDIRV.A
99.	<a href="#">MELT_HUMAN</a>	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.03	
Ventricular zone-expressed PH domain-containing protein homolog 1 OS=Homo sapiens GN=VEPH1 PE=2 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">492</a>	450.2693	898.5241	898.5097	16.1	2 28	0.046 1 U R.RDRSLPR.A
100.	<a href="#">TTBK1_HUMAN</a>	Mass: 142650	Score: 28	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.02
Tau-tubulin kinase 1 OS=Homo sapiens GN=TTBK1 PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">492</a>	450.2693	898.5241	898.5348	-11.90	1 28	0.048 2 U K.VATISPRR.H
101.	<a href="#">CENPH_HUMAN</a>	Score: 26	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11	
Centromere protein H OS=Homo sapiens GN=CENPH PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">1496</a>	622.8937	1243.7729	1243.7499	18.5	2 26	0.019 2 U R.LSTALKKNLEK.I
102.	<a href="#">ANM3_HUMAN</a>	Score: 23	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05	
Protein arginine N-methyltransferase 3 OS=Homo sapiens GN=PRMT3 PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">731</a>	508.8297	1015.6448	1015.6542	-9.25	1 23	0.034 2 U K.LINFIRLK.N
103.	<a href="#">HES2_HUMAN</a>	Mass: 18459	Score: 20	Matches: 1(1)	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="#">581</a>	476.3210	950.6275	950.6277	-0.14	0 20	0.0098 1 U K.GLILPLLGR.E
104.	<a href="#">TAAR2_HUMAN</a>	Mass: 40107	Score: 19	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07
Trace amine-associated receptor 2 OS=Homo sapiens GN=TAAR2 PE=2 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">562</a>	470.3154	938.6162	938.6277	-12.23	1 19	0.042 1 U K.ITIPVIKR.L
105.	<a href="#">CBPC1_HUMAN</a>	Score: 13	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.02	
Cytosolic carboxypeptidase 1 OS=Homo sapiens GN=AGTPBP1 PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">200</a>	391.2690	780.5234	780.5109	16.0	0 13	0.05 1 U R.LPLPTIK.S
106.	<a href="#">THMS2_HUMAN</a>	Score: 13	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04	
Protein THEMIS2 OS=Homo sapiens GN=THEMIS2 PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss Score	Expect Rank Unique Peptide
<a href="#">200</a>	391.2690	780.5234	780.5221	1.65	1 13	0.05 1 U R.LPKPKAK.T

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