

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_3_PMA.mgf
 Database : SwissProt_ID ID_2015_10 (549646 sequences; 195983064 residues)
 Taxonomy : Homo sapiens (human) (20197 sequences)
 Timestamp : 19 Jan 2016 at 19:26:41 GMT
 Enzyme : Trypsin
 Variable modifications : [Carboxymethyl \(C\)](#), [Deamidated \(NQ\)](#), [Oxidation \(M\)](#)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 20 ppm (# $^{13}\text{C} = 1$)
 Fragment Mass Tolerance : ± 0.5 Da
 Max Missed Cleavages : 2
 Instrument type : ESI-TRAP
 Number of queries : 4857

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
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
C03_HUMAN	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2
MX1_HUMAN	Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=4
EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4
K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
TERRA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
QSOX1_HUMAN	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3
CDH1_HUMAN	Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3
IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2
VPS35_HUMAN	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
ENPL_HUMAN	Endoplasmic reticulum protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1
RADI_HUMAN	Radixin OS=Homo sapiens GN=RDXX PE=1 SV=1
GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1
DPP3_HUMAN	Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=1 SV=2
K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2
PDC61_HUMAN	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1
COPG1_HUMAN	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1
H90B2_HUMAN	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2
A2M_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3
VASN_HUMAN	Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1
CD166_HUMAN	CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2
IQGAP1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1
K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5
HEP2_HUMAN	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3
PDIA4_HUMAN	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2
PSMD2_HUMAN	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3
PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2
NUCL_HUMAN	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3
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
LUM_HUMAN	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2
SYG_HUMAN	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3
K2C1B_HUMAN	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3
SLIK4_HUMAN	SLIT and NTRK-like protein 4 OS=Homo sapiens GN=SLITRK4 PE=2 SV=1
VTNC_HUMAN	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1
HBA_HUMAN	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2
K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2
TRFL_HUMAN	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6
BCAM_HUMAN	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2
PYGB_HUMAN	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5
CFAB_HUMAN	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2
ACPH_HUMAN	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4
GFPT1_HUMAN	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3
GNS_HUMAN	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3
PYGL_HUMAN	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4
UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3
TFR1_HUMAN	Transferrin receptor protein 1 OS=Homo sapiens GN=TFR1 PE=1 SV=2
K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
CROCC_HUMAN	Rootletin OS=Homo sapiens GN=CROCC PE=1 SV=1
PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2
STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2
FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4
COPB_HUMAN	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3

AFAM_HUMAN	Afamin OS=Homo sapiens GN=AFM PE=1 SV=1
G3PT_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2
HS71L_HUMAN	Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2
H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2
KATL2_HUMAN	Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens GN=KATNAL2 PE=2 SV=3
RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2
XPP3_HUMAN	Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1
GOGB1_HUMAN	Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2
C04A_HUMAN	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2
SEC23B_HUMAN	Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2
ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2
ABCA3_HUMAN	ATP-binding cassette sub-family A member 3 OS=Homo sapiens GN=ABCA3 PE=1 SV=2
EXOC3_HUMAN	Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2
FUBP2_HUMAN	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4
MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3
C06A1_HUMAN	Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3
SEMA3C_HUMAN	Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=2
SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2
MTNR5_HUMAN	Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=1 SV=3
DYM_HUMAN	Dymeclin OS=Homo sapiens GN=DYM PE=1 SV=1
MSL1_HUMAN	Male-specific lethal 1 homolog OS=Homo sapiens GN=MSL1 PE=1 SV=3
S31E1_HUMAN	Spermatogenesis-associated protein 31E1 OS=Homo sapiens GN=SPATA31E1 PE=2 SV=2
CC149_HUMAN	Coiled-coil domain-containing protein 149 OS=Homo sapiens GN=CCDC149 PE=2 SV=2
SKI_HUMAN	Ski oncogene OS=Homo sapiens GN=SKI PE=1 SV=1
AGRIN_HUMAN	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5
NEBU_HUMAN	Nebulin OS=Homo sapiens GN=NEB PE=1 SV=5
NRAP_HUMAN	Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2
ZN101_HUMAN	Zinc finger protein 101 OS=Homo sapiens GN=ZNF101 PE=1 SV=1
ZNF646_HUMAN	Zinc finger protein 646 OS=Homo sapiens GN=ZNF646 PE=1 SV=1
XYLB_HUMAN	Xylulose kinase OS=Homo sapiens GN=XYLB PE=1 SV=3
RPF1_HUMAN	Ribosome production factor 1 OS=Homo sapiens GN=RPF1 PE=1 SV=2
H2A1B_HUMAN	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
4F2_HUMAN	4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3
VNN1_HUMAN	Pantetheinase OS=Homo sapiens GN=VNN1 PE=1 SV=2
RASL2_HUMAN	Ras GTPase-activating protein 4 OS=Homo sapiens GN=RASA4 PE=2 SV=2
SEC23IP_HUMAN	SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1
RENT2_HUMAN	Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 PE=1 SV=1
CLCF1_HUMAN	Cardiotrophin-like cytokine factor 1 OS=Homo sapiens GN=CLCF1 PE=1 SV=1
KCA10_HUMAN	Potassium voltage-gated channel subfamily A member 10 OS=Homo sapiens GN=KCA10 PE=1 SV=2
NIBL1_HUMAN	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3
HS12B_HUMAN	Heat shock 70 kDa protein 12B OS=Homo sapiens GN=HSPA12B PE=1 SV=2
TAAR2_HUMAN	Trace amine-associated receptor 2 OS=Homo sapiens GN=TAAR2 PE=2 SV=2
STAB1_HUMAN	Stabilin-1 OS=Homo sapiens GN=STAB1 PE=1 SV=3
HES2_HUMAN	Transcription factor HES-2 OS=Homo sapiens GN=HES2 PE=2 SV=1

SwissProt_ID [Decoy](#) False discovery rate

Peptide matches above identity threshold	383	23	6.01 %
Peptide matches above homology or identity threshold	489	34	6.95 %

Select Summary Report

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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 All entries ▼

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

1. [HS90A_HUMAN](#) Mass: 84607 Score: 1114 Matches: 31(31) Sequences: 19(19) emPAI: 1.03

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

Query	Observed	Mr(calc)	Mr(expt)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
245	408.2598	814.5051	814.5065	-1.72	0	47	0.00065	1	U	R.ALLFVPR.R
523	474.7268	947.4390	947.4389	0.13	0	45	0.002	1	U	K.FYEQFSK.N 522
913	554.7731	1107.5317	1107.5349	-2.88	0	57	0.00015	1	U	R.APFDLFENR.K 914
1308	612.8172	1223.6198	1223.6186	1.00	0	57	0.00017	1	U	K.HIYYITGETK.D
1346	618.3016	1234.5887	1234.5942	-4.45	0	85	3e-007	1	U	K.DQVANSFVER.L 1347
1362	621.8561	1241.6977	1241.6979	-0.16	0	81	4.5e-007	1		K.ADLINNLGTIAK.S
1431	632.8261	1263.6375	1263.6360	1.22	1	38	0.015	1	U	R.RAPDFLFENR.K
1528	646.3231	1290.6317	1290.6303	1.08	0	76	2.8e-006	1	U	R.ELISNSSDALDK.I 1527
1750	683.3673	1364.7201	1364.7221	-1.52	0	107	1.7e-009	1	U	R.TLTIVDTGIGMTK.A 1754
1908	708.8207	1415.6268	1415.6303	-2.50	0	52	0.00029	1		K.EGLELPEDEEEK.K 1909
2231	757.3976	1512.7807	1512.7784	1.56	0	108	1.4e-009	1		R.GVVDSEDLPLNISR.E 2230
2270	764.3776	1526.7407	1526.7365	2.74	0	59	0.00011	1		K.SLTNDWEDHLAVK.H
2306	513.9208	1538.7407	1538.7464	-3.71	1	(42)	0.0059	1		R.YESLTDPKLDGK.E

2307	770.3783	1538.7420	1538.7464	-2.83	1	63	4.4e-005	1		R.YESLTDPSKLDGK.E
2382	520.9440	1559.8101	1559.8155	-3.45	1	(40)	0.011	1	U	R.ELISNSSDALDKIR.Y
2383	780.9130	1559.8114	1559.8155	-2.62	1	95	3.4e-008	1	U	R.ELISNSSDALDKIR.Y
2395	783.8547	1565.6949	1565.6919	1.91	0	85	1.8e-007	1	U	R.YYTSASGDEMVSLLK.D
3022	593.6522	1777.9348	1777.9403	-3.08	0	49	0.0012	1	U	K.HSQFIGYPITLFEK.E 3023 3024
3047	596.3198	1785.9375	1785.9373	0.08	0	45	0.003	1	U	K.HLEINPDHSIETLR.Q
3171	917.3962	1832.7778	1832.7741	2.04	0	86	1.2e-007	1	U	R.NPDDITNEEYGEFYK.S 3170
3352	479.5137	1914.0258	1914.0323	-3.37	1	32	0.044	1	U	K.KHLEINPDHSIETLR.Q

2. [HS90B_HUMAN](#) Mass: 83212 Score: 858 Matches: 24(24) Sequences: 20(20) emPAI: 1.06

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
295	415.2687	828.5228	828.5221	0.80	0	37	0.0072	1	U	R.ALLFIPR.R
401	443.7761	885.5376	885.5396	-2.25	1	32	0.031	1	U	R.RLSELLR.Y
407	446.2151	890.4157	890.4174	-1.86	0	44	0.0024	1	U	K.FYEAFSK.N
855	540.7719	1079.5293	1079.5287	0.49	0	43	0.0036	1	U	R.APFDLFENK.K
1104	580.7950	1159.5755	1159.5761	-0.47	0	43	0.0043	1		K.SIYYITGESK.E
1226	597.8276	1193.6407	1193.6404	0.26	0	64	2.2e-005	1	U	K.IDIIPNPQER.T
1362	621.8561	1241.6977	1241.6979	-0.16	0	81	4.5e-007	1		K.ADLINNLGTIAK.S
1379	625.3132	1248.6118	1248.6098	1.56	0	66	2.5e-005	1	U	K.EQVANSFAVER.V
1482	638.3233	1274.6321	1274.6354	-2.61	0	92	5.5e-008	1		R.ELISNASDALDK.I
1750	683.3673	1364.7201	1364.7221	-1.52	0	107	1.7e-009	1	U	R.TLTLVDTGIGMTK.A 1754
1908	708.8207	1415.6268	1415.6303	-2.50	0	52	0.00029	1		K.EGLELPEDEEEK.K 1909
2231	757.3976	1512.7807	1512.7784	1.56	0	108	1.4e-009	1		R.GVVDSEDLPLNISR.E 2230
2270	764.3776	1526.7407	1526.7365	2.74	0	59	0.00011	1		K.SLTNDWEDHLAVK.H
2306	513.9208	1538.7407	1538.7464	-3.71	1	(42)	0.0059	1		R.YESLTDPSKLDGK.E
2307	770.3783	1538.7420	1538.7464	-2.83	1	63	4.4e-005	1		R.YESLTDPSKLDGK.E
2338	772.9155	1543.8165	1543.8205	-2.62	1	76	2.2e-006	1		R.ELISNASDALDKIR.Y
3032	594.9880	1781.9423	1781.9424	-0.07	0	44	0.0027	1	U	K.HLEINPDHPIVETLR.Q
3111	603.6583	1807.9531	1807.9509	1.27	0	38	0.014	1	U	K.HSQFIGYPITLYLEK.E
3210	924.3995	1846.7845	1846.7897	-2.82	0	81	4.1e-007	1	U	R.NPDDITQEEYGEFYK.S
3344	478.5169	1910.0386	1910.0374	0.67	1	34	0.023	1	U	K.KHLEINPDHPIVETLR.Q
3924	731.6526	2191.9359	2191.9328	1.44	0	46	0.0016	1	U	R.YHTSQSGDEMTSLSEYVSR.M

3. [GRP78_HUMAN](#) Mass: 72288 Score: 546 Matches: 16(16) 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
1327	617.3130	1232.6114	1232.6183	-5.59	0	83	5e-007	1	U	K.DAGTIAGLNVMR.I
1948	715.8480	1429.6814	1429.6838	-1.67	0	84	2.7e-007	1	U	R.TWNPDSVQDIK.F
2271	510.2534	1527.7384	1527.7391	-0.46	1	33	0.049	1	U	R.AKFEELNMDFR.S
2358	776.8986	1551.7826	1551.7854	-1.84	0	74	3.7e-006	1	U	K.TFAPEEISAMVLTK.M 2359 2360
2371	519.2700	1554.7882	1554.7862	1.28	1	35	0.029	1	U	K.NGRVEIANDQGNR.I
2399	783.8969	1565.7793	1565.7726	4.28	0	42	0.0067	1	U	R.ITPSYVAFTPEGER.L
2523	535.6266	1603.8579	1603.8570	0.59	0	62	5.3e-005	1	U	K.TKPYIQVDIGGGQTK.T
2687	551.9979	1652.9718	1652.9712	0.33	2	39	0.0021	1	U	K.KKELEEIVQPIISK.L
2741	839.4094	1676.8042	1676.8006	2.15	0	86	2.5e-007	1	U	K.NQLTSNPENTVFDAK.R
3093	601.3043	1800.8910	1800.8893	0.89	1	35	0.033	1	U	R.IDTRNELESYAYSLK.N
3131	606.0052	1814.9937	1814.9890	2.61	1	44	0.002	1	U	R.IINEPTAAAIAYGLDKR.E
3288	629.9957	1886.9654	1886.9639	0.76	0	41	0.008	1	U	K.VTHAVVTPAYFNDQR.Q
3892	1082.9980	2163.9815	2163.9848	-1.50	0	102	5.7e-009	1	U	R.IEIESFYEGEDFSETLIR.A
3911	1088.4924	2174.9703	2174.9855	-6.99	1	86	2.3e-007	1	U	K.LYGSAGPPPTGEEDTAEKDEL.-

4. [EF2_HUMAN](#) Mass: 95277 Score: 523 Matches: 17(17) Sequences: 11(11) emPAI: 0.48

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
405	445.7585	889.5024	889.5022	0.21	0	42	0.0045	1	U	K.FSVSPVVR.V
877	546.2958	1090.5770	1090.5771	-0.11	0	78	1.6e-006	1	U	M.VNFTVDQIR.A
897	550.7744	1099.5342	1099.5372	-2.78	0	38	0.0093	1	U	K.VFDAIMNFK.K
901	551.7654	1101.5163	1101.5165	-0.12	0	36	0.012	1	U	K.QFAEMYVAK.F
909	554.3246	1106.6347	1106.6336	1.05	0	82	2.2e-007	1	U	R.VFSGLVSTGLK.V
1995	722.8868	1443.7591	1443.7609	-1.24	1	61	7e-005	1	U	K.EGIPALDNFLDKL.- 1996 1998
2609	544.5922	1630.7547	1630.7522	1.51	0	39	0.01	1	U	K.TGTITTFEHAHNM.R.V
3089	600.6381	1798.8925	1798.8890	1.97	0	(56)	0.00027	1	U	K.AYLPVNESFGFTADLR.S
3090	900.4556	1798.8967	1798.8890	4.29	0	100	9.6e-009	1	U	K.AYLPVNESFGFTADLR.S
3936	735.3794	2203.1164	2203.1048	5.23	0	48	0.0022	1	U	K.STAISLFYELSENDLNFILK.Q
3951	1110.5795	2219.1444	2219.1474	-1.34	0	87	2.1e-007	1	U	R.ALLELQLEPEELYQTFQR.I
3952	740.7253	2219.1540	2219.1474	3.00	0	(60)	0.00011	1	U	R.ALLELQLEPEELYQTFQR.I 3953
4384	872.8157	2615.4254	2615.4145	4.15	0	40	0.004	1	U	R.WLPAGDALLQMIHLPSPVTAQK.Y 4381

5. [ACTN1_HUMAN](#) Mass: 102993 Score: 470 Matches: 14(14) Sequences: 11(11) emPAI: 0.40

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
355	432.7452	863.4759	863.4752	0.71	0	43	0.0022	1	U	K.ALDFIASK.G
1274	608.3409	1214.6673	1214.6659	1.18	0	72	4.9e-006	1	U	K.LASDLEWIR.R
1531	431.9229	1292.7468	1292.7452	1.24	0	32	0.015	1	U	R.LAILGIHNEVSK.I
1819	693.8891	1385.7636	1385.7667	-2.20	0	87	1.4e-007	1	U	R.VGWEQLTTIAR.T 1821
1825	694.8958	1387.7770	1387.7745	1.80	0	59	7.5e-005	1	U	K.LMLLLEVISGER.L
1947	715.3837	1428.7528	1428.7572	-3.12	0	79	1e-006	1	U	R.TINEVENQILTR.D
2099	493.2462	1476.7167	1476.7143	1.63	0	36	0.027	1	U	R.LSNRPAPMPSEGR.M
2104	740.4005	1478.7864	1478.7989	-8.50	0	64	3.3e-005	1	U	K.MTLGMIWTIILR.F 2109
2302	769.3896	1536.7646	1536.7671	-1.64	0	75	3.2e-006	1	U	R.FAIQDISVEETSAK.E
2329	772.4162	1542.8178	1541.8301	641	0	41	0.0074	1	U	K.LVSI GAE EIVDGNVK.M
2826	571.3090	1710.9051	1710.9080	-1.70	0	(32)	0.048	1	U	K.LLETIDQLYLEYAK.R
2827	856.4607	1710.9068	1710.9080	-0.66	0	74	3.1e-006	1	U	K.LLETIDQLYLEYAK.R

6. [FETA_HUMAN](#) Mass: 68633 Score: 452 Matches: 12(12) 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
577	490.2569	978.4992	978.5022	-3.07	0	53	0.00042	1	U	K.GYQELLEK.C 578
1050	575.8102	1149.6058	1149.6030	2.49	0	42	0.0044	1	U	K.YIQESQALAK.R
3297	631.6635	1891.9685	1891.9720	-1.82	0	(59)	0.00016	1	U	K.LGEYYLQNAFLVAYTK.K 3301 3303
3298	946.9922	1891.9699	1891.9720	-1.07	0	91	9e-008	1	U	K.LGEYYLQNAFLVAYTK.K 3295 3296 3302 3305 3306

7. [CO3_HUMAN](#) Mass: 187030 Score: 439 Matches: 13(13) Sequences: 10(10) emPAI: 0.20

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
542	480.2769	958.5393	958.5447	-5.69	0	50	0.00083	1	U	K.GLEVTITAR.F
2076	735.8917	1469.7688	1469.7726	-2.58	0	78	1.2e-006	1	U	R.IPIEDGSGEVLSR.K
2221	504.6108	1510.8106	1510.8144	-2.49	0	(34)	0.028	1	U	R.LVAYYTLIGASGQR.E
2222	756.4134	1510.8122	1510.8144	-1.41	0	54	0.00029	1	U	R.LVAYYTLIGASGQR.E
3256	624.6840	1871.0302	1871.0265	2.01	0	56	0.00015	1	U	R.TELRPGETLNVNLLR.M
3271	939.9946	1877.9746	1877.9662	4.45	0	68	1.6e-005	1	U	K.EYVLPSEFIVEPTEK.F
3929	1099.5605	2197.1065	2197.1227	-7.35	0	99	1.5e-008	1	U	R.VPVAVQGEDTVQSLTQGDGVAK.L
3930	733.3779	2197.1118	2197.1227	-4.96	0	(56)	0.0003	1	U	R.VPVAVQGEDTVQSLTQGDGVAK.L
4207	1222.6632	2443.3119	2443.2999	4.90	0	61	4.8e-005	1	U	R.EPGQDLVVLPLSITTDIFPSFR.L 4205
4355	865.4423	2593.3050	2593.2959	3.51	0	45	0.0044	1	U	R.TMQALPYSTVGNSNNYLHLSVLR.T
4416	899.0862	2694.2369	2694.2424	-2.06	0	38	0.017	1	U	R.YYGGGYGSTQATFMVFQALAQYQK.D
4457	927.7759	2780.3058	2780.2979	2.86	0	37	0.03	1	U	K.YFKPGMFPDLMVFTVNPDPGPAYR.V

8. [MX1_HUMAN](#) Mass: 75473 Score: 432 Matches: 11(11) Sequences: 5(5) emPAI: 0.30

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
883	547.7821	1093.5497	1093.5556	-5.47	0	37	0.014	1	U	R.ELPGFVNRYR.T
1276	406.2221	1215.6446	1215.6459	-1.11	1	39	0.013	1	U	K.GTEDKVVDVVR.N
1661	666.3515	1330.6885	1330.6881	0.26	0	50	0.00095	1	U	R.VAVGNQPADIGYK.I 1660
2629	546.6419	1636.9039	1636.9036	0.18	0	(40)	0.0046	1	U	R.DVPDLTLIDLPGITR.V
2631	819.4608	1636.9071	1636.9036	2.13	0	87	9e-008	1	U	R.DVPDLTLIDLPGITR.V 2632 2633
3998	751.4077	2251.2013	2251.2060	-2.06	0	(65)	1.9e-005	1	U	R.ALGVEQDLALPAIAVIGDQSSGK.S
3999	1126.6099	2251.2052	2251.2060	-0.35	0	83	2.7e-007	1	U	R.ALGVEQDLALPAIAVIGDQSSGK.S 4000

9. [EZRI_HUMAN](#) Mass: 69370 Score: 421 Matches: 13(13) 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
411	447.7761	893.5376	893.5375	0.11	0	45	0.00042	1		K.LFFLQVK.E 410
460	457.7697	913.5248	913.5232	1.66	0	53	0.0002	1	U	K.IALLEEAR.R
566	488.7760	975.5374	975.5389	-1.59	0	63	3.9e-005	1		K.QLFDQVVK.T
835	357.5486	1069.6241	1069.6243	-0.22	1	35	0.0092	1	U	K.IALLEEAR.R
908	552.7945	1103.5744	1103.5764	-1.75	0	65	3.2e-005	1		K.IGFPWSEIR.N
1181	591.8016	1181.5887	1181.5869	1.50	0	68	1.2e-005	1		K.APDFVFYAPR.L
2001	723.4032	1444.7918	1444.7885	2.30	0	86	1.8e-007	1	U	R.QLLTSSSELSQAR.D
2679	826.4101	1650.8056	1650.8100	-2.66	0	76	2.8e-006	1	U	K.SQEQLAAELAEYTAI.I
3508	981.9827	1961.9509	1961.9444	3.30	0	59	0.00015	1	U	K.IAQDLEMYGINYFEIK.N
3710	680.0019	2036.9838	2036.9942	-5.10	0	(39)	0.018	1	U	K.FYPEDVAEELIQDITQK.L
3712	1019.5146	2037.0147	2036.9942	10.1	0	45	0.0041	1	U	K.FYPEDVAEELIQDITQK.L
3768	1041.5082	2081.0018	2080.9987	1.50	0	54	0.00048	1		R.VTTMDAELEFAIQNPNTGK.Q

10. [K2C1_HUMAN](#) Mass: 65999 Score: 340 Matches: 8(8) Sequences: 7(7) emPAI: 0.41

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
1174	590.3044	1178.5942	1178.5931	0.92	0	76	2.1e-006	1		K.YEELQITAGR.H
1550	651.8622	1301.7099	1301.7078	1.62	0	101	6.8e-009	1	U	R.SLDLSIIAEVK.A
1833	465.2483	1392.7230	1392.7249	-1.38	1	44	0.0038	1	U	R.TNAENFVTKK.D
2094	738.3795	1474.7445	1474.7416	1.95	0	85	3.7e-007	1	U	K.WELLQQVDTSTR.T
2096	738.3946	1474.7746	1474.7780	-2.27	0	83	4.8e-007	1		R.FLEQQNQVLQTK.W
2635	546.9566	1637.8480	1637.8525	-2.78	1	39	0.012	1	U	K.SLNNQFASFIDKVR.F
4155	1192.4746	2382.9347	2382.9447	-4.19	0	51	0.00012	1	U	R.GGGGGYSGSGSSYSGSGSGSGGGGGGR.G
4156	795.3188	2382.9347	2382.9447	-4.17	0	(50)	0.00015	1	U	R.GGGGGYSGSGSSYSGSGSGSGGGGGGR.G

11. [TERA_HUMAN](#) Mass: 89266 Score: 336 Matches: 15(15) Sequences: 10(10) emPAI: 0.47

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
521	474.2848	946.5551	946.5600	-5.19	1	31	0.029	1	U	R.KGDIFLVR.G
724	516.7819	1031.5493	1031.5499	-0.57	0	36	0.025	1	U	K.GDDLSTAILK.Q
789	525.2793	1048.5440	1048.5441	-0.02	0	59	9.5e-005	1	U	K.DVDLEFLAK.M
830	534.2626	1066.5107	1066.5117	-0.94	0	38	0.012	1	U	K.MDELQLFR.G
1151	586.8353	1171.6561	1171.6601	-3.42	0	49	0.00091	1	U	R.GILLYGPPGTGK.T
1652	665.3499	1328.6852	1328.6837	1.12	0	40	0.0076	1	U	R.WALSQSNPSALR.E
2004	723.9172	1445.8198	1445.8163	2.39	0	31	0.036	1	U	R.IVSQLLTMDGLK.Q
2374	778.9355	1555.8565	1555.8497	4.38	0	58	9.6e-005	1	U	R.LDQLIYIPLDEK.S
3112	604.3358	1809.9856	1809.9876	-1.10	0	(46)	0.0015	1	U	K.NAPAIIFIDELDAIAPK.R 3113
3114	906.0029	1809.9912	1809.9876	1.98	0	58	9.2e-005	1	U	K.NAPAIIFIDELDAIAPK.R 3116
4035	758.0479	2271.1219	2271.1245	-1.16	0	(52)	0.00083	1	U	R.AVANETGAFFFLINGPEIMSK.L 4037
4036	1136.5691	2271.1236	2271.1245	-0.40	0	89	1.5e-007	1	U	R.AVANETGAFFFLINGPEIMSK.L

12. [ALBU_HUMAN](#) Mass: 69321 Score: 334 Matches: 9(9) 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
496	464.2500	926.4855	926.4861	-0.67	0	45	0.0011	1	U	K.YLYEIAR.R 492 494 495
2224	756.4266	1510.8387	1510.8355	2.11	0	67	9.7e-006	1	U	K.VPQVSTPTLVEVSR.N
2638	547.3173	1638.9301	1638.9305	-0.21	1	(69)	3.5e-006	1	U	K.KVPQVSTPTLVEVSR.N 2637
2641	820.4743	1638.9341	1638.9305	2.18	1	91	2.6e-008	1	U	K.KVPQVSTPTLVEVSR.N 2639

13. [QSOX1_HUMAN](#) Mass: 82526 Score: 301 Matches: 8(8) Sequences: 6(6) emPAI: 0.32

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
1042	574.7911	1147.5677	1147.5662	1.33	0	38	0.015	1	U	R.SFYTAYLQR.L
1715	678.8442	1355.6738	1355.6721	1.24	0	37	0.016	1	U	R.LAGAPSEDQFPK.V
2118	741.8793	1481.7441	1481.7402	2.67	0	78	1.5e-006	1	U	R.NNEEYLALIFEK.G
3146	608.6484	1822.9233	1822.9287	-2.97	0	38	0.017	1	U	K.IYMDLESALHYILR.I
3234	620.3364	1857.9873	1857.9877	-0.21	0	87	1.7e-007	1	U	R.LDVPVMDVEATLNFLK.A
3235	930.0012	1857.9878	1857.9877	0.06	0	(66)	2e-005	1	U	R.LDVPVMDVEATLNFLK.A
3719	683.0280	2046.0622	2046.0633	-0.54	0	(33)	0.049	1	U	R.SALYSPDPLTLQADTVR.G
3720	1024.0397	2046.0648	2046.0633	0.72	0	92	6.5e-008	1	U	R.SALYSPDPLTLQADTVR.G

14. [CADH1_HUMAN](#) Mass: 97396 Score: 269 Matches: 4(4) Sequences: 3(3) emPAI: 0.09

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1951	716.3929	1430.7713	1430.7729	-1.12	0	96	2e-008	1	U	R.NTGVISVVTGLDR.E
2828	856.4673	1710.9201	1710.9152	2.88	0	76	1.6e-006	1	U	K.GQVPENANVITTLK.V
4136	1183.6284	2365.2423	2365.2318	4.42	0	99	9.7e-009	1	U	K.VFYITGGQADTPPVGFIER.E 4135

15. [IMB1_HUMAN](#) Mass: 97108 Score: 253 Matches: 9(9) 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
2526	803.4453	1604.8761	1604.8773	-0.79	0	62	4.4e-005	1	U	K.LAATNALLNSLEFTK.A
2604	543.9611	1628.8614	1628.8636	-1.39	0	34	0.035	1	U	K.YMEAFKPFGLGK.N
2692	553.6400	1657.8980	1657.9039	-3.54	0	(44)	0.0033	1	U	R.AAVENLPTFLVELSR.V 2694
2695	829.9621	1657.9096	1657.9039	3.46	0	89	7.6e-008	1	U	R.AAVENLPTFLVELSR.V 2693
2962	587.0173	1758.0302	1758.0291	0.60	0	39	0.0018	1	U	K.GALQYLVPIITQTLTK.Q
2965	880.0282	1758.0418	1758.0291	7.24	0	(27)	0.019	1	U	K.GALQYLVPIITQTLTK.Q
3674	672.6667	2014.9784	2014.9742	2.09	0	45	0.0036	1	U	R.LQQVLQMESHIQSTDR.I

16. [VPS35_HUMAN](#) Mass: 91649 Score: 230 Matches: 8(8) Sequences: 7(7) emPAI: 0.28

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
592	492.8130	983.6115	983.6128	-1.30	0	41	0.0014	1	U	R.ILVGTNLVR.L
663	506.2953	1010.5760	1010.5760	-0.04	0	45	0.00078	1	U	K.AELAEPLR.L
748	520.8273	1039.6400	1039.6389	1.00	0	38	0.0022	1	U	K.NIIIALIDR.L
1368	622.3356	1242.6566	1242.6568	-0.17	0	50	0.00069	1	U	R.LSQLEGVNVVER.Y
2514	801.9617	1601.9088	1601.9028	3.71	0	73	1.7e-006	1	U	K.IPVDTYNNILTVLK.L
2555	539.6517	1615.9334	1615.9297	2.26	0	34	0.01	1	U	K.AQLAAITLIIGTFER.M
3225	618.0048	1850.9925	1850.9891	1.83	0	69	8.5e-006	1	U	K.LFDIFSQQVATVIQSR.Q
3226	926.5057	1850.9969	1850.9891	4.25	0	(59)	8.3e-005	1	U	K.LFDIFSQQVATVIQSR.Q

17. [LG3BP_HUMAN](#) Mass: 65289 Score: 228 Matches: 7(7) Sequences: 5(5) emPAI: 0.30

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
107	352.2104	702.4063	702.4064	-0.15	0	35	0.021	1	U	K.SLGWLK.S
1637	442.8881	1325.6424	1325.6463	-2.96	0	(41)	0.0066	1	U	R.ASHEEVEGLVEK.I
1638	663.8322	1325.6499	1325.6463	-2.71	0	54	0.00035	1	U	R.ASHEEVEGLVEK.I
1713	678.3925	1354.7704	1354.7708	0.29	0	57	8.4e-005	1	U	R.SDLAVPSELALK.A
2482	796.8972	1591.7798	1591.7842	-2.78	0	97	2.4e-008	1	U	R.ELSEALGQIFDSQR.G 2483
3551	662.0396	1983.0970	1983.0942	1.43	0	56	0.00011	1	U	K.TLQALEFHTVPFQLLAR.Y

18. [K22E_HUMAN](#) Mass: 65393 Score: 226 Matches: 4(4) Sequences: 3(3) 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
1653	665.3680	1328.7215	1328.7187	2.12	0	86	1.9e-007	1		R.NLDLDSIIAEVK.A
1655	665.8557	1329.6969	1329.7027	-4.40	0	(52)	0.00059	1		R.NLDLDSIIAEVK.A
2043	730.9055	1459.7964	1459.7922	2.84	0	99	9.9e-009	1	U	K.VDLLNQIEIFLK.V
2096	738.3946	1474.7746	1474.7780	-2.27	0	83	4.8e-007	1		R.FLEQQNQVLQTK.W

19. [ENPL_HUMAN](#) Mass: 92411 Score: 220 Matches: 5(5) Sequences: 5(5) emPAI: 0.17

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
548	482.2957	962.5769	962.5800	-3.21	0	53	8.2e-005	1	U	K.LIINSLYK.N
1193	594.3428	1186.6711	1186.6710	0.09	0	41	0.005	1	U	K.SILFVPTSAPR.G
1482	638.3233	1274.6321	1274.6354	-2.61	0	92	5.5e-008	1		R.ELISNASDALDK.I
2132	743.3787	1484.7428	1484.7471	-2.92	0	75	2.7e-006	1	U	K.GVVDSDDLPLNVSRI.E
2338	772.9155	1543.8165	1543.8205	-2.62	1	76	2.2e-006	1		R.ELISNASDALDKIR.L

20. [RADI_HUMAN](#) Mass: 68521 Score: 218 Matches: 7(7) Sequences: 6(6) emPAI: 0.28

Radixin OS=Homo sapiens GN=RD3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
411	447.7761	893.5376	893.5375	0.11	0	45	0.00042	1		R.LFFLQVK.E 410
566	488.7760	975.5374	975.5389	-1.59	0	63	3.9e-005	1		K.QLFDQVVK.T
668	338.8773	1013.6099	1013.6120	-2.07	1	40	0.0037	1	U	K.IALLEEAKK.K
908	552.7945	1103.5744	1103.5764	-1.75	0	65	3.2e-005	1		K.IGFPWSEIR.N
1181	591.8016	1181.5887	1181.5869	1.50	0	68	1.2e-005	1		K.APDFVFYAPR.L
3768	1041.5082	2081.0018	2080.9987	1.50	0	54	0.00048	1		R.VTTMDAELEFAIQPNTTGK.Q

21. [GELS_HUMAN](#) Mass: 85644 Score: 214 Matches: 5(5) Sequences: 4(4) emPAI: 0.14

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1485	425.9095	1274.7068	1274.7095	-2.14	0	34	0.025	1	U	K.HVVPNEVVQR.L 1487
1616	660.3522	1318.6898	1318.6881	1.29	0	69	1.1e-005	1	U	K.AGALNSNDAFLVK.T
2858	861.9263	1721.8380	1721.8301	4.59	0	97	2.6e-008	1	U	R.EVQGFESATFLGYFK.S
3161	915.4846	1828.9546	1828.9571	-1.38	0	93	4.6e-008	1	U	K.QTQVSVLPEGGETPLFK.Q

22. [DPP3_HUMAN](#) Mass: 82538 Score: 213 Matches: 6(6) Sequences: 5(5) emPAI: 0.23

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
838	536.3243	1070.6340	1070.6335	0.45	0	30	0.038	1	U	R.LVASAEQLLK.E
2977	588.3069	1761.8990	1761.9009	-1.10	0	36	0.027	1	U	R.VILGSEAAQHPPEVR.G
3134	909.9743	1817.9341	1817.9258	4.53	0	64	4.1e-005	1	U	R.LASVLGSEPLDSEVTSK.L
3856	712.0407	2133.1003	2133.0953	2.33	0	(58)	0.00017	1	U	R.LEGSDVQLLEVEASAAGLIR.S
3857	1067.5581	2133.1017	2133.0953	2.97	0	114	3.9e-010	1	U	R.LEGSDVQLLEVEASAAGLIR.S
4462	941.8451	2822.5135	2822.5007	4.53	0	30	0.048	1	U	R.AAWYGLAVLLQTSPEAPYIALLSR.L

23. [K1C10_HUMAN](#) Mass: 58792 Score: 197 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
721	516.3016	1030.5887	1030.5910	-2.23	0	57	0.00013	1	U	R.VLDELTLTK.A
824	355.5406	1063.6000	1063.6026	-2.39	1	38	0.0064	1	U	R.LASYLDKVR.A
1803	691.3287	1380.6429	1380.6408	1.51	0	91	6.6e-008	1	U	R.ALEESNYELEGK.I
2816	854.3884	1706.7623	1706.7649	-1.53	0	73	4.2e-006	1	U	K.GSLGGGFSGGFSGGSFSR.G
4534	763.9120	3051.6188	3051.6200	-0.38	1	(37)	0.012	1	U	K.TIDDLKNQILNLTDTNANILLQIDNAR.L
4535	1018.2155	3051.6247	3051.6200	1.55	1	38	0.01	1	U	K.TIDDLKNQILNLTDTNANILLQIDNAR.L

24. [ITIH2_HUMAN](#) Mass: 106397 Score: 196 Matches: 4(4) 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
1675	669.3629	1336.7112	1336.7139	-2.07	0	49	0.00092	1	U	K.FYNQVSTPLLR.N 1674
2451	791.9326	1581.8506	1581.8474	1.97	0	116	1.8e-010	1	U	K.IQPSGGTNINEALLR.A
2809	852.4797	1702.9448	1702.9406	2.47	0	62	3.2e-005	1	U	K.LWAYLTINQLLAER.S

25. [PDC6I_HUMAN](#) Mass: 95963 Score: 196 Matches: 5(5) Sequences: 4(4) emPAI: 0.13

Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDC6IP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
701	341.5384	1021.5933	1021.5920	1.32	0	43	0.0011	1	U	R.LQHAAELIK.T 700
1621	660.8459	1319.6772	1319.6755	1.30	0	61	8.4e-005	1	U	K.TMQGSEVVNVLK.S
2879	864.4847	1726.9549	1726.9465	4.87	0	98	8.1e-009	1	U	R.SVIEQGGIQTVDQLIK.E
3315	948.0020	1893.9894	1893.9836	3.04	0	62	5.3e-005	1	U	K.NLATAYDNFVELVANLK.E

26. [COPG1_HUMAN](#) Mass: 97655 Score: 188 Matches: 4(4) Sequences: 3(3) emPAI: 0.09

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
1149	586.8307	1171.6469	1171.6448	1.80	0	50	0.00079	1	U	K.TLEEAVGNIVK.F
1375	622.8962	1243.7779	1243.7751	2.26	0	81	4.5e-008	1	U	R.SIATLAITTLK.T 1374
1817	693.8530	1385.6914	1385.6973	-4.26	0	46	0.0019	1	U	K.SVPLATAPMAEQR.T

27. [H90B2_HUMAN](#) Mass: 44321 Score: 169 Matches: 5(5) Sequences: 4(4) emPAI: 0.38

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
1104	580.7950	1159.5755	1159.5761	-0.47	0	43	0.0043	1		K.SIYYITGESK.E
1362	621.8561	1241.6977	1241.6979	-0.16	0	81	4.5e-007	1		K.ADLINNLTGIAK.F
2306	513.9208	1538.7407	1538.7464	-3.71	1	(42)	0.0059	1		R.YESLTDPSKLDGK.E
2307	770.3783	1538.7420	1538.7464	-2.83	1	63	4.4e-005	1		R.YESLTDPSKLDGK.E
3111	603.6583	1807.9531	1807.9509	1.27	0	38	0.014	1	U	K.HSQFLGYPTILYLEK.E

28. [A2MG_HUMAN](#) Mass: 163188 Score: 164 Matches: 5(5) 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
677	509.7999	1017.5852	1017.5859	-0.61	0	70	4e-006	1	U	K.ATVLNLYPK.C 678
949	558.8070	1115.5995	1115.5975	1.74	0	56	0.00022	1	U	R.QTVSWAVTPK.S
1255	605.8252	1209.6358	1209.6353	0.42	0	62	4.2e-005	1	U	K.LPPNVVEESAR.A 1254

29. [VASN_HUMAN](#) Mass: 71668 Score: 155 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
1051	575.8129	1149.6112	1149.6142	-2.64	0	61	6.2e-005	1	U	R.YLQGSVQLR.S
2418	785.4485	1568.8824	1568.8774	3.22	0	54	0.00016	1	U	R.SLTGLIEPVSPSLR.V
2845	858.9697	1715.9249	1715.9206	2.49	0	93	3.7e-008	1	U	R.LAGLGLQQLDEGLFSR.L

30. [CD166_HUMAN](#) Mass: 65061 Score: 154 Matches: 7(7) Sequences: 7(7) emPAI: 0.36

CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1218	596.3364	1190.6583	1190.6547	3.05	0	32	0.033	1	U	K.ALFLETEQLK.K
1494	639.3294	1276.6443	1276.6486	-3.37	0	50	0.001	1	U	R.LDVPQNLFGK.W
1897	471.5763	1411.7070	1411.7056	1.00	1	39	0.0095	1	U	R.SSNTYTLTDVRR.N
2296	512.3166	1533.9279	1533.9283	-0.22	0	44	0.00017	1	U	K.VLHPLGAVVIFK.K
2544	538.5859	1612.7358	1612.7369	-0.69	1	33	0.036	1	U	K.SVQYDDVPEYKDR.L

[2710](#) [416.5118](#) [1662.0180](#) [1662.0232](#) -3.14 1 44 0.00011 1 U [K.VLHPLEGAVVIFKK.E](#)
[4415](#) [897.7908](#) [2690.3507](#) [2690.3585](#) -2.92 0 51 0.0012 1 U [K.SMIASITVHYLDLSLNPSGEVTR.Q](#)

31. [IQGA1_HUMAN](#) Mass: 189134 Score: 154 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
3282	628.3430	1882.0070	1882.0047	1.24	0	(74)	2.7e-006	1	U	R.ILAIGLINEALDEGDAQK.T
3283	942.0145	1882.0145	1882.0047	5.20	0	79	8.5e-007	1	U	R.ILAIGLINEALDEGDAQK.T
3731	685.7017	2054.0833	2054.0796	1.80	0	41	0.006	1	U	K.LEGVLAEEVAHQYQDTLIR.A

32. [K2C6B_HUMAN](#) Mass: 60030 Score: 151 Matches: 3(3) Sequences: 2(2) emPAI: 0.15

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
1174	590.3044	1178.5942	1178.5931	0.92	0	76	2.1e-006	1		K.YEELQITAGR.H
1653	665.3680	1328.7215	1328.7187	2.12	0	86	1.9e-007	1		R.NLDLDSIIAEVK.A
1655	665.8557	1329.6969	1329.7027	-4.40	0	(52)	0.00059	1		R.NLDLDSIIAEVK.A

33. [HEP2_HUMAN](#) Mass: 57034 Score: 142 Matches: 3(3) Sequences: 1(1) emPAI: 0.10

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
2791	566.6394	1696.8964	1696.9300	-19.82	1	(54)	0.00029	1	U	R.LNILNAKFAFNLYR.V
2794	849.4573	1696.9000	1696.9300	-17.69	1	94	2.6e-008	1	U	R.LNILNAKFAFNLYR.V 2793

34. [PDIA4_HUMAN](#) Mass: 72887 Score: 141 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
1214	595.8216	1189.6286	1189.6302	-1.36	0	100	9e-009	1	U	K.IDATSASVLASR.F
2033	729.8818	1457.7491	1457.7548	-3.91	0	71	8.4e-006	1	U	K.VSQGQLVVMQPEK.F

35. [PSMD2_HUMAN](#) Mass: 100136 Score: 140 Matches: 6(6) Sequences: 5(5) emPAI: 0.19

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
676	508.8059	1015.5972	1015.5913	5.77	0	38	0.0078	1	U	R.LNILDTLSK.F
744	346.5417	1036.6033	1036.6029	0.39	0	34	0.0089	1	U	R.LAQGLTHLGK.G
2020	484.9442	1451.8109	1451.8096	0.87	0	36	0.0075	1	U	R.VGQAVDVVGAGKPK.T
3851	1067.0055	2131.9964	2131.9997	-1.53	0	(49)	0.0015	1	U	R.MNLASSFVNGFVNAAFQDK.L
3852	711.6745	2132.0017	2131.9997	0.93	0	56	0.00034	1	U	R.MNLASSFVNGFVNAAFQDK.L
4214	819.7972	2456.3697	2456.3566	5.32	0	32	0.019	1	U	R.AELATEEFLPVTPILEGFVILR.K

36. [PSA_HUMAN](#) Mass: 103211 Score: 140 Matches: 4(4) Sequences: 4(4) emPAI: 0.12

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
1203	595.3455	1188.6764	1188.6754	0.79	0	33	0.024	1	U	K.ATFDISLVVPK.D
1377	624.3254	1246.6363	1246.6340	1.90	0	45	0.0036	1	U	R.VALSNNMVIDR.K
1690	673.8760	1345.7375	1345.7354	1.59	0	86	1.8e-007	1	U	R.LGLQNDLFLSLAR.A
1801	690.9280	1379.8415	1379.8388	1.98	0	51	5.1e-005	1	U	R.VLGATLLPDLIQK.V

37. [NUCL_HUMAN](#) Mass: 76568 Score: 136 Matches: 5(5) Sequences: 3(3) emPAI: 0.16

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
510	469.2530	936.4915	936.4917	-0.17	0	47	0.001	1	U	K.TGISDVFAK.N
639	500.7742	999.5338	999.5349	-1.06	0	35	0.018	1	U	K.NDLAVVDVR.I
4087	771.3927	2311.1563	2311.1485	3.38	0	(48)	0.0017	1	U	K.VEGTEPTAFNLFVGNLNFNK.S 4086
4088	1156.5868	2311.1590	2311.1485	4.57	0	56	0.00032	1	U	K.VEGTEPTAFNLFVGNLNFNK.S

38. [TRAP1_HUMAN](#) Mass: 80060 Score: 135 Matches: 2(2) Sequences: 1(1) emPAI: 0.04

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
2231	757.3976	1512.7807	1512.7784	1.56	0	108	1.4e-009	1	U	R.GVVDSEIPLNLSR.E 2230

39. [GOLM1_HUMAN](#) Mass: 45306 Score: 135 Matches: 4(4) Sequences: 4(4) emPAI: 0.28

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
872	544.2896	1086.5647	1086.5669	-2.07	0	60	7.3e-005	1	U	R.DTINLLDQR.E

[1837](#) 697.8751 1393.7356 1393.7314 3.02 0 58 0.00011 1 U R.QQLQALSEPQPR.L
[4078](#) 766.7083 2297.1031 2297.1135 -4.52 1 41 0.0096 1 U R.QVEKEETNEIQVVNEEPQR.D
[4330](#) 643.0687 2568.2458 2568.2415 1.66 2 55 0.0005 1 U R.QVEKEETNEIQVVNEEPQRDR.L

40. [LUM_HUMAN](#) Mass: 38405 Score: 133 Matches: 3(3) 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
3485	653.0370	1956.0893	1956.0932	-1.96	0	(45)	0.0014	1	U	R.LPSGLPVSLTLTYLDNNK.I
3490	979.0599	1956.1052	1956.0932	6.16	0	63	1.4e-005	1	U	R.LPSGLPVSLTLTYLDNNK.I 3489

41. [SYG_HUMAN](#) Mass: 83113 Score: 131 Matches: 4(4) Sequences: 2(2) emPAI: 0.11

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
2028	729.3961	1456.7776	1456.7755	1.42	0	45	0.0026	1	U	R.TFFSFPVAVVAPFK.C 2029
3976	745.7328	2234.1767	2234.1695	3.21	0	55	0.00029	1	U	R.LGDAVEQGVINNTVLGYFGR.I
3977	1118.0974	2234.1803	2234.1695	4.80	0	(50)	0.00071	1	U	R.LGDAVEQGVINNTVLGYFGR.I

42. [K2C1B_HUMAN](#) Mass: 61864 Score: 128 Matches: 2(2) 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
1174	590.3044	1178.5942	1178.5931	0.92	0	76	2.1e-006	1	U	K.YQELQITAGR.H
2096	738.3946	1474.7746	1474.7780	-2.27	0	83	4.8e-007	1		R.FLEQQNQVLQTK.W

43. [SLIK4_HUMAN](#) Mass: 94271 Score: 120 Matches: 3(3) Sequences: 3(3) emPAI: 0.10

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
2151	745.9247	1489.8349	1489.8293	3.79	0	42	0.0029	1	U	K.SLPVYIFSGAPLAR.L
2608	815.9633	1629.9120	1629.9090	1.83	0	84	1.9e-007	1	U	K.LQNIIEGGAFLGLSALK.Q
3824	1058.5929	2115.1712	2115.1728	-0.74	0	35	0.014	1	U	K.VLILNDNLISFLPDNIFR.F

44. [VTNC_HUMAN](#) Mass: 54271 Score: 119 Matches: 3(3) Sequences: 1(1) emPAI: 0.05

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2668	823.9144	1645.8143	1645.8100	2.60	0	69	1.6e-005	1	U	R.DVWGIEGPIDAAFR.I 2664 2666

45. [HBA_HUMAN](#) Mass: 15248 Score: 116 Matches: 3(3) Sequences: 3(3) emPAI: 0.71

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
873	363.2134	1086.6184	1086.6186	-0.16	1	36	0.019	1	U	K.LRVDPVNFK.L
1401	626.8604	1251.7062	1251.7075	-1.04	0	82	2.2e-007	1	U	K.FLASVSTVLTSK.Y
2277	510.5802	1528.7189	1528.7270	-5.31	0	52	0.0005	1	U	K.VGAHAGEYGAEALER.M

46. [K1C9_HUMAN](#) Mass: 62027 Score: 112 Matches: 3(3) Sequences: 3(3) emPAI: 0.15

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
1079	579.2996	1156.5846	1156.5836	0.80	0	73	2.7e-006	1	U	R.QGVDADINGLR.Q
4481	968.1384	2901.3935	2901.4032	-3.36	1	35	0.044	1	U	K.NYSPYYNTIDDLKDQIVDLTVGNK.T
4579	1088.8462	3263.5167	3263.5066	3.12	0	50	0.0014	1	U	K.DIENQYETQITQIEHVSSSGQEVQSSAK.E

47. [CAND1_HUMAN](#) Mass: 136289 Score: 106 Matches: 3(3) Sequences: 3(3) emPAI: 0.07

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
1413	628.8931	1255.7716	1255.7751	-2.82	0	77	3.6e-007	1	U	K.LGTLSALDILIK.N
2127	742.4472	1482.8799	1482.8770	1.96	0	42	0.0011	1	U	K.ISGSILNELIGLVR.S
3750	689.0797	2064.2173	2064.2095	3.77	0	30	0.0051	1	U	K.IDLRPVLGEGVPILASFLR.K

48. [TRFL_HUMAN](#) Mass: 78132 Score: 105 Matches: 5(5) 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
52	318.1919	634.3692	634.3690	0.37	0	38	0.0047	1		K.DLLFK.D 51 53
887	549.2564	1096.4983	1096.4978	0.44	0	54	0.0002	1	U	R.YGYTGAFR.C 888

49. [BCAM_HUMAN](#) Mass: 67363 Score: 101 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
2577	812.4529	1622.8913	1622.8879	2.11	0	77	1e-006	1	U	R.EASGLLSLTSTLYLR.L
3860	712.6631	2134.9674	2134.9623	2.40	0	48	0.0016	1	U	R.LASAEHQGSELQVTMHDTR.G

50. [PYGB HUMAN](#) Mass: 96635 Score: 99 Matches: 4(4) Sequences: 4(4) emPAI: 0.13

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
796	527.2896	1052.5647	1052.5655	-0.75	0	50	0.0005	1		K.VIFLENYR.V
1857	700.9120	1399.8095	1399.8075	1.46	0	53	0.00019	1	U	K.LLPLVSDVEFIR.D
2568	540.9644	1619.8712	1619.8770	-3.57	1	32	0.046	1	U	K.IGEEFLTDSLQKK.L
3627	669.7126	2006.1161	2006.1200	-1.96	1	29	0.046	1		R.LKQEFVVAATLQDIIR.R

51. [CFAB HUMAN](#) Mass: 85479 Score: 95 Matches: 2(2) Sequences: 2(2) emPAI: 0.07

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
2204	754.8454	1507.6762	1507.6791	-1.87	0	72	4.3e-006	1	U	K.VSEADSSNADWVTK.Q
3199	921.9645	1841.9144	1841.9087	3.09	0	52	0.00067	1	U	K.EAGIPEFYDYDVALIK.L

52. [ACPH HUMAN](#) Mass: 81173 Score: 89 Matches: 2(2) Sequences: 2(2) emPAI: 0.07

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
1723	681.3308	1360.6471	1360.6470	0.04	0	72	5.3e-006	1	U	K.ALDVSASDDEIAR.L
2761	844.9453	1687.8761	1687.8781	-1.17	0	47	0.0024	1	U	R.QVLLSEPEEAAALYR.G

53. [GFPT1 HUMAN](#) Mass: 78756 Score: 79 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
2388	521.6351	1561.8834	1561.8868	-2.19	0	(35)	0.01	1	U	R.VIQQLEGAFALVFK.S
2389	781.9503	1561.8860	1561.8868	-0.54	0	67	6.8e-006	1	U	R.VIQQLEGAFALVFK.S

Proteins matching the same set of peptides:

[GFPT2 HUMAN](#) Mass: 76882 Score: 79 Matches: 2(2) Sequences: 1(1)

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

54. [GNS HUMAN](#) Mass: 62042 Score: 77 Matches: 2(2) Sequences: 2(2) emPAI: 0.10

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
2341	773.4109	1544.8073	1544.8086	-0.83	0	52	0.00062	1	U	R.WQTLLSVDDLVEK.L
2896	578.3388	1731.9946	1731.9923	1.31	1	51	0.00021	1	U	R.QLYEFDIKVPLLVR.G

55. [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
796	527.2896	1052.5647	1052.5655	-0.75	0	50	0.0005	1		K.VIFLENYR.V
2485	797.4142	1592.8139	1591.8246	622	0	43	0.0053	1	U	K.LVIDQIDNGFFSPK.Q
3627	669.7126	2006.1161	2006.1200	-1.96	1	29	0.046	1		R.LKQEFVVAATLQDIIR.R

56. [UBA1 HUMAN](#) Mass: 117774 Score: 72 Matches: 2(2) Sequences: 2(2) emPAI: 0.05

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
2578	812.4567	1622.8989	1622.8992	-0.16	0	32	0.03	1	U	R.LAGTQPLEVLEAVQR.S
4387	873.8052	2618.3937	2618.3778	6.08	0	63	3.6e-005	1	U	K.LAYVAAGDLAPINAFIGGLAAQEVMK.A

57. [TFR1 HUMAN](#) Mass: 84818 Score: 72 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
1960	717.4167	1432.8188	1432.8177	0.78	0	72	1.8e-006	1	U	K.VSASPLLYTLIEK.T

58. [K1C14 HUMAN](#) Mass: 51529 Score: 71 Matches: 2(2) Sequences: 2(2) emPAI: 0.12

Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
824	355.5406	1063.6000	1063.6026	-2.39	1	38	0.0064	1		R.LASYLDKVR.A
1542	651.3336	1300.6527	1300.6510	1.28	0	62	5.6e-005	1	U	R.ALEENADLEVK.I

Proteins matching the same set of peptides:

[K1C15 HUMAN](#) Mass: 49181 Score: 71 Matches: 2(2) Sequences: 2(2)

Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3

[K1C16 HUMAN](#) Mass: 51236 Score: 71 Matches: 2(2) Sequences: 2(2)

Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4

59.	CROCC HUMAN	Mass: 228388	Score: 62	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
460	457.7697	913.5248	913.5232	1.66	0	53 0.0002 1 U K.LALLEEAR.T
1706	677.8044	1353.5943	1353.5904	2.90	1	38 0.0081 1 U R.QMKMLDSENTR.L
60.	PABP1 HUMAN	Mass: 70626	Score: 62	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.08
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
507	467.7720	933.5294	933.5284	1.10	0	54 0.00019 1 U K.SGVGNIFIK.N
2323	514.9838	1541.9295	1541.9293	0.09	0	32 0.0063 1 U R.IVATKPLYVALAQR.K
61.	STAT1 HUMAN	Mass: 87280	Score: 56	Matches: 2(2)	Sequences: 2(2)	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
2815	853.9608	1705.9071	1705.9151	-4.73	0	38 0.012 1 U K.LLGPNASPDGLIPWTR.F
3698	677.0302	2028.0686	2028.0680	0.29	0	39 0.012 1 U R.TFSLFQQLIQSSFVVER.Q
62.	FBLN1 HUMAN	Mass: 77162	Score: 56	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
2433	525.9382	1574.7929	1574.7875	3.40	0	56 0.00028 1 U K.LEMNYVVGVSYSR.N
63.	COPB HUMAN	Mass: 107074	Score: 56	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.03
Coatamer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
1656	665.8757	1329.7368	1329.7326	3.14	0	42 0.0046 1 U R.VLQDLVMDILR.V 1657
64.	AFAM HUMAN	Score: 51	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.04	
Afamin OS=Homo sapiens GN=AFM PE=1 SV=1						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
305	416.7677	831.5209	831.5218	-1.09	0	51 0.00012 1 U R.FLVNLVK.L
65.	G3PT HUMAN	Mass: 44473	Score: 50	Matches: 1(1)	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
1113	581.3164	1160.6183	1160.6190	-0.60	0	50 0.00095 1 U K.AGIALNDNFVK.L
66.	HS71L HUMAN	Score: 49	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
2741	839.4094	1676.8042	1676.7828	12.7	0	49 0.0013 2 U K.NQVAMNPQNTVFDAK.R
67.	H4 HUMAN	Mass: 11360	Score: 49	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.60
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2						
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score Expect Rank Unique Peptide
1635	442.5894	1324.7463	1324.7463	0.04	0	43 0.0018 1 U R.DNIQGITKPAIR.R
1636	663.3812	1324.7478	1324.7463	1.13	0	(34) 0.012 1 U R.DNIQGITKPAIR.R
68.	KAT12 HUMAN	Mass: 61214	Score: 49	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
1151	586.8353	1171.6561	1171.6601	-3.42	0	49 0.00091 1 U K.GLLLYGPPGTGK.T
69.	RS27A HUMAN	Mass: 17953	Score: 48	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
3049	894.4697	1786.9248	1786.9200	2.67	0	48	0.0016	1	U	K.TITLEVEPSDTIENVK.A

Proteins matching the same set of peptides:

[RL40_HUMAN](#) Mass: 14719 Score: 48 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: 48 Matches: 1(1) Sequences: 1(1)

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

[UBC_HUMAN](#) Mass: 76992 Score: 48 Matches: 1(1) Sequences: 1(1)

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

70. [XPP3_HUMAN](#) Mass: 56997 Score: 47 Matches: 1(1) 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
245	408.2598	814.5051	814.5065	-1.72	0	47	0.00065	1	U	K.AILFVPR.R

71. [GOLGB1_HUMAN](#) Mass: 375790 Score: 46 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
2900	867.8986	1733.7827	1733.8141	-18.13	0	46	0.0021	1	U	K.MNLNQIQEELSR.V

72. [C04A_HUMAN](#) Mass: 192664 Score: 45 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
1758	684.3660	1366.7174	1366.7133	3.01	0	45	0.0024	1	U	R.DSSTWLTAFLVK.V

73. [SEC23B_HUMAN](#) Mass: 86424 Score: 44 Matches: 1(1) 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
3968	744.4098	2230.2075	2230.1958	5.29	0	44	0.002	1	U	R.STGVALSIAVGLLEGTFPNTGAR.I

74. [ITIH3_HUMAN](#) Mass: 99787 Score: 43 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
1517	645.8045	1289.5945	1289.5928	1.29	0	43	0.0036	1	U	R.DYIFGNVIER.L

75. [ABCA3_HUMAN](#) Score: 42 Matches: 1(1) Sequences: 1(1) emPAI: 0.02

ATP-binding cassette sub-family A member 3 OS=Homo sapiens GN=ABCA3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
131	379.7426	757.4706	757.4698	1.11	0	42	0.0027	1	U	R.LSLAVQK.G

76. [EXOC3_HUMAN](#) Mass: 86790 Score: 40 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
993	567.3040	1132.5934	1132.5975	-3.69	0	40	0.0089	1	U	R.QSINTIESLK.D

77. [FUBP2_HUMAN](#) Mass: 73070 Score: 39 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

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
1548	651.8521	1301.6897	1301.6827	5.36	0	39	0.013	1	U	R.SVSLTGAPESVQK.A

78. [MDHM_HUMAN](#) Mass: 35481 Score: 39 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
1334	617.3647	1232.7148	1232.7129	1.56	0	39	0.0042	1	U	K.IFGVTTLDIVR.A

79. [C06A1_HUMAN](#) Mass: 108462 Score: 38 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
3016	592.3129	1773.9168	1773.9122	2.58	0	38	0.017	1	U	R.VAVVQYSGTGQQRPER.A

80. [SEM3C_HUMAN](#) Mass: 85153 Score: 38 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1190	592.8719	1183.7293	1183.7288	0.43	0	38	0.0025	1	U	R.IIATSQGLLIR.S

81. [SEFQ_HUMAN](#) Mass: 76102 Score: 37 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1035	381.8813	1142.6219	1142.6196	2.02	0	37	0.013	1	U	R.FATHAAALSVR.N

82. [MTMR5_HUMAN](#) Mass: 208184 Score: 37 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2246	507.9422	1520.8047	1520.8133	-5.67	2	37	0.016	1	U	K.MQDKELRAVFLR.L

83. [DYM_HUMAN](#) Score: 36 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
1801	690.9280	1379.8415	1379.8176	17.3	1	36	0.0016	2	U	K.LVKTLTYNFIR.Q

84. [MSL1_HUMAN](#) 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
1385	625.3152	1248.6158	1248.6384	-18.04	2	35	0.033	1	U	R.MQLVKKDNEK.E

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
736	518.7678	1035.5210	1035.5236	-2.57	0	34	0.031	1	U	K.YNQLQLEK.G

86. [CC149_HUMAN](#) Mass: 52764 Score: 34 Matches: 1(1) Sequences: 1(1) emPAI: 0.06

Coiled-coil domain-containing protein 149 OS=Homo sapiens GN=CCDC149 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
715	514.8067	1027.5989	1026.5822	990	0	34	0.017	1	U	K.QANLAQLLR.D

87. [SKI_HUMAN](#) Mass: 79955 Score: 34 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
2266	509.6154	1525.8242	1524.8300	652	1	34	0.027	1	U	K.VVKELQELWPR.A

88. [AGRIN_HUMAN](#) Mass: 217092 Score: 33 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
793	526.3005	1050.5865	1050.5862	0.30	0	33	0.019	1	U	R.SFLAFTLR.A

89. [NEBU_HUMAN](#) Mass: 772428 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.00

Nebulin OS=Homo sapiens GN=NEB PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
904	551.8347	1101.6549	1101.6393	14.1	2	32	0.018	1	U	K.KAGEILSEKK.Y

90. [NRAP_HUMAN](#) Mass: 196950 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
904	551.8347	1101.6549	1101.6393	14.1	2	32	0.018	1	U	K.KAGELISEKK.Y

91. [ZN101_HUMAN](#) Mass: 50307 Score: 32 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
622	499.2763	996.5381	996.5392	-1.19	0	32	0.025	1	U	K.AFISAGYLR.T

92. [ZN646_HUMAN](#) Mass: 200636 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.01

Zinc finger protein 646 OS=Homo sapiens GN=ZNF646 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
566	488.7760	975.5374	975.5389	-1.54	0	32	0.046	2	U	K.QLFNAAALK.N

93. [XYLB_HUMAN](#) Mass: 40086 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
1635	442.5894	1324.7463	1324.7211	19.0	1	31	0.025	2	U	K.TKILATGGASHNR.E

94. [RPF1_HUMAN](#) Mass: 40086 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.07

Ribosome production factor 1 OS=Homo sapiens GN=RPF1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
553	485.2712	968.5278	968.5291	-1.32	0	31	0.028	1	U	K.VGIQELGPR.F

95. [H2A1B_HUMAN](#) Mass: 14127 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.21

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
3391	644.3951	1930.1636	1930.1615	1.07	0	31	0.0029	1	U	R.VTIAQGGVLPNIQAVLLPK.K

Proteins matching the same set of peptides:

[H2A1C_HUMAN](#) Mass: 14097 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2A1D_HUMAN](#) Mass: 14099 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2A1H_HUMAN](#) Mass: 13898 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2A1J_HUMAN](#) Mass: 13928 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2A1_HUMAN](#) Mass: 14083 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2A2A_HUMAN](#) Mass: 14087 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2A2C_HUMAN](#) Mass: 13980 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2A3_HUMAN](#) Mass: 14113 Score: 31 Matches: 1(1) Sequences: 1(1)

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

[H2AJ_HUMAN](#) Mass: 14011 Score: 31 Matches: 1(1) Sequences: 1(1)

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

96. [4F2_HUMAN](#) Mass: 67952 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1781	686.4197	1370.8249	1370.8286	-2.65	0	31	0.013	1	U	R.LLTSLPAQLLR.L

97. [VNN1_HUMAN](#) Mass: 56975 Score: 31 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
3704	678.4006	2032.1799	2032.1721	3.83	0	31	0.0093	1	U	R.LFSLKPTSGPVLTVTLFGR.L

98. [RASL2_HUMAN](#) Mass: 90401 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

Ras GTPase-activating protein 4 OS=Homo sapiens GN=RASA4 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
504	467.2751	932.5357	932.5291	7.07	1	30	0.039	1	U	R.TRETSIVK.K

Proteins matching the same set of peptides:

[RAS4B_HUMAN](#) Mass: 90350 Score: 30 Matches: 1(1) Sequences: 1(1)

Ras GTPase-activating protein 4B OS=Homo sapiens GN=RASA4B PE=3 SV=2

99. [S23IP_HUMAN](#) Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
553	485.2712	968.5278	968.5113	17.0	0	30	0.033	2	U	K.EMGIPLGPR.K

100. [RENT2_HUMAN](#) Mass: 147717 Score: 29 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
245	408.2598	814.5051	814.5065	-1.72	0	29	0.047	3	U	R.ALIVPR.Q

101. [CLCF1_HUMAN](#) Mass: 25160 Score: 28 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
341	428.7534	855.4923	855.4814	12.7	0	28	0.045	1	U	R.LGAETLPR.A

102. [KCA10_HUMAN](#) Mass: 57748 Score: 27 Matches: 1(1) Sequences: 1(1) emPAI: 0.05
Potassium voltage-gated channel subfamily A member 10 OS=Homo sapiens GN=KCA10 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
555	485.3067	968.5989	968.6018	-3.02	0	27	0.031	1	U	R.VIINIAGLR.F

103. [NIBL1_HUMAN](#) Mass: 84085 Score: 26 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
2130	742.9583	1483.9021	1483.9014	0.48	0	26	0.02	1	U	R.EALLQISIPFLK.K

104. [HS12B_HUMAN](#) Score: 26 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
592	492.8130	983.6115	983.5988	12.9	2	26	0.039	2	U	K.LLVDRGR.W

105. [TAAR2_HUMAN](#) Mass: 40107 Score: 18 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
513	470.3156	938.6166	938.6277	-11.78	1	18	0.046	1	U	K.ITIPVIKR.L

106. [STAB1_HUMAN](#) Mass: 275300 Score: 17 Matches: 1(1) Sequences: 1(1) emPAI: 0.01
Stabilin-1 OS=Homo sapiens GN=STAB1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
529	476.3211	950.6276	950.6277	-0.08	0	17	0.02	1	U	K.VAGLLPLLR.E

107. [HES2_HUMAN](#) Mass: 18459 Score: 15 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
528	476.3210	950.6275	950.6277	-0.14	0	15	0.033	1	U	K.GLILPLLGR.E

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