Mascot Search Results

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User                    : bo ek
Email                   : bo.ek@kemi.uu.se
Search title            : bo_21Ronqvist
MS data file            : data06.mgf
Database                : Swissprot2013 sprot (540261 sequences; 191876607 residues)
Taxonomy                : Homo sapiens (human) (20258 sequences)
Timestamp               : 16 Jun 2014 at 07:12:53 GMT
Enzyme                  : Trypsin
Fixed modifications     : Carbamidomethyl (C)
Variable modifications  : Oxidation (M)
Mass values             : Monoisotopic
Protein Mass            : Unrestricted
Peptide Mass Tolerance  : ± 10 ppm
Fragment Mass Tolerance : ± 0.4 Da
Max Missed Cleavages    : 1
Instrument type         : ESI-FTICR
Number of queries       : 5951
Protein hits            : AMPN_HUMAN  Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4
                          DPP4_HUMAN  Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4 PE=1 SV=2
                          NEP_HUMAN   Neprilysin OS=Homo sapiens GN=MME PE=1 SV=2
                          K1C9_HUMAN  Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
                          K22E_HUMAN  Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
                          GAPR1_HUMAN Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3
                          K2C1_HUMAN  Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
                          TMPS2_HUMAN Transmembrane protease serine 2 OS=Homo sapiens GN=TMPRSS2 PE=1 SV=3
                          BASP1_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2
                          ASM3B_HUMAN Acid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens GN=SMPDL3B PE=2 SV=2
                          IFM1_HUMAN  Interferon-induced transmembrane protein 1 OS=Homo sapiens GN=IFITM1 PE=1 SV=3
                          RAB3B_HUMAN Ras-related protein Rab-3B OS=Homo sapiens GN=RAB3B PE=1 SV=2
                          ADAM9_HUMAN Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1
                          TRFL_HUMAN  Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6
                          IDHC_HUMAN  Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2
                          CA2D1_HUMAN Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Homo sapiens GN=CACNA2D1 PE=1 SV=3
                          CD177_HUMAN CD177 antigen OS=Homo sapiens GN=CD177 PE=1 SV=2
                          1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1
                          S15A2_HUMAN Solute carrier family 15 member 2 OS=Homo sapiens GN=SLC15A2 PE=2 SV=2
                          PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1
                          AT8A1_HUMAN Probable phospholipid-transporting ATPase IA OS=Homo sapiens GN=ATP8A1 PE=1 SV=1
                          STEA4_HUMAN Metalloreductase STEAP4 OS=Homo sapiens GN=STEAP4 PE=1 SV=1
                          SEMG1_HUMAN Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2
                          ALBU_HUMAN  Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
                          SNP23_HUMAN Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=1 SV=1
                          1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1
                          PGK1_HUMAN  Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3
                          ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2
                          TGM4_HUMAN  Protein-glutamine gamma-glutamyltransferase 4 OS=Homo sapiens GN=TGM4 PE=1 SV=2
                          VPP1_HUMAN  V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3
                          GPC5C_HUMAN G-protein coupled receptor family C group 5 member C OS=Homo sapiens GN=GPRC5C PE=1 SV=2
                          EDIL3_HUMAN EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 PE=1 SV=1
                          FOLH1_HUMAN Glutamate carboxypeptidase 2 OS=Homo sapiens GN=FOLH1 PE=1 SV=1
                          NHRF1_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4
                          GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3
                          ATP9A_HUMAN Probable phospholipid-transporting ATPase IIA OS=Homo sapiens GN=ATP9A PE=1 SV=3
                          MYO1C_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4
                          GNAS1_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2
                          RHOG_HUMAN  Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1
                          MGA_HUMAN   Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=1 SV=5
                          ARRD1_HUMAN Arrestin domain-containing protein 1 OS=Homo sapiens GN=ARRDC1 PE=2 SV=1
                          HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1
                          SPIT1_HUMAN Kunitz-type protease inhibitor 1 OS=Homo sapiens GN=SPINT1 PE=1 SV=2
                          CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2
                          MPI_HUMAN   Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=2
                          PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2
                          HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5
                          ENOA_HUMAN  Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2
                          K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4
                          VP37B_HUMAN Vacuolar protein sorting-associated protein 37B OS=Homo sapiens GN=VPS37B PE=1 SV=1
                          ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2
                          ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2
                          CAN5_HUMAN  Calpain-5 OS=Homo sapiens GN=CAPN5 PE=1 SV=2
                          HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5
                          STOM_HUMAN  Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3
                          KINH_HUMAN  Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1
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ESPB1_HUMAN	Epididymal sperm-binding protein 1 OS=Homo sapiens GN=ELSPBP1 PE=1 SV=2
MELPH_HUMAN	Melanophilin OS=Homo sapiens GN=MLPH PE=1 SV=1
ANX11_HUMAN	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1
HSP76_HUMAN	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2
PPBT_HUMAN	Alkaline phosphatase, tissue-nonspecific isozyme OS=Homo sapiens GN=ALPL PE=1 SV=4
MFGM_HUMAN	Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2
IPSP_HUMAN	Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3
KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2
HSP72_HUMAN	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1
MYO5B_HUMAN	Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3
ANXA7_HUMAN	Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3
CBPO_HUMAN	Carboxypeptidase O OS=Homo sapiens GN=CPO PE=2 SV=1
DAF_HUMAN	Complement decay-accelerating factor OS=Homo sapiens GN=CD55 PE=1 SV=4
CBPM_HUMAN	Carboxypeptidase M OS=Homo sapiens GN=CPM PE=1 SV=2
SEMG2_HUMAN	Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1
KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3
GRP78_HUMAN	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2
RB27A_HUMAN	Ras-related protein Rab-27A OS=Homo sapiens GN=RAB27A PE=1 SV=3
MYO5A_HUMAN	Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=1 SV=2
PLS1_HUMAN	Phospholipid scramblase 1 OS=Homo sapiens GN=PLSCR1 PE=1 SV=1
ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
CAH4_HUMAN	Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2
KCRB_HUMAN	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1
RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1
VPS28_HUMAN	Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1
TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3
NIBAN_HUMAN	Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1
TS101_HUMAN	Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2
RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2
KPCD_HUMAN	Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2
NDRG1_HUMAN	Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1
VP37C_HUMAN	Vacuolar protein sorting-associated protein 37C OS=Homo sapiens GN=VPS37C PE=1 SV=2
APOC3_HUMAN	Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1
AT11B_HUMAN	Probable phospholipid-transporting ATPase IF OS=Homo sapiens GN=ATP11B PE=1 SV=2
PRDX6_HUMAN	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3
1433G_HUMAN	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2
YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3
DHSO_HUMAN	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4
CD63_HUMAN	CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2
LDHC_HUMAN	L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1 SV=4
ENTP3_HUMAN	Ectonucleoside triphosphate diphosphohydrolase 3 OS=Homo sapiens GN=ENTPD3 PE=1 SV=2
K1324_HUMAN	UPF0577 protein KIAA1324 OS=Homo sapiens GN=KIAA1324 PE=2 SV=2
GPR64_HUMAN	G-protein coupled receptor 64 OS=Homo sapiens GN=GPR64 PE=1 SV=2
CAPG_HUMAN	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2
PPAP_HUMAN	Prostatic acid phosphatase OS=Homo sapiens GN=ACPP PE=1 SV=3
5NTD_HUMAN	5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1
LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2
1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3
RAB3D_HUMAN	Ras-related protein Rab-3D OS=Homo sapiens GN=RAB3D PE=1 SV=1
CYFP1_HUMAN	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1
DDAH2_HUMAN	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens GN=DDAH2 PE=1 SV=1
GNA13_HUMAN	Guanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2
GGT1_HUMAN	Gamma-glutamyltranspeptidase 1 OS=Homo sapiens GN=GGT1 PE=1 SV=2
TSN7_HUMAN	Tetraspanin-7 OS=Homo sapiens GN=TSPAN7 PE=1 SV=2
TERA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4
CD38_HUMAN	ADP-ribosyl cyclase 1 OS=Homo sapiens GN=CD38 PE=1 SV=2
CIB1_HUMAN	Calcium and integrin-binding protein 1 OS=Homo sapiens GN=CIB1 PE=1 SV=4
HEBP1_HUMAN	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1
MYO1D_HUMAN	Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2
MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4
MYH11_HUMAN	Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3
RAB1A_HUMAN	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3
NHRF2_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=2
G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4
GNAI1_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2
CD9_HUMAN	CD9 antigen OS=Homo sapiens GN=CD9 PE=1 SV=4
FLOT1_HUMAN	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3
S52A3_HUMAN	Solute carrier family 52, riboflavin transporter, member 3 OS=Homo sapiens GN=SLC52A3 PE=1 SV=4
1433F_HUMAN	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4
1433S_HUMAN	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1
RAB8A_HUMAN	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1
CNDP2_HUMAN	Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2
PLS3_HUMAN	Phospholipid scramblase 3 OS=Homo sapiens GN=PLSCR3 PE=1 SV=2
PCY2_HUMAN	Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens GN=PCYT2 PE=1 SV=1
MRP_HUMAN	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2
FAS_HUMAN	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3
RB27B_HUMAN	Ras-related protein Rab-27B OS=Homo sapiens GN=RAB27B PE=1 SV=4
CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

TSN31_HUMAN	Tetraspanin-31 OS=Homo sapiens GN=TSPAN31 PE=2 SV=1
FXL20_HUMAN	F-box/LRR-repeat protein 20 OS=Homo sapiens GN=FBXL20 PE=1 SV=2
TCPR1_HUMAN	Tectonin beta-propeller repeat-containing protein 1 OS=Homo sapiens GN=TECPR1 PE=1 SV=1
RAB3A_HUMAN	Ras-related protein Rab-3A OS=Homo sapiens GN=RAB3A PE=1 SV=1
CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3
WFDC8_HUMAN	WAP four-disulfide core domain protein 8 OS=Homo sapiens GN=WFDC8 PE=2 SV=2
MT1G_HUMAN	Metallothionein-1G OS=Homo sapiens GN=MT1G PE=1 SV=2
PROF2_HUMAN	Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3
ADAM7_HUMAN	Disintegrin and metalloproteinase domain-containing protein 7 OS=Homo sapiens GN=ADAM7 PE=1 SV=3
PRSS8_HUMAN	Prostasin OS=Homo sapiens GN=PRSS8 PE=1 SV=1
RAB8B_HUMAN	Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2
HORN_HUMAN	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2
KIF5A_HUMAN	Kinesin heavy chain isoform 5A OS=Homo sapiens GN=KIF5A PE=1 SV=2
KIF5C_HUMAN	Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1
1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1
RRAS2_HUMAN	Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=1 SV=1
K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
MT1E_HUMAN	Metallothionein-1E OS=Homo sapiens GN=MT1E PE=1 SV=1
TBB2A_HUMAN	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
PSCA_HUMAN	Prostate stem cell antigen OS=Homo sapiens GN=PSCA PE=1 SV=1
PODXL_HUMAN	Podocalyxin OS=Homo sapiens GN=PODXL PE=1 SV=2
STXB2_HUMAN	Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=1 SV=2
RAB35_HUMAN	Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1
GNA12_HUMAN	Guanine nucleotide-binding protein subunit alpha-12 OS=Homo sapiens GN=GNA12 PE=1 SV=4
CTL2_HUMAN	Choline transporter-like protein 2 OS=Homo sapiens GN=SLC44A2 PE=1 SV=3
DOP2_HUMAN	Protein dopey-2 OS=Homo sapiens GN=DOPEY2 PE=1 SV=5
PLSL_HUMAN	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6
HCK_HUMAN	Tyrosine-protein kinase HCK OS=Homo sapiens GN=HCK PE=1 SV=5
FA84A_HUMAN	Protein FAM84A OS=Homo sapiens GN=FAM84A PE=2 SV=2
K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
PTGR1_HUMAN	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2
GBG12_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3
RAB5C_HUMAN	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2
PACN3_HUMAN	Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens GN=PACSIN3 PE=1 SV=2
PHP14_HUMAN	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1
LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3
TSN9_HUMAN	Tetraspanin-9 OS=Homo sapiens GN=TSPAN9 PE=1 SV=1
GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4
EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4
SERC5_HUMAN	Serine incorporator 5 OS=Homo sapiens GN=SERINC5 PE=2 SV=1
STAT3_HUMAN	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2
RAB3C_HUMAN	Ras-related protein Rab-3C OS=Homo sapiens GN=RAB3C PE=2 SV=1
WDR48_HUMAN	WD repeat-containing protein 48 OS=Homo sapiens GN=WDR48 PE=1 SV=1
CD47_HUMAN	Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1
GMPPA_HUMAN	Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1
ANXA4_HUMAN	Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4
S26A3_HUMAN	Chloride anion exchanger OS=Homo sapiens GN=SLC26A3 PE=1 SV=1
LY6K_HUMAN	Lymphocyte antigen 6K OS=Homo sapiens GN=LY6K PE=1 SV=2
POTEE_HUMAN	POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3
DHAK_HUMAN	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
LRC47_HUMAN	Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1
GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2
CD59_HUMAN	CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1
NPT2B_HUMAN	Sodium-dependent phosphate transport protein 2B OS=Homo sapiens GN=SLC34A2 PE=1 SV=3
LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2
PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1
WFDC2_HUMAN	WAP four-disulfide core domain protein 2 OS=Homo sapiens GN=WFDC2 PE=1 SV=2
CC50A_HUMAN	Cell cycle control protein 50A OS=Homo sapiens GN=TMEM30A PE=1 SV=1
GDIB_HUMAN	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2
CB072_HUMAN	Uncharacterized protein C2orf72 OS=Homo sapiens GN=C2orf72 PE=2 SV=2
LELP1_HUMAN	Late cornified envelope-like proline-rich protein 1 OS=Homo sapiens GN=LELP1 PE=2 SV=1
FNTA_HUMAN	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens GN=FNTA PE=1 SV=1
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2
CHM2A_HUMAN	Charged multivesicular body protein 2a OS=Homo sapiens GN=CHMP2A PE=1 SV=1
K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5
AGM1_HUMAN	Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1
RAP1A_HUMAN	Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1
CAMP_HUMAN	Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1
GBG5_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3
TMC5_HUMAN	Transmembrane channel-like protein 5 OS=Homo sapiens GN=TMC5 PE=2 SV=3
CRIS1_HUMAN	Cysteine-rich secretory protein 1 OS=Homo sapiens GN=CRISP1 PE=1 SV=1
GNAL_HUMAN	Guanine nucleotide-binding protein G(olf) subunit alpha OS=Homo sapiens GN=GNAL PE=1 SV=1
ENOB_HUMAN	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5
SH3B4_HUMAN	SH3 domain-binding protein 4 OS=Homo sapiens GN=SH3BP4 PE=1 SV=1
DCXR_HUMAN	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3

ZA2G_HUMAN	Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2
CHM4B_HUMAN	Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1
LDH6A_HUMAN	L-lactate dehydrogenase A-like 6A OS=Homo sapiens GN=LDHAL6A PE=2 SV=1
PRIO_HUMAN	Major prion protein OS=Homo sapiens GN=PRNP PE=1 SV=1
TCPQ_HUMAN	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4
LSR_HUMAN	Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LSR PE=1 SV=4
P20D2_HUMAN	Peptidase M20 domain-containing protein 2 OS=Homo sapiens GN=PM20D2 PE=1 SV=2
CTNB1_HUMAN	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1
PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2
K1C25_HUMAN	Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1
K1C28_HUMAN	Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2
S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2
RAB5A_HUMAN	Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2
S26A2_HUMAN	Sulfate transporter OS=Homo sapiens GN=SLC26A2 PE=1 SV=2
MT1F_HUMAN	Metallothionein-1F OS=Homo sapiens GN=MT1F PE=1 SV=1
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2
SYTL1_HUMAN	Synaptotagmin-like protein 1 OS=Homo sapiens GN=SYTL1 PE=1 SV=1
KAD1_HUMAN	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3
RAB10_HUMAN	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1
RAB15_HUMAN	Ras-related protein Rab-15 OS=Homo sapiens GN=RAB15 PE=1 SV=1
GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3
MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4
TMM8A_HUMAN	Transmembrane protein 8A OS=Homo sapiens GN=TMEM8A PE=1 SV=3
HIN1L_HUMAN	Putative HIN1-like protein OS=Homo sapiens GN=HIN1L PE=5 SV=1
LG3BP_HUMAN	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1
ZCCHV_HUMAN	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3
BCAS1_HUMAN	Breast carcinoma-amplified sequence 1 OS=Homo sapiens GN=BCAS1 PE=1 SV=2
CBR1_HUMAN	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3
DNJB2_HUMAN	DnaJ homolog subfamily B member 2 OS=Homo sapiens GN=DNAJB2 PE=1 SV=3
TSN6_HUMAN	Tetraspanin-6 OS=Homo sapiens GN=TSPAN6 PE=1 SV=1
TXNL1_HUMAN	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3
CD36_HUMAN	Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2
UBL3_HUMAN	Ubiquitin-like protein 3 OS=Homo sapiens GN=UBL3 PE=1 SV=1
TR10C_HUMAN	Tumor necrosis factor receptor superfamily member 10C OS=Homo sapiens GN=TNFRSF10C PE=1 SV=3
CD14_HUMAN	Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2
ALDR_HUMAN	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3
K22O_HUMAN	Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2
K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4
INADL_HUMAN	InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3
MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4
COLL1_HUMAN	Colipase-like protein 1 OS=Homo sapiens GN=CLPSL1 PE=2 SV=1
MYOF_HUMAN	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1
APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1
PTTG_HUMAN	Pituitary tumor-transforming gene 1 protein-interacting protein OS=Homo sapiens GN=PTTG1IP PE=1 SV=1
BAIP2_HUMAN	Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2 PE=1 SV=1
AT8A2_HUMAN	Probable phospholipid-transporting ATPase IB OS=Homo sapiens GN=ATP8A2 PE=2 SV=2
SORT_HUMAN	Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3
P2RX4_HUMAN	P2X purinoceptor 4 OS=Homo sapiens GN=P2RX4 PE=1 SV=2
REPS2_HUMAN	RalBP1-associated Eps domain-containing protein 2 OS=Homo sapiens GN=REPS2 PE=1 SV=2
SMIM1_HUMAN	Small integral membrane protein 1 OS=Homo sapiens GN=SMIM1 PE=1 SV=1
LFG3_HUMAN	Protein lifeguard 3 OS=Homo sapiens GN=TMBIM1 PE=1 SV=2
SORCN_HUMAN	Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1
PGK2_HUMAN	Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3
GNA11_HUMAN	Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2
SO2A1_HUMAN	Solute carrier organic anion transporter family member 2A1 OS=Homo sapiens GN=SLCO2A1 PE=1 SV=2
HYES_HUMAN	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2
GTR5_HUMAN	Solute carrier family 2, facilitated glucose transporter member 5 OS=Homo sapiens GN=SLC2A5 PE=1 SV=1
CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4
ZDHC2_HUMAN	Palmitoyltransferase ZDHHC2 OS=Homo sapiens GN=ZDHHC2 PE=2 SV=1
DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2
CC181_HUMAN	Coiled-coil domain-containing protein 181 OS=Homo sapiens GN=CCDC181 PE=2 SV=1
TRI34_HUMAN	Tripartite motif-containing protein 34 OS=Homo sapiens GN=TRIM34 PE=1 SV=2
RRAS_HUMAN	Ras-related protein R-Ras OS=Homo sapiens GN=RRAS PE=1 SV=1
PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1
PRS8_HUMAN	26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1
KI2L4_HUMAN	Killer cell immunoglobulin-like receptor 2DL4 OS=Homo sapiens GN=KIR2DL4 PE=1 SV=3
GNAQ_HUMAN	Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo sapiens GN=GNAQ PE=1 SV=4
RAB14_HUMAN	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4
IGS21_HUMAN	Immunoglobulin superfamily member 21 OS=Homo sapiens GN=IGSF21 PE=2 SV=1
TSN8_HUMAN	Tetraspanin-8 OS=Homo sapiens GN=TSPAN8 PE=1 SV=1
VIGLN_HUMAN	Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2
MIF_HUMAN	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4
PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4
PTPRJ_HUMAN	Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3
FLOT2_HUMAN	Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2
RB39B_HUMAN	Ras-related protein Rab-39B OS=Homo sapiens GN=RAB39B PE=1 SV=1
RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3
RB33B_HUMAN	Ras-related protein Rab-33B OS=Homo sapiens GN=RAB33B PE=1 SV=1

GP2_HUMAN	Pancreatic secretory granule membrane major glycoprotein GP2 OS=Homo sapiens GN=GP2 PE=2 SV=3
PEPD_HUMAN	Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3
SGTA_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1
PPME1_HUMAN	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3
AT1A2_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1
FKB1A_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2
ANO7_HUMAN	Anoctamin-7 OS=Homo sapiens GN=ANO7 PE=1 SV=2
UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3
GNAZ_HUMAN	Guanine nucleotide-binding protein G(z) subunit alpha OS=Homo sapiens GN=GNAZ PE=2 SV=3
IMPA1_HUMAN	Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1 PE=1 SV=1
NPDC1_HUMAN	Neural proliferation differentiation and control protein 1 OS=Homo sapiens GN=NPDC1 PE=1 SV=2
PTPRB_HUMAN	Receptor-type tyrosine-protein phosphatase beta OS=Homo sapiens GN=PTPRB PE=1 SV=3
SUIS_HUMAN	Sucrase-isomaltase, intestinal OS=Homo sapiens GN=SI PE=1 SV=6
PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5
AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3
CK052_HUMAN	Uncharacterized protein C11orf52 OS=Homo sapiens GN=C11orf52 PE=2 SV=2
NCALD_HUMAN	Neurocalcin-delta OS=Homo sapiens GN=NCALD PE=2 SV=2
MEGF9_HUMAN	Multiple epidermal growth factor-like domains protein 9 OS=Homo sapiens GN=MEGF9 PE=2 SV=3
COL12_HUMAN	Collectin-12 OS=Homo sapiens GN=COLEC12 PE=1 SV=3
T106B_HUMAN	Transmembrane protein 106B OS=Homo sapiens GN=TMEM106B PE=1 SV=2
GSH1_HUMAN	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2
ENOG_HUMAN	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3
AL1A3_HUMAN	Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens GN=ALDH1A3 PE=1 SV=2
SUCB2_HUMAN	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2
AT1A4_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Homo sapiens GN=ATP1A4 PE=1 SV=3
TB10A_HUMAN	TBC1 domain family member 10A OS=Homo sapiens GN=TBC1D10A PE=1 SV=1
LPP1_HUMAN	Lipid phosphate phosphohydrolase 1 OS=Homo sapiens GN=PPAP2A PE=1 SV=1
LSAMP_HUMAN	Limbic system-associated membrane protein OS=Homo sapiens GN=LSAMP PE=1 SV=2
ENPP3_HUMAN	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Homo sapiens GN=ENPP3 PE=1 SV=2
LAMP2_HUMAN	Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2
PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4
IQGA2_HUMAN	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4
ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3
DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3
SPIT3_HUMAN	Kunitz-type protease inhibitor 3 OS=Homo sapiens GN=SPINT3 PE=2 SV=3
WDR1_HUMAN	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4
COPT1_HUMAN	High affinity copper uptake protein 1 OS=Homo sapiens GN=SLC31A1 PE=1 SV=1
ANXA6_HUMAN	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3
ANO6_HUMAN	Anoctamin-6 OS=Homo sapiens GN=ANO6 PE=1 SV=2
I5P1_HUMAN	Type I inositol 1,4,5-trisphosphate 5-phosphatase OS=Homo sapiens GN=INPP5A PE=2 SV=1
GMPR1_HUMAN	GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1
LFA3_HUMAN	Lymphocyte function-associated antigen 3 OS=Homo sapiens GN=CD58 PE=1 SV=1
ISK2_HUMAN	Serine protease inhibitor Kazal-type 2 OS=Homo sapiens GN=SPINK2 PE=1 SV=2
AQP5_HUMAN	Aquaporin-5 OS=Homo sapiens GN=AQP5 PE=1 SV=1
GSHB_HUMAN	Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1
MAL2_HUMAN	Protein MAL2 OS=Homo sapiens GN=MAL2 PE=1 SV=1
SC5A1_HUMAN	Sodium/glucose cotransporter 1 OS=Homo sapiens GN=SLC5A1 PE=1 SV=1
NFH_HUMAN	Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4
MP2K2_HUMAN	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1
RAB13_HUMAN	Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4
TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1
ZN263_HUMAN	Zinc finger protein 263 OS=Homo sapiens GN=ZNF263 PE=2 SV=2
CHMP5_HUMAN	Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1
RINI_HUMAN	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2
SYT7_HUMAN	Synaptotagmin-7 OS=Homo sapiens GN=SYT7 PE=1 SV=3
EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
VAS1_HUMAN	V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2
GSTP1_HUMAN	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2
TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3
QOR_HUMAN	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1
TCPD_HUMAN	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4
GPC4_HUMAN	Glypican-4 OS=Homo sapiens GN=GPC4 PE=1 SV=4
CO4A5_HUMAN	Collagen alpha-5(IV) chain OS=Homo sapiens GN=COL4A5 PE=1 SV=2
LIN7C_HUMAN	Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1
KGP2_HUMAN	cGMP-dependent protein kinase 2 OS=Homo sapiens GN=PRKG2 PE=1 SV=1
CHM1B_HUMAN	Charged multivesicular body protein 1b OS=Homo sapiens GN=CHMP1B PE=1 SV=1
MB12B_HUMAN	Multivesicular body subunit 12B OS=Homo sapiens GN=MVB12B PE=1 SV=2
SYTL4_HUMAN	Synaptotagmin-like protein 4 OS=Homo sapiens GN=SYTL4 PE=1 SV=2
SDCB1_HUMAN	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1
HID1_HUMAN	Protein HID1 OS=Homo sapiens GN=HID1 PE=1 SV=1
ZG16B_HUMAN	Zymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3
NPC2_HUMAN	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1
KLK3_HUMAN	Prostate-specific antigen OS=Homo sapiens GN=KLK3 PE=1 SV=2
CN37_HUMAN	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2
CKAP5_HUMAN	Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3
FERM2_HUMAN	Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1
SERA_HUMAN	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4

TALDO_HUMAN	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2
CTL4_HUMAN	Choline transporter-like protein 4 OS=Homo sapiens GN=SLC44A4 PE=2 SV=2
ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2
GTR3_HUMAN	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1
LANC1_HUMAN	LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1
CHM2B_HUMAN	Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B PE=1 SV=1
DB126_HUMAN	Beta-defensin 126 OS=Homo sapiens GN=DEFB126 PE=2 SV=2
LEG3_HUMAN	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5
GBG4_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-4 OS=Homo sapiens GN=GNG4 PE=1 SV=1
PROM2_HUMAN	Prominin-2 OS=Homo sapiens GN=PROM2 PE=1 SV=1
ZNT4_HUMAN	Zinc transporter 4 OS=Homo sapiens GN=SLC30A4 PE=2 SV=2
AT8B1_HUMAN	Probable phospholipid-transporting ATPase IC OS=Homo sapiens GN=ATP8B1 PE=1 SV=3
TM63A_HUMAN	Transmembrane protein 63A OS=Homo sapiens GN=TMEM63A PE=2 SV=3
SERC1_HUMAN	Serine incorporator 1 OS=Homo sapiens GN=SERINC1 PE=1 SV=1
PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2
RAB44_HUMAN	Ras-related protein Rab-44 OS=Homo sapiens GN=RAB44 PE=3 SV=3
ITCH_HUMAN	E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens GN=ITCH PE=1 SV=2
MYO1B_HUMAN	Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3
K2C7_HUMAN	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5
DDAH1_HUMAN	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3
FUCM_HUMAN	Fucose mutarotase OS=Homo sapiens GN=FUOM PE=1 SV=2
YES_HUMAN	Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=1 SV=3
UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3
RHOA_HUMAN	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1
ABCB6_HUMAN	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1
MGRN1_HUMAN	E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 PE=1 SV=2
NCKP1_HUMAN	Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1
UBR2_HUMAN	E3 ubiquitin-protein ligase UBR2 OS=Homo sapiens GN=UBR2 PE=1 SV=1
AP1B1_HUMAN	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2
RALB_HUMAN	Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1
VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4
TNAP3_HUMAN	Tumor necrosis factor alpha-induced protein 3 OS=Homo sapiens GN=TNFAIP3 PE=1 SV=1
CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1
PTHB1_HUMAN	Protein PTHB1 OS=Homo sapiens GN=BBS9 PE=1 SV=1
SARG_HUMAN	Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2
VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2
SPTN2_HUMAN	Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3
K1609_HUMAN	TLD domain-containing protein KIAA1609 OS=Homo sapiens GN=KIAA1609 PE=1 SV=2
EPM2A_HUMAN	Laforin OS=Homo sapiens GN=EPM2A PE=1 SV=2
SRP54_HUMAN	Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1
SYCC_HUMAN	Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=3
RNF14_HUMAN	E3 ubiquitin-protein ligase RNF14 OS=Homo sapiens GN=RNF14 PE=1 SV=1
MPP10_HUMAN	U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=1 SV=2
UBP30_HUMAN	Ubiquitin carboxyl-terminal hydrolase 30 OS=Homo sapiens GN=USP30 PE=1 SV=1
SMAG2_HUMAN	Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1
AIMP1_HUMAN	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2
NRAP_HUMAN	Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2
SPRE_HUMAN	Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1
ABHEB_HUMAN	Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1
ZBT32_HUMAN	Zinc finger and BTB domain-containing protein 32 OS=Homo sapiens GN=ZBTB32 PE=1 SV=1
CD151_HUMAN	CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3
TSN11_HUMAN	Tetraspanin-11 OS=Homo sapiens GN=TSPAN11 PE=2 SV=2
FILA_HUMAN	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3
CRLD2_HUMAN	Cysteine-rich secretory protein LCCL domain-containing 2 OS=Homo sapiens GN=CRISPLD2 PE=1 SV=1
TR49C_HUMAN	Tripartite motif-containing protein 49C OS=Homo sapiens GN=TRIM49C PE=2 SV=1
FA73B_HUMAN	Protein FAM73B OS=Homo sapiens GN=FAM73B PE=1 SV=1
TMED2_HUMAN	Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=1 SV=1
BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2
UNC80_HUMAN	Protein unc-80 homolog OS=Homo sapiens GN=UNC80 PE=2 SV=2
FAT2_HUMAN	Protocadherin Fat 2 OS=Homo sapiens GN=FAT2 PE=1 SV=2
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2
WNT3A_HUMAN	Protein Wnt-3a OS=Homo sapiens GN=WNT3A PE=1 SV=2
CS018_HUMAN	Uncharacterized protein C19orf18 OS=Homo sapiens GN=C19orf18 PE=2 SV=1
ANXA3_HUMAN	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3
FA43A_HUMAN	Protein FAM43A OS=Homo sapiens GN=FAM43A PE=2 SV=2
AT2B3_HUMAN	Plasma membrane calcium-transporting ATPase 3 OS=Homo sapiens GN=ATP2B3 PE=1 SV=3
AT2B4_HUMAN	Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2
BCOR_HUMAN	BCL-6 corepressor OS=Homo sapiens GN=BCOR PE=1 SV=1
TBCB_HUMAN	Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2
SH3R3_HUMAN	SH3 domain-containing RING finger protein 3 OS=Homo sapiens GN=SH3RF3 PE=1 SV=2
PRAX_HUMAN	Periaxin OS=Homo sapiens GN=PRX PE=1 SV=2
INT1_HUMAN	Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2
FA83H_HUMAN	Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3
MTMR6_HUMAN	Myotubularin-related protein 6 OS=Homo sapiens GN=MTMR6 PE=1 SV=3
SRCAP_HUMAN	Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3
WDR35_HUMAN	WD repeat-containing protein 35 OS=Homo sapiens GN=WDR35 PE=1 SV=3
DPOD1_HUMAN	DNA polymerase delta catalytic subunit OS=Homo sapiens GN=POLD1 PE=1 SV=2
PM2PB_HUMAN	Putative postmeiotic segregation increased 2-like protein 11 OS=Homo sapiens GN=PMS2P11 PE=5 SV=1

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CC170_HUMAN Coiled-coil domain-containing protein 170 OS=Homo sapiens GN=CCDC170 PE=2 SV=3
CR3L2_HUMAN Cyclic AMP-responsive element-binding protein 3-like protein 2 OS=Homo sapiens GN=CREB3L2 PE=1 SV=3
NUDC2_HUMAN NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1
RPC3_HUMAN  DNA-directed RNA polymerase III subunit RPC3 OS=Homo sapiens GN=POLR3C PE=1 SV=1
UBP24_HUMAN Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3
5NT3B_HUMAN 7-methylguanosine phosphate-specific 5'-nucleotidase OS=Homo sapiens GN=NT5C3B PE=1 SV=4
OR4A5_HUMAN Olfactory receptor 4A5 OS=Homo sapiens GN=OR4A5 PE=2 SV=4
GPRL1_HUMAN GLIPR1-like protein 1 OS=Homo sapiens GN=GLIPR1L1 PE=1 SV=2
BRD7_HUMAN  Bromodomain-containing protein 7 OS=Homo sapiens GN=BRD7 PE=1 SV=1
VKGC_HUMAN  Vitamin K-dependent gamma-carboxylase OS=Homo sapiens GN=GGCX PE=1 SV=2
H1BP3_HUMAN HCLS1-binding protein 3 OS=Homo sapiens GN=HS1BP3 PE=1 SV=1
MIPEP_HUMAN Mitochondrial intermediate peptidase OS=Homo sapiens GN=MIPEP PE=1 SV=2
MDR3_HUMAN  Multidrug resistance protein 3 OS=Homo sapiens GN=ABCB4 PE=1 SV=2
F151A_HUMAN Protein FAM151A OS=Homo sapiens GN=FAM151A PE=2 SV=2
QSOX1_HUMAN Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3
CTR4_HUMAN  Cationic amino acid transporter 4 OS=Homo sapiens GN=SLC7A4 PE=2 SV=3
AP4A_HUMAN  Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] OS=Homo sapiens GN=NUDT2 PE=1 SV=3
AT2B2_HUMAN Plasma membrane calcium-transporting ATPase 2 OS=Homo sapiens GN=ATP2B2 PE=1 SV=2
KANK1_HUMAN KN motif and ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=KANK1 PE=1 SV=3
RHG35_HUMAN Rho GTPase-activating protein 35 OS=Homo sapiens GN=ARHGAP35 PE=1 SV=3
RUFY3_HUMAN Protein RUFY3 OS=Homo sapiens GN=RUFY3 PE=1 SV=1
STK4_HUMAN  Serine/threonine-protein kinase 4 OS=Homo sapiens GN=STK4 PE=1 SV=2
CCD41_HUMAN Coiled-coil domain-containing protein 41 OS=Homo sapiens GN=CCDC41 PE=2 SV=2
TXLNB_HUMAN Beta-taxilin OS=Homo sapiens GN=TXLNB PE=1 SV=3
DYST_HUMAN  Dystonin OS=Homo sapiens GN=DST PE=1 SV=4
F117B_HUMAN Protein FAM117B OS=Homo sapiens GN=FAM117B PE=1 SV=2
MA1B1_HUMAN Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens GN=MAN1B1 PE=1 SV=2
TRY3_HUMAN  Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2
WDR67_HUMAN WD repeat-containing protein 67 OS=Homo sapiens GN=WDR67 PE=2 SV=2
INP4B_HUMAN Type II inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4
M3K9_HUMAN  Mitogen-activated protein kinase kinase kinase 9 OS=Homo sapiens GN=MAP3K9 PE=1 SV=3
PD2R2_HUMAN Prostaglandin D2 receptor 2 OS=Homo sapiens GN=PTGDR2 PE=1 SV=3
K1671_HUMAN Uncharacterized protein KIAA1671 OS=Homo sapiens GN=KIAA1671 PE=1 SV=2
DPYD_HUMAN  Dihydropyrimidine dehydrogenase [NADP(+)] OS=Homo sapiens GN=DPYD PE=1 SV=2
PADI6_HUMAN Protein-arginine deiminase type-6 OS=Homo sapiens GN=PADI6 PE=1 SV=3
RRP36_HUMAN Ribosomal RNA processing protein 36 homolog OS=Homo sapiens GN=RRP36 PE=1 SV=1
UBP54_HUMAN Inactive ubiquitin carboxyl-terminal hydrolase 54 OS=Homo sapiens GN=USP54 PE=1 SV=4
NEBL_HUMAN  Nebulette OS=Homo sapiens GN=NEBL PE=1 SV=1
TIM21_HUMAN Mitochondrial import inner membrane translocase subunit Tim21 OS=Homo sapiens GN=TIMM21 PE=1 SV=1
LINES_HUMAN Protein Lines homolog OS=Homo sapiens GN=LINS PE=2 SV=2
POP1_HUMAN  Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2
PEG3_HUMAN  Paternally-expressed gene 3 protein OS=Homo sapiens GN=PEG3 PE=1 SV=1
DJB14_HUMAN DnaJ homolog subfamily B member 14 OS=Homo sapiens GN=DNAJB14 PE=2 SV=1
PITM2_HUMAN Membrane-associated phosphatidylinositol transfer protein 2 OS=Homo sapiens GN=PITPNM2 PE=1 SV=1
CMBL_HUMAN  Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1
KDM2A_HUMAN Lysine-specific demethylase 2A OS=Homo sapiens GN=KDM2A PE=1 SV=3
ZCHC4_HUMAN Zinc finger CCHC domain-containing protein 4 OS=Homo sapiens GN=ZCCHC4 PE=1 SV=3
EXD2_HUMAN  Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2
TILB_HUMAN  Protein TILB homolog OS=Homo sapiens GN=LRRC6 PE=1 SV=3
I22R1_HUMAN Interleukin-22 receptor subunit alpha-1 OS=Homo sapiens GN=IL22RA1 PE=1 SV=1
ANKH1_HUMAN Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1
LRC45_HUMAN Leucine-rich repeat-containing protein 45 OS=Homo sapiens GN=LRRC45 PE=2 SV=1
ACOC_HUMAN  Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3
PARI_HUMAN  PCNA-interacting partner OS=Homo sapiens GN=PARPBP PE=1 SV=3
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	Swissprot2013	Decoy	False discovery rate
Peptide matches above identity threshold	2017	132	6.54 %
Peptide matches above homology or identity threshold	2030	145	7.14 %

Select Summary Report

Format As	Select Summary (protein hits)		Help
	Significance threshold p< 0.05	Max. number of hits AUTO	
	Standard scoring ○ MudPIT scoring ●	Ions score or expect cut-off 0	Show sub-sets 0
	Show pop-ups ● Suppress pop-ups ○	Sort unassigned Decreasing Score	Require bold red ☐

1. AMPN_HUMAN **Mass:** 109870 **Score:** 5650 **Queries matched:** 129 **emPAI:** 2.88

Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
413	443.76	885.51	885.50	3.45	0	70	1e-006	1	K.IQTQLQR.D 399 400 401 402 403 404 405 407 408 409 410 411 412
480	451.25	900.49	900.49	2.31	0	73	3.2e-007	1	R.ALEQALEK.T
551	455.72	909.43	909.43	1.16	0	39	0.00066	1	R.SEVYGPMK.N
575	457.26	912.51	912.51	1.53	1	27	0.014	1	M.AKGFYISK.S 573
614	463.72	925.42	925.42	-3.92	0	(5)	0.95	1	R.SEVYGPMK.N
711	472.28	942.54	942.53	8.47	0	32	0.0041	1	K.ELWILNR.Y 710
753	479.28	956.55	956.54	5.81	0	63	4.9e-006	1	K.QASNGVLIR.I 751
1066	507.80	1013.59	1013.59	1.99	0	30	0.0091	1	R.SIQLPTTVR.D
1067	507.81	1013.60	1013.60	1.16	1	53	1.6e-005	1	R.KIQTQLQR.D
1453	542.74	1083.47	1083.47	1.53	0	(58)	4.7e-006	1	R.SEYMEGNVR.K 1450 1452 1454
1530	550.74	1099.46	1099.46	-0.76	0	65	4.1e-007	1	R.SEYMEGNVR.K 1529 1531 1532 1533 1534
1646	561.31	1120.61	1120.60	6.06	0	62	5.2e-006	1	R.DHSAIPVINR.A 1645
1693	565.82	1129.63	1129.63	-0.97	1	68	9.2e-007	1	R.ALEQALEKTK.A
1950	585.29	1168.57	1168.57	-0.27	0	49	0.0001	1	R.GVGGSQPPDIDK.T 1946 1947 1948 1951
2103	601.83	1201.64	1201.64	-0.27	0	(74)	3.7e-007	1	K.DLTALSNMLPK.G 2104
2153	606.79	1211.57	1211.56	5.71	1	(38)	0.00086	1	R.SEYMEGNVRK.V 2152
2187	609.83	1217.64	1217.63	2.90	0	76	2.9e-007	1	K.DLTALSNMLPK.G 2186 2188
2212	612.77	1223.52	1223.52	1.03	0	69	3.3e-007	1	R.VNYDEENWR.K 2213
2225	613.35	1224.68	1224.67	3.77	0	72	2.8e-007	1	K.EATDVIIIHSK.K 2223 2224
2234	614.78	1227.56	1227.56	-0.07	1	38	0.00055	1	R.SEYMEGNVRK.V 2233 2235 2236
2299	619.32	1236.62	1236.62	2.20	0	(26)	0.022	1	K.DLMVLNDVYR.V
2389	627.31	1252.61	1252.61	0.58	0	60	1e-005	1	K.DLMVLNDVYR.V
2467	635.27	1268.53	1268.53	-1.43	0	103	8.6e-011	1	K.DNEETGFGSGTR.A 2460 2461 2462 2463 2464 2465 2466 2468 2469 2470 2471 2472 2473
2690	657.36	1312.71	1312.71	-1.29	1	52	4.2e-005	1	R.GLYVFKGSSTVR.F 2691
2750	664.79	1327.56	1327.56	1.67	0	65	5.2e-007	1	K.SFPCFDEPAMK.A
2823	672.79	1343.56	1343.55	6.16	0	(45)	4e-005	1	K.SFPCFDEPAMK.A 2822
2870	676.81	1351.61	1351.62	-1.68	1	65	1.6e-006	1	R.VNYDEENWRK.I
2919	681.34	1360.68	1360.68	-1.20	0	132	5.9e-013	1	K.VVATTQMQAADAR.K 2908 2909 2910 2911 2912 2913 2914 2915 2916 2917 2918 2920 2921 2922 2923 2924 2925 2926 2927
2988	689.34	1376.67	1376.67	0.91	0	(129)	8.3e-013	1	K.VVATTQMQAADAR.K 2979 2980 2981 2982 2983 2985 2986 2987 2989 2990 2991
3211	722.90	1443.79	1443.78	2.38	0	25	0.019	1	R.VTLRPYLTPNDR.G
3246	728.83	1455.65	1455.65	-2.32	1	74	1.4e-007	1	R.KSFPCFDEPAMK.A
3279	732.37	1462.73	1462.72	6.82	0	73	4.5e-007	1	R.QQQDYWLIDVR.A 3278
3300	734.40	1466.78	1466.78	-0.88	0	61	4.4e-006	1	R.YLSYTLNPDLIR.K
3360	745.39	1488.77	1488.77	-1.74	1	(98)	1.5e-009	1	R.KVVATTQMQAADAR.K 3361 3363
3416	753.39	1504.76	1504.77	-5.73	1	116	1.9e-011	1	R.KVVATTQMQAADAR.K 3417 3418 3419
4090	862.92	1723.83	1723.83	2.31	0	83	3.5e-008	1	R.ENSLLFDPLSSSSSNK.E
4619	663.98	1988.93	1988.93	0.16	0	27	0.011	1	K.QWMENPNNNPIHPNLR.S
4666	1005.49	2008.97	2008.97	-0.88	1	95	2.2e-009	1	R.ENSLLFDPLSSSSSNKER.V 4668

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2. DPP4_HUMAN **Mass:** 88907 **Score:** 3597 **Queries matched:** 98 **emPAI:** 2.40

Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
44	405.70	809.38	809.37	2.50	0	44	0.00018	1	K.MGFVDNK.R
49	406.18	810.35	810.35	0.23	0	73	1.5e-007	1	R.GSGYQGDK.I 48 50 51 52 53
130	413.69	825.37	825.37	-1.68	0	(34)	0.0014	1	K.MGFVDNK.R
266	427.74	853.46	853.46	2.49	0	39	0.0007	1	K.IMHAINR.R
274	428.75	855.48	855.48	-1.78	0	69	6e-007	1	K.AGAVNPTVK.F 269 270 271 272 273 275 276 277 278 279
389	442.72	883.42	883.41	7.48	0	51	5.9e-005	1	K.DCTFITK.G 387 388
421	444.75	887.48	887.47	5.37	0	47	0.00031	1	R.QLITEER.I 420
581	458.28	914.54	914.53	4.63	0	45	0.00024	1	R.ISLQWLR.R
588	459.74	917.46	917.45	6.24	0	38	0.0015	1	R.WNCLVAR.Q 587
767	480.29	958.56	958.56	1.82	1	47	0.00012	1	K.TVRVPYPK.A

804	483.75	965.48	965.48	0.92	1	(48)	0.00015	1	K.MGFVDNKR.I 807
813	484.26	966.50	966.50	0.92	0	48	9.3e-005	1	K.IQLSDYTK.V 812 814
886	491.74	981.47	981.47	0.42	1	51	5.4e-005	1	K.MGFVDNKR.I
1026	504.71	1007.41	1007.42	-0.93	0	94	9.5e-010	1	K.GTDDATADSR.K 1023 1024 1025 1027 1028 1029 1030 1031 1032 1033
1130	515.28	1028.55	1028.54	7.93	0	65	3.1e-006	1	K.CGIAVAPVSR.W 1129
1427	540.77	1079.52	1079.52	-0.52	0	69	9.1e-007	1	K.IISNEEGYR.H 1429
1479	544.79	1087.57	1087.57	0.07	0	42	0.00066	1	K.IEPNLPSYR.I 1478 1480
1553	552.28	1102.55	1102.55	3.91	0	82	6.4e-008	1	R.VLEDNSALDK.M 1548 1549 1550 1551 1552 1554
1979	588.30	1174.58	1174.58	-1.87	0	(72)	5e-007	1	K.MLQNVQMPSK.K
2041	596.30	1190.58	1190.58	-2.50	0	73	3.5e-007	1	K.MLQNVQMPSK.K 2043 2044 2048 2049 2050 2054
2053	596.30	1190.58	1190.58	1.91	0	(65)	2.3e-006	1	K.MLQNVQMPSK.K 2045 2046 2047 2051 2052 2055
2123	604.29	1206.57	1206.57	-0.88	0	(62)	4e-006	1	K.MLQNVQMPSK.K 2118 2119 2120 2121 2122 2124 2125 2126
2459	634.79	1267.56	1267.55	8.17	0	60	4.2e-006	1	R.CQYYSVSFSK.E 2458
2878	677.33	1352.64	1352.64	-1.60	0	5	2.2	1	R.WISDHEYLYK.Q
3326	739.35	1476.68	1476.67	8.22	0	76	1.5e-007	1	K.VTCLSCELNPER.C 3324 3325
3389	749.39	1496.77	1496.77	1.79	0	47	0.00015	1	K.LAYVWNNDIYVK.I
3433	755.83	1509.64	1509.64	2.27	0	72	1.4e-007	1	R.WEYYDSVYTER.Y
3643	789.39	1576.77	1576.77	-1.70	0	104	3.1e-010	1	R.LGTFEVEDQIEAAR.Q 3644
4107	578.63	1732.88	1732.87	2.97	1	30	0.007	1	R.RLGTFEVEDQIEAAR.Q
4510	648.99	1943.94	1943.94	0.88	0	25	0.017	1	R.CSGPGLPLYTLHSSVNDK.G
4925	759.38	2275.12	2275.12	1.75	1	(36)	0.0015	1	R.VLEDNSALDKMLQNVQMPSK.K
4932	764.71	2291.12	2291.11	2.49	1	49	7.5e-005	1	R.VLEDNSALDKMLQNVQMPSK.K

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3. NEP_HUMAN **Mass:** 86144 **Score:** 1683 **Queries matched:** 58 **emPAI:** 2.12

Neprilysin OS=Homo sapiens GN=MME PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
6	400.75	799.49	799.49	0.16	1	49	9.3e-005	1	K.ALAIKER.I
72	406.78	811.55	811.55	-0.63	0	28	0.0014	1	K.LKPILTK.Y 73
133	414.73	827.44	827.44	-1.10	0	44	0.00015	1	K.DVLQEPK.T 132 134
222	422.75	843.48	843.48	3.81	0	57	2.9e-005	1	K.AIAQLNSK.Y 219 220 221
743	477.73	953.44	953.44	-4.75	0	17	0.11	1	K.YACGGWLK.R
880	491.72	981.42	981.42	-0.83	0	(39)	0.00036	1	K.NSYMNPEK.K 877 878 879 881 882
965	499.72	997.42	997.42	1.34	0	46	6.6e-005	1	K.NSYMNPEK.K 964 966
989	501.76	1001.51	1001.51	-2.34	0	38	0.0018	1	R.NVIPETSSR.Y 985 986 987 988 990 993 994 995 996
1000	501.78	1001.54	1001.54	2.21	0	59	1.6e-005	1	K.TEDIVAVQK.A 999
1054	506.74	1011.47	1011.47	5.09	0	70	4.8e-007	1	K.YGASWTAEK.A 1053
1120	514.28	1026.55	1026.55	2.72	1	48	9.2e-005	1	R.AYQNYIKK.N
1579	554.28	1106.54	1106.54	1.49	0	50	8.1e-005	1	R.NDPMLLYNK.M
1585	555.77	1109.52	1109.52	4.78	1	52	3.3e-005	1	K.NSYMNPEKK.C 1584
1684	565.27	1128.53	1128.53	-2.61	0	38	0.00071	1	K.TDVHSPGNFR.I 1685
2538	642.83	1283.64	1283.64	0.29	0	84	2.6e-008	1	R.LYVEAAFAGESK.H
2678	656.28	1310.55	1310.55	2.17	0	53	9.7e-006	1	R.DYYECTGIYK.E
3223	725.35	1448.69	1448.68	6.14	0	118	1.2e-011	1	R.IGYPDDIVSNDNK.L 3222
3247	728.86	1455.70	1455.70	1.95	0	75	1.9e-007	1	K.ALYGTTSETATWR.R
3802	814.42	1626.83	1626.83	0.26	0	97	1.4e-009	1	R.LPIDENQLALEMNK.V
3851	822.42	1642.83	1642.82	2.68	0	(87)	1.6e-008	1	R.LPIDENQLALEMNK.V
3913	834.86	1667.71	1667.71	-4.95	0	108	2.9e-011	1	R.CANYVNGNMENAVGR.L 3915
3944	842.86	1683.71	1683.71	-1.45	0	(95)	5.3e-010	1	R.CANYVNGNMENAVGR.L 3943
4299	902.44	1802.86	1802.87	-7.56	0	95	2.2e-009	1	K.SESQMDITDINTPKPK.K 4300
4617	663.67	1987.99	1987.99	2.33	1	(43)	0.00029	1	M.GKSESQMDITDINTPKPK.K
4654	669.00	2003.98	2003.98	-0.12	1	51	4.5e-005	1	M.GKSESQMDITDINTPKPK.K
4748	1023.96	2045.91	2045.91	2.15	0	35	0.00078	1	R.LIQNMDATTEPCTDFFK.Y
4856	724.04	2169.09	2169.07	5.85	1	(7)	1.3	1	R.QEERLPIDENQLALEMNK.V
4864	729.36	2185.07	2185.07	-1.37	1	23	0.026	1	R.QEERLPIDENQLALEMNK.V

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4. K1C9_HUMAN **Mass:** 62255 **Score:** 1606 **Queries matched:** 32 **emPAI:** 0.89

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	Peptide
464	449.21	896.41	896.41	-0.79	0	53	2.1e-005	1	R.MTLDDFR.I
884	491.72	981.43	981.43	0.72	0	86	7.7e-009	1	R.FSSSGGGGGGGR.F 883 885
1334	530.79	1059.56	1059.56	1.36	0	26	0.028	1	K.TLLDIDNTR.M
1362	533.25	1064.49	1064.49	-2.86	0	(73)	2.8e-007	1	K.STMQELNSR.L 1361 1363 1364 1365 1366 1367 1368
1436	541.25	1080.49	1080.49	-0.38	0	74	1.7e-007	1	K.STMQELNSR.L 1437 1438
1644	561.30	1120.58	1120.58	6.74	0	23	0.046	1	R.QEYEQLIAK.N
1880	579.30	1156.59	1156.58	6.81	0	61	5.9e-006	1	R.QGVDADINGLR.Q 1878 1879
2114	603.81	1205.60	1205.60	6.57	0	28	0.019	1	R.QVLDNLTMEK.S
2263	616.80	1231.59	1231.59	-2.49	0	105	2.3e-010	1	R.SGGGGGGGLGSGGSIR.S 2262 2264 2265
2280	618.27	1234.52	1234.52	-0.89	0	82	1.1e-008	1	R.FSSSSGYGGGSSR.V 2278 2279 2281 2282
4275	896.37	1790.72	1790.72	2.01	0	139	1.4e-014	1	R.GGSGGSYGGGGSGGGYGGGSGSR.G 4276

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5. K22E_HUMAN **Mass:** 65678 **Score:** 1404 **Queries matched:** 27 **emPAI:** 0.47

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	Peptide
159	416.25	830.48	830.49	-8.23	0	20	0.092	2	R.SLVGLGGTK.S
1204	521.28	1040.55	1040.55	-0.77	0	42	0.00029	1	K.VDPEIQNVK.A 1199 1200 1201 1202 1203 1205 1206
1376	533.76	1065.51	1065.51	1.11	1	14	0.33	4	K.YEDEINKR.T
1576	554.27	1106.53	1106.54	-1.53	0	51	7.1e-005	1	K.AQYEEIAQR.S 1575 1577 1578
2076	599.28	1196.54	1196.54	0.31	0	98	7.3e-010	1	K.GGSISGGGYGSGGGK.H 2075
2396	627.81	1253.60	1253.60	-0.67	0	90	6.5e-009	1	R.GFSSGSAVVSGGSR.R 2395 2397 2399 2400
3691	794.85	1587.68	1587.68	0.60	0	132	1.2e-013	1	R.GGSSSGGGYGSGGGGSSSVK.G 3692
4117	870.86	1739.70	1739.70	0.36	0	156	2.8e-016	1	R.GSSSGGGYSSGSSSYGSGGR.Q 4121
4139	871.38	1740.74	1740.74	-0.09	0	161	1.3e-016	1	R.GGSGGGGSISGGGYGSGGGSGGR.Y 4138

---

6. GAPR1_HUMAN **Mass:** 17322 **Score:** 1292 **Queries matched:** 26 **emPAI:** 1.24

Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2	400.19	798.37	798.36	5.91	0	25	0.013	1	K.HSPESSR.G 1
126	413.21	824.40	824.41	-6.36	0	11	0.34	2	R.WYSEIK.N 125 127 129
2381	627.31	1252.60	1252.60	-1.71	0	116	2.3e-011	1	K.ASASDGSSFVVAR.Y 2382 2384 2385 2386 2387 2388 2390
3239	727.35	1452.69	1452.68	4.44	0	103	3.5e-010	1	R.EAQQYSEALASTR.I 3229 3230 3231 3232 3233 3234 3236 3237 3238 3240
4439	942.92	1883.82	1883.81	2.89	0	63	1.1e-006	1	R.GQCGENLAWASYDQTGK.E

---

7. K2C1_HUMAN **Mass:** 66170 **Score:** 1243 **Queries matched:** 34 **emPAI:** 0.93

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	Peptide
18	401.73	801.44	801.43	2.65	1	26	0.044	1	R.EREQIK.S
353	437.75	873.49	873.49	0.63	0	46	0.00031	1	R.SLVNLGGSK.S
973	500.23	998.44	998.44	6.73	0	63	1.9e-006	1	K.DVDGAYMTK.V 968 969 970 972
1070	508.22	1014.43	1014.43	1.76	0	(30)	0.0018	1	K.DVDGAYMTK.V 1069
1152	517.26	1032.51	1032.51	1.33	0	54	4.2e-005	1	R.TLLEGEESR.M
1369	533.26	1064.51	1064.51	-2.33	0	60	7e-006	1	K.AQYEDIAQK.S 1370 1371 1372 1373 1374
1376	533.76	1065.51	1065.51	1.11	1	14	0.33	4	K.YEDEINKR.T
1498	546.75	1091.50	1091.50	-0.34	0	97	1.1e-009	1	R.GSGGGSSGGSIGGR.G 1499 1500
1658	563.28	1124.54	1124.53	0.61	0	76	1.5e-007	1	K.AEAESLYQSK.Y 1656 1657 1659
1874	579.26	1156.50	1156.51	-7.04	0	6	0.73	1	R.DYQELMNTK.L
1999	590.31	1178.60	1178.59	3.62	0	53	4.3e-005	1	K.YEELQITAGR.H
2774	666.76	1331.51	1331.51	-0.83	0	60	1e-006	1	K.NMQDMVEDYR.N 2773 2775 2776 2777
5008	1192.48	2382.95	2382.94	1.24	0	82	5.8e-009	1	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G 5007 5010

```
8.   TMPS2_HUMAN      Mass: 55079     Score: 1170    Queries matched: 23    emPAI: 0.48
     Transmembrane protease serine 2 OS=Homo sapiens GN=TMPRSS2 PE=1 SV=3
    Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      653    466.76    931.50    931.50  -1.47    0    72   6.7e-007    1   K.TSEVLNAAK.V 650 651 652 654 655 656 657 658
      820    486.30    970.59    970.58   6.26    0    57   1.5e-005    1   K.VLLIETQR.C 819
     1098    512.24   1022.47   1022.47   0.04    0    75   1.6e-007    1   K.SPSGTVCTSK.T 1099
     1938    584.26   1166.50   1166.50  -0.06    0    47     5e-005    1   K.LYHSDACSSK.A
     3845    821.44   1640.86   1640.86   2.28    0   119   7.2e-012    1   R.VLTQASNPVVCTQPK.S 3837 3839 3840 3841 3842 3843 3846 3847
```

```
9.   BASP1_HUMAN      Mass: 22680     Score: 1038    Queries matched: 31    emPAI: 3.76
     Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2
    Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      680    469.71    937.41    937.41  -0.14    0    52   2.1e-005    1   K.GYNVNDEK.A 678 681 683 684
     1376    533.76   1065.51   1065.51   1.09    1    46    0.00023    1   K.KGYNVNDEK.A
     2535    642.82   1283.64   1283.64  -0.47    0     9       0.74    1   K.TEAPAAPAAQETK.S
     2572    645.30   1288.58   1288.58   0.16    0   109   4.1e-011    1   K.AEGAATEEEGTPK.E 2573 2574
     3023    693.84   1385.67   1385.67  -0.94    0    73   2.7e-007    1   K.ETPAATEAPSSTPK.A 3022 3024 3025
     3159    714.34   1426.66   1426.66   0.78    0    69   5.3e-007    1   K.ESEPQAAAEPAEAK.E 3153 3154 3155 3156 3157 3158 3160
     4239    888.43   1774.85   1774.85  -1.35    0    49   7.8e-005    1   K.APEQEQAAPGPAAGGEAPK.A
     4495    966.94   1931.87   1931.87  -0.76    0    77   9.8e-008    1   K.SDGAPASDSKPGSSEAAPSSK.E 4494 4496
     4937    766.72   2297.14   2297.13   5.58    1    38    0.00083    1   K.AEPPKAPEQEQAAPGPAAGGEAPK.A 4935 4936
     5164    879.42   2635.23   2635.22   2.68    1    25       0.01    1   K.AAEAAAAPAESAAPAAGEEPSKEEGEPK.K 5165
```

```
10.  ASM3B_HUMAN      Mass: 51237     Score: 1032    Queries matched: 22    emPAI: 0.23
     Acid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens GN=SMPDL3B PE=2 SV=2
    Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       54    406.22    810.43    810.43  -6.26    0    71     5e-007    1   K.LPGPSGAGR.I 55 56 57 58 59 60 61 62 63 64 65 66 67
     1472    544.79   1087.56   1087.56  -5.00    0   101   7.9e-010    1   R.IAGDQSTLQR.Y 1473 1474 1475 1476 1477
     3712    797.44   1592.86   1592.86  -1.73    0    96   1.1e-009    1   K.TTLPGVVNGANNPAIR.V 3713
```

```
11.  IFM1_HUMAN      Mass: 14126     Score: 1008    Queries matched: 11    emPAI: 0.63
     Interferon-induced transmembrane protein 1 OS=Homo sapiens GN=IFITM1 PE=1 SV=3
    Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
     3632    785.38   1568.75   1568.75   0.24    0  (151)  5.3e-015    1   K.MVGDVTGAQAYASTAK.C 3629 3631 3633 3634 3635 3636
     3675    793.38   1584.74   1584.75  -1.03    0   154   1.8e-015    1   K.MVGDVTGAQAYASTAK.C 3671 3676 3677


     Proteins matching the same set of peptides:
     IFM2_HUMAN      Mass: 14794     Score: 1008    Queries matched: 11
     Interferon-induced transmembrane protein 2 OS=Homo sapiens GN=IFITM2 PE=1 SV=2
     IFM3_HUMAN      Mass: 14794     Score: 1008    Queries matched: 11
     Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=1 SV=2
```

```
12.  RAB3B_HUMAN      Mass: 24970     Score: 960     Queries matched: 16    emPAI: 1.34
     Ras-related protein Rab-3B OS=Homo sapiens GN=RAB3B PE=1 SV=2
    Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      816    484.68    967.34    967.34  -0.70    0   (46)  2.4e-005    1   K.CDMEEER.V 817
      897    492.67    983.33    983.33   0.44    0    61   7.6e-007    1   K.CDMEEER.V
     1538    550.84   1099.66   1099.66   3.69    0    68   5.1e-007    1   K.LLIIGNSSVGK.T 1537
     2701    658.83   1315.65   1315.65   1.50    0    74   3.2e-007    1   K.LQIWDTAGQER.Y
     3919    835.87   1669.72   1669.72   2.12    0   (99)  2.6e-010    1   K.MSDSLDTDPSMLGSSK.N
     3959    843.86   1685.72   1685.71   1.64    0   126   4.5e-013    1   K.MSDSLDTDPSMLGSSK.N 3954 3955 3956 3957 3958 3960 3961 3962
```

```
13.  ADAM9_HUMAN      Mass: 93006     Score: 944     Queries matched: 18    emPAI: 0.17
```

Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1275	526.23	1050.45	1050.46	-7.84	0	69	3.4e-007	1	K.CATGNALCGK.L 1277 1278 1279 1280 1281
2227	613.77	1225.52	1225.52	0.68	0	(41)	0.00016	1	K.SCIMNSGASGSR.N 2226
2319	621.76	1241.51	1241.51	1.02	0	62	8.4e-007	1	K.SCIMNSGASGSR.N 2318
3569	775.82	1549.63	1549.64	-5.66	0	98	1.4e-010	1	K.LVDAGEECDCGTPK.E 3568 3570 3571 3572 3573 3574 3575

---

14. TRFL_HUMAN **Mass:** 80014 **Score:** 927 **Queries matched:** 30 **emPAI:** 1.16

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
155	415.70	829.39	829.39	-0.99	0	35	0.0011	1	K.SCHTGLR.R
261	426.71	851.42	851.41	1.65	0	57	1.4e-005	1	K.DSAIGFSR.V
285	429.23	856.44	856.45	-4.15	0	21	0.055	1	R.GPPVSCIK.R 284 286
435	445.71	889.41	889.41	0.14	0	47	0.00014	1	K.SEEEVAAR.R 436
668	468.27	934.54	934.53	0.23	0	59	4.6e-006	1	R.VPSHAVVAR.S
726	475.22	948.43	948.43	0.49	0	52	4.1e-005	1	R.LCAGTGENK.C 725
844	488.22	974.43	974.42	1.15	0	38	0.00028	1	K.CVPNSNER.Y 845 846
1082	509.76	1017.51	1017.51	-0.28	1	52	6.5e-005	1	R.KSEEEVAAR.R
1089	510.76	1019.50	1019.50	0.32	0	89	1.5e-008	1	R.DGAGDVAFIR.E 1090
1358	532.82	1063.62	1063.61	1.54	0	14	0.1	1	K.QVLLHQQAK.F
1830	575.82	1149.62	1149.62	3.42	0	40	0.00068	1	R.THYYAVAVVK.K 1829
2298	619.31	1236.61	1236.60	6.49	0	65	2.6e-006	1	R.SDTSLTWNSVK.G
2933	681.86	1361.71	1361.70	6.96	0	68	1.4e-006	1	K.CGLVPVLAENYK.S 2932
3043	697.35	1392.68	1392.67	5.88	0	102	5.6e-010	1	R.CLAENAGDVAFVK.D
3214	723.36	1444.71	1444.71	-3.59	0	63	3.9e-006	1	R.VVWCAVGEQELR.K
3649	790.38	1578.74	1578.75	-2.29	0	82	4e-008	1	K.NLLFNDNTECLAR.L
3706	795.89	1589.76	1589.75	8.78	0	62	4.6e-006	1	R.SVQWCAVSQPEATK.C 3705
3773	807.90	1613.79	1613.78	1.47	0	45	0.00021	1	R.DSPIQCIQAIAENR.A
4311	904.40	1806.78	1806.79	-3.81	0	0	3.2	2	R.SNLCALCIGDEQGENK.C
4405	931.89	1861.76	1861.76	0.68	0	94	4.4e-010	1	K.FDEYFSQSCAPGSDPR.S

---

15. IDHC_HUMAN **Mass:** 46915 **Score:** 852 **Queries matched:** 23 **emPAI:** 0.85

Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
182	419.21	836.40	836.40	-2.06	0	32	0.005	1	K.SQFEAQK.I 181 183
932	496.24	990.46	990.46	0.02	0	42	0.00035	1	R.DATNDQVTK.D 931
1466	544.29	1086.57	1086.57	0.59	0	42	0.0007	1	R.ATDFVVPGPGK.V
2276	617.81	1233.61	1233.61	-1.68	0	77	1.8e-007	1	R.LIDDMVAQAMK.S
3193	719.86	1437.70	1437.70	1.84	0	68	1.3e-006	1	K.VEITYTPSDGTQK.V 3194 3195
3983	848.39	1694.76	1694.76	1.43	0	(92)	2.4e-009	1	K.ISGGSVVEMQGDEMTR.I
4037	856.38	1710.75	1710.76	-3.68	0	(103)	1.5e-010	1	K.ISGGSVVEMQGDEMTR.I 4036 4038 4041 4044
4042	856.39	1710.76	1710.76	3.53	0	120	4.1e-012	1	K.ISGGSVVEMQGDEMTR.I 4039 4040 4043 4045
4092	864.38	1726.74	1726.75	-7.56	0	(17)	0.04	1	K.ISGGSVVEMQGDEMTR.I 4093

---

16. CA2D1_HUMAN **Mass:** 125630 **Score:** 778 **Queries matched:** 27 **emPAI:** 0.26

Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Homo sapiens GN=CACNA2D1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
793	483.21	964.41	964.42	-3.35	0	17	0.046	1	K.MIDGESGEK.T 788 790 791 792 795 796
799	483.69	965.37	965.37	0.02	0	50	9.9e-006	1	K.GTCPCDTR.L 800 801
1333	530.78	1059.55	1059.56	-1.85	0	47	0.00026	1	K.LEETITQAR.Y
1357	532.79	1063.57	1063.57	0.82	0	64	3.7e-006	1	R.FVVTDGGITR.V
3009	691.83	1381.65	1381.65	-4.68	0	58	7.9e-006	1	K.SGPGAYESGIMVSK.A
3673	793.38	1584.74	1584.73	3.46	0	105	1.2e-010	1	K.TPNNPSCNADLINR.V 3667 3668 3669 3670 3671 3672 3674
3924	836.37	1670.72	1670.72	-1.41	0	75	4.9e-008	1	K.SYDYQSVCEPGAAPK.Q 3920 3921 3923 3925
4782	1058.51	2115.00	2115.00	0.24	0	33	0.0021	1	R.LLIQAEQTSDGPNPCDMVK.Q

```
17.   CD177_HUMAN     Mass:  47929     Score:  743     Queries matched:  22     emPAI:  1.28
      CD177 antigen OS=Homo sapiens GN=CD177 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss  Score    Expect  Rank  Peptide
       438    446.26    890.50    890.50   3.72     0     41   0.00053     1  R.QIGIFSAR.E
       594    460.75    919.49    919.49   1.42     0     67  1.8e-006     1  R.GGGIFSNLR.V
       722    474.72    947.43    947.43   1.32     0     29    0.0055     1  K.DFLTCHR.G
      2039    595.34   1188.67   1188.67  -2.18     1     19     0.045     1  R.LRGGGIFSNLR.V
      2289    618.79   1235.56   1235.56   0.72     0     68  5.9e-007     1  K.GCSTVGAQNSQK.T 2288 2290 2291
      2577    645.79   1289.56   1289.57  -3.61     1     43  8.7e-005     1  K.GCTEAKDQEPR.V 2578 2579
      2592    646.81   1291.60   1291.60  -0.61     0     55  1.9e-005     1  K.GTTHCYDGLLR.L
      4624    996.44   1990.86   1990.87  -1.54     0    103  8.5e-011     1  R.QCPTCVQPLGTCSSGSPR.M 4622 4623 4625 4626 4627 4628 4629 4630
      5074   1235.52   2469.03   2469.04  -0.76     0     89  1.7e-009     1  R.CPVCLSMEGCLEGTTEEICPK.G
```

```
18.   1433Z_HUMAN     Mass:  27899     Score:  743     Queries matched:  20     emPAI:  1.15
      14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss  Score    Expect  Rank  Peptide
        86    408.71    815.41    815.41   0.04     0     56  1.8e-005     1  K.LAEQAER.Y 83 84 85
       428    445.25    888.49    888.49  -0.65     0     46   0.00026     1  R.VVSSIEQK.T 425 426 427 430
       538    454.27    906.53    906.52   8.47     0     37    0.0012     1  R.NLLSVAYK.N
      1735    568.71   1135.40   1135.40   1.72     0     54  3.9e-006     1  R.YDDMAACMK.S 1733 1734
      2508    640.33   1278.65   1278.65   7.01     1     74  2.9e-007     1  R.YLAEVAAGDDKK.G
      2656    652.85   1303.68   1303.68   1.90     0     19      0.12     2  K.FLIPNASQAESK.V
      3567    774.87   1547.72   1547.71   9.12     0    105  1.6e-010     1  K.SVTEQGAELSNEER.N 3563 3564 3565 3566
```

```
19.   S15A2_HUMAN     Mass:  82415     Score:  688     Queries matched:  24     emPAI:  0.30
      Solute carrier family 15 member 2 OS=Homo sapiens GN=SLC15A2 PE=2 SV=2
     Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss  Score    Expect  Rank  Peptide
       470    450.24    898.48    898.48  -1.07     0     40   0.00047     1  K.IEDIPANK.M 467 468 469 471
       868    490.74    979.47    979.48  -2.07     0     77  1.5e-007     1  R.TTNGMTTVR.F 865 866 867 869
       952    498.74    995.47    995.47   0.31     0   (61)  4.3e-006     1  R.TTNGMTTVR.F 951
      2622    649.30   1296.58   1296.57   5.16     0     62  2.4e-006     1  R.EDGNSISSMMVK.D 2621
      2684    657.29   1312.56   1312.56  -5.26     0   (51)  1.3e-005     1  R.EDGNSISSMMVK.D 2682 2683 2685 2686 2687 2688 2689
      2766    665.29   1328.56   1328.56  -2.02     0   (53)  9.3e-006     1  R.EDGNSISSMMVK.D 2767
```

```
20.   PDC6I_HUMAN     Mass:  96590     Score:  672     Queries matched:  25     emPAI:  0.40
      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  Peptide
        82    408.25    814.49    814.49  -1.25     1     44   0.00027     1  K.KQEGLLK.N
       431    445.26    888.51    888.51   4.73     1     22     0.049     1  K.MKDAIIAK.L
       579    458.25    914.48    914.48  -0.46     0     53  3.6e-005     1  K.AVQADGQVK.E 580
       836    487.29    972.57    972.56   7.61     0     36     0.001     1  K.EVFPVLAAK.H 835
      1959    585.33   1168.65   1168.65   3.59     0     52  2.8e-005     1  K.STPVNVPISQK.F 1953 1954 1955 1956 1958
      2657    652.85   1303.69   1303.68   8.00     0     70    7e-007     1  K.TMQGSEVVNVLK.S 2655 2656
      3490    766.86   1531.71   1531.70   3.83     0     85    2e-008     1  R.LLDEEEATDNDLR.A
      4831   1081.48   2160.95   2160.95  -1.35     0    105  7.5e-011     1  K.FIQQTYPSGGEEQAQYCR.A 4829 4830 4833 4834 4835 4836 4837 4838
```

```
21.   AT8A1_HUMAN     Mass:  132597     Score:  661     Queries matched:  17     emPAI:  0.21
      Probable phospholipid-transporting ATPase IA OS=Homo sapiens GN=ATP8A1 PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss  Score    Expect  Rank  Peptide
        69    406.71    811.41    811.41   2.06     0     30    0.0045     1  K.YPELYK.T
      1006    502.73   1003.44   1003.44   0.58     0     58  3.6e-006     1  R.IECESPNR.H 1005
```

1392	535.80	1069.58	1069.58	5.91	0	36	0.0014	1	K.SQDPGAVVLGK.S 1390
1813	574.28	1146.55	1146.55	1.23	0	88	1.4e-008	1	K.TSLADQEEVR.T 1809 1810 1812 1814 1815 1816 1817
2646	651.88	1301.74	1301.73	2.36	0	69	4.7e-007	1	R.TIFINQPQLTK.F
2771	666.35	1330.68	1330.67	2.65	0	87	1.7e-008	1	R.TSNLNEELGQVK.Y
2970	687.36	1372.71	1372.71	-0.77	0	85	2.9e-008	1	K.TLVDEVQELEAK.S 2971

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22. STEA4_HUMAN **Mass:** 52518 **Score:** 659 **Queries matched:** 17 **emPAI:** 0.73

Metalloreductase STEAP4 OS=Homo sapiens GN=STEAP4 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
659	467.26	932.51	932.51	1.72	0	23	0.042	1	R.FLSPSNLR.W 660
714	472.75	943.49	943.50	-5.33	1	7	1.7	2	R.IRQGWER.N
1679	564.84	1127.66	1127.65	2.06	0	52	3.1e-005	1	K.ILVDISNNLK.I
1848	577.27	1152.52	1152.52	-3.89	0	55	1.3e-005	1	R.QVFVCGNDSK.A 1849 1850 1851 1853 1854
3861	823.92	1645.82	1645.82	2.08	0	90	8.5e-009	1	R.NLGLTPMDQGSLMAAK.E
3902	831.92	1661.82	1661.81	6.15	0	(72)	5.1e-007	1	R.NLGLTPMDQGSLMAAK.E
3936	839.91	1677.81	1677.81	3.00	0	(88)	1.1e-008	1	R.NLGLTPMDQGSLMAAK.E 3937
3938	840.40	1678.79	1678.79	0.68	0	83	2.3e-008	1	K.TCIDALPLTMNSSEK.Q
4375	918.99	1835.97	1835.95	8.78	0	101	4e-010	1	K.TTLLPSGAEVLSYSEAAK.K 4374

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23. SEMG1_HUMAN **Mass:** 52157 **Score:** 651 **Queries matched:** 15 **emPAI:** 0.51

Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
890	491.77	981.52	981.52	-2.11	0	65	1.8e-006	1	K.SQIQAPNPK.Q 889 891
1165	517.76	1033.50	1033.50	-0.11	0	56	2.2e-005	1	K.EQTSVSGAQK.G 1166 1167
2546	643.80	1285.58	1285.58	-1.34	0	74	1.5e-007	1	K.ISYQSSSTEER.R 2544 2545 2547
2960	685.81	1369.61	1369.61	-3.67	0	82	2e-008	1	K.GISSQYSNTEER.L 2959
3722	801.36	1600.71	1600.71	0.60	0	92	1.6e-009	1	R.GTQNPSQDQGNSPSGK.G 3720 3721

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24. ALBU_HUMAN **Mass:** 71317 **Score:** 606 **Queries matched:** 16 **emPAI:** 0.36

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
898	492.74	983.47	983.48	-6.34	0	17	0.12	1	K.TYETTLEK.C
1064	507.30	1012.59	1012.59	2.51	0	37	0.0011	1	K.LVAASQAALGL.- 1062 1063
2962	686.29	1370.56	1370.56	0.49	0	55	2.9e-006	1	K.AAFTECCQAADK.A 2961
3178	717.77	1433.52	1433.53	-3.08	0	49	1.1e-005	1	R.ETYGEMADCCAK.Q 3179 3180
3206	722.32	1442.63	1442.63	-0.67	0	73	1.4e-007	1	K.YICENQDSISSK.L 3203 3204 3205 3207
3392	749.79	1497.57	1497.57	1.12	0	111	7.9e-012	1	K.TCVADESAENCDK.S 3391

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25. SNP23_HUMAN **Mass:** 23682 **Score:** 598 **Queries matched:** 12 **emPAI:** 0.16

Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1152	517.26	1032.51	1032.52	-9.56	1	1	8.4	4	R.ITDKADTNR.D
4309	904.40	1806.78	1806.78	-2.38	0	95	1.2e-009	1	K.TTWGDGGENSPCNVVSK.Q 4307 4308 4310 4311 4312 4313 4314 4315 4316 4317

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26. 1433T_HUMAN **Mass:** 28032 **Score:** 558 **Queries matched:** 12 **emPAI:** 0.66

14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
86	408.71	815.41	815.41	0.04	0	56	1.8e-005	1	K.LAEQAER.Y 83 84 85
498	452.26	902.51	902.51	0.50	0	49	0.00011	1	R.VISSIEQK.T 499
538	454.27	906.53	906.52	8.47	0	37	0.0012	1	R.NLLSVAYK.N
3491	766.86	1531.71	1531.71	-2.87	0	109	6.5e-011	1	K.AVTEQGAELSNEER.N 3489 3492 3494 3495

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27. PGK1_HUMAN **Mass:** 44985 **Score:** 543 **Queries matched:** 16 **emPAI:** 0.38

Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
38	405.21	808.40	808.41	-3.88	0	58	1.2e-005	1	K.YAEAVTR.A 39 40 41 42 43
390	442.73	883.45	883.44	1.46	0	18	0.086	1	K.ELNYFAK.A
1143	516.74	1031.46	1031.46	3.51	0	54	1.1e-005	1	K.DCVGPEVEK.A 1140 1141 1142
1523	549.32	1096.62	1096.61	2.84	0	12	0.23	1	K.VLPGVDALSNI.-
1539	551.27	1100.53	1100.53	-0.83	0	58	1e-005	1	K.NNQITNNQR.I 1540
4162	877.90	1753.79	1753.78	6.68	0	100	3.8e-010	1	R.GCITIIGGGDTATCCAK.W 4161

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28. ANXA2_HUMAN **Mass:** 38808 **Score:** 538 **Queries matched:** 12 **emPAI:** 0.20

Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2203	611.80	1221.59	1221.59	-1.77	0	71	5e-007	1	K.TPAQYDASELK.A 2201 2202 2204 2205 2207
2329	622.82	1243.62	1243.62	2.10	0	74	3.3e-007	1	R.TNQELQEINR.V 2324 2325 2326 2327 2328

Proteins matching the same set of peptides:

AXA2L_HUMAN **Mass:** 38806 **Score:** 538 **Queries matched:** 12

Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2

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29. TGM4_HUMAN **Mass:** 77951 **Score:** 521 **Queries matched:** 9 **emPAI:** 0.38

Protein-glutamine gamma-glutamyltransferase 4 OS=Homo sapiens GN=TGM4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1270	525.31	1048.60	1048.60	-0.29	0	57	4e-006	1	K.HTLVVLDPR.T
2020	592.85	1183.68	1183.68	2.18	0	61	4.1e-006	1	K.NTLAIPLTDVK.F
3140	711.32	1420.62	1420.62	-3.16	0	87	4.7e-009	1	R.SVTGFDSAHDTER.N
3716	798.38	1594.75	1594.75	0.65	0	95	1.6e-009	1	R.NLTVDTYVNENGEK.I
3974	846.88	1691.75	1691.75	-3.30	0	88	5.1e-009	1	K.GYDGWQAVDATPQER.S 3975
4151	875.43	1748.84	1748.83	4.61	0	69	6.6e-007	1	R.SQGVFCCGPSPLTAIR.K 4150
4500	967.50	1932.99	1933.00	-4.58	0	102	4.5e-010	1	K.TSQIQGQVSEVTLTLDSK.T

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30. VPP1_HUMAN **Mass:** 97148 **Score:** 518 **Queries matched:** 14 **emPAI:** 0.21

V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
785	482.73	963.44	963.44	-0.82	0	52	3.7e-005	1	K.EMASGVNTR.I 786
864	490.73	979.44	979.44	1.08	0	(47)	7.2e-005	1	K.EMASGVNTR.I
3144	711.84	1421.66	1421.66	1.09	0	79	6e-008	1	R.MQTNQTPPTYNK.T 3141 3142 3143 3145
3190	719.84	1437.66	1437.66	0.36	0	(68)	6.4e-007	1	R.MQTNQTPPTYNK.T 3189 3191 3192
3548	774.36	1546.71	1546.71	0.25	0	43	0.00023	1	R.ASLYPCPETPQER.K 3549

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31. GPC5C_HUMAN **Mass:** 48732 **Score:** 517 **Queries matched:** 10 **emPAI:** 0.16

G-protein coupled receptor family C group 5 member C OS=Homo sapiens GN=GPRC5C PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4148	873.38	1744.74	1744.74	3.67	0	90	1.7e-009	1	K.SSPEQSYQGDMYPTR.G 4144 4145 4146 4147
4185	881.37	1760.73	1760.73	-1.18	0	(81)	7.3e-009	1	K.SSPEQSYQGDMYPTR.G 4180 4182 4183 4184

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32. EDIL3_HUMAN **Mass:** 55098 **Score:** 514 **Queries matched:** 22 **emPAI:** 0.93

EGF-like repeat and discoidin I-like domain-containing protein 3 OS=Homo sapiens GN=EDIL3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
315	434.21	866.41	866.41	-0.36	0	35	0.0036	1	K.IAYSNDGK.T 313 314
523	453.75	905.49	905.49	1.62	0	37	0.0011	1	R.IGSPEYIK.S
666	468.24	934.47	934.47	-1.06	0	41	0.00066	1	R.LYPQVCR.R 667
834	487.29	972.56	972.56	0.55	0	77	1.3e-007	1	R.VTGVITQGAK.R 828 829 830 831 832 833 835
1380	534.74	1067.47	1067.47	0.53	0	58	6.4e-006	1	K.GTNEDMVFR.G

1881	579.32	1156.63	1156.62	1.34	0	32	0.005	1	K.NVIDPPIYAR.H 1882
1888	580.28	1158.54	1158.54	4.40	0	46	0.00014	1	R.GDTFIGYVCK.C
1923	583.75	1165.48	1165.48	-1.93	0	36	0.00033	1	R.SELLGCTEEE.- 1922
4560	981.98	1961.95	1961.95	0.03	0	41	0.00052	1	R.GNIDNNTPYANSFTPPIK.A 4561

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33. FOLH1_HUMAN **Mass:** 84506 **Score:** 504 **Queries matched:** 17 **emPAI:** 0.47

Glutamate carboxypeptidase 2 OS=Homo sapiens GN=FOLH1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
586	459.24	916.47	916.48	-2.06	0	12	0.66	1	K.QIQSQWK.E
789	483.21	964.41	964.41	-1.89	0	37	0.00046	1	K.SPDEGFEGK.S 794 797
1266	524.82	1047.62	1047.61	8.72	0	52	2.2e-005	1	R.IYNVIGTLR.G 1265
1900	581.29	1160.57	1160.57	-0.06	0	71	6.3e-007	1	K.SSNEATNITPK.H 1897
2040	596.28	1190.54	1190.54	0.95	0	(26)	0.0094	1	K.SPSPEFSGMPR.I
2117	604.27	1206.54	1206.53	1.21	0	63	1.9e-006	1	K.SPSPEFSGMPR.I 2116
2345	624.28	1246.55	1246.54	5.24	0	63	1.5e-006	1	K.MGGSAPPDSSWR.G
2438	632.28	1262.54	1262.53	3.79	0	(58)	2.9e-006	1	K.MGGSAPPDSSWR.G 2436 2437
3735	801.89	1601.77	1601.76	4.79	0	41	0.0005	1	K.SYPDGWNLPGGGVQR.G
4326	906.47	1810.93	1810.91	7.28	0	42	0.00036	1	K.GVILYSDPADYFAPGVK.S

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34. NHRF1_HUMAN **Mass:** 39130 **Score:** 494 **Queries matched:** 17 **emPAI:** 0.32

Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1115	513.78	1025.54	1025.54	-2.05	0	46	0.00017	1	R.LVEPGSPAEK.A 1113 1114
3076	700.84	1399.66	1399.66	-1.22	0	76	1.4e-007	1	R.SVDPDSPAEASGLR.A 3075 3077 3078 3079 3080 3081
5108	1294.59	2587.17	2587.19	-7.00	0	96	5.9e-010	1	R.AQEAPGQAEPPAAAEVQGAGNENEPR.E 5109 5110 5111 5112 5113 5114

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35. GNAI3_HUMAN **Mass:** 41076 **Score:** 484 **Queries matched:** 10 **emPAI:** 0.42

Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
547	455.22	908.42	908.42	2.56	0	53	3.1e-005	1	K.MFDVGGQR.S
1316	529.32	1056.62	1056.62	0.47	0	73	2.5e-007	1	K.LLLLGAGESGK.S 1317
1518	548.75	1095.48	1095.48	-0.32	0	76	6.3e-008	1	R.DGGVQACFSR.S 1515 1516 1517 1519 1520
4188	881.46	1760.91	1760.91	4.32	0	41	0.00065	1	R.ISQSNYIPTQQDVLR.T

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36. ATP9A_HUMAN **Mass:** 119989 **Score:** 483 **Queries matched:** 27 **emPAI:** 0.20

Probable phospholipid-transporting ATPase IIA OS=Homo sapiens GN=ATP9A PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
143	415.23	828.44	828.45	-2.28	0	17	0.13	1	R.NVINNQK.Y 145 146 147 148 149 150 151 152
713	472.75	943.49	943.49	-2.32	0	48	0.00015	1	R.LPVACTQR.L 715
787	482.73	963.44	963.44	-0.31	0	59	7.3e-006	1	R.DQSSMQLR.T 781 782 783 784
1015	503.24	1004.47	1004.47	2.98	0	68	1.2e-006	1	R.SVMNTSNPR.S 1009 1010 1011 1012 1013 1014
1092	511.24	1020.47	1020.47	3.25	0	(16)	0.1	1	R.SVMNTSNPR.S 1091
1346	531.30	1060.58	1060.57	4.16	0	50	7.4e-005	1	R.VPADMIFLR.T
2671	654.29	1306.57	1306.57	3.82	0	73	1.7e-007	1	R.TDQLDGETDWK.L

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37. MYO1C_HUMAN **Mass:** 122461 **Score:** 473 **Queries matched:** 10 **emPAI:** 0.13

Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
914	494.26	986.51	986.50	8.67	0	53	5.6e-005	1	R.LGTDEISPR.V
1408	538.26	1074.51	1074.51	-2.20	0	54	2.3e-005	1	K.DNYPQSVPR.L 1406 1407 1409 1410
1630	559.79	1117.57	1117.57	1.79	0	53	5.5e-005	1	K.IICDLVEEK.F
2855	675.32	1348.63	1348.63	-0.56	0	119	8e-012	1	R.DQAVMISGESGAGK.T 2852 2853

38. GNAS1_HUMAN **Mass:** 111697 **Score:** 461 **Queries matched:** 15 **emPAI:** 0.14
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
296	432.22	862.42	862.41	1.28	0	67	2.1e-006	1	R.ISTASGDGR.H 295 298 300 303 306
1316	529.32	1056.62	1056.62	0.47	0	73	2.5e-007	1	R.LLLLGAGESGK.S 1317
1509	547.81	1093.61	1093.60	6.90	0	64	1.7e-006	1	R.VLTSGIFETK.F
4232	887.89	1773.77	1773.77	-1.35	0	65	8.5e-007	1	R.YTTPEDATPEPGEDPR.V 4231 4233 4234 4235 4236

Proteins matching the same set of peptides:
GNAS2_HUMAN **Mass:** 46092 **Score:** 461 **Queries matched:** 15
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1

39. RHOG_HUMAN **Mass:** 21751 **Score:** 455 **Queries matched:** 14 **emPAI:** 0.38
Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1326	530.78	1059.54	1059.54	-1.74	0	69	1.7e-006	1	K.CVVVGDGAVGK.T 1324 1325 1327 1328 1329 1330 1331
4213	882.97	1763.92	1763.92	0.28	0	65	1.6e-006	1	K.EQGQAPITPQQGQALAK.Q 4211 4212 4214 4215 4216

40. MGA_HUMAN **Mass:** 211031 **Score:** 447 **Queries matched:** 29 **emPAI:** 0.11
Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
21	402.70	803.38	803.38	0.40	0	18	0.13	1	R.DQPPGYK.K 22 24
189	419.71	837.40	837.40	-1.80	0	44	0.0002	1	R.STFPSSGR.W 184 185 186 188 190 191 192 193 194 195 196 197
563	456.74	911.46	911.46	0.12	0	43	0.00027	1	R.NHNTIGTR.R
770	481.24	960.46	960.46	-0.15	0	55	2.3e-005	1	K.LTDQTNNR.F 771
1264	524.79	1047.56	1047.56	-0.14	0	53	5e-005	1	R.QLDFTLSPK.F
2526	641.83	1281.64	1281.64	-0.06	0	63	3.9e-006	1	R.INCIPDQPPTK.A 2524 2525 2527 2528 2529 2530
4142	872.91	1743.81	1743.81	1.49	0	59	5.2e-006	1	R.EIEELYNNPQNPER.S
4742	682.34	2043.99	2043.99	1.80	0	11	0.42	1	K.HNGVPSQTSPTVTYDSNLK.V

41. ARRD1_HUMAN **Mass:** 46352 **Score:** 446 **Queries matched:** 9 **emPAI:** 0.36
Arrestin domain-containing protein 1 OS=Homo sapiens GN=ARRDC1 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
333	435.76	869.51	869.51	1.88	0	39	0.0006	1	R.LGAPLPFR.A
875	491.27	980.53	980.53	3.43	1	1	4.4	6	K.RWIHDVR.T
1403	537.29	1072.57	1072.58	-1.63	0	78	1.5e-007	1	R.TIAEVEGAGVK.A
2520	641.30	1280.58	1280.59	-3.26	0	93	2.4e-009	1	R.VTCIGSCGVSNK.A 2521 2522 2523
3209	722.89	1443.77	1443.77	-3.29	0	72	4.6e-007	1	R.VVYSPGEPLAGTVR.V 3210

42. HSP7C_HUMAN **Mass:** 71082 **Score:** 443 **Queries matched:** 14 **emPAI:** 0.36
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
26	402.73	803.44	803.44	0.24	0	30	0.016	1	K.ITITNDK.G 27
171	417.70	833.40	833.40	0.03	0	32	0.0062	1	R.MVQEAEK.Y 172
716	472.77	943.52	943.52	2.20	0	43	0.00046	1	K.VCNPIITK.L
2238	614.81	1227.61	1227.62	-6.20	0	75	2.6e-007	1	K.VEIIANDQGNR.T 2239 2240 2241 2242 2244
2647	652.30	1302.59	1302.59	0.00	0	55	1.4e-005	1	K.NSLESYAFNMK.A
3871	825.41	1648.80	1648.79	6.54	0	56	1.8e-005	1	K.NQVAMNPTNTVFDAK.R
4267	596.67	1786.98	1786.98	-0.33	1	7	0.39	1	R.IINEPTAAAIAYGLDKK.V

43. SPIT1_HUMAN **Mass:** 60128 **Score:** 434 **Queries matched:** 12 **emPAI:** 0.27
Kunitz-type protease inhibitor 1 OS=Homo sapiens GN=SPINT1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

110	411.73	821.45	821.45	4.71	1	8	0.67	3	R.SYRQLR.T
1156	517.73	1033.45	1033.45	4.27	0	33	0.0014	1	K.DVENTDWR.L
1228	522.80	1043.58	1043.57	6.44	1	9	1.1	4	R.LLRGDTDVR.V
1263	524.78	1047.54	1047.53	7.42	0	48	0.00015	1	R.TQGFGGSGIPK.A 1262
1831	575.85	1149.68	1149.68	1.49	0	10	0.21	1	K.VQPQEPLVLK.D
2752	664.79	1327.57	1327.57	-3.14	0	91	1.9e-009	1	K.QTEDYCLASNK.V 2751 2753 2754 2758
3411	751.84	1501.66	1501.65	1.06	0	57	5.1e-006	1	R.WYYDPTEQICK.S

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44. CDC42_HUMAN **Mass:** 21587 **Score:** 424 **Queries matched:** 13 **emPAI:** 0.39

Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
500	452.72	903.42	903.42	-0.52	0	15	0.15	1	R.DDPSTIEK.L
1326	530.78	1059.54	1059.54	-1.74	0	69	1.7e-006	1	K.CVVVGDGAVGK.T 1324 1325 1327 1328 1329 1330 1331
2085	599.79	1197.57	1197.57	1.90	0	81	4.3e-008	1	K.YVECSALTQK.G 2082 2083 2086

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45. MPI_HUMAN **Mass:** 47196 **Score:** 417 **Queries matched:** 5 **emPAI:** 0.08

Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4225	887.34	1772.66	1772.66	-1.57	0	112	5.8e-012	1	K.GDCVECMACSDNTVR.A 4226 4227 4228 4229

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46. PCBP1_HUMAN **Mass:** 37987 **Score:** 417 **Queries matched:** 10 **emPAI:** 0.21

Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1463	543.78	1085.55	1085.55	-0.83	0	61	5.1e-006	1	K.IANPVEGSSGR.Q 1462
2557	644.80	1287.59	1287.59	1.53	0	67	8.4e-007	1	R.INISEGNCPER.I 2551 2552 2553 2554 2555 2556 2558

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47. HSP71_HUMAN **Mass:** 70294 **Score:** 415 **Queries matched:** 17 **emPAI:** 0.29

Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
26	402.73	803.44	803.44	0.24	0	30	0.016	1	K.ITITNDK.G 27
171	417.70	833.40	833.40	0.03	0	32	0.0062	1	R.MVQEAEK.Y 172
484	451.74	901.47	901.48	-1.65	0	29	0.013	1	R.STLEPVEK.A 485
719	474.24	946.46	946.46	-0.06	0	42	0.00051	1	K.SAVEDEGLK.G 720 721
1708	566.79	1131.57	1131.58	-3.69	1	3	5	5	K.SAVEDEGLKGK.I 1709
2238	614.81	1227.61	1227.62	-6.20	0	75	2.6e-007	1	K.VEIIANDQGNR.T 2239 2240 2241 2242 2244

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48. ENOA_HUMAN **Mass:** 47481 **Score:** 410 **Queries matched:** 12 **emPAI:** 0.70

Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
32	403.73	805.45	805.44	1.45	0	29	0.007	1	K.YNQLLR.I
45	405.73	809.44	809.44	1.99	0	43	0.00018	1	K.AVEHINK.T
504	452.73	903.45	903.45	-1.18	0	53	6.3e-005	1	R.IEEELGSK.A 501 502 503 505 506
1022	504.25	1006.50	1006.49	1.25	0	36	0.0019	1	K.SCNCLLLK.V
3091	703.86	1405.71	1405.71	1.24	0	98	1.5e-009	1	R.GNPTVEVDLFTSK.G
3149	713.37	1424.72	1424.72	1.97	0	37	0.0018	1	R.YISPDQLADLYK.S
3812	817.42	1632.83	1632.81	6.99	0	121	6.1e-012	1	K.VNQIGSVTESLQACK.L

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49. K1C16_HUMAN **Mass:** 51578 **Score:** 409 **Queries matched:** 6 **emPAI:** 0.15

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1566	553.77	1105.52	1105.52	0.27	0	65	2.2e-006	1	K.VTMQNLNDR.L 1567
4771	1052.48	2102.95	2102.95	0.26	0	99	4.6e-010	1	R.GQTGGDVNVEMDAAPGVDLSR.I 4770 4772 4773

50. VP37B_HUMAN **Mass:** 31345 **Score:** 388 **Queries matched:** 7 **emPAI:** 0.41
Vacuolar protein sorting-associated protein 37B OS=Homo sapiens GN=VPS37B PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
597	461.23	920.44	920.44	4.28	0	25	0.025	1	K.EMTLASNR.S
2785	667.32	1332.63	1332.63	-0.06	0	96	1.8e-009	1	K.MEETQNVQLNK.E 2783 2784 2786
2854	675.32	1348.63	1348.63	-1.46	0	(88)	1.1e-008	1	K.MEETQNVQLNK.E 2856

51. ANXA1_HUMAN **Mass:** 38918 **Score:** 386 **Queries matched:** 10 **emPAI:** 0.44
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
153	415.26	828.51	828.51	2.88	0	12	0.39	1	R.NALLSLAK.G
583	458.75	915.49	915.48	1.46	0	47	0.00025	1	K.ILVALCGGN.- 582
1426	540.75	1079.48	1079.48	1.90	0	30	0.0055	1	R.SEIDMNDIK.A
2154	607.27	1212.52	1212.53	-4.25	0	78	3.2e-008	1	K.DITSDTSGDFR.N 2155 2156 2157 2158
2430	631.81	1261.60	1261.59	2.01	0	90	8e-009	1	K.TPAQFDADELR.A

52. ALDOA_HUMAN **Mass:** 39851 **Score:** 384 **Queries matched:** 11 **emPAI:** 0.88
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
12	401.25	800.48	800.48	7.00	0	46	0.00033	1	R.ALQASALK.A
617	464.21	926.42	926.42	-1.56	0	36	0.00065	1	R.CQYVTEK.V
1227	522.79	1043.56	1043.56	-0.68	0	47	0.00018	1	R.QLLLTADDR.V
1368	533.26	1064.50	1064.50	-3.72	1	6	1.7	3	K.DGADFAKWR.C 1367
1505	547.29	1092.56	1092.56	0.03	1	16	0.19	1	K.AAQEEYVKR.A
1709	566.80	1131.58	1131.57	7.37	0	85	3.1e-008	1	R.ALANSLACQGK.Y 1708
2780	666.86	1331.70	1331.69	7.04	0	91	6.3e-009	1	K.GILAADESTGSIAK.R
3596	521.61	1561.81	1561.81	0.10	1	25	0.024	1	M.PYQYPALTPEQKK.E
4924	1136.58	2271.15	2271.13	5.41	0	132	3.9e-013	1	K.GVVPLAGTNGETTTQGLDGLSER.C

53. CAN5_HUMAN **Mass:** 74092 **Score:** 381 **Queries matched:** 18 **emPAI:** 0.28
Calpain-5 OS=Homo sapiens GN=CAPN5 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
16	401.69	801.36	801.36	0.50	0	34	0.001	1	R.TDQPEGR.Y 15 17
241	423.69	845.37	845.37	-0.64	0	36	0.0004	1	K.GICEDPR.L 237 238 239 240 242
1161	517.75	1033.49	1033.49	6.81	0	76	1.9e-007	1	K.AVTAADMEAR.L 1157 1158 1160
1512	548.27	1094.52	1094.52	-1.46	0	44	0.00023	1	K.GTSTPEYNVK.G 1510 1511 1513
2068	597.78	1193.54	1193.55	-8.00	0	45	0.00016	1	R.VFTDVPSNCR.E

54. HS90A_HUMAN **Mass:** 85006 **Score:** 355 **Queries matched:** 21 **emPAI:** 0.24
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	Peptide
302	432.22	862.42	862.42	-1.75	0	(21)	0.083	1	R.EMLQQSK.I 297 298 299 301 303 304 305 306
367	440.22	878.42	878.42	1.36	0	36	0.0024	1	R.EMLQQSK.I 366
520	453.71	905.40	905.40	1.12	1	8	0.69	2	K.EDKEEEK.E
774	482.21	962.41	962.41	-0.50	0	(43)	0.00016	1	R.TDTGEPMGR.G 775
861	490.21	978.41	978.41	-1.54	0	49	2.6e-005	1	R.TDTGEPMGR.G 860 862
2194	610.75	1219.49	1219.48	1.14	0	57	2e-006	1	R.DNSTMGYMAAK.K
2283	618.30	1234.59	1234.59	-3.06	0	80	6.7e-008	1	K.DQVANSAFVER.L 2284 2285

55. STOM_HUMAN **Mass:** 31882 **Score:** 351 **Queries matched:** 8 **emPAI:** 0.75
Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1020	503.73	1005.45	1005.45	-0.75	0	85	1.6e-008	1	R.AMAAAEAEASR.E 1018 1019
1097	511.73	1021.45	1021.45	1.18	0	(73)	2.1e-007	1	R.AMAAAEAEASR.E
2346	624.31	1246.60	1246.60	-0.03	0	(43)	0.00042	1	K.VIAAEGEMNASR.A 2347
2439	632.30	1262.59	1262.59	0.32	0	72	4.5e-007	1	K.VIAAEGEMNASR.A
4486	965.51	1929.00	1928.99	6.84	0	35	0.0018	1	R.VQNATLAVANITNADSATR.L

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56. KINH_HUMAN **Mass:** 110358 **Score:** 348 **Queries matched:** 4 **emPAI:** 0.07

Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1892	580.79	1159.57	1159.57	2.47	0	102	5.9e-010	1	K.TGAEGAVLDEAK.N 1891
3578	776.34	1550.67	1550.67	1.13	0	116	6.5e-012	1	K.SAEIDSDDTGGSAAQK.Q 3577

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57. ESPB1_HUMAN **Mass:** 27001 **Score:** 344 **Queries matched:** 9 **emPAI:** 0.30

Epididymal sperm-binding protein 1 OS=Homo sapiens GN=ELSPBP1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2173	609.25	1216.48	1216.48	-1.48	0	57	2e-006	1	K.YCQSEDYPR.C 2170 2172 2174 2175 2177 2178 2179
3546	773.83	1545.65	1545.65	-0.37	0	85	5.3e-009	1	K.FCETNEYGGNSLR.K

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58. MELPH_HUMAN **Mass:** 66593 **Score:** 343 **Queries matched:** 6 **emPAI:** 0.11

Melanophilin OS=Homo sapiens GN=MLPH PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3310	736.84	1471.67	1471.67	-1.91	0	68	6.9e-007	1	K.SPQDPGDPVQYNR.T 3309 3311
3654	791.83	1581.65	1581.65	0.78	0	94	4.7e-010	1	R.DSPQSLTDESCSEK.A 3652 3653

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59. ANX11_HUMAN **Mass:** 54697 **Score:** 342 **Queries matched:** 8 **emPAI:** 0.14

Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
158	416.23	830.45	830.45	-1.26	0	8	2	1	K.TLEEAIR.S
2137	605.31	1208.61	1208.61	3.50	1	4	2.9	4	K.FNAVLCSRSR.A
2790	668.81	1335.60	1335.61	-0.66	0	87	1e-008	1	R.DAQELYAAGENR.L 2788 2789 2791 2792
3290	733.33	1464.65	1464.65	-2.91	0	62	1.2e-006	1	R.DESTNVDMSLAQR.D

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60. HSP76_HUMAN **Mass:** 71440 **Score:** 341 **Queries matched:** 10 **emPAI:** 0.16

Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
26	402.73	803.44	803.44	0.24	0	30	0.016	1	K.ITITNDK.G 27
484	451.74	901.47	901.48	-1.65	0	29	0.013	1	R.STLEPVEK.A 485
2238	614.81	1227.61	1227.62	-6.20	0	75	2.6e-007	1	R.VEILANDQGNR.T 2239 2240 2241 2242 2244

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61. PPBT_HUMAN **Mass:** 57611 **Score:** 338 **Queries matched:** 6 **emPAI:** 0.13

Alkaline phosphatase, tissue-nonspecific isozyme OS=Homo sapiens GN=ALPL PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
648	466.74	931.46	931.46	1.15	0	30	0.0095	1	R.DQAQETLK.Y
2907	681.34	1360.66	1360.66	-1.41	0	101	9.1e-010	1	K.ANEGTVGVSAATER.S 2904 2905 2906 2908

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62. MFGM_HUMAN **Mass:** 43894 **Score:** 338 **Queries matched:** 14 **emPAI:** 0.77

Lactadherin OS=Homo sapiens GN=MFGE8 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
899	492.75	983.49	983.49	-1.13	0	32	0.0039	1	K.QITASSSYK.T 900 901
1739	568.75	1135.48	1135.47	5.38	0	58	1.8e-006	1	K.GYAGNHCETK.C
1790	572.82	1143.63	1143.62	7.21	0	72	5.4e-007	1	K.EVTGIITQGAR.N 1788 1789

1973	587.34	1172.66	1172.66	0.55	0	13	0.3	1	K.NLFETPILAR.Y
2840	673.84	1345.67	1345.67	1.77	0	42	0.00065	1	R.NFGSVQFVASYK.V
3038	696.36	1390.70	1390.70	0.69	0	104	2.9e-010	1	R.MWVTGVVTQGASR.L
3547	774.35	1546.68	1546.68	1.05	0	38	0.00041	1	R.GDVFPSYTCTCLK.G
3648	527.25	1578.73	1578.73	1.55	0	3	2.3	1	R.LYPTSCHTACTLR.F
5034	806.40	2416.16	2416.15	6.98	0	(11)	0.33	1	K.CVEPLGMENGNIANSQIAASSVR.V
5057	811.73	2432.16	2432.14	5.61	0	20	0.052	1	K.CVEPLGMENGNIANSQIAASSVR.V

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63. IPSP_HUMAN **Mass:** 45760 **Score:** 337 **Queries matched:** 7 **emPAI:** 0.08
Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1898	581.29	1160.57	1160.57	-1.35	0	83	3.7e-008	1	K.AVVEVDESGTR.A 1895 1896 1899 1901 1902 1903

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64. KAP2_HUMAN **Mass:** 45832 **Score:** 335 **Queries matched:** 13 **emPAI:** 0.48
cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
100	410.21	818.41	818.41	-9.86	0	7	2.7	6	K.SLEVSER.M 102
683	469.72	937.42	937.43	-7.12	0	22	0.023	2	R.SVGQYDNR.G 684
1285	526.28	1050.54	1050.53	5.89	0	96	1.9e-009	1	R.AASAYAVGDVK.C 1283 1284
2028	594.29	1186.56	1186.56	-0.60	0	48	6.9e-005	1	K.DGGNQEVEIAR.C 2027
2739	662.81	1323.62	1323.61	1.73	0	(40)	0.00064	1	K.MFGSSVDLGNLGQ.- 2740 2741
2813	670.81	1339.61	1339.61	0.68	0	47	9.4e-005	1	K.MFGSSVDLGNLGQ.-

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65. HSP72_HUMAN **Mass:** 70263 **Score:** 334 **Queries matched:** 12 **emPAI:** 0.11
Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
26	402.73	803.44	803.44	0.24	0	30	0.016	1	K.ITITNDK.G 27
1416	538.75	1075.49	1075.49	0.43	1	3	1.8	3	K.DEYEHKQK.E 1417
2238	614.81	1227.61	1227.62	-6.20	0	75	2.6e-007	1	K.VEIIANDQGNR.T 2239 2240 2241 2242 2244
3938	840.40	1678.79	1678.80	-4.01	0	4	2	2	K.NQVAMNPTNTIFDAK.R
4267	596.67	1786.98	1786.98	-0.33	1	7	0.39	1	R.IINEPTAAAIAYGLDKK.G

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66. MYO5B_HUMAN **Mass:** 215135 **Score:** 334 **Queries matched:** 9 **emPAI:** 0.03
Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
351	437.22	872.43	872.44	-0.64	0	6	1.7	4	K.NDLNELR.K
506	452.74	903.46	903.45	8.47	0	1	7.4	7	R.LNVGMENK.V
981	501.27	1000.53	1000.53	2.26	1	35	0.0033	1	K.NDLNELRK.A
2843	673.85	1345.68	1345.68	0.32	0	96	2.4e-009	1	K.NQSIIVSGESGAGK.T 2841 2842 2844 2845 2846

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67. ANXA7_HUMAN **Mass:** 52991 **Score:** 329 **Queries matched:** 8 **emPAI:** 0.31
Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
448	447.23	892.44	892.44	0.84	0	50	0.00011	1	R.LYQAGEGR.L 446 447
1260	524.75	1047.48	1047.48	0.40	0	85	1.6e-008	1	K.AMQGAGTQER.V 1259
1356	532.74	1063.48	1063.47	3.45	0	(62)	2.5e-006	1	K.AMQGAGTQER.V 1355
1496	546.27	1090.53	1090.53	3.81	0	55	2.4e-005	1	K.GAGTDDSTLVR.I

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68. CBPO_HUMAN **Mass:** 43015 **Score:** 329 **Queries matched:** 10 **emPAI:** 0.28
Carboxypeptidase O OS=Homo sapiens GN=CPO PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
622	464.25	926.48	926.48	1.41	0	41	0.00044	1	K.ISQPSGNPK.K 621 623

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      4496     644.96    1931.87    1931.87    2.13    1      2          3    2    K.SRSPHNNGTCFGTDLNR.N
      4817    1077.96    2153.90    2153.90   -1.20    0    112   6.8e-012    1    R.NCQDQTFCGTGPVSEPETK.A 4816 4818 4819 4820 4821
```

```
69.   DAF_HUMAN     Mass:  42400     Score:  328     Queries matched:  13    emPAI:  0.53
      Complement decay-accelerating factor OS=Homo sapiens GN=CD55 PE=1 SV=4
      Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss  Score      Expect  Rank   Peptide
        246     424.70     847.39     847.39    0.26    0     42     0.00041    1    R.SCEVPTR.L 244 245
        574     457.26     912.51     912.50    2.60    1     33      0.0037    1    R.REPSLSPK.L
       1128     515.24    1028.47    1028.47   -0.11    0     49    4.2e-005    1    K.SCPNPGEIR.N 1121 1122 1123 1127
       1386     535.75    1069.49    1069.49    0.29    0     62    2.3e-006    1    R.QSVTYACNK.G 1384 1385
       3082     700.86    1399.70    1399.69    6.62    0     63    3.4e-006    1    R.TSFPEDTVITYK.C
```

```
70.   CBPM_HUMAN     Mass:  50938     Score:  326     Queries matched:  12    emPAI:  0.33
      Carboxypeptidase M OS=Homo sapiens GN=CPM PE=1 SV=2
      Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss  Score      Expect  Rank   Peptide
         20     402.24     802.46     802.46    4.06    0     33      0.0054    1    R.IGIPEFK.Y
        229     423.21     844.40     844.40    1.83    0     19       0.071    1    K.HICPYR.T
       1085     509.76    1017.51    1017.52   -2.84    0     40     0.00086    1    R.QPETVAVMK.W 1084
       1288     526.76    1051.51    1051.50    5.82    0     51    5.1e-005    1    R.QEGMEAFLK.T
       2756     664.79    1327.57    1327.58   -3.63    0     61    1.9e-006    1    R.ENYNQYDLNR.N 2755 2757 2759 2760 2761 2762
```

```
71.   SEMG2_HUMAN     Mass:  65519     Score:  325     Queries matched:  9     emPAI:  0.18
      Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1
      Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss  Score      Expect  Rank   Peptide
         39     405.21     808.41     808.41   -3.13    0      7         1.5    8    K.ISYPSSR.T 43
        854     488.74     975.46     975.46    0.77    0     38       0.001    1    K.EQASASGAQK.G
       2141     605.77    1209.53    1209.53    0.87    0     66    8.6e-007    1    K.GLSSQCSNTEK.R 2140
       2546     643.80    1285.58    1285.58   -1.34    0     74    1.5e-007    1    K.ISYQSSSTEER.H 2544 2545 2547
```

```
72.   KCY_HUMAN     Mass:  22436     Score:  324     Queries matched:  7    emPAI:  0.37
      UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3
      Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss  Score      Expect  Rank   Peptide
       2797     669.30    1336.58    1336.58    1.14    0   (65)    6.4e-007    1    R.EMDQTMAANAQK.N 2795 2796 2798
       2875     677.29    1352.57    1352.57    0.10    0   (71)    1.4e-007    1    R.EMDQTMAANAQK.N
       2876     677.29    1352.57    1352.57    2.54    0     75    6.4e-008    1    R.EMDQTMAANAQK.N 2874
```

```
73.   GRP78_HUMAN     Mass:  72402     Score:  323     Queries matched:  7     emPAI:  0.05
      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   Peptide
        496     452.24     902.47     902.47    1.85    0      9         1.3    7    R.VMEHFIK.L
       2238     614.81    1227.61    1227.62   -6.20    0     75    2.6e-007    1    R.VEIIANDQGNR.I 2239 2240 2241 2242 2244
```

```
74.   RB27A_HUMAN     Mass:  25137     Score:  323     Queries matched:  7     emPAI:  0.53
      Ras-related protein Rab-27A OS=Homo sapiens GN=RAB27A PE=1 SV=3
      Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss  Score      Expect  Rank   Peptide
        293     431.70     861.38     861.38    0.33    0     57    5.6e-006    1    K.SDLEDQR.V
        417     444.71     887.41     887.41    1.02    0     74    1.2e-007    1    R.ASGPDGATGR.G 415 416 418 419
       1354     532.30    1062.58    1062.57    6.14    0     31      0.0067    2    K.FLALGDSGVGK.T
```

```
75.   MYO5A_HUMAN     Mass:  216979     Score:  322     Queries matched:  8     emPAI:  0.02
      Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=1 SV=2
```

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
965	499.72	997.42	997.41	9.21	0	1	2.1	6	K.EMTETMEK.K 966
2843	673.85	1345.68	1345.68	0.32	0	96	2.4e-009	1	R.NQSIIVSGESGAGK.T 2841 2842 2844 2845 2846

---

76. PLS1_HUMAN **Mass:** 36052 **Score:** 315 **Queries matched:** 9 **emPAI:** 0.22

Phospholipid scramblase 1 OS=Homo sapiens GN=PLSCR1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1725	567.78	1133.54	1133.54	-1.19	0	69	1e-006	1	K.SLDEQCVVGK.I 1720 1721 1722 1724 1726 1727 1728
3746	804.33	1606.64	1606.64	2.69	0	82	6.4e-009	1	R.VYFAAEDTDCCTR.N

---

77. ACTA_HUMAN **Mass:** 42381 **Score:** 314 **Queries matched:** 10 **emPAI:** 0.53

Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
853	488.73	975.44	975.44	2.57	0	85	1.6e-008	1	K.AGFAGDDAPR.A 852
1905	581.32	1160.62	1160.61	6.08	0	52	5.1e-005	1	K.EITALAPSTMK.I 1904
1989	589.31	1176.61	1176.61	7.62	0	(44)	0.00036	1	K.EITALAPSTMK.I 1988
2081	599.77	1197.52	1197.51	1.46	0	66	7e-007	1	K.DSYVGDEAQSK.R
2883	677.82	1353.62	1353.62	-0.18	1	66	1.4e-006	1	K.DSYVGDEAQSKR.G 2882
3400	750.85	1499.69	1499.70	-8.41	0	3	2.7	3	K.QEYDEAGPSIVHR.K

Proteins matching the same set of peptides:

ACTC_HUMAN **Mass:** 42334 **Score:** 314 **Queries matched:** 10

Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1

ACTS_HUMAN **Mass:** 42366 **Score:** 314 **Queries matched:** 10

Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1

---

78. CAH4_HUMAN **Mass:** 35295 **Score:** 310 **Queries matched:** 9 **emPAI:** 0.66

Carbonic anhydrase 4 OS=Homo sapiens GN=CA4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
252	425.19	848.36	848.36	1.34	0	33	0.00069	1	K.WGGNCQK.D 251
1353	532.29	1062.57	1062.57	1.00	0	35	0.0025	1	R.EQILAFSQK.L
1535	550.82	1099.62	1099.62	0.81	0	71	7.9e-007	1	R.QSPINIVTTK.A 1536
3132	708.88	1415.74	1415.74	0.57	0	68	1.1e-006	1	K.ASISGGGLPAPYQAK.Q 3133
3350	742.85	1483.69	1483.69	2.00	0	57	1.1e-005	1	R.YLGSLTTPTCDEK.V 3351

---

79. KCRB_HUMAN **Mass:** 42902 **Score:** 310 **Queries matched:** 6 **emPAI:** 0.52

Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
360	439.76	877.50	877.50	-0.52	1	17	0.092	1	K.FSEVLKR.L
1133	516.28	1030.55	1030.55	-0.25	0	60	9.7e-006	1	K.LLIEMEQR.L
1258	524.28	1046.55	1046.54	3.10	0	(38)	0.0013	1	K.LLIEMEQR.L
3684	793.93	1585.84	1585.83	4.25	0	121	4.9e-012	1	K.LAVEALSSLDGDLAGR.Y
3887	828.92	1655.83	1655.82	3.97	0	87	1.4e-008	1	R.LEQGQAIDDLMPAQK.-
4565	982.97	1963.92	1963.92	-1.82	0	88	9.1e-009	1	R.GTGGVDTAAVGGVFDVSNADR.L

---

80. RAC1_HUMAN **Mass:** 21835 **Score:** 305 **Queries matched:** 10 **emPAI:** 0.62

Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
870	490.78	979.55	979.55	2.04	0	50	5.1e-005	1	R.AVLCPPPVK.K
1326	530.78	1059.54	1059.54	-1.74	0	69	1.7e-006	1	K.CVVVGDGAVGK.T 1324 1325 1327 1328 1329 1330 1331
2315	620.80	1239.59	1239.59	1.99	0	76	1.5e-007	1	K.YLECSALTQR.G

Proteins matching the same set of peptides:

```
          RAC3_HUMAN     Mass: 21764     Score: 305     Queries matched: 10
          Ras-related C3 botulinum toxin substrate 3 OS=Homo sapiens GN=RAC3 PE=1 SV=1

81.       VPS28_HUMAN     Mass: 25694     Score: 305     Queries matched: 7     emPAI: 0.51
          Vacuolar protein sorting-associated protein 28 homolog OS=Homo sapiens GN=VPS28 PE=1 SV=1
          Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
            105    410.72    819.42    819.42  0.94    0    52  7.6e-005    1   K.TMQALEK.A
            177    418.71    835.41    835.41  0.65    0   (47)  0.00023    1   K.TMQALEK.A 175 176
           3729    801.83   1601.65   1601.65  0.60    0    95  3.3e-010    1   K.DCVSPSEYTAACSR.L 3727 3728

82.       TPIS_HUMAN     Mass: 31057     Score: 302     Queries matched: 5     emPAI: 0.26
          Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3
          Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
           2275    617.80   1233.59   1233.59 -1.28    0    97  1.5e-009    1   K.SNVSDAVAQSTR.I 2273 2274
           2747    663.84   1325.67   1325.66  4.19    0    79  9.6e-008    1   R.IIYGGSVTGATCK.E
           3293    489.58   1465.72   1465.72  0.00    0    17      0.16    1   K.TATPQQAQEVHEK.L

83.       NIBAN_HUMAN     Mass: 104039     Score: 297     Queries matched: 7     emPAI: 0.15
          Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1
          Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
            422    445.22    888.43    888.43  1.98    0    36    0.0019    1   R.TEVEQQR.D
            768    480.74    959.47    959.47 -2.81    0    33    0.0047    1   K.AMVAQPAEK.S
           1845    576.76   1151.51   1151.51 -0.26    0    59  5.4e-006    1   R.SDMDQIVNSK.N 1844
           3456    762.37   1522.72   1522.73 -3.24    0   100  6.2e-010    1   K.EVNEVSQNFQTTK.D 3457 3458

84.       TS101_HUMAN     Mass: 44088     Score: 296     Queries matched: 13     emPAI: 0.63
          Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2
          Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
            443    447.22    892.43    892.43 -3.62    0    31    0.0067    1   K.LEEMVTR.L 442 446
            812    484.26    966.50    966.50  0.54    1    56  1.7e-005    1   R.KTAGLSDLY.-
            926    495.78    989.54    989.54 -1.82    0    38    0.0017    1   R.ASLISAVSDK.L
           1574    553.77   1105.53   1105.53  1.54    0    61  7.5e-006    1   R.DGTISEDTIR.A 1569 1570 1571 1572 1573
           1598    557.32   1112.63   1112.63  1.49    1    52  2.7e-005    1   R.AQAELNALKR.T
           2003    590.34   1178.66   1178.65  2.04    0    40   0.00038    1   R.ETVNVITLYK.D

85.       RS27A_HUMAN     Mass: 18296     Score: 296     Queries matched: 14     emPAI: 1.60
          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  Peptide
           1195    520.26   1038.51   1038.51  0.08    0    36     0.002    1   K.EGIPPDQQR.L 1188 1189 1191 1192 1193 1194 1196
           1379    534.32   1066.62   1066.61  5.17    0    62  2.5e-006    1   K.ESTLHLVLR.L
           3459    762.39   1522.77   1522.77 -4.45    1    90  6.6e-009    1   K.IQDKEGIPPDQQR.L 3461 3462
           4266    894.47   1786.93   1786.92  8.34    0    70  6.5e-007    1   K.TITLEVEPSDTIENVK.A
           4611    663.03   1986.07   1986.05  8.52    1     2       2.2    1   K.TITLEVEPSDTIENVKAK.I


          Proteins matching the same set of peptides:
          RL40_HUMAN     Mass: 15004     Score: 296     Queries matched: 14
          Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2
          UBB_HUMAN     Mass: 25803     Score: 296     Queries matched: 14
          Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1
          UBC_HUMAN     Mass: 76992     Score: 296     Queries matched: 14
          Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3

86.       KPCD_HUMAN     Mass: 78652     Score: 295     Queries matched: 6     emPAI: 0.05
          Protein kinase C delta type OS=Homo sapiens GN=PRKCD PE=1 SV=2
```

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
736	476.23	950.45	950.45	2.22	0	15	0.21	2	K.ENIFGESR.A 735
4098	865.38	1728.74	1728.73	6.04	0	90	1.3e-009	1	K.TGVAGEDMQDNSGTYGK.I 4095 4096 4097

---

87. NDRG1_HUMAN **Mass:** 43264 **Score:** 294 **Queries matched:** 5 **emPAI:** 0.18

Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2801	669.83	1337.64	1337.64	-2.73	0	105	2.4e-010	1	R.TASGSSVTSLDGTR.S 2800 2802 2803
3693	794.88	1587.74	1587.74	2.07	0	67	9.8e-007	1	K.MADCGGLPQISQPAK.L

---

88. VP37C_HUMAN **Mass:** 38692 **Score:** 292 **Queries matched:** 9 **emPAI:** 0.20

Vacuolar protein sorting-associated protein 37C OS=Homo sapiens GN=VPS37C PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
596	461.23	920.44	920.44	-1.09	0	18	0.12	1	R.EMALATNR.S 595
2519	641.28	1280.55	1280.54	0.67	0	77	2.3e-008	1	K.IEEESEAMAEK.F 2516 2517 2518
3088	701.88	1401.74	1401.73	8.62	0	71	6.4e-007	1	R.NLEFQGPLEISR.S 3086 3087

---

89. APOC3_HUMAN **Mass:** 10846 **Score:** 288 **Queries matched:** 4 **emPAI:** 0.87

Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4056	858.93	1715.84	1715.84	-0.84	0	115	2.7e-011	1	K.DALSSVQESQVAQQAR.G 4057 4058 4059

---

90. AT11B_HUMAN **Mass:** 135415 **Score:** 288 **Queries matched:** 7 **emPAI:** 0.03

Probable phospholipid-transporting ATPase IF OS=Homo sapiens GN=ATP11B PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
96	409.25	816.48	816.48	0.46	1	3	2.3	10	R.NSSKILR.F
2062	597.75	1193.49	1193.50	-5.30	0	67	2.6e-007	1	K.SDSECAEQLR.Q 2063 2064 2065 2066 2067

---

91. PRDX6_HUMAN **Mass:** 25133 **Score:** 284 **Queries matched:** 7 **emPAI:** 0.33

Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
580	458.25	914.48	914.49	-3.53	0	5	2.1	3	R.VATPVDWK.D 579
3052	698.33	1394.65	1394.65	2.95	0	85	1.7e-008	1	R.DFTPVCTTELGR.A
3657	791.84	1581.66	1581.66	-3.13	0	84	5.1e-009	1	K.DINAYNCEEPTEK.L 3655 3656 3658

---

92. 1433G_HUMAN **Mass:** 28456 **Score:** 284 **Queries matched:** 9 **emPAI:** 0.65

14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
86	408.71	815.41	815.41	0.04	0	56	1.8e-005	1	R.LAEQAER.Y 83 84 85
498	452.26	902.51	902.51	0.50	0	49	0.00011	1	R.VISSIEQK.T 499
538	454.27	906.53	906.52	8.47	0	37	0.0012	1	R.NLLSVAYK.N
2335	623.26	1244.50	1244.50	0.38	0	56	2.4e-006	1	K.NCSETQYESK.V 2336

---

93. YBOX1_HUMAN **Mass:** 35903 **Score:** 274 **Queries matched:** 4 **emPAI:** 0.10

Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3991	848.44	1694.86	1694.86	1.13	0	104	2.9e-010	1	K.GAEAANVTGPGGVPVQGSK.Y 3988 3989 3990

---

94. DHSO_HUMAN **Mass:** 38927 **Score:** 272 **Queries matched:** 13 **emPAI:** 0.74

Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

110	411.73	821.45	821.45	4.69	0	35	0.0014	1	K.HLKPGDR.V
548	455.26	908.51	908.51	0.90	0	55	1.2e-005	1	R.VAIEPGAPR.E 549
636	465.24	928.46	928.46	-1.69	0	62	3.5e-006	1	K.ESPQEIAR.K 633 635 637
701	471.19	940.36	940.36	-0.82	0	30	0.001	1	R.ENDEFCK.M 699 700
3700	795.42	1588.83	1588.82	2.24	0	56	1.7e-005	1	K.AMGAAQVVVTDLSATR.L
4371	611.29	1830.86	1830.86	0.33	1	18	0.068	1	R.VAIEPGAPRENDEFCK.M
4529	975.52	1949.03	1949.03	0.54	0	70	4.9e-007	1	R.LENYPIPEPGPNEVLLR.M

---

95. CD63_HUMAN **Mass:** 26474 **Score:** 265 **Queries matched:** 14 **emPAI:** 0.71

CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
656	466.76	931.50	931.49	8.69	1	3	4.5	6	K.IPSMSKNR.V 651 655
1177	519.24	1036.46	1036.46	-2.76	0	42	0.00019	1	R.QQMENYPK.N 1176 1178 1179 1180
1293	527.24	1052.46	1052.46	-0.68	0	(36)	0.00088	1	R.QQMENYPK.N 1291 1292
2411	629.29	1256.56	1256.56	3.28	0	72	2.6e-007	1	K.VMSEFNNNFR.Q
2489	637.28	1272.55	1272.56	-1.69	0	(61)	1.8e-006	1	K.VMSEFNNNFR.Q 2490

---

96. LDHC_HUMAN **Mass:** 36630 **Score:** 264 **Queries matched:** 8 **emPAI:** 0.22

L-lactate dehydrogenase C chain OS=Homo sapiens GN=LDHC PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
215	421.76	841.50	841.50	1.55	0	3	2.2	5	K.ISGLPVTR.V
967	499.73	997.45	997.45	5.05	0	8	0.62	1	K.DYSVSANSR.I
2354	624.81	1247.60	1247.59	5.12	0	68	1.1e-006	1	R.VIGSGCNLDSAR.F 2352 2353
2859	675.79	1349.57	1349.58	-3.72	0	90	1.4e-009	1	K.LIEDDENSQCK.I 2858 2860

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97. ENTP3_HUMAN **Mass:** 59809 **Score:** 263 **Queries matched:** 6 **emPAI:** 0.06

Ectonucleoside triphosphate diphosphohydrolase 3 OS=Homo sapiens GN=ENTPD3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3864	824.39	1646.76	1646.76	-1.03	0	72	3.7e-007	1	K.GSGISSYGNNPQDVPR.A 3863 3865 3866 3867 3868

---

98. K1324_HUMAN **Mass:** 114445 **Score:** 262 **Queries matched:** 4 **emPAI:** 0.03

UPF0577 protein KIAA1324 OS=Homo sapiens GN=KIAA1324 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2619	649.28	1296.54	1296.54	2.84	0	91	8.8e-010	1	R.SNDVTQSCSSGR.S 2617 2618 2620

---

99. GPR64_HUMAN **Mass:** 113232 **Score:** 258 **Queries matched:** 8 **emPAI:** 0.10

G-protein coupled receptor 64 OS=Homo sapiens GN=GPR64 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
5	400.67	799.33	799.34	-2.61	0	22	0.0062	1	R.YLCCGK.L
160	416.73	831.45	831.45	1.42	0	47	0.00026	1	K.TSIQDLR.S
1933	583.75	1165.49	1165.48	7.78	0	55	5.2e-006	1	R.GGWSDNGCSVK.D 1925 1927 1928 1931 1932

---

100. CAPG_HUMAN **Mass:** 38760 **Score:** 257 **Queries matched:** 4 **emPAI:** 0.10

Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2444	632.81	1263.61	1263.61	-1.17	0	102	4.4e-010	1	K.VSDATGQMNLTK.V 2443 2445 2446

---

101. PPAP_HUMAN **Mass:** 44880 **Score:** 251 **Queries matched:** 16 **emPAI:** 0.75

Prostatic acid phosphatase OS=Homo sapiens GN=ACPP PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
373	441.27	880.52	880.52	2.12	0	32	0.002	1	K.FVTLVFR.H
528	454.25	906.48	906.48	-2.97	0	47	0.00014	1	R.ATQIPSYK.K 530 531 532 533 534 536

714	472.75	943.49	943.49	6.57	0	31	0.007	1	K.HEQVYIR.S
1173	518.30	1034.58	1034.58	4.84	1	40	0.00049	1	R.ATQIPSYKK.L 1172
2210	612.31	1222.61	1222.61	1.41	0	54	4.1e-005	1	R.FQELESETLK.S 2211
2770	665.85	1329.68	1329.68	1.72	0	35	0.0027	1	R.SPIDTFPTDPIK.E
4570	657.99	1970.95	1970.95	3.79	1	36	0.0013	1	R.FQELESETLKSEEFQK.R 4569

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102. 5NTD_HUMAN **Mass:** 63898 **Score:** 251 **Queries matched:** 7 **emPAI:** 0.18

5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
248	424.73	847.44	847.45	-6.39	0	21	0.08	1	K.LDVLCTK.C
1650	562.26	1122.50	1122.50	0.73	0	53	2e-005	1	R.LEQTSEDSSK.C 1648 1649 1651
3354	743.36	1484.70	1484.69	4.04	0	92	3.5e-009	1	K.TIVYLDGSSQSCR.F
4104	866.48	1730.94	1730.95	-0.89	0	65	1.6e-006	1	K.VLPVGDEVVGIVGYTSK.E

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103. LDHB_HUMAN **Mass:** 36900 **Score:** 242 **Queries matched:** 7 **emPAI:** 0.47

L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
766	480.28	958.55	958.54	2.77	0	32	0.0067	1	R.GLTSVINQK.L
1985	588.80	1175.58	1175.58	-2.07	0	35	0.003	1	K.SADTLWDIQK.D
2354	624.81	1247.60	1247.59	5.12	0	68	1.1e-006	1	R.VIGSGCNLDSAR.F 2352 2353
3981	847.95	1693.89	1693.89	2.25	0	89	5.7e-009	1	K.LIAPVAEEEATVPNNK.I 3980

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104. 1433B_HUMAN **Mass:** 28179 **Score:** 241 **Queries matched:** 8 **emPAI:** 0.66

14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
86	408.71	815.41	815.41	0.04	0	56	1.8e-005	1	K.LAEQAER.Y 83 84 85
498	452.26	902.51	902.51	0.50	0	49	0.00011	1	R.VISSIEQK.T 499
538	454.27	906.53	906.52	8.47	0	37	0.0012	1	R.NLLSVAYK.N
2011	591.78	1181.55	1181.56	-5.10	0	54	2.6e-005	1	R.YLSEVASGDNK.Q

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105. RAB3D_HUMAN **Mass:** 24480 **Score:** 237 **Queries matched:** 7 **emPAI:** 0.78

Ras-related protein Rab-3D OS=Homo sapiens GN=RAB3D PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
209	421.72	841.43	841.43	-3.58	0	4	2.3	1	R.VVPAEDGR.R
672	468.69	935.36	935.37	-1.23	0	56	2.7e-006	1	K.CDLEDER.V
848	488.26	974.51	974.51	0.68	0	53	5e-005	1	R.LVDVICEK.M 849
1538	550.84	1099.66	1099.66	3.69	0	68	5.1e-007	1	K.LLLIGNSSVGK.T 1537
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.LQIWDTAGQER.Y

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106. CYFP1_HUMAN **Mass:** 146742 **Score:** 235 **Queries matched:** 5 **emPAI:** 0.03

Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2408	628.30	1254.58	1254.58	-2.11	0	113	2.6e-011	1	R.YSNSEVVTGSGR.Q 2404 2405 2406 2409

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107. DDAH2_HUMAN **Mass:** 29911 **Score:** 233 **Queries matched:** 8 **emPAI:** 0.27

N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens GN=DDAH2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
842	487.74	973.46	973.47	-2.69	0	6	1.7	4	-.MGTPGEGLGR.C 843
1718	567.30	1132.58	1132.57	3.72	0	73	5.5e-007	1	R.TVVAGSSDAAQK.A 1717 1719
1840	576.31	1150.61	1150.62	-7.32	1	1	5.6	8	K.AQREHGVLGGK.L
3117	707.35	1412.68	1412.69	-4.50	0	68	9.9e-007	1	R.GGGDLPNSQEALQK.L 3118

108. GNA13_HUMAN **Mass:** 44364 **Score:** 232 **Queries matched:** 6 **emPAI:** 0.27
Guanine nucleotide-binding protein subunit alpha-13 OS=Homo sapiens GN=GNA13 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
356	439.21	876.41	876.41	-1.58	0	51	6.6e-005	1	K.MVDVGGQR.S 355
1316	529.32	1056.62	1056.62	0.47	0	73	2.5e-007	1	K.ILLLGAGESGK.S 1317
2503	639.31	1276.60	1276.59	4.44	0	50	6.2e-005	1	R.APMAAQGMVETR.V 2502

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109. GGT1_HUMAN **Mass:** 61714 **Score:** 229 **Queries matched:** 9 **emPAI:** 0.34
Gamma-glutamyltranspeptidase 1 OS=Homo sapiens GN=GGT1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1147	516.75	1031.48	1031.48	0.29	0	40	0.00053	1	R.ESVESPEQK.G 1144 1145 1146
1210	521.81	1041.60	1041.59	4.28	1	45	0.00023	1	K.GLAAALENKR.T
1354	532.30	1062.58	1062.57	6.12	0	40	0.00085	1	K.FVDVTEVVR.N
1864	577.83	1153.65	1153.65	1.55	0	42	0.00029	1	K.GGLSVAVPGEIR.G
1970	586.85	1171.68	1171.67	6.28	0	74	1.9e-007	1	R.LFQPSIQLAR.Q 1969

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110. TSN7_HUMAN **Mass:** 28183 **Score:** 225 **Queries matched:** 3 **emPAI:** 0.13
Tetraspanin-7 OS=Homo sapiens GN=TSPAN7 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4250	889.86	1777.71	1777.72	-5.72	0	105	2.9e-011	1	R.TYTDAMQTYNGNDER.S 4251 4252

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111. TERA_HUMAN **Mass:** 89950 **Score:** 223 **Queries matched:** 4 **emPAI:** 0.08
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1411	538.27	1074.53	1074.53	-2.52	0	71	6.5e-007	1	K.LAGESESNLR.K 1412
1614	558.76	1115.50	1115.50	1.10	0	83	1.6e-008	1	R.GGNIGDGGGAADR.V 1615

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112. CD38_HUMAN **Mass:** 35218 **Score:** 222 **Queries matched:** 12 **emPAI:** 0.66
ADP-ribosyl cyclase 1 OS=Homo sapiens GN=CD38 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1481	544.81	1087.61	1087.61	0.05	1	45	0.00018	1	K.RFPETVLAR.C
1486	545.27	1088.52	1088.52	-1.59	0	24	0.022	1	R.DLCQDPTIK.E 1485
1621	559.29	1116.56	1116.56	-2.48	0	51	7.3e-005	1	K.LGTQTVPCNK.I 1620 1622 1623 1624 1625 1626
2300	619.75	1237.48	1237.48	0.24	0	21	0.0078	1	K.NPEDSSCTSEI.-
2799	669.80	1337.59	1337.58	4.19	0	62	1.9e-006	1	K.INYQSCPDWR.K

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113. CIB1_HUMAN **Mass:** 21861 **Score:** 222 **Queries matched:** 5 **emPAI:** 0.91
Calcium and integrin-binding protein 1 OS=Homo sapiens GN=CIB1 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
178	418.73	835.44	835.44	-0.25	0	32	0.0052	1	R.VFSTSPAK.D
902	493.24	984.46	984.46	2.89	0	63	2.1e-006	1	R.SPDFASSFK.I
2710	660.33	1318.64	1318.63	6.43	0	44	0.00034	1	R.FCELLPQEQR.S
3275	732.34	1462.67	1462.67	1.67	0	93	2.7e-009	1	R.LVNCLTGEGEDTR.L 3277

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114. HEBP1_HUMAN **Mass:** 21198 **Score:** 221 **Queries matched:** 6 **emPAI:** 0.39
Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1652	562.27	1122.52	1122.53	-6.67	0	35	0.002	1	K.EADYVAQATR.L
3835	820.90	1639.79	1639.78	3.70	0	62	4.5e-006	1	R.IPNQFQSDPPAPSDK.S 3831 3832 3833 3834

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115. MYO1D_HUMAN **Mass:** 116927 **Score:** 219 **Queries matched:** 15 **emPAI:** 0.10

Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
463	448.72	895.43	895.43	-2.19	0	16	0.19	4	R.DTIEQYK.G 461 462
736	476.23	950.45	950.45	-1.36	0	62	4.4e-006	1	K.CTVSVETR.L 735
925	495.77	989.52	989.52	4.65	0	2	6.3	1	R.SGFILSVPGN.-
1111	513.29	1024.57	1024.57	5.68	0	46	0.00011	1	R.VIVQQPGER.S 1107 1108 1109 1110
2029	594.30	1186.59	1186.60	-5.76	0	42	0.00054	1	R.LNQPQPDFTK.N 2030 2032 2033

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116. MYH9_HUMAN **Mass:** 227646 **Score:** 217 **Queries matched:** 6 **emPAI:** 0.03

Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
439	446.75	891.48	891.47	9.33	1	11	0.78	4	K.KLEMDLK.D
1242	523.29	1044.56	1044.56	-2.61	0	3	3.9	2	R.LEVNLQAMK.A
2277	618.25	1234.49	1234.49	-4.15	0	2	0.61	1	K.GAGDGSDEEVDGK.A
3708	796.35	1590.70	1590.69	0.57	0	93	1.1e-009	1	R.NTDQASMPDNTAAQK.V 3707
3748	804.35	1606.69	1606.69	0.61	0	(62)	1.1e-006	1	R.NTDQASMPDNTAAQK.V

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117. MYH11_HUMAN **Mass:** 228054 **Score:** 217 **Queries matched:** 6 **emPAI:** 0.03

Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
89	409.21	816.40	816.40	-2.52	0	4	2.7	8	R.NALQDEK.R
1854	577.27	1152.53	1152.53	-0.58	0	6	1.4	3	K.MTESSLPSASK.T 1851
3708	796.35	1590.70	1590.69	0.57	0	93	1.1e-009	1	R.NTDQASMPDNTAAQK.V 3707
3748	804.35	1606.69	1606.69	0.61	0	(62)	1.1e-006	1	R.NTDQASMPDNTAAQK.V

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118. RAB1A_HUMAN **Mass:** 22891 **Score:** 214 **Queries matched:** 7 **emPAI:** 0.86

Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1247	523.75	1045.49	1045.49	-0.40	0	51	4.2e-005	1	R.MGPGATAGGAEK.S 1245
1348	531.75	1061.48	1061.48	-3.09	0	(46)	0.00011	1	R.MGPGATAGGAEK.S 1349 1350
1398	536.33	1070.64	1070.63	3.27	0	51	4.5e-005	1	K.LLLIGDSGVGK.S
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.LQIWDTAGQER.F

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119. NHRF2_HUMAN **Mass:** 37619 **Score:** 211 **Queries matched:** 9 **emPAI:** 0.21

Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
750	478.74	955.47	955.47	-0.43	0	48	9.8e-005	1	R.SVDPGSPAAR.S 748 749
2941	683.81	1365.61	1365.60	3.39	0	59	3.5e-006	1	R.QLTCTEEMAQR.G 2938 2939 2940 2942
4312	904.40	1806.78	1806.79	-4.62	1	1	2.8	3	R.SDLPGSDKDTEDGSAWK.Q

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120. G6PI_HUMAN **Mass:** 63335 **Score:** 211 **Queries matched:** 8 **emPAI:** 0.12

Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
225	423.20	844.39	844.39	-3.14	0	54	1.8e-005	1	K.SPEDLER.L 226 227 228
260	426.71	851.41	851.41	-0.62	0	44	0.00036	1	K.INYTEGR.A 258 259 261

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121. GNAI1_HUMAN **Mass:** 40905 **Score:** 210 **Queries matched:** 4 **emPAI:** 0.30

Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
547	455.22	908.42	908.42	2.56	0	53	3.1e-005	1	K.MFDVGGQR.S
1316	529.32	1056.62	1056.62	0.47	0	73	2.5e-007	1	K.LLLLGAGESGK.S 1317
1846	577.26	1152.50	1152.50	-2.07	0	73	1.2e-007	1	K.DSGVQACFNR.S

122. CD9_HUMAN **Mass:** 25969 **Score:** 209 **Queries matched:** 12 **emPAI:** 1.27
CD9 antigen OS=Homo sapiens GN=CD9 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
168	**417.23**	**832.45**	**832.45**	**2.26**	**1**	**5**	**2.3**	**3**	**-.MPVKGGTK.C** 163 164
351	437.22	872.43	872.44	-0.66	1	41	0.00048	1	K.TKDEPQR.E
705	**471.73**	**941.45**	**941.45**	**5.78**	**0**	**33**	**0.0028**	**1**	**K.EVQEFYK.D** 704
1287	**526.29**	**1050.56**	**1050.56**	**-0.53**	**0**	**39**	**0.00088**	**1**	**K.DVLETFTVK.S**
1607	**558.29**	**1114.56**	**1114.56**	**1.45**	**1**	**29**	**0.0082**	**1**	**K.DEPQRETLK.A** 1608
2002	**590.33**	**1178.65**	**1178.65**	**-0.36**	**1**	**82**	**3.1e-008**	**1**	**K.KDVLETFTVK.S** 2004
3598	**782.37**	**1562.73**	**1562.73**	**1.52**	**1**	**51**	**4e-005**	**1**	**K.EVQEFYKDTYNK.L**

123. FLOT1_HUMAN **Mass:** 47554 **Score:** 209 **Queries matched:** 8 **emPAI:** 0.16
Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
390	442.73	883.45	883.44	1.42	0	5	1.8	5	K.FSEQVFK.V
643	**465.74**	**929.46**	**929.46**	**0.20**	**0**	**48**	**0.0001**	**1**	**K.QQIEEQR.V** 644
1497	**546.28**	**1090.54**	**1090.54**	**-2.86**	**0**	**16**	**0.27**	**1**	**R.GEAEAFAIGAR.A**
2508	640.33	1278.65	1278.66	-1.77	1	6	2.1	5	K.KAAYDIEVNTR.R
3303	**735.39**	**1468.76**	**1468.76**	**-3.14**	**0**	**85**	**2.1e-008**	**1**	**R.AQQVAVQEQEIAR.R** 3304 3305

124. S52A3_HUMAN **Mass:** 51741 **Score:** 208 **Queries matched:** 8 **emPAI:** 0.15
Solute carrier family 52, riboflavin transporter, member 3 OS=Homo sapiens GN=SLC52A3 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
5045	**1212.05**	**2422.08**	**2422.08**	**0.02**	**0**	**79**	**2.4e-008**	**1**	**R.EENDLGPAGTVDSSQGQGYLEEK.A** 5042 5043 5044 5047 5049 5050 5051

125. 1433F_HUMAN **Mass:** 28372 **Score:** 208 **Queries matched:** 8 **emPAI:** 0.46
14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
86	408.71	815.41	815.41	0.04	0	56	1.8e-005	1	R.LAEQAER.Y 83 84 85
498	452.26	902.51	902.51	0.50	0	49	0.00011	1	R.VISSIEQK.T 499
538	454.27	906.53	906.52	8.47	0	37	0.0012	1	R.NLLSVAYK.N
1040	**505.23**	**1008.45**	**1008.45**	**-4.32**	**1**	**3**	**2.4**	**4**	**K.TMADGNEKK.L**

126. 1433S_HUMAN **Mass:** 27871 **Score:** 208 **Queries matched:** 7 **emPAI:** 0.47
14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
86	408.71	815.41	815.41	0.04	0	56	1.8e-005	1	K.LAEQAER.Y 83 84 85
498	452.26	902.51	902.51	0.50	0	49	0.00011	1	R.VLSSIEQK.S 499
538	454.27	906.53	906.52	8.47	0	37	0.0012	1	R.NLLSVAYK.N

127. RAB8A_HUMAN **Mass:** 23824 **Score:** 206 **Queries matched:** 16 **emPAI:** 0.56
Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
141	**415.23**	**828.44**	**828.43**	**2.27**	**0**	**15**	**0.16**	**1**	**K.ITPDQQK.R** 135 136 137 139 140 142
1398	536.33	1070.64	1070.63	3.27	0	51	4.5e-005	1	K.LLLIGDSGVGK.T
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.LQIWDTAGQER.F
3090	**703.84**	**1405.66**	**1405.67**	**-5.61**	**1**	**(0)**	**5.1**	**2**	**K.MILGNKCDVNDK.R**
3126	**707.85**	**1413.69**	**1413.68**	**3.35**	**0**	**73**	**3.4e-007**	**1**	**K.LEGNSPQGSNQGVK.I** 3125
3141	711.83	1421.65	1421.66	-8.07	1	4	1.6	4	K.MILGNKCDVNDK.R 3143 3144 3145

128. CNDP2_HUMAN **Mass:** 53187 **Score:** 206 **Queries matched:** 6 **emPAI:** 0.23

Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1595	556.81	1111.61	1111.60	6.51	0	66	1.3e-006	1	K.TGQEIPVNVR.F 1593
2270	617.33	1232.64	1232.64	-1.59	0	27	0.016	1	K.TVFGVEPDLTR.E 2271
4108	867.95	1733.88	1733.88	0.45	0	78	1.3e-007	1	R.EGGSIPVTLTFQEATGK.N 4109

129. PLS3_HUMAN **Mass:** 32369 **Score:** 206 **Queries matched:** 3 **emPAI:** 0.12

Phospholipid scramblase 3 OS=Homo sapiens GN=PLSCR3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4557	981.92	1961.82	1961.83	-5.64	0	97	2.4e-010	1	R.SGAGQPLGQAAEESNCCAR.L 4558 4559

130. PCY2_HUMAN **Mass:** 44264 **Score:** 206 **Queries matched:** 3 **emPAI:** 0.08

Ethanolamine-phosphate cytidylyltransferase OS=Homo sapiens GN=PCYT2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2009	591.29	1180.56	1180.56	-0.77	0	92	4e-009	1	R.GAAGGAEQPGPGGR.R 2008 2010

131. MRP_HUMAN **Mass:** 19574 **Score:** 205 **Queries matched:** 3 **emPAI:** 0.43

MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2749	664.33	1326.64	1326.64	-1.62	0	45	0.00019	1	K.AAATPESQEPQAK.G
2968	687.33	1372.64	1372.65	-4.14	0	108	7.5e-011	1	R.GDVTAEEAAGASPAK.A 2969

132. FAS_HUMAN **Mass:** 275877 **Score:** 202 **Queries matched:** 7 **emPAI:** 0.04

Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
26	402.73	803.44	803.44	0.25	0	4	5.9	7	K.LQELSSK.A
248	424.73	847.44	847.45	-6.37	0	8	1.6	4	R.DIMLATGK.L
527	454.23	906.44	906.44	0.34	0	58	1.4e-005	1	R.AAEQYTPK.A 526
2056	596.79	1191.56	1191.56	1.18	0	9	0.86	1	R.LGMLSPEGTCK.A
3035	694.82	1387.62	1387.63	-6.72	0	60	4e-006	1	K.ADEASELACPTPK.E
4268	895.38	1788.75	1788.75	-1.86	0	84	6.1e-009	1	R.GNAGQSNYGFANSAMER.I

133. RB27B_HUMAN **Mass:** 24820 **Score:** 199 **Queries matched:** 9 **emPAI:** 0.53

Ras-related protein Rab-27B OS=Homo sapiens GN=RAB27B PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
75	407.70	813.40	813.40	-3.48	0	49	6.3e-005	1	K.ADLPDQR.E 76 77 78 79
603	462.20	922.39	922.39	0.47	0	(44)	8.1e-005	1	R.MEQCVEK.T 604
690	470.20	938.39	938.38	2.17	0	44	6.9e-005	1	R.MEQCVEK.T 689

134. CLUS_HUMAN **Mass:** 53031 **Score:** 198 **Queries matched:** 8 **emPAI:** 0.23

Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1394	536.29	1070.57	1070.57	-4.91	0	52	4.4e-005	1	K.EIQNAVNGVK.Q 1395 1396
2559	644.82	1287.63	1287.63	3.10	0	60	6.9e-006	1	R.ELDESLQVAER.L
4205	881.92	1761.83	1761.82	4.56	0	63	3e-006	1	R.EILSVDCSTNNPSQAK.L 4201 4202 4203

135. TSN31_HUMAN **Mass:** 23665 **Score:** 198 **Queries matched:** 4 **emPAI:** 0.16

Tetraspanin-31 OS=Homo sapiens GN=TSPAN31 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3106	706.78	1411.55	1411.55	-2.47	0	77	2.2e-008	1	K.SQSPTCQMCGEK.F 3107 3108 3109

```
136.  FXL20_HUMAN     Mass: 50216     Score: 198     Queries matched: 4    emPAI: 0.07
      F-box/LRR-repeat protein 20 OS=Homo sapiens GN=FBXL20 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
      2017    592.78   1183.54   1183.54 -1.89    0    82  2.8e-008    1    K.TTDATCTSLSK.F 2016 2018 2019

137.  TCPR1_HUMAN     Mass: 131439    Score: 197     Queries matched: 4    emPAI: 0.03
      Tectonin beta-propeller repeat-containing protein 1 OS=Homo sapiens GN=TECPR1 PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
      4026    854.36   1706.70   1706.71 -3.25    0    85  4.3e-009    1    R.TAEDTVEDACPAEGSR.E 4027 4028 4029

138.  RAB3A_HUMAN     Mass: 25196     Score: 195     Queries matched: 5    emPAI: 0.53
      Ras-related protein Rab-3A OS=Homo sapiens GN=RAB3A PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
       848    488.26    974.51    974.51  0.68    0    53    5e-005    1    R.LVDVICEK.M 849
      1538    550.84   1099.66   1099.66  3.69    0    68  5.1e-007    1    K.ILIIGNSSVGK.T 1537
      2701    658.83   1315.65   1315.65  1.50    0    74  3.2e-007    1    K.LQIWDTAGQER.Y

139.  CAZA1_HUMAN     Mass: 33073     Score: 195     Queries matched: 4    emPAI: 0.24
      F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
       521    453.72    905.42    905.43 -2.96    1    11      0.48    1    K.IGKEMQNA.-
      3528    771.85   1541.68   1541.68 -1.65    0    89    4e-009    1    K.EASDPQPEEADGGLK.S 3527
      4022    853.41   1704.81   1704.82 -4.87    0    57  1.4e-005    1    K.DVQDSLTVSNEAQTAK.E

140.  WFDC8_HUMAN     Mass: 29516     Score: 193     Queries matched: 3    emPAI: 0.44
      WAP four-disulfide core domain protein 8 OS=Homo sapiens GN=WFDC8 PE=2 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
      3452    760.34   1518.67   1518.67  1.04    0    84    1e-008    1    K.CLQDEECPLVEK.C
      4378    920.87   1839.73   1839.73  4.04    0   115  2.8e-012    1    R.GCEGNANNFLNEDACR.T
      5217    909.05   2724.13   2724.14 -1.44    1    22    0.0061    1    R.LTCTTELPDSCNTDFDCKEYQK.C

141.  MT1G_HUMAN     Mass: 7277      Score: 193     Queries matched: 5    emPAI: 1.46
      Metallothionein-1G OS=Homo sapiens GN=MT1G PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
       949    498.71    995.40    995.40 -0.65    0    44  4.6e-005    1    K.CAQGCICK.G 950
      3213    723.26   1444.50   1444.50  0.20    0    79  1.3e-008    1    K.SCCSCCPVGCAK.C 3212
      3301    734.82   1467.62   1467.63 -4.85    1     7      0.41    1    K.CAQGCICKGASEK.C

142.  PROF2_HUMAN     Mass: 15378     Score: 188     Queries matched: 2    emPAI: 0.25
      Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
      3183    717.85   1433.69   1433.69  0.09    0   109  8.1e-011    1    K.SQGGEPTYNVAVGR.A 3182

143.  ADAM7_HUMAN     Mass: 88122     Score: 187     Queries matched: 4    emPAI: 0.04
      Disintegrin and metalloproteinase domain-containing protein 7 OS=Homo sapiens GN=ADAM7 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank   Peptide
      3792    813.92   1625.82   1625.83 -4.68    0    97  1.4e-009    1    K.QVQSPPTETLGVENK.G 3793 3794 3795

144.  PRSS8_HUMAN     Mass: 37093     Score: 183     Queries matched: 6    emPAI: 0.21
      Prostasin OS=Homo sapiens GN=PRSS8 PE=1 SV=1
```

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
211	**421.74**	**841.46**	**841.47**	**-2.28**	**0**	**48**	**0.0001**	**1**	**K.VTELQPR.V** 212 213 214
3498	**511.91**	**1532.72**	**1532.71**	**5.42**	**0**	**60**	**6.3e-006**	**1**	**K.LGAHQLDSYSEDAK.V** 3497

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145. RAB8B_HUMAN **Mass:** 23740 **Score:** 182 **Queries matched:** 3 **emPAI:** 0.56

Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1398	536.33	1070.64	1070.63	3.27	0	51	4.5e-005	1	K.LLLIGDSGVGK.T
2651	**652.80**	**1303.59**	**1303.58**	**2.68**	**0**	**98**	**7.1e-010**	**1**	**K.MNDSNSAGAGGPVK.I**
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.LQIWDTAGQER.F

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146. HORN_HUMAN **Mass:** 283140 **Score:** 180 **Queries matched:** 3 **emPAI:** 0.03

Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1756	**570.26**	**1138.50**	**1138.50**	**1.20**	**0**	**78**	**5.4e-008**	**1**	**R.GSGSGQSPSYGR.H**
3051	**698.32**	**1394.62**	**1394.62**	**1.88**	**0**	**92**	**2.5e-009**	**1**	**R.YGQQGSGSGQSPSR.G** 3050

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147. KIF5A_HUMAN **Mass:** 118161 **Score:** 179 **Queries matched:** 4 **emPAI:** 0.03

Kinesin heavy chain isoform 5A OS=Homo sapiens GN=KIF5A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
367	440.22	878.42	878.42	1.38	1	9	1.1	2	K.EAKEGAMK.D 366
1892	580.79	1159.57	1159.57	2.47	0	102	5.9e-010	1	K.TGAEGAVLDEAK.N 1891

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148. KIF5C_HUMAN **Mass:** 109997 **Score:** 179 **Queries matched:** 6 **emPAI:** 0.03

Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
421	444.75	887.48	887.47	5.37	0	3	7.5	8	K.IQEELTR.L
1892	580.79	1159.57	1159.57	2.47	0	102	5.9e-010	1	K.TGAEGAVLDEAK.N 1891
2504	**639.79**	**1277.57**	**1277.57**	**-0.95**	**0**	**6**	**0.92**	**2**	**K.QLESAQMDSNR.K** 2505 2506

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149. 1433E_HUMAN **Mass:** 29326 **Score:** 178 **Queries matched:** 6 **emPAI:** 0.44

14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
86	408.71	815.41	815.41	0.04	0	56	1.8e-005	1	K.LAEQAER.Y 83 84 85
538	454.27	906.53	906.52	8.47	0	37	0.0012	1	R.NLLSVAYK.N
2069	**597.81**	**1193.60**	**1193.59**	**9.29**	**0**	**42**	**0.00069**	**1**	**K.EAAENSLVAYK.A**

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150. RRAS2_HUMAN **Mass:** 23613 **Score:** 178 **Queries matched:** 3 **emPAI:** 0.16

Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3028	**693.85**	**1385.69**	**1385.69**	**-2.54**	**0**	**78**	**1.2e-007**	**1**	**R.QVTQEEGQQLAR.Q** 3026 3027

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151. K1C10_HUMAN **Mass:** 59020 **Score:** 177 **Queries matched:** 3 **emPAI:** 0.13

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	Peptide
1566	553.77	1105.52	1105.52	0.27	0	65	2.2e-006	1	K.VTMQNLNDR.L 1567
2429	**631.80**	**1261.59**	**1261.59**	**2.68**	**0**	**88**	**8.8e-009**	**1**	**R.SLLEGEGSSGGGGR.G**

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152. MT1E_HUMAN **Mass:** 7150 **Score:** 176 **Queries matched:** 3 **emPAI:** 1.52

Metallothionein-1E OS=Homo sapiens GN=MT1E PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

```
          876     491.70    981.38    981.38   1.78   0    57  2.2e-006    1   K.CAQGCVCK.G
         3213     723.26   1444.50   1444.50   0.20   0    79  1.3e-008    1   K.SCCSCCPVGCAK.C 3212

153.   TBB2A_HUMAN     Mass: 50274    Score: 175    Queries matched: 4   emPAI: 0.33
       Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1430    541.22   1080.42   1080.42   0.41   0   (37)  0.00026    1   K.NMMAACDPR.H
       1522    549.21   1096.41   1096.41   0.14   0    43  4.7e-005    1   K.NMMAACDPR.H
       3217    723.85   1445.68   1445.68  -3.24   0   (66) 1.7e-006    1   K.EVDEQMLNVQNK.N
       3273    731.85   1461.68   1461.68   0.86   0    75  1.6e-007    1   K.EVDEQMLNVQNK.N


       Proteins matching the same set of peptides:
       TBB2B_HUMAN     Mass: 50377    Score: 175    Queries matched: 4
       Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1
       TBB4B_HUMAN     Mass: 50255    Score: 175    Queries matched: 4
       Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1
       TBB5_HUMAN     Mass: 50095    Score: 175    Queries matched: 4
       Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2

154.   PSCA_HUMAN     Mass: 13474    Score: 175    Queries matched: 2   emPAI: 0.29
       Prostate stem cell antigen OS=Homo sapiens GN=PSCA PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
       4600    990.40   1978.79   1978.80  -5.50   0   100  1e-010   1   K.GCSLNCVDDSQDYYVGK.K 4601

155.   PODXL_HUMAN     Mass: 59055    Score: 175    Queries matched: 3   emPAI: 0.06
       Podocalyxin OS=Homo sapiens GN=PODXL PE=1 SV=2
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       3295    734.32   1466.62   1466.62   0.58   0    73  6.1e-008    1   K.CEDLETQTQSEK.Q 3294 3296

156.   STXB2_HUMAN     Mass: 66867    Score: 175    Queries matched: 15   emPAI: 0.11
       Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=1 SV=2
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
         42    405.21    808.41    808.41  -1.54   0     8       1.1    9   R.AAYEVTR.A 38 39 40 41 43
        311    434.20    866.39    866.40  -9.56   0    14      0.12    1   R.ILSSCCK.M 312
       2062    597.75   1193.49   1193.49   4.10   0     7      0.31    2   K.DVMEDAVEDR.L 2063 2064 2065
       2091    600.79   1199.56   1199.57  -1.93   0    63    2e-006    1   K.ADTPSLGEGPEK.T 2090
       4492    966.48   1930.95   1930.93   5.54   0   104  2.6e-010    1   R.NLEQLGGTVTNPGGSGTSSR.L

157.   RAB35_HUMAN     Mass: 23296    Score: 173    Queries matched: 5   emPAI: 0.58
       Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1398    536.33   1070.64   1070.63   3.27   0    51  4.5e-005    1   K.LLIIGDSGVGK.S
       1914    582.79   1163.57   1163.57   1.59   1     3       4.1    2   M.ARDYDHLFK.L
       2701    658.83   1315.65   1315.65   1.50   0    74  3.2e-007    1   K.LQIWDTAGQER.F
       2820    671.84   1341.66   1341.66   0.34   0    71  4.3e-007    1   K.QQQQQNDVVK.L 2819

158.   GNA12_HUMAN     Mass: 44422    Score: 173    Queries matched: 5   emPAI: 0.18
       Guanine nucleotide-binding protein subunit alpha-12 OS=Homo sapiens GN=GNA12 PE=1 SV=4
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        356    439.21    876.41    876.41  -1.58   0    51  6.6e-005    1   K.MVDVGGQR.S 355
       1316    529.32   1056.62   1056.62   0.47   0    73  2.5e-007    1   K.ILLLGAGESGK.S 1317
       1646    561.31   1120.61   1120.60   3.04   1     6         2    3   -.MSGVVRTLSR.C
```

```
159.  CTL2_HUMAN     Mass: 81610     Score: 169     Queries matched: 9    emPAI: 0.14
      Choline transporter-like protein 2 OS=Homo sapiens GN=SLC44A2 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       121    413.18    824.34    824.35  -5.29    0    35   0.00047    1   R.GEFCGQK.G 122 123 124
       733    475.75    949.49    949.49   5.48    0    21      0.09    1   K.VIYPTDSR.G 732
       751    479.28    956.54    956.54  -0.04    1    13      0.35    7   K.KANGVLEAR.Q
      3059    699.33   1396.64   1396.63   2.24    0    66  1.2e-006    1   K.IFDDSPCPFTAK.T
      3790    813.35   1624.68   1624.68  -1.99    0    64  7.5e-007    1   K.TCNPETFPSSNESR.Q

160.  DOP2_HUMAN     Mass: 260348     Score: 169     Queries matched: 7    emPAI: 0.03
      Protein dopey-2 OS=Homo sapiens GN=DOPEY2 PE=1 SV=5
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       563    456.74    911.46    911.46  -2.81    0     4         2    8   R.SYSSVIEK.A
      1133    516.28   1030.55   1030.54   3.03    1     5       2.9    9   K.EPEKYPLR.G
      1702    566.77   1131.53   1131.53   0.35    0    38    0.0009    1   K.TMAAGDPANLR.N 1703 1704
      2928    681.81   1361.61   1361.61   1.92    0    87  7.3e-009    1   K.SSESPSSSPSSPAR.K 2929

161.  PLSL_HUMAN     Mass: 70814     Score: 166     Queries matched: 10    emPAI: 0.29
      Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      1482    545.23   1088.46   1088.46  -0.22    0    40   0.00016    1   K.ALENDPDCR.H 1483
      1732    568.31   1134.61   1134.60   4.21    0    31    0.0065    1   R.QFVTATDVVR.G
      2369    626.27   1250.53   1250.54  -2.95    0     2       1.5    4   R.AECMLQQAER.L
      3120    707.80   1413.58   1413.58   5.69    0    16     0.024    1   R.GSVSDEEMMELR.E 3119 3123
      3412    751.88   1501.75   1501.74   1.12    0    31    0.0072    1   K.MINLSVPDTIDER.T
      3678    793.42   1584.83   1584.84  -6.14    0    61  4.3e-006    1   R.VYALPEDLVEVNPK.M 3679

162.  HCK_HUMAN     Mass: 60075     Score: 166     Queries matched: 6    emPAI: 0.06
      Tyrosine-protein kinase HCK OS=Homo sapiens GN=HCK PE=1 SV=5
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       398    443.72    885.43    885.43  -2.10    0     1       4.2    5   K.DAWEIPR.E
      2135    605.29   1208.57   1208.57   6.00    0    61  5.1e-006    1   R.VIEDNEYTAR.E 2131 2132 2133 2136


      Proteins matching the same set of peptides:
      LYN_HUMAN     Mass: 58993     Score: 166     Queries matched: 6
      Tyrosine-protein kinase Lyn OS=Homo sapiens GN=LYN PE=1 SV=3

163.  FA84A_HUMAN     Mass: 32870     Score: 164     Queries matched: 3    emPAI: 0.11
      Protein FAM84A OS=Homo sapiens GN=FAM84A PE=2 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      3436    756.83   1511.65   1511.65  -0.77    0    73  1.2e-007    1   K.APPGCTPCPESPSR.H 3435 3437

164.  K1C14_HUMAN     Mass: 51872     Score: 164     Queries matched: 4    emPAI: 0.15
      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  Peptide
      1566    553.77   1105.52   1105.52   0.27    0    65  2.2e-006    1   K.VTMQNLNDR.L 1567
      2924    681.35   1360.68   1360.68  -5.09    0    11       0.6    2   R.EVATNSELVQSGK.S
      3147    713.35   1424.69   1424.69  -2.84    0    76  1.9e-007    1   R.APSTYGGGLSVSSSR.F

165.  PTGR1_HUMAN     Mass: 36075     Score: 163     Queries matched: 4    emPAI: 0.22
      Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
```

```
         2601     647.79   1293.57   1293.57   1.78    0     63    2e-006    1    K.EGDTMMGQQVAK.V 2602 2603
         2676     655.79   1309.57   1309.56   2.85    0   (51) 2.4e-005    1    K.EGDTMMGQQVAK.V
```

```
166.   GBG12_HUMAN     Mass: 8115      Score: 160     Queries matched: 3    emPAI: 0.51
       Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
        1802    573.80   1145.58   1145.58   -0.89    0     70  9.5e-007    1    K.TASTNNIAQAR.R 1801 1803
```

```
167.   RAB5C_HUMAN     Mass: 23696     Score: 160     Queries matched: 7    emPAI: 0.35
       Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
        2147    606.29   1210.57   1210.57   -0.49    0     44   0.00024    1    K.NEPQNATGAPGR.N 2148 2149 2150
        2635    650.31   1298.62   1298.62   -4.92    0     62  2.9e-006    1    R.GVDLQENNPASR.S 2634 2636
```

```
168.   PACN3_HUMAN     Mass: 48799     Score: 159     Queries matched: 4    emPAI: 0.16
       Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens GN=PACSIN3 PE=1 SV=2
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
         646    466.72    931.44    931.44   -0.81    0     56  1.4e-005    1    K.LQGQDSER.V
        2106    602.30   1202.59   1202.59    0.59    0     80  1.1e-007    1    K.ADSAVSQEQLR.K 2105
        2771    666.35   1330.68   1330.68   -5.79    1     14      0.37    2    K.ADSAVSQEQLRK.L
```

```
169.   PHP14_HUMAN     Mass: 13995     Score: 158     Queries matched: 2    emPAI: 0.28
       14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
        2948    684.76   1367.50   1367.50   -0.53    0     91  8.2e-010    1    K.QGCDCECLGGGR.I 2949
```

```
170.   LAMP1_HUMAN     Mass: 45367     Score: 156     Queries matched: 4    emPAI: 0.17
       Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
        1154    517.28   1032.55   1032.55    6.39    0     61    6e-006    1    K.TVESITDIR.A 1153
        1839    576.31   1150.60   1150.60    3.94    0     66  2.3e-006    1    R.ALQATVGNSYK.C 1836
```

```
171.   TSN9_HUMAN     Mass: 27559     Score: 156     Queries matched: 2    emPAI: 0.14
       Tetraspanin-9 OS=Homo sapiens GN=TSPAN9 PE=1 SV=1
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
        2896    679.74   1357.46   1357.46    0.68    0     91  8.3e-010    1    R.CCMENSQGCGR.N 2895
```

```
172.   GBB1_HUMAN     Mass: 38151     Score: 155     Queries matched: 4    emPAI: 0.33
       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
          26    402.73    803.44    803.44   -5.61    1      6       3.6    4    R.IQMRTR.R
        1043    505.26   1008.51   1008.51   -0.53    0     56  1.7e-005    1    R.AGVLAGHDNR.V
        1078    509.29   1016.56   1016.55    7.85    0     69    1e-006    1    R.LLVSASQDGK.L
        2222    613.30   1224.59   1224.58    9.90    0     72  4.7e-007    1    R.LFVSGACDASAK.L
```

```
173.   KPYM_HUMAN     Mass: 58470     Score: 155     Queries matched: 4    emPAI: 0.13
       Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4
       Query  Observed   Mr(expt)  Mr(calc)    ppm  Miss Score    Expect Rank   Peptide
         922    495.76    989.50    989.50    0.53    0     71  8.1e-007    1    K.GSGTAEVELK.K 921 924
        4859   1088.07   2174.12   2174.11    3.60    0     66  1.2e-006    1    R.LAPITSDPTEATAVGAVEASFK.C
```

---

174. EZRI_HUMAN **Mass:** 69484 **Score:** 155 **Queries matched:** 17 **emPAI:** 0.37

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
9	401.23	800.44	800.44	0.81	0	35	0.0023	1	R.QAVDQIK.S 7 8 10 11
243	424.68	847.34	847.35	-4.75	0	15	0.034	1	R.DQWEDR.I
354	438.23	874.44	874.44	-0.32	0	38	0.0013	1	R.QQLETEK.K
466	449.72	897.43	897.42	8.88	0	36	0.0014	1	K.SGYLSSER.L
798	483.26	964.50	964.50	-0.63	1	20	0.079	1	R.NISFNDKK.F
995	501.77	1001.52	1001.51	1.70	0	15	0.35	2	R.ELSEQIQR.A 985 986 988 993
1004	502.29	1002.56	1002.55	7.89	1	38	0.001	1	R.KENPLQFK.F 1003
2012	591.80	1181.59	1181.59	-0.67	0	71	4.8e-007	1	K.APDFVFYAPR.L

---

175. SERC5_HUMAN **Mass:** 48574 **Score:** 153 **Queries matched:** 4 **emPAI:** 0.16

Serine incorporator 5 OS=Homo sapiens GN=SERINC5 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
592	460.73	919.44	919.44	0.11	0	71	5.4e-007	1	R.SSSDALQGR.Y 591 593
1710	566.80	1131.59	1131.59	0.11	0	62	5.9e-006	1	R.YAAPELEIAR.C

---

176. STAT3_HUMAN **Mass:** 88810 **Score:** 152 **Queries matched:** 3 **emPAI:** 0.04

Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1840	576.31	1150.61	1150.60	8.73	0	7	1.6	3	K.FPELNYQLK.I
4409	932.42	1862.82	1862.82	0.27	0	126	5.4e-013	1	K.SQGDMQDLNGNNQSVTR.Q 4407

---

177. RAB3C_HUMAN **Score:** 151 **Queries matched:** 5

Ras-related protein Rab-3C OS=Homo sapiens GN=RAB3C PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
848	488.26	974.51	974.51	0.68	0	21	0.082	2	R.LVDIICDK.M 849
1538	550.84	1099.66	1099.66	3.69	0	68	5.1e-007	1	K.LLIIGNSSVGK.T 1537
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.LQIWDTAGQER.Y

---

178. WDR48_HUMAN **Mass:** 77018 **Score:** 151 **Queries matched:** 2 **emPAI:** 0.05

WD repeat-containing protein 48 OS=Homo sapiens GN=WDR48 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3581	777.35	1552.68	1552.68	0.26	0	89	4.1e-009	1	R.DGTQCLSGSSDGTIR.L 3580

---

179. CD47_HUMAN **Mass:** 35590 **Score:** 150 **Queries matched:** 7 **emPAI:** 0.11

Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
641	465.29	928.56	928.56	3.01	0	20	0.054	1	K.IEVSQLLK.G
1762	570.28	1138.55	1138.55	3.01	0	55	1.9e-005	1	K.STVPTDFSSAK.I 1757 1759 1760 1763 1764

---

180. GMPPA_HUMAN **Mass:** 46604 **Score:** 149 **Queries matched:** 5 **emPAI:** 0.08

Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1234	523.24	1044.47	1044.46	4.36	0	5	1	3	R.YQDTHPER.L
3381	747.84	1493.67	1493.67	-0.16	0	58	6e-006	1	R.VEGTPSDPNPNDPR.A 3380 3382 3384

---

181. ANXA4_HUMAN **Mass:** 36088 **Score:** 146 **Queries matched:** 3 **emPAI:** 0.10

Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

```
       2964    686.34   1370.66   1370.66   3.79    0     70  5.7e-007    1    R.ISQTYQQQYGR.S 2963 2965

182.  S26A3_HUMAN     Mass: 85021     Score: 145     Queries matched: 3    emPAI: 0.09
      Chloride anion exchanger OS=Homo sapiens GN=SLC26A3 PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        894    492.30    982.58    982.58  -1.53    0     69  3.4e-007    1    K.QGLLQVTPK.G 896
        935    496.25    990.49    990.49   0.14    0     53  3.3e-005    1    K.CSTLANIGR.T

183.  LY6K_HUMAN     Mass: 19288     Score: 144     Queries matched: 4    emPAI: 0.20
      Lymphocyte antigen 6K OS=Homo sapiens GN=LY6K PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       2597    647.77   1293.53   1293.54  -6.07    0     53  5.1e-006    1    R.ENTFECQNPR.R 2598 2599 2600

184.  POTEE_HUMAN     Mass: 122882     Score: 143     Queries matched: 5    emPAI: 0.03
      POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        853    488.73    975.44    975.44   2.57    0     85  1.6e-008    1    K.AGFAGDDAPR.A 852
       1575    554.27   1106.53   1106.53   5.13    0     12      0.47    2    K.MSQELEINK.D 1576 1578

185.  DHAK_HUMAN     Mass: 59252     Score: 140     Queries matched: 3    emPAI: 0.13
      Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        723    474.74    947.46    947.46   0.92    0     60  7.7e-006    1    K.SAEAAAEATK.N
       4502    970.96   1939.91   1939.91   0.77    0     74  2.5e-007    1    R.VAPAEPQEAPDSTAAGGSASK.R 4503

186.  G3P_HUMAN     Mass: 36201     Score: 138     Queries matched: 7    emPAI: 0.22
      Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         28    403.22    804.42    804.42  -9.52    0      2     9.1    1   K.VGVNGFGR.I
        138    415.22    828.43    828.43  -0.95    0     34  0.0023    1   K.QASEGPLK.G 136 139 140 142
       4372    917.47   1832.92   1832.91   2.74    0    115  2e-011    1   K.IISNASCTTNCLAPLAK.V

187.  LRC47_HUMAN     Mass: 64004     Score: 138     Queries matched: 3    emPAI: 0.06
      Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1859    577.33   1152.65   1152.66  -6.67    1      8      0.53    3    R.LRELPADLAR.C
       3365    745.81   1489.60   1489.59   7.82    0     82  6.3e-009    1    R.EGGDGEEQDVGDAGR.L 3364

188.  GSTO1_HUMAN     Mass: 27833     Score: 137     Queries matched: 4    emPAI: 0.14
      Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       2712    660.85   1319.68   1319.68  -0.96    0     62  6.2e-006    1    K.GSAPPGPVPEGSIR.I 2711 2713 2714

189.  CD59_HUMAN     Mass: 14795     Score: 137     Queries matched: 3    emPAI: 0.60
      CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        440    446.75    891.49    891.48   6.60    0     63  4.6e-006    1    K.AGLQVYNK.C 439
       2996    690.29   1378.56   1378.55   4.08    0     51  9.5e-006    1    R.ENELTYYCCK.K

190.  NPT2B_HUMAN     Mass: 77363     Score: 137     Queries matched: 7    emPAI: 0.05
```

Sodium-dependent phosphate transport protein 2B OS=Homo sapiens GN=SLC34A2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2440	632.31	1262.61	1262.62	-8.01	0	1	6.3	3	K.VISQIAMNDEK.A
3542	773.38	1544.75	1544.75	2.20	0	2	4.8	1	K.YLEGAAGQQPTAPDK.S
4442	946.93	1891.84	1891.85	-5.43	1	55	8.5e-006	1	R.EAQGEVPASDSKTECTAL.- 4443 4444 4445 4446

---

191. LDHA_HUMAN **Mass:** 36950 **Score:** 134 **Queries matched:** 5 **emPAI:** 0.21

L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1631	559.80	1117.58	1117.58	0.65	0	5	2.9	1	K.SADTLWGIQK.E
1729	567.79	1133.56	1133.56	0.61	0	41	0.00079	1	K.VTLTSEEEAR.L
2354	624.81	1247.60	1247.59	5.12	0	68	1.1e-006	1	R.VIGSGCNLDSAR.F 2352 2353

---

192. PIP_HUMAN **Mass:** 16847 **Score:** 133 **Queries matched:** 2 **emPAI:** 0.23

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2890	678.78	1355.54	1355.55	-3.62	0	75	3.4e-008	1	K.YTACLCDDNPK.T 2891

---

193. WFDC2_HUMAN **Mass:** 13953 **Score:** 132 **Queries matched:** 2 **emPAI:** 0.28

WAP four-disulfide core domain protein 2 OS=Homo sapiens GN=WFDC2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3939	840.84	1679.66	1679.67	-3.74	0	77	1.8e-008	1	R.DQCQVDSQCPGQMK.C 3940

---

194. CC50A_HUMAN **Mass:** 41057 **Score:** 130 **Queries matched:** 2 **emPAI:** 0.19

Cell cycle control protein 50A OS=Homo sapiens GN=TMEM30A PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3401	500.91	1499.72	1499.71	2.67	1	75	1.9e-007	1	K.FRNPPGGDNLEER.F
4501	970.43	1938.85	1938.85	-1.58	0	73	9.9e-008	1	R.EIEIDYTGTEPSSPCNK.C

---

195. GDIB_HUMAN **Mass:** 51087 **Score:** 130 **Queries matched:** 8 **emPAI:** 0.15

Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2004	590.34	1178.67	1178.67	0.10	1	5	1.3	6	R.IKLYSESLAR.Y
2937	683.36	1364.70	1364.69	5.81	0	83	4.2e-008	1	K.DLGTESQIFISR.T
4874	1100.04	2198.06	2198.05	3.60	0	38	0.00098	1	K.NTNDANSCQIIIPQNQVNR.K 4870 4871 4872 4873 4875

---

196. CB072_HUMAN **Mass:** 30918 **Score:** 128 **Queries matched:** 2 **emPAI:** 0.12

Uncharacterized protein C2orf72 OS=Homo sapiens GN=C2orf72 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
974	500.27	998.52	998.53	-3.63	0	84	2.4e-008	1	R.AAGAAGAAAAAAR.A 975

---

197. LELP1_HUMAN **Mass:** 11659 **Score:** 127 **Queries matched:** 6 **emPAI:** 0.34

Late cornified envelope-like proline-rich protein 1 OS=Homo sapiens GN=LELP1 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4518	973.89	1945.76	1945.76	-1.16	0	59	1.3e-006	1	K.CPSSCPHACPPPCPPPE.- 4513 4515 4516 4517 4519

---

198. FNTA_HUMAN **Mass:** 44495 **Score:** 127 **Queries matched:** 3 **emPAI:** 0.08

Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens GN=FNTA PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3245	728.82	1455.62	1455.62	0.02	0	62	1.4e-006	1	K.HSTENDSPTNVQQ.- 3243 3244

```
199.  HPRT_HUMAN     Mass: 24792     Score: 126     Queries matched: 2    emPAI: 0.15
      Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      3030    694.29   1386.58   1386.57   2.08   0    77  2.8e-008    1   K.SYCNDQSTGDIK.V 3029
```

```
200.  CHM2A_HUMAN     Mass: 25088     Score: 125     Queries matched: 9    emPAI: 0.33
      Charged multivesicular body protein 2a OS=Homo sapiens GN=CHMP2A PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       590    460.72    919.42    919.42  -0.04   0    51  4.5e-005    1   K.QGQMDAVR.I
      1002    502.27   1002.53   1002.53  -5.32   1     8       1.9    7   R.QKLETQEK.K
      1434    541.24   1080.47   1080.47   0.15   0    54  1.4e-005    1   K.SNNSMAQAMK.G 1432 1433 1435
      2009    591.29   1180.56   1180.57  -9.88   1    10      0.53    2   K.GVTKAMGTMNR.Q 2010
      3340    741.86   1481.70   1481.70   2.97   1     0       5.4    2   K.SNNSMAQAMKGVTK.A
```

```
201.  K2C6B_HUMAN     Mass: 60315     Score: 124     Queries matched: 6    emPAI: 0.13
      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  Peptide
      1376    533.76   1065.51   1065.51   1.11   1    14      0.33    4   K.YEDEINKR.T
      1576    554.27   1106.53   1106.54  -1.53   0    51  7.1e-005    1   K.AQYEEIAQR.S 1575 1577 1578
      1999    590.31   1178.60   1178.59   3.62   0    53  4.3e-005    1   K.YEELQITAGR.H
```

```
202.  AGM1_HUMAN     Mass: 60270     Score: 124     Queries matched: 5    emPAI: 0.06
      Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       248    424.73    847.44    847.45  -6.37   0     8       1.6    4   -.MDLGAITK.Y
      1961    586.73   1171.45   1171.46  -2.70   0    56  2.2e-006    1   K.QASCSGDEYR.S 1962 1963
      2560    644.84   1287.66   1287.67  -1.64   1     1       6.5    7   K.IKQSAEQLEDK.K
```

```
203.  RAP1A_HUMAN     Mass: 21316     Score: 123     Queries matched: 4    emPAI: 0.64
      Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       577    458.24    914.46    914.46  -0.70   0    51  4.1e-005    1   K.EQGQNLAR.Q 578
       672    468.69    935.36    935.37  -1.23   0    56  2.7e-006    1   K.CDLEDER.V
       907    493.31    984.60    984.60   0.22   0    28    0.0047    1   K.LVVLGSGGVGK.S


      Proteins matching the same set of peptides:
      RAP1B_HUMAN     Mass: 21040     Score: 123     Queries matched: 4
      Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1
```

```
204.  CAMP_HUMAN     Mass: 19517     Score: 123     Queries matched: 3    emPAI: 0.43
      Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       612    463.22    924.43    924.43   0.20   0    69  6.9e-007    1   R.SSDANLYR.L 613
      2455    633.81   1265.60   1265.59   8.02   0    26     0.019    1   R.CMGTVTLNQAR.G
```

```
205.  GBG5_HUMAN     Mass: 7428     Score: 122     Queries matched: 3    emPAI: 0.56
      Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       489    451.75    901.49    901.49  -1.59   0    67  2.9e-006    1   K.VSQAAADLK.Q 487 491
```

```
206.  TMC5_HUMAN     Mass: 115636    Score: 122     Queries matched: 7    emPAI: 0.06
      Transmembrane channel-like protein 5 OS=Homo sapiens GN=TMC5 PE=2 SV=3
```

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
398	443.72	885.43	885.43	2.44	0	11	0.48	2	R.SVQEGNPR.A
868	490.74	979.47	979.47	1.41	0	4	2.9	2	R.SNPYSVASR.T 865
2097	601.35	1200.69	1200.69	-1.19	0	46	9.9e-005	1	K.LIASLIPMTSR.D 2098
2180	609.35	1216.68	1216.68	-0.21	0	(45)	0.00016	1	K.LIASLIPMTSR.D 2181

---

207. CRIS1_HUMAN **Mass:** 29432 **Score:** 122 **Queries matched:** 6 **emPAI:** 0.27

Cysteine-rich secretory protein 1 OS=Homo sapiens GN=CRISP1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1313	528.30	1054.59	1054.58	2.74	0	9	0.77	1	R.VVPPASNMLK.M
1397	536.30	1070.58	1070.58	-1.45	0	(0)	7.7	7	R.VVPPASNMLK.M
2142	605.78	1209.54	1209.54	0.81	0	58	6.8e-006	1	K.ATCLCDTEIK.- 2143
4088	862.34	1722.66	1722.66	-1.27	0	57	2.2e-006	1	K.TGVPCEACPSNCEDK.L 4087

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208. GNAL_HUMAN **Score:** 122 **Queries matched:** 4

Guanine nucleotide-binding protein G(olf) subunit alpha OS=Homo sapiens GN=GNAL PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
172	417.70	833.40	833.40	0.17	0	0	8.3	10	K.QDMLAEK.V
690	470.20	938.39	938.39	-9.82	0	8	0.24	6	-.MGCLGGNSK.T
1316	529.32	1056.62	1056.62	0.47	0	73	2.5e-007	1	R.LLLLGAGESGK.S 1317

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209. ENOB_HUMAN **Mass:** 47299 **Score:** 121 **Queries matched:** 1 **emPAI:** 0.08

Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3812	817.42	1632.83	1632.81	6.99	0	121	6.1e-012	1	K.VNQIGSVTESIQACK.L

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210. SH3B4_HUMAN **Mass:** 108397 **Score:** 121 **Queries matched:** 12 **emPAI:** 0.11

SH3 domain-binding protein 4 OS=Homo sapiens GN=SH3BP4 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1153	517.28	1032.54	1032.54	5.25	0	24	0.035	2	K.STVGLQCLR.S
1234	523.24	1044.47	1044.47	-5.09	0	36	0.00088	1	R.AELDSEPER.V 1232 1233 1235 1236 1237
1799	573.78	1145.55	1145.55	0.18	0	42	0.00048	1	K.SPAPEQFQSR.E 1796 1797 1798 1800

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211. DCXR_HUMAN **Mass:** 26182 **Score:** 119 **Queries matched:** 1 **emPAI:** 0.15

L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3895	829.92	1657.83	1657.82	4.00	0	119	8e-012	1	R.GVPGAIVNVSSQCSQR.A

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212. PEBP1_HUMAN **Mass:** 21158 **Score:** 117 **Queries matched:** 1 **emPAI:** 0.18

Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4528	975.48	1948.95	1948.94	4.46	0	117	1.3e-011	1	K.GNDISSGTVLSDYVGSGPPK.G

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213. ZA2G_HUMAN **Mass:** 34465 **Score:** 116 **Queries matched:** 5 **emPAI:** 0.23

Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
9	401.23	800.44	800.44	-4.19	1	13	0.34	2	K.YLKYSK.N 8
1671	564.29	1126.56	1126.56	1.55	0	49	6.7e-005	1	R.AGEVQEPELR.G 1672
3225	726.35	1450.68	1450.68	1.89	0	71	3.8e-007	1	K.AYLEEECPATLR.K

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214. CHM4B_HUMAN **Mass:** 24935 **Score:** 116 **Queries matched:** 3 **emPAI:** 0.15

```
             Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
             1856    577.30   1152.59   1152.59 -1.49    0     58  1.5e-005    1  K.GGPTPQEAIQR.L 1857 1858

215.     LDH6A_HUMAN     Mass: 36826     Score: 115     Queries matched: 5   emPAI: 0.10
             L-lactate dehydrogenase A-like 6A OS=Homo sapiens GN=LDHAL6A PE=2 SV=1
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
             2354    624.81   1247.60   1247.59  5.12    0     68  1.1e-006    1  R.VIGSGCNLDSAR.F 2352 2353
             3190    719.84   1437.66   1437.66 -5.08    0      1       3.5    6  K.NFAEEEAIHHNK.I 3189

216.     PRIO_HUMAN     Mass: 27871     Score: 115     Queries matched: 5   emPAI: 0.14
             Major prion protein OS=Homo sapiens GN=PRNP PE=1 SV=1
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
             1224    522.74   1043.47   1043.47 -1.81    0     52  1.7e-005    1  R.ESQAYYQR.G 1219 1220 1222 1223

217.     TCPQ_HUMAN     Mass: 60153     Score: 114     Queries matched: 1   emPAI: 0.06
             T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
             2967    686.88   1371.74   1371.74  0.18    0    114  3.2e-011    1  K.AIADTGANVVVTGGK.V

218.     LSR_HUMAN     Mass: 72534     Score: 113     Queries matched: 6   emPAI: 0.05
             Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LSR PE=1 SV=4
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
             1465    544.28   1086.54   1086.53  8.73    1      5       2.3    2  R.EQAGGGWRAR.R
             1898    581.29   1160.57   1160.56  4.26    0      4       3.4    4  -.MQQDGLGVGTR.N
             2506    639.79   1277.57   1277.57  0.09    0     61  3.4e-006    1  R.IQASQQDDSMR.V 2504 2505
             3523    771.37   1540.73   1540.73 -0.87    0      6       1.4    1  K.QGNAVTLGDYYQGR.R

219.     P20D2_HUMAN     Mass: 48088     Score: 113     Queries matched: 3   emPAI: 0.08
             Peptidase M20 domain-containing protein 2 OS=Homo sapiens GN=PM20D2 PE=1 SV=2
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
              818    484.74    967.46    967.45  5.73    1      1       3.7    9  K.AYMENGRK.L
             2358    625.77   1249.53   1249.52  3.37    0     71  1.5e-007    1  R.SAECIDEAAER.L 2357

220.     CTNB1_HUMAN     Mass: 86069     Score: 112     Queries matched: 2   emPAI: 0.04
             Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
             3048    698.31   1394.60   1394.61 -4.21    0     69  4e-007    1  R.TMQNTNDVETAR.C 3049

221.     PGAM1_HUMAN     Mass: 28900     Score: 111     Queries matched: 3   emPAI: 0.28
             Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2
            Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
              847    488.25    974.49    974.49  0.96    0   (52)  6.8e-005    1  K.AMEAVAAQGK.A
              934    496.25    990.48    990.48  2.19    0     60  1.2e-005    1  K.AMEAVAAQGK.A 933


             Proteins matching the same set of peptides:
             PGAM2_HUMAN     Mass: 28919     Score: 111     Queries matched: 3
             Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3

222.     K1C25_HUMAN     Mass: 49858     Score: 109     Queries matched: 4   emPAI: 0.07
             Keratin, type I cytoskeletal 25 OS=Homo sapiens GN=KRT25 PE=1 SV=1
```

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
92	**409.23**	**816.44**	**816.43**	**4.86**	**0**	**3**	**7.2**	**1**	**R.GLLSGNEK.V** 91
1566	553.77	1105.52	1105.52	0.27	0	65	2.2e-006	1	K.VTMQNLNDR.L 1567

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223. K1C28_HUMAN **Mass:** 51163 **Score:** 109 **Queries matched:** 3 **emPAI:** 0.07

Keratin, type I cytoskeletal 28 OS=Homo sapiens GN=KRT28 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1566	553.77	1105.52	1105.52	0.27	0	65	2.2e-006	1	K.VTMQNLNDR.L 1567
3474	**762.87**	**1523.72**	**1523.72**	**-2.69**	**1**	**1**	**5.7**	**2**	**K.GFGSGSPGNSSKDLSK.T**

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224. S10AB_HUMAN **Mass:** 11847 **Score:** 108 **Queries matched:** 4 **emPAI:** 0.78

Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1086	**510.25**	**1018.49**	**1018.49**	**0.05**	**0**	**42**	**0.00056**	**1**	**K.ISSPTETER.C** 1087
1321	**530.75**	**1059.48**	**1059.49**	**-3.34**	**0**	**53**	**1.6e-005**	**1**	**K.DGYNYTLSK.T** 1320

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225. RAB5A_HUMAN **Mass:** 23872 **Score:** 107 **Queries matched:** 3 **emPAI:** 0.16

Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2392	**627.79**	**1253.57**	**1253.57**	**-1.10**	**0**	**54**	**1.7e-005**	**1**	**K.NEPQNPGANSAR.G** 2393 2394

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226. S26A2_HUMAN **Mass:** 82635 **Score:** 106 **Queries matched:** 3 **emPAI:** 0.09

Sulfate transporter OS=Homo sapiens GN=SLC26A2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
776	**482.70**	**963.39**	**963.39**	**0.77**	**0**	**52**	**6.9e-006**	**1**	**K.NCQCSPAK.A** 777
1112	**513.32**	**1024.63**	**1024.63**	**-0.99**	**0**	**33**	**0.00051**	**1**	**K.QTVNPILIK.V**

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227. MT1F_HUMAN **Mass:** 7222 **Score:** 106 **Queries matched:** 3 **emPAI:** 1.49

Metallothionein-1F OS=Homo sapiens GN=MT1F PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
876	491.70	981.38	981.38	1.78	0	57	2.2e-006	1	K.CAQGCVCK.G
3271	**731.26**	**1460.50**	**1460.50**	**1.67**	**0**	**48**	**1.5e-005**	**1**	**K.SCCSCCPVGCSK.C** 3270

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228. IF5A1_HUMAN **Mass:** 17049 **Score:** 106 **Queries matched:** 4 **emPAI:** 0.50

Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
459	**447.74**	**893.46**	**893.45**	**5.25**	**0**	**(41)**	**0.00075**	**1**	**K.IVEMSTSK.T** 458
552	**455.73**	**909.45**	**909.45**	**1.01**	**0**	**51**	**4.6e-005**	**1**	**K.IVEMSTSK.T** 553

Proteins matching the same set of peptides:

IF5A2_HUMAN **Mass:** 17124 **Score:** 106 **Queries matched:** 4

Eukaryotic translation initiation factor 5A-2 OS=Homo sapiens GN=EIF5A2 PE=1 SV=3

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229. SYTL1_HUMAN **Mass:** 62104 **Score:** 105 **Queries matched:** 4 **emPAI:** 0.06

Synaptotagmin-like protein 1 OS=Homo sapiens GN=SYTL1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1995	**590.30**	**1178.59**	**1178.59**	**-2.11**	**0**	**47**	**0.00015**	**1**	**R.VPPSPDDLPSR.G** 1997 2000 2001

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230. KAD1_HUMAN **Mass:** 21735 **Score:** 104 **Queries matched:** 7 **emPAI:** 0.38

Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
362	**440.21**	**878.41**	**878.41**	**1.43**	**0**	**43**	**0.00045**	**1**	**R.SEVSSGSAR.G** 361 363 364 365

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          2361     625.79   1249.56   1249.56   0.19    0     29   0.0055    2   R.EVQQGEEFER.R 2360

231.   RAB10_HUMAN      Score: 104     Queries matched: 4
       Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
          8    401.23    800.44    800.44   0.54    0    11      0.54    2  K.ANINIEK.A 9
       1398    536.33   1070.64   1070.63   3.27    0    51  4.5e-005    1  K.LLLIGDSGVGK.T
       2701    658.83   1315.65   1315.65   1.50    0    74  3.2e-007    1  K.LQIWDTAGQER.F

232.   RAB15_HUMAN      Mass: 24660     Score: 104     Queries matched: 2    emPAI: 0.33
       Ras-related protein Rab-15 OS=Homo sapiens GN=RAB15 PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1398    536.33   1070.64   1070.63   3.27    0    51  4.5e-005    1  R.LLLIGDSGVGK.T
       2701    658.83   1315.65   1315.65   1.50    0    74  3.2e-007    1  R.IQIWDTAGQER.Y

233.   GBB2_HUMAN      Mass: 38048     Score: 104     Queries matched: 4    emPAI: 0.21
       Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
         26    402.73    803.44    803.44  -5.61    1     6       3.6    4  R.IQMRTR.R
       1043    505.26   1008.51   1008.51  -0.53    0    56  1.7e-005    1  R.AGVLAGHDNR.V
       1078    509.29   1016.56   1016.55   7.85    0    69    1e-006    1  R.LLVSASQDGK.L
       2410    628.30   1254.60   1254.59   3.08    0     5       1.6    1  R.TFVSGACDASIK.L

234.   MARCS_HUMAN      Mass: 31707     Score: 104     Queries matched: 2    emPAI: 0.12
       Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       3399    750.85   1499.68   1499.67   1.19    0    66  1.1e-006    1  K.AEDGATPSPSNETPK.K 3398

235.   TMM8A_HUMAN      Mass: 86359     Score: 104     Queries matched: 3    emPAI: 0.04
       Transmembrane protein 8A OS=Homo sapiens GN=TMEM8A PE=1 SV=3
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1941    584.26   1166.51   1166.51  -0.15    0    53  1.6e-005    1  R.VCSDTPSVMR.L 1939 1940

236.   HIN1L_HUMAN      Mass: 50162     Score: 104     Queries matched: 3    emPAI: 0.07
       Putative HIN1-like protein OS=Homo sapiens GN=HIN1L PE=5 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        262    427.69    853.37    853.38  -1.53    0    48  5.5e-005    1  K.DGSCLFR.A 263 264

       Proteins matching the same set of peptides:
       OTUD4_HUMAN      Mass: 124695    Score: 104     Queries matched: 3
       OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=3

237.   LG3BP_HUMAN      Mass: 66202     Score: 103     Queries matched: 2    emPAI: 0.06
       Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1319    530.26   1058.51   1058.51   1.95    0    81  4.4e-008    1  R.LADGGATNQGR.V 1318

238.   ZCCHV_HUMAN      Mass: 103135    Score: 102     Queries matched: 2    emPAI: 0.04
       Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
       3440    758.34   1514.67   1514.67  -0.31    0    66 1e-006    1  R.QQICNQQPPCSR.L 3441
```

239. BCAS1_HUMAN **Mass:** 61957 **Score:** 101 **Queries matched:** 10 **emPAI:** 0.06
Breast carcinoma-amplified sequence 1 OS=Homo sapiens GN=BCAS1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
457	**447.72**	**893.43**	**893.43**	**-0.32**	**1**	**3**	**4.1**	**2**	**K.KSAAEMNK.Q** 450 451 453 455 456
497	**452.24**	**902.47**	**902.47**	**-0.86**	**1**	**7**	**2.1**	**4**	**K.DIVDGKEK.E**
3595	**781.91**	**1561.80**	**1561.80**	**3.45**	**0**	**61**	**6e-006**	**1**	**K.TITPPEPEPTGAPQK.G** 3593 3594

240. CBR1_HUMAN **Mass:** 30641 **Score:** 100 **Queries matched:** 3 **emPAI:** 0.12
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1416	538.75	1075.49	1075.50	-2.72	0	50	3.6e-005	1	K.SCSPELQQK.F 1417 1418

241. DNJB2_HUMAN **Mass:** 35672 **Score:** 99 **Queries matched:** 7 **emPAI:** 0.11
DnaJ homolog subfamily B member 2 OS=Homo sapiens GN=DNAJB2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
30	**403.70**	**805.38**	**805.38**	**-5.00**	**0**	**3**	**3.3**	**8**	**R.SASADDIK.K** 29
296	432.22	862.42	862.42	-3.37	0	4	4.7	7	R.SPEEVFR.E
1706	**566.78**	**1131.55**	**1131.55**	**-1.24**	**0**	**57**	**1.4e-005**	**1**	**R.EGLTGTGTGPSR.A** 1703 1704 1705

242. TSN6_HUMAN **Mass:** 28172 **Score:** 99 **Queries matched:** 4 **emPAI:** 0.13
Tetraspanin-6 OS=Homo sapiens GN=TSPAN6 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1080	**509.73**	**1017.45**	**1017.45**	**-0.07**	**0**	**65**	**1e-006**	**1**	**K.LEDCTPQR.D** 1081
1917	**582.80**	**1163.58**	**1163.58**	**2.12**	**0**	**17**	**0.17**	**1**	**R.AITNNQYEIV.-** 1916

243. TXNL1_HUMAN **Mass:** 32630 **Score:** 98 **Queries matched:** 3 **emPAI:** 0.12
Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1782	**572.77**	**1143.53**	**1143.53**	**-3.13**	**0**	**48**	**6e-005**	**1**	**K.FQGPDNGQGPK.Y** 1781 1783

244. CD36_HUMAN **Mass:** 53589 **Score:** 98 **Queries matched:** 4 **emPAI:** 0.07
Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
125	413.21	824.40	824.40	-2.84	0	41	0.0003	1	K.TGTEVYR.Q 126 127 129

245. UBL3_HUMAN **Mass:** 13263 **Score:** 97 **Queries matched:** 4 **emPAI:** 0.30
Ubiquitin-like protein 3 OS=Homo sapiens GN=UBL3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2889	**678.33**	**1354.65**	**1354.65**	**-0.19**	**0**	**48**	**0.00011**	**1**	**R.ETLPEPNSQGQR.N** 2886 2887 2888

246. TR10C_HUMAN **Mass:** 28244 **Score:** 96 **Queries matched:** 4 **emPAI:** 0.29
Tumor necrosis factor receptor superfamily member 10C OS=Homo sapiens GN=TNFRSF10C PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
550	**455.69**	**909.37**	**909.37**	**1.94**	**0**	**39**	**0.00018**	**1**	**R.DTVCQCK.E**
1737	**568.73**	**1135.44**	**1135.44**	**0.39**	**0**	**45**	**3.3e-005**	**1**	**R.NENSPEMCR.K** 1736 1738

247. CD14_HUMAN **Mass:** 40678 **Score:** 96 **Queries matched:** 3 **emPAI:** 0.09
Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

```
        564     456.75    911.48    911.48   -1.35   0    54  2.2e-005   1   R.ATVNPSAPR.C 565 566

248.  ALDR_HUMAN    Mass: 36230     Score: 93     Queries matched: 2    emPAI: 0.10
      Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1591    556.80   1111.58   1111.59  -5.79   0    57  1.2e-005   1   K.SPPGQVTEAVK.V 1592

249.  K22O_HUMAN    Mass: 66370     Score: 93     Queries matched: 12    emPAI: 0.06
      Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       1243    523.29   1044.56   1044.56   6.20   0     2       7.1   8   K.LGELQTTAGR.H
       1376    533.76   1065.51   1065.51   1.11   1    14      0.33   4   K.YEDEINKR.T
       1576    554.27   1106.53   1106.54  -1.53   0    51  7.1e-005   1   R.AQYEEIAQR.S 1575 1577 1578
       1759    570.28   1138.55   1138.55  -2.64   0    12       0.4   3   K.SEAEALYQTK.L 1757 1760 1762 1763 1764

250.  K2C4_HUMAN    Mass: 57649     Score: 93     Queries matched: 5    emPAI: 0.06
      Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        946    497.76    993.50    993.49   6.25   0     4       3.9  10   K.SISMSVAGSR.Q
       1576    554.27   1106.53   1106.54  -1.53   0    51  7.1e-005   1   R.AQYEEIAQR.S 1575 1577 1578

251.  INADL_HUMAN     Mass: 197046     Score: 91     Queries matched: 3    emPAI: 0.02
      InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       3269    730.85   1459.69   1459.68   4.26   0    54  2.6e-005   1   K.TSSSTSPLEPPSDR.G 3267 3268

252.  MDHC_HUMAN    Mass: 36631     Score: 90     Queries matched: 3    emPAI: 0.22
      Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        585    458.76    915.51    915.50   7.92   0    35  0.0042   1   K.LGVTANDVK.N
       4174    879.47   1756.93   1756.91   6.39   0    57  1e-005   1   K.VIVVGNPANTNCLTASK.S 4173

253.  COLL1_HUMAN     Mass: 14674     Score: 90     Queries matched: 2    emPAI: 0.27
      Colipase-like protein 1 OS=Homo sapiens GN=CLPSL1 PE=2 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       3150    714.26   1426.50   1426.50  -2.81   0    59  1.2e-006   1   R.NQDCETGCCQR.A 3151

254.  MYOF_HUMAN    Mass: 236100    Score: 89     Queries matched: 4    emPAI: 0.03
      Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        461    448.72    895.42    895.42  -2.55   0    43  0.0004   1   K.CGQYIQK.G 462 463
       3485    765.37   1528.73   1528.72   7.46   0    38   0.001   1   R.ELPDSVPQECTVR.I

255.  APOD_HUMAN    Mass: 21547     Score: 89     Queries matched: 1    emPAI: 0.18
      Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1
      Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
       2591    646.80   1291.58   1291.59  -9.46   0    89  4.1e-009   1   K.MTVTDQVNCPK.L

256.  PTTG_HUMAN    Mass: 21109     Score: 89     Queries matched: 2    emPAI: 0.18
      Pituitary tumor-transforming gene 1 protein-interacting protein OS=Homo sapiens GN=PTTG1IP PE=1 SV=1
```

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4621	996.01	1990.00	1989.99	3.11	0	89	7.5e-009	1	K.ACLDYPVTSVLPPASLCK.L 4620

---

257. BAIP2_HUMAN **Mass:** 61115 **Score:** 88 **Queries matched:** 6 **emPAI:** 0.13

Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
101	410.21	818.41	818.41	-1.65	0	25	0.041	1	K.TALTEER.R 103
116	412.70	823.38	823.38	-0.59	0	45	0.00016	1	K.YQTEQR.S 117 118
1352	531.77	1061.52	1061.53	-6.57	1	8	1.6	2	K.NSAAYHSKGK.E

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258. AT8A2_HUMAN **Mass:** 130641 **Score:** 87 **Queries matched:** 2 **emPAI:** 0.03

Probable phospholipid-transporting ATPase IB OS=Homo sapiens GN=ATP8A2 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1840	576.31	1150.61	1150.62	-9.64	0	5	2.3	6	K.VYQEASTILK.D
2771	666.35	1330.68	1330.67	2.65	0	87	1.7e-008	1	R.TSNLNEELGQVK.Y

---

259. SORT_HUMAN **Mass:** 92979 **Score:** 86 **Queries matched:** 3 **emPAI:** 0.04

Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2111	603.74	1205.46	1205.46	1.33	0	52	5.6e-006	1	R.SAPGEDEECGR.V 2112
3209	722.89	1443.77	1443.78	-8.29	1	0	6	4	K.VVLTAEVSGGSRGGR.I

---

260. P2RX4_HUMAN **Mass:** 44139 **Score:** 86 **Queries matched:** 4 **emPAI:** 0.18

P2X purinoceptor 4 OS=Homo sapiens GN=P2RX4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
268	428.70	855.38	855.38	0.90	0	29	0.0043	1	K.SCIYDAK.T
482	451.72	901.43	901.43	-0.01	0	43	0.00026	1	R.DLAGNEQR.T 481 483

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261. REPS2_HUMAN **Mass:** 72002 **Score:** 85 **Queries matched:** 1 **emPAI:** 0.05

RalBP1-associated Eps domain-containing protein 2 OS=Homo sapiens GN=REPS2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3512	770.35	1538.69	1538.69	-2.01	0	85	9e-009	1	R.CAGAAGGGPGSGPPEAAR.V

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262. SMIM1_HUMAN **Mass:** 8915 **Score:** 85 **Queries matched:** 1 **emPAI:** 0.46

Small integral membrane protein 1 OS=Homo sapiens GN=SMIM1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3610	782.88	1563.74	1563.74	3.13	0	85	1.9e-008	1	R.DGVSLGAVSSTEEASR.C

---

263. LFG3_HUMAN **Mass:** 34927 **Score:** 85 **Queries matched:** 1 **emPAI:** 0.11

Protein lifeguard 3 OS=Homo sapiens GN=TMBIM1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3511	769.33	1536.65	1536.65	2.34	0	85	5.5e-009	1	R.AVSDSFGPGEWDDR.K

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264. SORCN_HUMAN **Mass:** 21947 **Score:** 85 **Queries matched:** 2 **emPAI:** 0.17

Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2095	601.31	1200.60	1200.60	-1.55	0	53	3.1e-005	1	R.SGTVDPQELQK.A 2096

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265. PGK2_HUMAN **Mass:** 45166 **Score:** 85 **Queries matched:** 4 **emPAI:** 0.17

Phosphoglycerate kinase 2 OS=Homo sapiens GN=PGK2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
913	494.25	986.49	986.49	1.63	0	44	0.00026	1	K.NQITNNQR.I 912
1017	503.73	1005.45	1005.44	2.90	0	38	0.00064	1	K.DCVGAEVEK.A 1016

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266. GNA11_HUMAN **Mass:** 42382 **Score:** 85 **Queries matched:** 4 **emPAI:** 0.18

Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
356	439.21	876.41	876.41	-1.58	0	51	6.6e-005	1	R.MVDVGGQR.S 355
1198	520.75	1039.48	1039.48	-1.55	0	29	0.0078	1	R.EYQLSDSAK.Y 1197

Proteins matching the same set of peptides:

GNA14_HUMAN **Mass:** 42000 **Score:** 85 **Queries matched:** 4

Guanine nucleotide-binding protein subunit alpha-14 OS=Homo sapiens GN=GNA14 PE=2 SV=1

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267. SO2A1_HUMAN **Mass:** 71367 **Score:** 82 **Queries matched:** 1 **emPAI:** 0.05

Solute carrier organic anion transporter family member 2A1 OS=Homo sapiens GN=SLCO2A1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2454	633.80	1265.59	1265.58	4.08	0	82	4.3e-008	1	K.LGASQGSDTSTSR.A

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268. HYES_HUMAN **Mass:** 63316 **Score:** 82 **Queries matched:** 4 **emPAI:** 0.06

Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
230	423.21	844.41	844.40	1.60	0	54	2.3e-005	1	K.GGPEGATTR.L 229 231
888	491.75	981.48	981.48	-0.45	0	15	0.25	2	K.EMVTFLDK.L

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269. GTR5_HUMAN **Mass:** 55394 **Score:** 81 **Queries matched:** 3 **emPAI:** 0.22

Solute carrier family 2, facilitated glucose transporter member 5 OS=Homo sapiens GN=SLC2A5 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
154	415.27	828.52	828.52	8.09	1	43	0.00014	1	K.KALQTLR.G
170	417.69	833.37	833.37	6.60	0	28	0.0059	1	R.GWDSVDR.E
513	453.28	904.54	904.54	-1.43	0	45	7.1e-005	1	K.AAGFISVLK.L

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270. CLIC1_HUMAN **Mass:** 27248 **Score:** 81 **Queries matched:** 2 **emPAI:** 0.14

Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2764	664.83	1327.64	1327.64	1.69	0	81	5.5e-008	1	K.NSNPALNDNLEK.G
4395	922.99	1843.97	1843.97	0.82	0	17	0.12	1	K.LAALNPESNTAGLDIFAK.F

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271. ZDHC2_HUMAN **Mass:** 42906 **Score:** 81 **Queries matched:** 5 **emPAI:** 0.18

Palmitoyltransferase ZDHHC2 OS=Homo sapiens GN=ZDHHC2 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
396	443.72	885.43	885.43	1.61	0	36	0.0015	1	M.APSGPGSSAR.R 397 398
1151	517.24	1032.47	1032.47	7.76	0	32	0.0036	1	-.MAPSGPGSSAR.R
3289	733.31	1464.61	1464.62	-8.11	0	1	0.77	1	K.AGMSNPALTMENET.-

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272. DCD_HUMAN **Mass:** 11391 **Score:** 80 **Queries matched:** 4 **emPAI:** 0.35

Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1675	564.77	1127.52	1127.52	0.57	0	51	3.8e-005	1	K.ENAGEDPGLAR.Q 1673 1674 1677

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273. CC181_HUMAN **Mass:** 60408 **Score:** 80 **Queries matched:** 7 **emPAI:** 0.06

Coiled-coil domain-containing protein 181 OS=Homo sapiens GN=CCDC181 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
18	401.73	801.44	801.43	2.65	1	19	0.22	9	K.QLEEKR.E
505	452.73	903.45	903.45	-0.96	1	36	0.0028	2	K.IEEEKEK.K 501 502 503 504 506

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274. TRI34_HUMAN **Score:** 80 **Queries matched:** 7

Tripartite motif-containing protein 34 OS=Homo sapiens GN=TRIM34 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
96	409.25	816.48	816.49	-8.61	1	9	0.67	6	K.KPKMVSK.K
505	452.73	903.45	903.45	-0.96	1	36	0.0028	2	R.LEEEEKK.T 501 502 503 504 506

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275. RRAS_HUMAN **Mass:** 23637 **Score:** 80 **Queries matched:** 3 **emPAI:** 0.16

Ras-related protein R-Ras OS=Homo sapiens GN=RRAS PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3986	**848.42**	**1694.83**	**1694.83**	**2.75**	**0**	**51**	**6.1e-005**	**1**	**K.YQEQELPPSPPSAPR.K** 3984 3985

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276. PRDX1_HUMAN **Mass:** 22324 **Score:** 79 **Queries matched:** 4 **emPAI:** 0.37

Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
102	410.21	818.41	818.41	-1.15	0	5	3.5	2	R.SVDETLR.L
1914	582.79	1163.57	1163.56	8.33	0	34	0.0032	1	K.ATAVMPDGQFK.D 1913
2151	**606.34**	**1210.67**	**1210.67**	**2.80**	**0**	**49**	**7.6e-005**	**1**	**R.QITVNDLPVGR.S**

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277. PRS8_HUMAN **Mass:** 45768 **Score:** 79 **Queries matched:** 1 **emPAI:** 0.08

26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2580	**645.80**	**1289.59**	**1289.58**	**2.96**	**0**	**79**	**5.2e-008**	**1**	**R.LEGGSGGDSEVQR.T**

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278. KI2L4_HUMAN **Score:** 78 **Queries matched:** 14

Killer cell immunoglobulin-like receptor 2DL4 OS=Homo sapiens GN=KIR2DL4 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
412	443.76	885.51	885.50	3.04	1	31	0.0089	2	R.KITGPSQR.S 399 400 401 402 403 404 405 407 408 409 410 411 413

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279. GNAQ_HUMAN **Mass:** 42400 **Score:** 78 **Queries matched:** 5 **emPAI:** 0.18

Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo sapiens GN=GNAQ PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
356	439.21	876.41	876.41	-1.58	0	51	6.6e-005	1	R.MVDVGGQR.S 355
1388	**535.75**	**1069.49**	**1069.49**	**-0.67**	**0**	**23**	**0.021**	**1**	**R.EYQLSDSTK.Y** 1387 1389

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280. RAB14_HUMAN **Mass:** 24110 **Score:** 77 **Queries matched:** 2 **emPAI:** 0.34

Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
352	**437.25**	**872.49**	**872.50**	**-4.66**	**0**	**25**	**0.032**	**1**	**R.IIEVSGQK.I**
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.LQIWDTAGQER.F

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281. IGS21_HUMAN **Score:** 77 **Queries matched:** 8

Immunoglobulin superfamily member 21 OS=Homo sapiens GN=IGSF21 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1817	574.29	1146.56	1146.55	3.65	0	35	0.0026	2	R.TPSSDGTVEVR.A 1809 1810 1812 1813 1814 1815 1816

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282. TSN8_HUMAN **Mass:** 26711 **Score:** 76 **Queries matched:** 2 **emPAI:** 0.14

Tetraspanin-8 OS=Homo sapiens GN=TSPAN8 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1168	517.77	1033.53	1033.53	-2.81	0	52	5.5e-005	1	K.LLSATGESEK.Q 1169

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283. VIGLN_HUMAN **Mass:** 141995 **Score:** 76 **Queries matched:** 1 **emPAI:** 0.03

Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2474	635.33	1268.64	1268.64	0.58	0	76	1.5e-007	1	R.IEGDPQGVQQAK.R

---

284. MIF_HUMAN **Mass:** 12639 **Score:** 76 **Queries matched:** 2 **emPAI:** 0.72

Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1228	522.80	1043.58	1043.58	-0.62	0	48	0.00012	1	K.LLCGLLAER.L
2548	644.35	1286.69	1286.68	5.21	0	49	0.00011	1	M.PMFIVNTNVPR.A

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285. PLST_HUMAN **Mass:** 71279 **Score:** 75 **Queries matched:** 4 **emPAI:** 0.11

Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1482	545.23	1088.46	1088.46	-0.22	0	40	0.00016	1	K.ALENDPDCR.H 1483
1652	562.27	1122.52	1122.52	0.33	0	2	3.9	4	M.DEMATTQISK.D
3412	751.88	1501.75	1501.74	1.12	0	31	0.0072	1	K.MINLSVPDTIDER.A

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286. PTPRJ_HUMAN **Mass:** 147048 **Score:** 75 **Queries matched:** 3 **emPAI:** 0.05

Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
926	495.78	989.54	989.54	-1.82	0	7	2.1	7	R.SQSLSEVLK.Y
942	497.27	992.53	992.53	0.79	0	69	7.9e-007	1	R.TGTFIAIDR.L
2804	669.89	1337.76	1337.76	0.73	0	25	0.01	1	K.VITEPIPVSDLR.V

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287. FLOT2_HUMAN **Mass:** 47434 **Score:** 75 **Queries matched:** 9 **emPAI:** 0.16

Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
359	439.74	877.46	877.46	2.61	1	7	1.8	5	K.KEMLDVK.F 357 358
494	451.76	901.50	901.50	-0.26	0	43	0.0005	1	K.TQTAVVQR.D 493
571	457.24	912.46	912.47	-2.50	0	24	0.021	1	R.EVAAPDVGR.M 568 569 570

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288. RB39B_HUMAN **Mass:** 24835 **Score:** 74 **Queries matched:** 3 **emPAI:** 0.15

Ras-related protein Rab-39B OS=Homo sapiens GN=RAB39B PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
524	454.20	906.38	906.39	-5.08	0	8	0.4	1	K.CDLDTQR.Q
1129	515.28	1028.54	1028.54	4.35	1	11	0.82	3	R.SITRAYYR.N
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.LQIWDTAGQER.F

---

289. RAB6A_HUMAN **Mass:** 23692 **Score:** 74 **Queries matched:** 3 **emPAI:** 0.16

Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1249	523.76	1045.51	1045.50	8.89	0	1	9.4	5	R.QVSIEEGER.K
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	R.LQLWDTAGQER.F
3272	731.35	1460.68	1460.69	-7.92	0	4	2.5	1	R.VAAALPGMESTQDR.S

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290. RB33B_HUMAN **Score:** 74 **Queries matched:** 1
Ras-related protein Rab-33B OS=Homo sapiens GN=RAB33B PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2701	658.83	1315.65	1315.65	1.50	0	74	3.2e-007	1	K.IQLWDTAGQER.F

---

291. GP2_HUMAN **Mass:** 61095 **Score:** 74 **Queries matched:** 2 **emPAI:** 0.13
Pancreatic secretory granule membrane major glycoprotein GP2 OS=Homo sapiens GN=GP2 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
895	492.30	982.58	982.58	2.69	0	51	2.6e-005	1	R.VLDLGPITR.R
1391	535.80	1069.58	1069.58	0.35	0	42	0.00036	1	R.SEVPAIDLAR.V

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292. PEPD_HUMAN **Mass:** 55311 **Score:** 74 **Queries matched:** 2 **emPAI:** 0.07
Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1833	576.26	1150.50	1150.50	0.57	0	52	2.1e-005	1	R.GVNTDSGSVCR.E 1832

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293. SGTA_HUMAN **Mass:** 34270 **Score:** 74 **Queries matched:** 1 **emPAI:** 0.11
Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3135	709.31	1416.60	1416.60	-0.87	0	74	7.1e-008	1	R.TPPSEEDSAEAER.L

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294. PPME1_HUMAN **Mass:** 42687 **Score:** 72 **Queries matched:** 2 **emPAI:** 0.09
Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2589	646.79	1291.57	1291.57	-2.87	0	51	1.7e-005	1	K.QCEGITSPEGSK.S 2590

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295. AT1A2_HUMAN **Mass:** 113505 **Score:** 72 **Queries matched:** 2 **emPAI:** 0.03
Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1002	502.27	1002.53	1002.52	5.90	1	8	1.9	6	K.EKELDELK.K
3781	810.38	1618.75	1618.74	3.12	0	72	3e-007	1	K.VDNSSLTGESEPQTR.S

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296. FKB1A_HUMAN **Mass:** 12000 **Score:** 72 **Queries matched:** 2 **emPAI:** 0.33
Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2698	657.84	1313.66	1313.66	-1.20	0	48	0.00012	1	M.GVQVETISPGDGR.T 2699

---

297. ANO7_HUMAN **Mass:** 106661 **Score:** 71 **Queries matched:** 2 **emPAI:** 0.03
Anoctamin-7 OS=Homo sapiens GN=ANO7 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1268	525.27	1048.53	1048.53	-2.24	0	46	0.00025	1	K.TPPEGPQAPR.L 1269

---

298. UBP14_HUMAN **Mass:** 56489 **Score:** 71 **Queries matched:** 5 **emPAI:** 0.07
Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
145	415.23	828.44	828.45	-1.71	0	8	1	2	K.QSPTLQR.N 148 151
2811	670.78	1339.54	1339.54	-0.20	0	71	8.9e-008	1	K.CTESEEEEVTK.G
3189	719.83	1437.65	1437.64	8.23	1	2	2.9	4	K.QDEWIKFDDDK.V

---

299. GNAZ_HUMAN **Mass:** 41411 **Score:** 71 **Queries matched:** 3 **emPAI:** 0.09

Guanine nucleotide-binding protein G(z) subunit alpha OS=Homo sapiens GN=GNAZ PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
356	439.21	876.41	876.41	-1.58	0	51	6.6e-005	1	K.MVDVGGQR.S 355
595	461.23	920.44	920.44	0.77	0	1	7.7	9	R.QFEDLNR.N

---

300. IMPA1_HUMAN **Mass:** 30568 **Score:** 71 **Queries matched:** 1 **emPAI:** 0.12

Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2560	644.84	1287.66	1287.67	-1.67	0	71	7e-007	1	K.LQVSQQEDITK.S

---

301. NPDC1_HUMAN **Mass:** 35122 **Score:** 70 **Queries matched:** 4 **emPAI:** 0.11

Neural proliferation differentiation and control protein 1 OS=Homo sapiens GN=NPDC1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
112	**412.23**	**822.44**	**822.43**	**4.83**	**0**	**49**	**8e-005**	**1**	**K.APGSPAAPR.I** 111
2820	671.84	1341.66	1341.66	-0.28	1	5	2.1	3	R.QQMLCLERHK.E
3537	**772.40**	**1542.79**	**1542.78**	**9.02**	**1**	**0**	**7.2**	**2**	**K.ADYATAKAPGSPAAPR.I**

---

302. PTPRB_HUMAN **Score:** 69 **Queries matched:** 1

Receptor-type tyrosine-protein phosphatase beta OS=Homo sapiens GN=PTPRB PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
942	497.27	992.53	992.53	0.79	0	69	7.9e-007	1	R.TGTFIALDR.I

Proteins matching the same set of peptides:

PTPRO_HUMAN **Score:** 69 **Queries matched:** 1

---

303. SUIS_HUMAN **Mass:** 210746 **Score:** 69 **Queries matched:** 7 **emPAI:** 0.02

Sucrase-isomaltase, intestinal OS=Homo sapiens GN=SI PE=1 SV=6

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
21	402.70	803.38	803.38	0.40	0	18	0.13	1	R.DQPPGYK.L 22 24
320	**434.71**	**867.41**	**867.41**	**-0.68**	**0**	**19**	**0.067**	**1**	**R.STYPTSGR.W** 321 322
2314	**620.78**	**1239.55**	**1239.55**	**0.57**	**0**	**69**	**4.8e-007**	**1**	**R.QDNSYSVNSAR.Y**

---

304. PRDX2_HUMAN **Mass:** 22049 **Score:** 68 **Queries matched:** 2 **emPAI:** 0.38

Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
611	**462.72**	**923.43**	**923.43**	**-7.66**	**0**	**39**	**0.00062**	**1**	**K.TDEGIAYR.G**
2151	606.34	1210.67	1210.67	2.80	0	49	7.6e-005	1	R.QITVNDLPVGR.S

---

305. AL9A1_HUMAN **Mass:** 54679 **Score:** 67 **Queries matched:** 2 **emPAI:** 0.07

4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1546	**552.26**	**1102.51**	**1102.51**	**-0.08**	**0**	**50**	**5.2e-005**	**1**	**R.VEPADASGTEK.A** 1547

---

306. CK052_HUMAN **Mass:** 14140 **Score:** 66 **Queries matched:** 2 **emPAI:** 0.28

Uncharacterized protein C11orf52 OS=Homo sapiens GN=C11orf52 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1968	**586.80**	**1171.60**	**1171.59**	**0.76**	**0**	**53**	**4e-005**	**1**	**R.VLQQQGSQER.S** 1967

---

307. NCALD_HUMAN **Mass:** 22345 **Score:** 65 **Queries matched:** 1 **emPAI:** 0.17

Neurocalcin-delta OS=Homo sapiens GN=NCALD PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2734	**661.80**	**1321.59**	**1321.60**	**-1.75**	**0**	**65**	**1.3e-006**	**1**	**R.LLQCDPSSAGQF.-**

```
308.  MEGF9_HUMAN     Mass: 65338     Score: 64     Queries matched: 1   emPAI: 0.06
      Multiple epidermal growth factor-like domains protein 9 OS=Homo sapiens GN=MEGF9 PE=2 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      3770    807.85   1613.69   1613.68   1.06    0    64  4.7e-007    1  R.CPCSAVTSTGSCSIK.S
```

```
309.  COL12_HUMAN     Mass: 82035     Score: 64     Queries matched: 7   emPAI: 0.05
      Collectin-12 OS=Homo sapiens GN=COLEC12 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
        50    406.18    810.35    810.36 -8.36    0     6      0.77    3  K.LFCEDK.S 48 49 51 52 53
      2191    610.30   1218.59   1218.58  3.54    0    64  2.5e-006    1  R.SVDDTSQAIQR.I
```

```
310.  T106B_HUMAN     Mass: 31393     Score: 63     Queries matched: 1   emPAI: 0.12
      Transmembrane protein 106B OS=Homo sapiens GN=TMEM106B PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      3188    719.81   1437.60   1437.60  5.04    0    63  8.8e-007    1  R.DSVTCPTCQGTGR.I
```

```
311.  GSH1_HUMAN     Mass: 73518     Score: 63     Queries matched: 3   emPAI: 0.05
      Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
      1149    517.24   1032.47   1032.47  0.76    0    40  0.00043    1  K.GGNAVVDGCGK.A 1148 1150
```

```
312.  ENOG_HUMAN     Score: 63     Queries matched: 1
      Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      3091    703.86   1405.71   1405.71  1.25    0    63  4.7e-006    2  R.GNPTVEVDLYTAK.G
```

```
313.  AL1A3_HUMAN     Mass: 56871     Score: 61     Queries matched: 4   emPAI: 0.14
      Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens GN=ALDH1A3 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score  Expect Rank  Peptide
       850    488.27    974.52    974.51  8.12    1     4      3.9    6  K.EAASRSNLK.R
      1299    527.24   1052.47   1052.47 -4.07    0    36  0.00087    1  K.FATCNPSTR.E 1298
      1780    572.29   1142.56   1142.56 -0.13    0    44  0.00024    1  K.TEQGPQIDQK.Q
```

```
314.  SUCB2_HUMAN     Mass: 46824     Score: 61     Queries matched: 3   emPAI: 0.08
      Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
      1251    523.77   1045.52   1045.52 -1.57    0    38  0.0017    1  -.MASPVAAQAGK.L 1249 1250
```

```
315.  AT1A4_HUMAN     Mass: 115119     Score: 60     Queries matched: 3   emPAI: 0.03
      Sodium/potassium-transporting ATPase subunit alpha-4 OS=Homo sapiens GN=ATP1A4 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      1915    582.80   1163.58   1163.57  8.38    0     6       1.9    4  K.GTVAPHDQSPR.R
      3741    803.37   1604.73   1604.73  1.42    0    55  1.3e-005    1  K.VDNSSLTGESEPQSR.S 3742
```

```
316.  TB10A_HUMAN     Mass: 57595     Score: 60     Queries matched: 1   emPAI: 0.06
      TBC1 domain family member 10A OS=Homo sapiens GN=TBC1D10A PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score    Expect Rank  Peptide
      2881    677.81   1353.60   1353.60 -1.30    0    60  3.5e-006    1  K.ACQGQYETIER.L
```

---

317. LPP1_HUMAN **Mass:** 32535 **Score:** 60 **Queries matched:** 7 **emPAI:** 0.12

Lipid phosphate phosphohydrolase 1 OS=Homo sapiens GN=PPAP2A PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
298	432.22	862.42	862.41	7.45	1	18	0.16	1	R.MKGDWAR.L 297 299 301 302
361	440.21	878.41	878.41	2.40	1	(2)	4.7	6	R.MKGDWAR.L
1944	**584.77**	**1167.53**	**1167.52**	**5.56**	**0**	**60**	**5.1e-006**	**1**	**R.GVFCNDESIK.Y**

---

318. LSAMP_HUMAN **Mass:** 37883 **Score:** 60 **Queries matched:** 2 **emPAI:** 0.10

Limbic system-associated membrane protein OS=Homo sapiens GN=LSAMP PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1490	**545.77**	**1089.53**	**1089.53**	**-3.20**	**0**	**60**	**1e-005**	**1**	**K.AANEVSSADVK.Q**
2932	681.86	1361.70	1361.69	9.71	1	0	7.1	8	K.SNEATTGRQASLK.C

---

319. ENPP3_HUMAN **Mass:** 101998 **Score:** 59 **Queries matched:** 4 **emPAI:** 0.07

Ectonucleotide pyrophosphatase/phosphodiesterase family member 3 OS=Homo sapiens GN=ENPP3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
340	**436.23**	**870.45**	**870.44**	**1.95**	**0**	**26**	**0.012**	**1**	**R.VPPSESQK.C** 339 341
645	**466.17**	**930.32**	**930.32**	**-2.57**	**0**	**42**	**5.7e-005**	**1**	**K.DCCADYK.S**

---

320. LAMP2_HUMAN **Mass:** 45503 **Score:** 59 **Queries matched:** 1 **emPAI:** 0.08

Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
916	**494.29**	**986.56**	**986.55**	**2.54**	**0**	**59**	**1.4e-005**	**1**	**R.IPLNDLFR.C**

---

321. PRDX5_HUMAN **Mass:** 22301 **Score:** 58 **Queries matched:** 1 **emPAI:** 0.17

Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2208	**611.83**	**1221.64**	**1221.64**	**-2.37**	**0**	**58**	**1.1e-005**	**1**	**R.FSMVVQDGIVK.A**

---

322. IQGA2_HUMAN **Mass:** 181036 **Score:** 57 **Queries matched:** 2 **emPAI:** 0.02

Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2639	**651.29**	**1300.56**	**1300.56**	**-0.45**	**0**	**40**	**0.0002**	**1**	**K.EACNVPEPEEK.F** 2638

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323. ACLY_HUMAN **Mass:** 121674 **Score:** 57 **Queries matched:** 3 **emPAI:** 0.03

ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
492	**451.75**	**901.49**	**901.49**	**3.20**	**0**	**57**	**3.4e-005**	**1**	**R.LGQEATVGK.A** 487 491

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324. DESP_HUMAN **Mass:** 334021 **Score:** 57 **Queries matched:** 6 **emPAI:** 0.01

Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
354	438.23	874.44	874.44	-0.31	0	7	1.9	6	K.QSLEEAAK.T
1294	**527.24**	**1052.46**	**1052.46**	**3.37**	**1**	**3**	**1.8**	**2**	**K.RTASEDSCK.R**
1576	554.27	1106.53	1106.54	-1.53	1	8	1.3	3	K.AEFQEEAKR.R 1575 1578
2197	**610.79**	**1219.57**	**1219.57**	**3.14**	**0**	**57**	**1.4e-005**	**1**	**R.ETQSQLETER.S**

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325. SPIT3_HUMAN **Mass:** 10644 **Score:** 57 **Queries matched:** 2 **emPAI:** 0.38

Kunitz-type protease inhibitor 3 OS=Homo sapiens GN=SPINT3 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1680	**565.24**	**1128.47**	**1128.47**	**0.53**	**0**	**45**	**5.4e-005**	**1**	**K.GPCQTYMTR.W** 1681

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326. WDR1_HUMAN **Mass:** 66836 **Score:** 56 **Queries matched:** 4 **emPAI:** 0.06

WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
740	**476.74**	**951.46**	**951.47**	**-1.93**	**0**	**33**	**0.0035**	**1**	**R.DYSGQGVVK.L** 739 741 742

---

327. COPT1_HUMAN **Mass:** 21190 **Score:** 55 **Queries matched:** 1 **emPAI:** 0.18

High affinity copper uptake protein 1 OS=Homo sapiens GN=SLC31A1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
96	409.25	816.48	816.48	0.44	1	55	1.8e-005	1	R.KSQVSIR.Y

---

328. ANXA6_HUMAN **Mass:** 76168 **Score:** 54 **Queries matched:** 10 **emPAI:** 0.05

Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1033	504.72	1007.42	1007.42	1.69	0	54	1.6e-005	1	K.AMEGAGTDEK.A 1024 1025 1026 1027 1028 1029 1030 1031 1032

---

329. ANO6_HUMAN **Mass:** 107180 **Score:** 54 **Queries matched:** 3 **emPAI:** 0.03

Anoctamin-6 OS=Homo sapiens GN=ANO6 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1049	**505.80**	**1009.59**	**1009.60**	**-1.81**	**0**	**0**	**2.2**	**3**	**R.IVYFILSR.V**
2708	**659.77**	**1317.52**	**1317.53**	**-2.81**	**0**	**48**	**1.7e-005**	**1**	**R.QSEDPSCPNER.Y** 2709

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330. I5P1_HUMAN **Mass:** 48359 **Score:** 54 **Queries matched:** 3 **emPAI:** 0.08

Type I inositol 1,4,5-trisphosphate 5-phosphatase OS=Homo sapiens GN=INPP5A PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
717	**473.75**	**945.48**	**945.48**	**0.01**	**0**	**52**	**7.2e-005**	**1**	**R.AADTNEVVK.L** 718
942	497.27	992.53	992.53	0.81	1	2	4.4	10	K.ELSVFKDR.L

---

331. GMPR1_HUMAN **Mass:** 37851 **Score:** 54 **Queries matched:** 1 **emPAI:** 0.10

GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2038	**595.30**	**1188.58**	**1188.59**	**-7.51**	**0**	**54**	**3.6e-005**	**1**	**K.VGVGPGSVCTTR.T**

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332. LFA3_HUMAN **Mass:** 28756 **Score:** 54 **Queries matched:** 6 **emPAI:** 0.13

Lymphocyte function-associated antigen 3 OS=Homo sapiens GN=CD58 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
838	**487.73**	**973.45**	**973.45**	**-0.15**	**0**	**37**	**0.00098**	**1**	**K.MENDLPQK.I** 837 839 840 841 842

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333. ISK2_HUMAN **Mass:** 9627 **Score:** 53 **Queries matched:** 1 **emPAI:** 0.42

Serine protease inhibitor Kazal-type 2 OS=Homo sapiens GN=SPINK2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1106	**513.23**	**1024.44**	**1024.44**	**0.29**	**0**	**53**	**1.5e-005**	**1**	**R.TPNCSQYR.L**

---

334. AQP5_HUMAN **Mass:** 28445 **Score:** 53 **Queries matched:** 1 **emPAI:** 0.13

Aquaporin-5 OS=Homo sapiens GN=AQP5 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1422	**539.28**	**1076.54**	**1076.54**	**0.88**	**0**	**53**	**4.4e-005**	**1**	**R.SFGPAVVMNR.F**

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335. GSHB_HUMAN **Mass:** 52523 **Score:** 53 **Queries matched:** 1 **emPAI:** 0.07

Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3086	701.87	1401.72	1401.73	-4.34	1	53	5.4e-005	1	K.CPDIATQLAGTKK.V

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336. MAL2_HUMAN **Mass:** 19341 **Score:** 51 **Queries matched:** 1 **emPAI:** 0.20

Protein MAL2 OS=Homo sapiens GN=MAL2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1842	**576.34**	**1150.67**	**1150.67**	**0.31**	**0**	**51**	**1.6e-005**	**1**	**R.VTLPAGPDILR.T**

---

337. SC5A1_HUMAN **Mass:** 74305 **Score:** 51 **Queries matched:** 2 **emPAI:** 0.05

Sodium/glucose cotransporter 1 OS=Homo sapiens GN=SLC5A1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2587	**646.31**	**1290.60**	**1290.59**	**5.12**	**0**	**38**	**0.001**	**1**	**K.IACVVPSECEK.Y** 2586

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338. NFH_HUMAN **Mass:** 112639 **Score:** 51 **Queries matched:** 2 **emPAI:** 0.03

Neurofilament heavy polypeptide OS=Homo sapiens GN=NEFH PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
109	**411.69**	**821.37**	**821.37**	**3.35**	**0**	**5**	**1.9**	**10**	**K.VNTDAMR.S**
1915	582.80	1163.58	1163.58	-0.11	0	51	6.6e-005	1	R.TSVSSVSASPSR.F

---

339. MP2K2_HUMAN **Mass:** 44681 **Score:** 51 **Queries matched:** 2 **emPAI:** 0.08

Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
892	**492.27**	**982.52**	**982.52**	**-1.46**	**0**	**41**	**0.00074**	**1**	**R.LNQPGTPTR.T** 893

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340. RAB13_HUMAN **Score:** 51 **Queries matched:** 6

Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
430	445.25	888.49	888.49	0.32	1	8	1.4	6	R.TVDIEGKK.I 425 426 427 428
1398	536.33	1070.64	1070.63	3.27	0	51	4.5e-005	1	K.LLLIGDSGVGK.T

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341. 2AAA_HUMAN **Mass:** 66065 **Score:** 51 **Queries matched:** 1 **emPAI:** 0.06

Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1893	**580.80**	**1159.58**	**1159.57**	**4.23**	**0**	**51**	**8.3e-005**	**1**	**K.LTQDQDVDVK.Y**

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342. TBA1A_HUMAN **Mass:** 50788 **Score:** 50 **Queries matched:** 1 **emPAI:** 0.07

Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1072	**508.29**	**1014.57**	**1014.57**	**0.14**	**0**	**50**	**7.3e-005**	**1**	**K.DVNAAIATIK.T**

Proteins matching the same set of peptides:

TBA1B_HUMAN **Mass:** 50804 **Score:** 50 **Queries matched:** 1
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1
TBA1C_HUMAN **Mass:** 50548 **Score:** 50 **Queries matched:** 1
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1
TBA3C_HUMAN **Mass:** 50612 **Score:** 50 **Queries matched:** 1
Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3
TBA3E_HUMAN **Mass:** 50568 **Score:** 50 **Queries matched:** 1
Tubulin alpha-3E chain OS=Homo sapiens GN=TUBA3E PE=1 SV=2

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343. ZN263_HUMAN **Score:** 50 **Queries matched:** 6

Zinc finger protein 263 OS=Homo sapiens GN=ZNF263 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
287	**429.72**	**857.42**	**857.42**	**5.04**	**0**	**0**	**4.7**	**3**	**R.QGMHLTR.H**
415	444.71	887.41	887.41	-0.82	0	27	0.006	2	M.ASGPGSQER.E 416 417 418 419

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344. CHMP5_HUMAN **Mass:** 24612 **Score:** 50 **Queries matched:** 2 **emPAI:** 0.15

Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1657	563.27	1124.53	1124.54	-3.18	1	0	4.8	4	K.DTKTTVDAMK.L
3952	**843.42**	**1684.82**	**1684.81**	**7.97**	**0**	**50**	**6.5e-005**	**1**	**K.APPPSLTDCIGTVDSR.A**

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345. RINI_HUMAN **Mass:** 51766 **Score:** 49 **Queries matched:** 2 **emPAI:** 0.15

Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
180	**419.17**	**836.33**	**836.33**	**0.83**	**0**	**15**	**0.041**	**1**	**K.GCGDLCR.V**
3058	**699.29**	**1396.57**	**1396.57**	**-3.74**	**0**	**48**	**1.7e-005**	**1**	**K.LESCGVTSDNCR.D**

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346. SYT7_HUMAN **Mass:** 45815 **Score:** 49 **Queries matched:** 1 **emPAI:** 0.08

Synaptotagmin-7 OS=Homo sapiens GN=SYT7 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2877	**677.32**	**1352.63**	**1352.63**	**1.66**	**0**	**49**	**7.7e-005**	**1**	**K.AMDIGGTSDPYVK.V**

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347. EF1A1_HUMAN **Mass:** 50451 **Score:** 49 **Queries matched:** 2 **emPAI:** 0.07

Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
334	**435.77**	**869.53**	**869.53**	**-1.22**	**0**	**5**	**0.86**	**4**	**K.QLIVGVNK.M**
576	**457.79**	**913.57**	**913.56**	**6.60**	**0**	**49**	**6.5e-005**	**1**	**R.QTVAVGVIK.A**

Proteins matching the same set of peptides:

EF1A2_HUMAN **Mass:** 50780 **Score:** 49 **Queries matched:** 2

Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1

EF1A3_HUMAN **Mass:** 50495 **Score:** 49 **Queries matched:** 2

Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1

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348. VAS1_HUMAN **Mass:** 52164 **Score:** 49 **Queries matched:** 1 **emPAI:** 0.07

V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
218	**422.28**	**842.54**	**842.53**	**3.28**	**1**	**49**	**3.9e-005**	**1**	**K.KGSLLVAR.T**

---

349. GSTP1_HUMAN **Mass:** 23569 **Score:** 48 **Queries matched:** 1 **emPAI:** 0.16

Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1747	**568.79**	**1135.57**	**1135.57**	**1.60**	**0**	**48**	**0.00012**	**1**	**K.ASCLYGQLPK.F**

---

350. TLN1_HUMAN **Mass:** 271766 **Score:** 48 **Queries matched:** 1 **emPAI:** 0.01

Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1061	**507.25**	**1012.49**	**1012.49**	**0.37**	**0**	**48**	**9.6e-005**	**1**	**R.SAQPASAEPR.Q**

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351. QOR_HUMAN **Mass:** 35356 **Score:** 48 **Queries matched:** 1 **emPAI:** 0.11

Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2107	602.31	1202.61	1202.61	-1.96	0	48	0.00018	1	K.ILGTAGTEEGQK.I

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352. TCPD_HUMAN **Mass:** 58401 **Score:** 48 **Queries matched:** 3 **emPAI:** 0.06

T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
437	445.72	889.44	889.43	2.84	0	48	0.00016	1	K.ITGCASPGK.T
1324	530.77	1059.53	1059.54	-7.74	1	5	3.8	4	R.SGATAGAAGGRGK.G 1329

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353. GPC4_HUMAN **Mass:** 63455 **Score:** 47 **Queries matched:** 1 **emPAI:** 0.06

Glypican-4 OS=Homo sapiens GN=GPC4 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4505	972.38	1942.75	1942.75	0.94	0	47	2e-005	1	K.ICPQGSTCCSQEMEEK.Y

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354. CO4A5_HUMAN **Mass:** 162083 **Score:** 47 **Queries matched:** 3 **emPAI:** 0.02

Collagen alpha-5(IV) chain OS=Homo sapiens GN=COL4A5 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
579	458.25	914.48	914.48	-0.46	0	35	0.0023	2	K.GLQGEQGVK.G 580
3893	829.44	1656.86	1656.86	-3.18	0	1	4.8	1	K.GQPGLPGFPGTPGPPGPK.G

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355. LIN7C_HUMAN **Mass:** 21935 **Score:** 47 **Queries matched:** 2 **emPAI:** 0.38

Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
206	421.22	840.43	840.43	-6.26	0	28	0.0052	1	R.SGEVPPQK.L
940	496.74	991.46	991.46	-5.38	0	38	0.0012	1	K.VLEEMESR.F

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356. KGP2_HUMAN **Mass:** 88061 **Score:** 46 **Queries matched:** 2 **emPAI:** 0.04

cGMP-dependent protein kinase 2 OS=Homo sapiens GN=PRKG2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
811	484.22	966.43	966.43	2.82	0	10	0.51	2	R.GSFDEPTSK.F
918	494.76	987.50	987.50	0.17	0	46	0.00022	1	K.AGVSAEPTTR.T

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357. CHM1B_HUMAN **Mass:** 22152 **Score:** 46 **Queries matched:** 1 **emPAI:** 0.17

Charged multivesicular body protein 1b OS=Homo sapiens GN=CHMP1B PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
663	467.75	933.49	933.50	-2.51	0	46	0.00027	1	R.VQTAVTMGK.V

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358. MB12B_HUMAN **Mass:** 35996 **Score:** 45 **Queries matched:** 1 **emPAI:** 0.10

Multivesicular body subunit 12B OS=Homo sapiens GN=MVB12B PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2360	625.79	1249.56	1249.56	-4.08	0	45	0.00012	1	R.DSTEAAICDIR.I

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359. SYTL4_HUMAN **Mass:** 76603 **Score:** 45 **Queries matched:** 2 **emPAI:** 0.05

Synaptotagmin-like protein 4 OS=Homo sapiens GN=SYTL4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
818	484.74	967.46	967.46	-1.07	0	45	0.00015	1	K.AGGTSDSFVK.G
1490	545.77	1089.53	1089.52	5.87	0	1	7.8	5	R.IQESNGTWR.C

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360. SDCB1_HUMAN **Mass:** 32595 **Score:** 45 **Queries matched:** 8 **emPAI:** 0.24

Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
34	**405.20**	**808.38**	**808.38**	**-1.94**	**0**	**22**	**0.03**	**1**	**R.MAPSIMK.S** 33 35 36 37
100	410.21	818.41	818.40	2.22	0	19	0.14	1	R.DRPFER.T
1775	**571.28**	**1140.55**	**1140.55**	**1.22**	**0**	**20**	**0.063**	**1**	**K.SLMDHTIPEV.-**
2654	**652.82**	**1303.64**	**1303.64**	**-6.88**	**1**	**41**	**0.00062**	**1**	**R.EVILCKDQDGK.I**

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361. HID1_HUMAN **Score:** 45 **Queries matched:** 2

Protein HID1 OS=Homo sapiens GN=HID1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
806	**483.75**	**965.48**	**965.49**	**-3.57**	**0**	**3**	**3.7**	**5**	**K.SLSMVTANK.L**
916	494.29	986.56	986.56	-0.88	0	45	0.00035	2	K.LPLQTIMR.L

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362. ZG16B_HUMAN **Mass:** 22725 **Score:** 44 **Queries matched:** 1 **emPAI:** 0.17

Zymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
589	**460.23**	**918.45**	**918.44**	**0.44**	**0**	**44**	**0.00026**	**1**	**K.LGDSWDVK.L**

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363. NPC2_HUMAN **Mass:** 16902 **Score:** 44 **Queries matched:** 3 **emPAI:** 0.23

Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1074	**508.77**	**1015.52**	**1015.51**	**5.72**	**0**	**14**	**0.29**	**1**	**K.SGINCPIQK.D** 1073
4383	**922.43**	**1842.85**	**1842.86**	**-4.76**	**0**	**44**	**0.00024**	**1**	**K.EVNVSPCPTQPCQLSK.G**

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364. KLK3_HUMAN **Mass:** 29293 **Score:** 44 **Queries matched:** 2 **emPAI:** 0.28

Prostate-specific antigen OS=Homo sapiens GN=KLK3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
265	**427.70**	**853.40**	**853.39**	**1.61**	**0**	**28**	**0.0061**	**1**	**K.FMLCAGR.W**
1421	**539.26**	**1076.50**	**1076.50**	**2.94**	**0**	**34**	**0.0022**	**1**	**R.IVGGWECEK.H**

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365. CN37_HUMAN **Mass:** 47948 **Score:** 43 **Queries matched:** 2 **emPAI:** 0.08

2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
385	**442.71**	**883.40**	**883.41**	**-7.75**	**0**	**(0)**	**3.6**	**4**	**K.MVSADAYK.I**
476	**450.71**	**899.40**	**899.41**	**-2.85**	**0**	**43**	**0.00018**	**1**	**K.MVSADAYK.I**

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366. CKAP5_HUMAN **Mass:** 227062 **Score:** 43 **Queries matched:** 3 **emPAI:** 0.02

Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
647	**466.74**	**931.46**	**931.46**	**0.19**	**0**	**3**	**4.6**	**9**	**R.SQQELEAK.L**
1949	**585.29**	**1168.57**	**1168.57**	**5.02**	**0**	**43**	**0.00044**	**1**	**K.MQGQSPPAPTR.G**
4069	**859.97**	**1717.92**	**1717.93**	**-4.55**	**1**	**5**	**1.4**	**1**	**R.DAAFEALGTALKVVGEK.A**

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367. FERM2_HUMAN **Mass:** 78438 **Score:** 43 **Queries matched:** 1 **emPAI:** 0.05

Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3415	**752.36**	**1502.70**	**1502.70**	**0.53**	**0**	**43**	**0.0003**	**1**	**R.GCEVTPDVNISGQK.F**

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368. SERA_HUMAN **Mass:** 57356 **Score:** 42 **Queries matched:** 3 **emPAI:** 0.13

D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
910	**493.81**	**985.60**	**985.60**	**3.72**	**0**	**29**	**0.0053**	**1**	**R.DLPLLLFR.T**

```
        1397     536.30   1070.58   1070.57   5.46   0     33  0.0036    1   K.QADVNLVNAK.L
        1405     537.78   1073.56   1073.55   1.27   0     21     0.11   1   R.QIPQATASMK.D

369.   TALDO_HUMAN      Mass: 37688      Score: 42      Queries matched: 1    emPAI: 0.10
       Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score   Expect Rank   Peptide
         647     466.74     931.46     931.46   0.19    0     42  0.00063    1    K.AAQASDLEK.I

370.   CTL4_HUMAN      Mass: 80741      Score: 41      Queries matched: 7    emPAI: 0.05
       Choline transporter-like protein 4 OS=Homo sapiens GN=SLC44A4 PE=2 SV=2
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score   Expect Rank   Peptide
         381     442.71     883.40     883.40  -1.51    0     17     0.08    1    K.NEAPPDNK.K 380 382 383 384 385
        3870     824.90    1647.78    1647.78   4.07    0     41  0.00054    1    K.NEFSQTVGEVFYTK.N

371.   ANXA5_HUMAN      Mass: 35971      Score: 41      Queries matched: 1    emPAI: 0.10
       Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score   Expect Rank   Peptide
        2812     670.81    1339.61    1339.60   1.63    0     41  0.00041    1    R.GTVTDFPGFDER.A

372.   GTR3_HUMAN      Mass: 54345      Score: 41      Queries matched: 1    emPAI: 0.07
       Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score   Expect Rank   Peptide
        1560     552.83    1103.64    1103.63   1.65    0     41  0.00038    1    K.QVTVLELFR.V


       Proteins matching the same set of peptides:
       GTR14_HUMAN      Mass: 56854      Score: 41      Queries matched: 1
       Solute carrier family 2, facilitated glucose transporter member 14 OS=Homo sapiens GN=SLC2A14 PE=2 SV=1

373.   LANC1_HUMAN      Mass: 45995      Score: 41      Queries matched: 2    emPAI: 0.08
       LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score   Expect Rank   Peptide
         938     496.73     991.44     991.44  -1.33    0     41  0.00034    1    K.QAEDCITR.L 939

374.   CHM2B_HUMAN      Mass: 23948      Score: 41      Queries matched: 1    emPAI: 0.16
       Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B PE=1 SV=1
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score   Expect Rank   Peptide
         887     491.75     981.48     981.48  -2.26    0     41  0.00057    1    K.VTSMSTQTK.V

375.   DB126_HUMAN      Mass: 12565      Score: 40      Queries matched: 2    emPAI: 0.32
       Beta-defensin 126 OS=Homo sapiens GN=DEFB126 PE=2 SV=2
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score  Expect Rank   Peptide
         937     496.70     991.39     991.39   1.98    0     28  0.0016    1   R.DCCVPADR.R 936

376.   LEG3_HUMAN      Mass: 26193      Score: 40      Queries matched: 9    emPAI: 0.15
       Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score  Expect Rank   Peptide
         165     417.23     832.45     832.45  -1.19    0     30  0.0082    1   R.VIVCNTK.L 161 162 163 164 166 167 168 169

377.   GBG4_HUMAN      Mass: 8554      Score: 40      Queries matched: 2    emPAI: 1.18
       Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-4 OS=Homo sapiens GN=GNG4 PE=1 SV=1
       Query   Observed   Mr(expt)   Mr(calc)    ppm   Miss Score  Expect Rank   Peptide
```

82	408.25	814.49	814.49	-1.25	1	29	0.0072	4	R.KAVEQLK.M
562	456.67	911.33	911.33	-1.67	0	27	0.0019	1	K.MEACMDR.V

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378. PROM2_HUMAN **Mass:** 93079 **Score:** 40 **Queries matched:** 1 **emPAI:** 0.04

Prominin-2 OS=Homo sapiens GN=PROM2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1302	527.78	1053.55	1053.56	-2.40	0	40	0.00074	1	K.AVAQQPEGVR.T

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379. ZNT4_HUMAN **Mass:** 47852 **Score:** 40 **Queries matched:** 1 **emPAI:** 0.08

Zinc transporter 4 OS=Homo sapiens GN=SLC30A4 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4112	869.86	1737.70	1737.70	-0.82	1	40	0.0001	1	R.QEVDRTCANCQSSSP.-

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380. AT8B1_HUMAN **Mass:** 144802 **Score:** 40 **Queries matched:** 1 **emPAI:** 0.03

Probable phospholipid-transporting ATPase IC OS=Homo sapiens GN=ATP8B1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1100	512.26	1022.51	1022.50	2.63	0	40	0.00094	1	K.GADTVIYER.L

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381. TM63A_HUMAN **Mass:** 93549 **Score:** 39 **Queries matched:** 4 **emPAI:** 0.04

Transmembrane protein 63A OS=Homo sapiens GN=TMEM63A PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
605	462.21	922.40	922.40	-1.14	0	32	0.0023	1	K.CQSLQCK.G 604
1437	541.25	1080.49	1080.49	-7.33	0	7	0.82	2	K.GEPQPSSHSR.E 1436

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382. SERC1_HUMAN **Mass:** 51488 **Score:** 39 **Queries matched:** 2 **emPAI:** 0.07

Serine incorporator 1 OS=Homo sapiens GN=SERINC1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
282	429.23	856.44	856.44	1.02	0	36	0.0014	1	K.IQESQPR.S 283

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383. PROF1_HUMAN **Mass:** 15216 **Score:** 39 **Queries matched:** 1 **emPAI:** 0.26

Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2999	690.36	1378.71	1378.71	2.43	0	39	0.0012	1	K.STGGAPTFNVTVTK.T

---

384. RAB44_HUMAN **Score:** 38 **Queries matched:** 3

Ras-related protein Rab-44 OS=Homo sapiens GN=RAB44 PE=3 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
816	484.68	967.34	967.34	-0.70	0	(20)	0.009	2	K.MDCEEER.Q 817
897	492.67	983.33	983.33	0.44	0	25	0.0033	2	K.MDCEEER.Q

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385. ITCH_HUMAN **Mass:** 103593 **Score:** 38 **Queries matched:** 1 **emPAI:** 0.04

E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens GN=ITCH PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4273	895.88	1789.74	1789.74	1.30	0	38	0.00015	1	R.VSTNGSDDPEDAGAGENR.R

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386. MYO1B_HUMAN **Mass:** 132928 **Score:** 37 **Queries matched:** 3 **emPAI:** 0.03

Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
915	494.27	986.52	986.51	9.72	0	4	4.6	7	K.MPSLSPIDK.N 914
1040	505.23	1008.45	1008.45	-1.01	0	37	0.00087	1	R.DQFTDQQK.L

```
387.  K2C7_HUMAN     Score: 37     Queries matched: 7
      Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
       973    500.23    998.44    998.44  6.75    0   (21)   0.03    2  K.DVDAAYMSK.V 968 969 970 972
      1070    508.22   1014.43   1014.43  1.78    0    24  0.0078    2  K.DVDAAYMSK.V 1069

388.  DDAH1_HUMAN     Mass: 31444     Score: 36     Queries matched: 2   emPAI: 0.12
      N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
      1826    575.76   1149.51   1149.52 -4.93    0    30  0.0039    1  R.TPEEYPESAK.V 1827

389.  FUCM_HUMAN     Score: 35     Queries matched: 2
      Fucose mutarotase OS=Homo sapiens GN=FUOM PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         6    400.75    799.49    799.49  0.16    1    35  0.0023    2  R.ALAKIER.F
      2559    644.82   1287.63   1287.62  7.66    1     2     4.1    5  K.IERFEFYER.A

390.  YES_HUMAN     Mass: 61276     Score: 34     Queries matched: 3   emPAI: 0.06
      Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=1 SV=3
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
       398    443.72    885.43    885.43 -2.10    0     1     4.2    5  K.DAWEIPR.E
       732    475.75    949.49    949.49 -0.30    0     4     3.1    2  R.AQFDTLQK.L
      1104    512.80   1023.58   1023.58  0.47    0    34  0.0013    1  R.LLLNPGNQR.G

391.  UBA1_HUMAN     Mass: 118858    Score: 34     Queries matched: 2   emPAI: 0.03
      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  Peptide
      2361    625.79   1249.56   1249.56  0.20    0    34  0.0018    1  R.AENYDIPSADR.H
      2560    644.84   1287.66   1287.66  0.29    0     1       7    9  R.QLYVLGHEAMK.R

392.  RHOA_HUMAN     Score: 34     Queries matched: 3
      Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
      1480    544.79   1087.57   1087.57  3.55    0    34  0.0039    2  K.LVIVGDGACGK.T 1478 1479


      Proteins matching the same set of peptides:
      RHOC_HUMAN     Score: 34     Queries matched: 3

393.  ABCB6_HUMAN     Score: 34     Queries matched: 1
      ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
        12    401.25    800.48    800.48  7.00    0    34  0.0047    2  R.AIQASLAK.V

394.  MGRN1_HUMAN     Mass: 61456     Score: 33     Queries matched: 3   emPAI: 0.06
      E3 ubiquitin-protein ligase MGRN1 OS=Homo sapiens GN=MGRN1 PE=1 SV=2
     Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
      2610    648.28   1294.55   1294.55 -7.45    0    23  0.0079    1  R.YQANNCPICR.L 2609 2611


      Proteins matching the same set of peptides:
      RN157_HUMAN     Mass: 74731     Score: 33     Queries matched: 3
```

```
        RING finger protein 157 OS=Homo sapiens GN=RNF157 PE=1 SV=3

395.    NCKP1_HUMAN     Mass: 130018     Score: 33     Queries matched: 2    emPAI: 0.03
        Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1
       Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
         946    497.76    993.50    993.51  -9.10   1     4     3.5    8   R.KYGPVMQR.Y
        2631    649.84   1297.67   1297.67  -2.28   0    33  0.0028    1   R.NNNQQLAQLQK.E


396.    UBR2_HUMAN     Score: 33     Queries matched: 2
        E3 ubiquitin-protein ligase UBR2 OS=Homo sapiens GN=UBR2 PE=1 SV=1
       Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
         440    446.75    891.49    891.49  -1.71   0    31  0.0072    2   R.AGIMPFLK.C 439


397.    AP1B1_HUMAN     Mass: 105482     Score: 33     Queries matched: 2    emPAI: 0.04
        AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2
       Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
         939    496.73    991.44    991.44  -0.76   0    33   0.002    1   R.EAQSICER.V 938


        Proteins matching the same set of peptides:
        AP2B1_HUMAN     Mass: 105398     Score: 33     Queries matched: 2
        AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1

398.    RALB_HUMAN     Mass: 23508     Score: 33     Queries matched: 5    emPAI: 0.16
        Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1
       Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
         626    464.25    926.49    926.48   4.24   0    29  0.0073    1   R.QVPVEEAR.S 620 621 624 625


399.    VINC_HUMAN     Mass: 124292     Score: 32     Queries matched: 2    emPAI: 0.03
        Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4
       Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        2475    635.34   1268.67   1268.67  -2.98   0    32  0.0034    1   K.AVAGNISDPGLQK.S 2476


400.    TNAP3_HUMAN     Score: 32     Queries matched: 6
        Tumor necrosis factor alpha-induced protein 3 OS=Homo sapiens GN=TNFAIP3 PE=1 SV=1
       Query  Observed  Mr(expt)  Mr(calc)     ppm  Miss Score Expect Rank  Peptide
         471    450.25    898.48    898.48    1.04   0    27  0.0092    2   K.LDEANLPK.E 467 468 469 470
         639    465.26    928.50    928.51  -10.00   1     5       4    7   K.SDPSRLVR.S


401.    CYTC_HUMAN     Mass: 16017     Score: 32     Queries matched: 1    emPAI: 0.24
        Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1
       Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
        2231    613.81   1225.60   1225.60   0.49   0    32  0.0053    1   R.ALDFAVGEYNK.A


402.    PTHB1_HUMAN     Mass: 100415     Score: 32     Queries matched: 4    emPAI: 0.04
        Protein PTHB1 OS=Homo sapiens GN=BBS9 PE=1 SV=1
       Query  Observed  Mr(expt)  Mr(calc)    ppm  Miss Score Expect Rank  Peptide
          26    402.73    803.44    803.44   0.24   0    30   0.016    1   K.ITIDTNK.S 27
        1251    523.77   1045.52   1045.52   5.51   1     2     7.3    3   K.RQETEQQK.L
        2191    610.30   1218.59   1218.58   5.61   0     5     1.8    4   K.LMYEHNLQR.T


403.    SARG_HUMAN     Mass: 64211     Score: 32     Queries matched: 1    emPAI: 0.06
```

```
         Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         3538    772.85   1543.68   1543.68  2.38    0    32 0.0025    1  R.AEDAPLSSGEDPNSR.L

404.     VAT1_HUMAN    Mass: 42122     Score: 31     Queries matched: 1    emPAI: 0.09
         Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         2071    597.84   1193.66   1193.67 -2.31    1    31 0.0026    1  K.VLLVPGPEKEN.-

405.     SPTN2_HUMAN    Mass: 272526    Score: 31     Queries matched: 7    emPAI: 0.01
         Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
          158    416.23    830.45    830.45 -1.26    0     1    8.9    4  K.LTALEER.E
          435    445.71    889.41    889.41  0.14    0    14    0.3    3  R.EESLGEAR.R 436
         1787    572.82   1143.62   1143.61  8.02    1    26  0.024    1  R.GEMSGRLGPLK.L 1784 1785 1786

406.     K1609_HUMAN    Mass: 51588     Score: 31     Queries matched: 1    emPAI: 0.07
         TLD domain-containing protein KIAA1609 OS=Homo sapiens GN=KIAA1609 PE=1 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         1261    524.77   1047.53   1047.53  0.27    0    31 0.0074    1  K.MISATEGPVK.A

407.     EPM2A_HUMAN    Score: 31     Queries matched: 7
         Laforin OS=Homo sapiens GN=EPM2A PE=1 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         3141    711.83   1421.65   1421.66 -2.99    0    23   0.02    2  R.YPEPMTPDTMIK.L 3142 3143 3144 3145
         3190    719.84   1437.66   1437.65  3.04    0   (6)      1    4  R.YPEPMTPDTMIK.L 3192

408.     SRP54_HUMAN    Score: 31     Queries matched: 4
         Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         3381    747.84   1493.67   1493.68 -2.98    1    26 0.0078    2  K.LNQQMAKMMDPR.V 3380 3382 3384

409.     SYCC_HUMAN    Score: 31     Queries matched: 2
         Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=3
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         1033    504.72   1007.42   1007.43 -9.48    0    31 0.0037    2  -.MADSSGQQGK.G
         1709    566.80   1131.58   1131.59 -9.68    0     7      2    3  R.LAFLMHSWK.D

410.     RNF14_HUMAN    Score: 30     Queries matched: 1
         E3 ubiquitin-protein ligase RNF14 OS=Homo sapiens GN=RNF14 PE=1 SV=1
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         3538    772.85   1543.68   1543.68  1.79    0    30 0.0033    2  R.DGQVQCLNCPEPK.C

411.     MPP10_HUMAN    Mass: 78930     Score: 30     Queries matched: 2    emPAI: 0.05
         U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=1 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
          898    492.74    983.47    983.48 -7.23    0     2    3.9    2  K.MMDSLFLK.L
         1002    502.27   1002.53   1002.53 -5.32    1    30  0.012    1  K.AGDIKTAAEK.T

412.     UBP30_HUMAN    Score: 30     Queries matched: 4
```

```
         Ubiquitin carboxyl-terminal hydrolase 30 OS=Homo sapiens GN=USP30 PE=1 SV=1
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
         1018    503.73   1005.45   1005.45  -1.50    0   (14)    0.2    3   R.AEAAMTAADR.A 1019 1020
         1097    511.73   1021.45   1021.45   1.17    0    30  0.0051    2   R.AEAAMTAADR.A


413.    SMAG2_HUMAN     Mass: 75892     Score: 30     Queries matched: 1   emPAI: 0.05
         Protein Smaug homolog 2 OS=Homo sapiens GN=SAMD4B PE=1 SV=1
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
          159    416.25    830.48    830.47   8.55    1    30   0.011    1   R.VTRTQAR.F


414.    AIMP1_HUMAN     Score: 30     Queries matched: 5
         Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
           82    408.25    814.49    814.49  -1.27    0    30  0.0069    2   K.QQVSLLK.E
          934    496.25    990.48    990.48   2.19    0     2     6.6    4   -.MANNDAVLK.R
         1903    581.29   1160.57   1160.57   2.03    1     6     1.8    3   K.EQIKGGTGDEK.K 1898 1901


415.    NRAP_HUMAN     Score: 30     Queries matched: 1
         Nebulin-related-anchoring protein OS=Homo sapiens GN=NRAP PE=2 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
           82    408.25    814.49    814.49  -1.25    1    30  0.0069    2   R.KKPDSIK.F


416.    SPRE_HUMAN     Score: 29     Queries matched: 2
         Sepiapterin reductase OS=Homo sapiens GN=SPR PE=1 SV=1
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
           82    408.25    814.49    814.49  -1.25    1    29  0.0072    4   R.KGLQELK.A
         1258    524.28   1046.55   1046.55  -7.66    0    17    0.18    2   R.AVCLLTGASR.G


417.    ABHEB_HUMAN     Mass: 22446     Score: 29     Queries matched: 2   emPAI: 0.17
         Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
          905    493.25    984.50    984.50  -3.56    0    29  0.0073    1   R.EALPGSGQAR.F 903


418.    ZBT32_HUMAN     Mass: 53671     Score: 29     Queries matched: 4   emPAI: 0.07
         Zinc finger and BTB domain-containing protein 32 OS=Homo sapiens GN=ZBTB32 PE=1 SV=1
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
          325    434.75    867.49    867.49   1.20    0    23    0.02    1   R.LQAPVGQR.G 323 324 327


419.    CD151_HUMAN     Mass: 29132     Score: 29     Queries matched: 5   emPAI: 0.13
         CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
          307    432.22    862.43    862.42   4.30    0    29   0.015    1   K.VEGGCITK.L
          778    482.71    963.41    963.42  -0.60    0    16   0.063    1   R.VVPDSCCK.T 779 780
         1002    502.27   1002.53   1002.53   1.15    0    13    0.54    3   K.TVVALCGQR.D


420.    TSN11_HUMAN     Score: 29     Queries matched: 1
         Tetraspanin-11 OS=Homo sapiens GN=TSPAN11 PE=2 SV=2
        Query  Observed  Mr(expt)  Mr(calc)   ppm  Miss Score Expect Rank  Peptide
          307    432.22    862.43    862.42   4.30    0    29   0.015    1   K.VEGGCLTK.L
```

421. FILA_HUMAN **Mass:** 435036 **Score:** 29 **Queries matched:** 6 **emPAI:** 0.01
Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
110	411.73	821.45	821.46	-8.98	1	4	2	6	R.HSGIPRR.Q
1002	502.27	1002.53	1002.53	-5.31	1	8	1.6	5	R.LSERLEEK.E
1089	510.76	1019.50	1019.51	-6.73	1	5	3.3	9	K.SSSQVNRSR.H
2806	**670.30**	**1338.59**	**1338.60**	**-8.72**	**1**	**25**	**0.013**	**1**	**R.HHEASSRADSSR.H** 2805 2807

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422. CRLD2_HUMAN **Mass:** 57366 **Score:** 29 **Queries matched:** 3 **emPAI:** 0.06
Cysteine-rich secretory protein LCCL domain-containing 2 OS=Homo sapiens GN=CRISPLD2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1274	**525.74**	**1049.48**	**1049.47**	**0.76**	**0**	**29**	**0.0066**	**1**	**K.IGCAVNTCR.K** 1272
2328	622.82	1243.62	1243.62	1.59	0	3	3.9	7	R.NGVQSESLGTPR.D

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423. TR49C_HUMAN **Score:** 29 **Queries matched:** 9
Tripartite motif-containing protein 49C OS=Homo sapiens GN=TRIM49C PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
651	466.76	931.50	931.50	-1.93	0	29	0.015	2	K.STEQINLK.T 650 652 653 654 655 656 657 658

Proteins matching the same set of peptides:
TRI49_HUMAN **Score:** 29 **Queries matched:** 9

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424. FA73B_HUMAN **Score:** 29 **Queries matched:** 2
Protein FAM73B OS=Homo sapiens GN=FAM73B PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1005	502.73	1003.44	1003.44	-1.64	0	24	0.011	2	R.GDSGSTPMPR.D 1006

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425. TMED2_HUMAN **Mass:** 22860 **Score:** 29 **Queries matched:** 1 **emPAI:** 0.17
Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1007	**502.74**	**1003.47**	**1003.47**	**3.20**	**0**	**29**	**0.0061**	**1**	**R.AINDNTNSR.V**

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426. BASI_HUMAN **Mass:** 42573 **Score:** 29 **Queries matched:** 1 **emPAI:** 0.09
Basigin OS=Homo sapiens GN=BSG PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1065	**507.75**	**1013.49**	**1013.49**	**1.53**	**0**	**29**	**0.0084**	**1**	**R.FFVSSSQGR.S**

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427. UNC80_HUMAN **Mass:** 367152 **Score:** 28 **Queries matched:** 5 **emPAI:** 0.01
Protein unc-80 homolog OS=Homo sapiens GN=UNC80 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
633	465.24	928.46	928.45	8.09	0	3	3	3	K.EAHGNVFR.R
847	488.25	974.49	974.48	8.54	0	9	1.3	5	R.SSPINSQSR.T
1466	544.29	1086.57	1086.56	9.75	0	2	6.8	7	R.WNLIHYNK.T
1694	**566.29**	**1130.57**	**1130.58**	**-6.81**	**1**	**28**	**0.011**	**1**	**K.RSSPINSQSR.T**
2254	**615.78**	**1229.55**	**1229.54**	**3.43**	**0**	**7**	**0.66**	**2**	**R.QDELMYMLR.K**

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428. FAT2_HUMAN **Mass:** 482097 **Score:** 28 **Queries matched:** 4 **emPAI:** 0.01
Protocadherin Fat 2 OS=Homo sapiens GN=FAT2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
109	411.69	821.37	821.38	-6.22	0	7	1.1	8	K.GNNGSAFR.V
116	412.70	823.38	823.38	-0.61	0	1	4.7	7	R.DGQVSYR.L
850	488.27	974.52	974.51	8.10	0	28	0.017	1	K.SSNTALLNR.E
1634	**560.27**	**1118.52**	**1118.53**	**-6.76**	**1**	**1**	**5.4**	**5**	**K.LDRENSTER.V**

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429. PPIA_HUMAN **Mass:** 18229 **Score:** 28 **Queries matched:** 3 **emPAI:** 0.47
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	Peptide
247	**424.71**	**847.41**	**847.41**	**8.06**	**0**	**23**	**0.048**	**1**	**K.TEWLDGK.H**
1634	560.27	1118.52	1118.53	-3.35	0	22	0.037	1	K.ITIADCGQLE.-
3772	**807.88**	**1613.74**	**1613.73**	**2.23**	**0**	**14**	**0.17**	**1**	**R.IIPGFMCQGGDFTR.H**

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430. WNT3A_HUMAN **Score:** 28 **Queries matched:** 2
Protein Wnt-3a OS=Homo sapiens GN=WNT3A PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1839	576.31	1150.60	1150.59	9.62	0	28	0.015	2	R.QAIASHMHLK.C 1836

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431. CS018_HUMAN **Score:** 28 **Queries matched:** 4
Uncharacterized protein C19orf18 OS=Homo sapiens GN=C19orf18 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
86	408.71	815.41	815.41	0.04	0	25	0.025	2	R.LAQAEER.Q 83 84 85

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432. ANXA3_HUMAN **Mass:** 36524 **Score:** 28 **Queries matched:** 1 **emPAI:** 0.10
Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
859	**489.77**	**977.52**	**977.52**	**-0.51**	**0**	**28**	**0.015**	**1**	**K.QDAQILYK.A**

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433. FA43A_HUMAN **Mass:** 46203 **Score:** 27 **Queries matched:** 1 **emPAI:** 0.08
Protein FAM43A OS=Homo sapiens GN=FAM43A PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3640	**786.84**	**1571.66**	**1571.67**	**-6.61**	**0**	**27**	**0.0023**	**1**	**R.AAEGDPAEEEAEAQR.A**

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434. AT2B3_HUMAN **Mass:** 135253 **Score:** 27 **Queries matched:** 15 **emPAI:** 0.06
Plasma membrane calcium-transporting ATPase 3 OS=Homo sapiens GN=ATP2B3 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
42	405.21	808.41	808.41	-5.73	0	24	0.026	2	K.SMSTVIR.M 38 39 40 41 43
2048	596.30	1190.58	1190.57	5.96	0	(0)	7.8	6	R.MVTGDNINTAR.A
2122	604.29	1206.57	1206.57	2.71	0	22	0.043	2	R.MVTGDNINTAR.A 2118 2119 2120 2121
3471	**762.85**	**1523.69**	**1523.69**	**1.61**	**1**	**6**	**1**	**1**	**K.QQDGAMESSQTKAK.K** 3472
3837	821.43	1640.85	1640.84	6.93	0	0	5.9	3	R.QVVAVTGDGTNDGPALK.K

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435. AT2B4_HUMAN **Score:** 27 **Queries matched:** 14
Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
42	405.21	808.41	808.41	-5.73	0	24	0.026	2	K.SMSTVIR.N 38 39 40 41 43
368	**440.22**	**878.42**	**878.42**	**-0.10**	**0**	**4**	**3.7**	**8**	**K.QDYQAVR.N**
2048	596.30	1190.58	1190.57	5.96	0	(0)	7.8	6	R.MVTGDNINTAR.A
2122	604.29	1206.57	1206.57	2.71	0	22	0.043	2	R.MVTGDNINTAR.A 2118 2119 2120 2121
3837	821.43	1640.85	1640.84	6.93	0	0	5.9	3	R.QVVAVTGDGTNDGPALK.K

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436. BCOR_HUMAN **Score:** 27 **Queries matched:** 1
BCL-6 corepressor OS=Homo sapiens GN=BCOR PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
981	501.27	1000.53	1000.53	2.25	0	27	0.022	2	K.NAGETLLQR.A

---

437. TBCB_HUMAN **Mass:** 27594 **Score:** 27 **Queries matched:** 3 **emPAI:** 0.14
Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1402	**536.79**	**1071.56**	**1071.57**	**-6.29**	**0**	**27**	**0.014**	**1**	**K.AQASSIPVGSR.C** 1401
1539	551.27	1100.53	1100.52	9.39	0	3	3.2	5	R.AQQEAEAAQR.L

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438. SH3R3_HUMAN **Score:** 27 **Queries matched:** 3
SH3 domain-containing RING finger protein 3 OS=Homo sapiens GN=SH3RF3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
388	442.71	883.41	883.41	0.23	0	24	0.022	2	K.DCLTFTK.D 387 389

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439. PRAX_HUMAN **Score:** 27 **Queries matched:** 5
Periaxin OS=Homo sapiens GN=PRX PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
73	406.79	811.56	811.55	8.02	1	22	0.0071	2	K.LKLPTIK.M 72
1958	585.33	1168.65	1168.65	-3.55	1	3	1.9	2	K.VPDMKLPEIK.L 1959
2107	602.31	1202.61	1202.60	6.66	1	4	3.6	4	K.VPEMKVPEMK.L

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440. INT1_HUMAN **Score:** 26 **Queries matched:** 1
Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
480	451.25	900.49	900.49	2.31	0	26	0.019	2	R.LAEAAVAEK.R

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441. FA83H_HUMAN **Score:** 25 **Queries matched:** 4
Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
460	**448.22**	**894.42**	**894.43**	**-6.97**	**1**	**3**	**3**	**4**	**K.QDSFRSR.L**
592	460.73	919.44	919.44	0.09	0	25	0.022	2	R.SDSLGTQGR.L 591 593

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442. MTMR6_HUMAN **Score:** 25 **Queries matched:** 1
Myotubularin-related protein 6 OS=Homo sapiens GN=MTMR6 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
352	437.25	872.49	872.50	-4.66	0	25	0.032	1	K.LLEVNGTK.G

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443. SRCAP_HUMAN **Mass:** 344996 **Score:** 25 **Queries matched:** 1 **emPAI:** 0.01
Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
760	**479.79**	**957.56**	**957.56**	**2.08**	**0**	**25**	**0.016**	**1**	**K.LTLTGAQVR.Q**

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444. WDR35_HUMAN **Mass:** 135229 **Score:** 25 **Queries matched:** 6 **emPAI:** 0.03
WD repeat-containing protein 35 OS=Homo sapiens GN=WDR35 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
496	452.24	902.47	902.47	-0.89	1	25	0.031	1	K.IADEEAKK.G 497
2843	673.85	1345.68	1345.69	-2.66	0	3	5.4	4	K.EISALSWEGGGLK.I 2846
4043	856.39	1710.76	1710.77	-7.51	1	5	1.1	3	K.WAKDNPDLFAMMEK.T 4042

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445. DPOD1_HUMAN **Score:** 25 **Queries matched:** 3
DNA polymerase delta catalytic subunit OS=Homo sapiens GN=POLD1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

462	448.72	895.43	895.43	-4.08	0	24	0.027	2	R.ESELYQK.E 461 463

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446. PM2PB_HUMAN **Mass:** 29106 **Score:** 25 **Queries matched:** 1 **emPAI:** 0.13

Putative postmeiotic segregation increased 2-like protein 11 OS=Homo sapiens GN=PMS2P11 PE=5 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3074	**700.83**	**1399.64**	**1399.65**	**-7.50**	**0**	**25**	**0.015**	**1**	**K.LSAASGYSDVTDSK.A**

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447. CC170_HUMAN **Score:** 24 **Queries matched:** 4

Coiled-coil domain-containing protein 170 OS=Homo sapiens GN=CCDC170 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
496	452.24	902.47	902.47	-0.91	0	24	0.037	2	K.LADTNELK.I 497
1240	**523.29**	**1044.56**	**1044.56**	**-0.55**	**1**	**1**	**6.2**	**6**	**K.AIEDLNKSR.D**
2481	**635.85**	**1269.68**	**1269.69**	**-2.93**	**1**	**5**	**1.9**	**2**	**K.ELHMSLLRQK.I**

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448. CR3L2_HUMAN **Score:** 24 **Queries matched:** 2

Cyclic AMP-responsive element-binding protein 3-like protein 2 OS=Homo sapiens GN=CREB3L2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
496	452.24	902.47	902.47	-0.91	0	24	0.037	2	K.LEGNETLK.V 497

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449. NUDC2_HUMAN **Score:** 24 **Queries matched:** 3

NudC domain-containing protein 2 OS=Homo sapiens GN=NUDCD2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
884	491.72	981.43	981.42	4.69	0	24	0.011	2	-.MSAPFEER.S 883 885

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450. RPC3_HUMAN **Score:** 24 **Queries matched:** 4

DNA-directed RNA polymerase III subunit RPC3 OS=Homo sapiens GN=POLR3C PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
105	410.72	819.42	819.42	0.94	0	(24)	0.049	2	-.MTQAEIK.L
177	418.71	835.41	835.41	0.65	0	24	0.045	2	-.MTQAEIK.L 175 176

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451. UBP24_HUMAN **Score:** 24 **Queries matched:** 2

Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
574	457.26	912.51	912.50	2.58	1	24	0.028	2	K.KDSVSLHK.K 573

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452. 5NT3B_HUMAN **Score:** 24 **Queries matched:** 1

7-methylguanosine phosphate-specific 5'-nucleotidase OS=Homo sapiens GN=NT5C3B PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1168	517.77	1033.53	1033.52	3.50	1	24	0.035	2	K.IISEECRK.E

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453. OR4A5_HUMAN **Score:** 24 **Queries matched:** 15

Olfactory receptor 4A5 OS=Homo sapiens GN=OR4A5 PE=2 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
2046	596.30	1190.58	1190.57	5.59	1	(17)	0.16	2	R.NSEMRNAIEK.L 2045 2047 2048 2051 2052 2053
2120	604.29	1206.57	1206.57	0.83	1	24	0.022	2	R.NSEMRNAIEK.L 2118 2119 2121 2122 2123 2124 2125

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454. GPRL1_HUMAN **Mass:** 27989 **Score:** 24 **Queries matched:** 4 **emPAI:** 0.14

GLIPR1-like protein 1 OS=Homo sapiens GN=GLIPR1L1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
707	**471.74**	**941.46**	**941.46**	**-0.72**	**0**	**24**	**0.023**	**1**	**K.VNPPAADMK.Y** 706

754	479.73	957.45	957.46	-6.75	0	(16)	0.095	1	K.VNPPAADMK.Y 756

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455. BRD7_HUMAN **Score:** 24 **Queries matched:** 1
Bromodomain-containing protein 7 OS=Homo sapiens GN=BRD7 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1040	505.23	1008.45	1008.44	6.81	1	24	0.019	2	K.DKDMLEDK.F

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456. VKGC_HUMAN **Score:** 24 **Queries matched:** 4
Vitamin K-dependent gamma-carboxylase OS=Homo sapiens GN=GGCX PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
211	421.74	841.46	841.47	-2.26	0	24	0.026	2	K.AELISGPR.Q 212 213 214

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457. H1BP3_HUMAN **Score:** 24 **Queries matched:** 2
HCLS1-binding protein 3 OS=Homo sapiens GN=HS1BP3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
582	458.75	915.48	915.48	7.14	0	24	0.055	2	R.SPGAAGLTSR.D 583

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458. MIPEP_HUMAN **Score:** 23 **Queries matched:** 1
Mitochondrial intermediate peptidase OS=Homo sapiens GN=MIPEP PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
12	401.25	800.48	800.48	6.98	0	23	0.056	3	R.ALQGTIAK.N

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459. MDR3_HUMAN **Score:** 23 **Queries matched:** 4
Multidrug resistance protein 3 OS=Homo sapiens GN=ABCB4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1143	516.74	1031.46	1031.46	-0.36	0	21	0.021	2	K.FESMYVEK.L 1140 1141 1142

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460. F151A_HUMAN **Score:** 23 **Queries matched:** 10
Protein FAM151A OS=Homo sapiens GN=FAM151A PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
408	443.76	885.50	885.50	-0.11	0	23	0.049	3	K.QLALNATR.K 400 401 402 404 405 410 411 412 413

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461. QSOX1_HUMAN **Score:** 23 **Queries matched:** 1
Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
82	408.25	814.49	814.49	-1.25	1	23	0.032	6	R.KEGAVLAK.K

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462. CTR4_HUMAN **Mass:** 68680 **Score:** 23 **Queries matched:** 1 **emPAI:** 0.05
Cationic amino acid transporter 4 OS=Homo sapiens GN=SLC7A4 PE=2 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
3606	**782.41**	**1562.81**	**1562.79**	**9.61**	**0**	**23**	**0.045**	**1**	**K.SSPPSSPGPASPGPLTK.Q**

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463. AP4A_HUMAN **Score:** 23 **Queries matched:** 1
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical] OS=Homo sapiens GN=NUDT2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
547	455.22	908.42	908.42	-4.60	0	23	0.035	2	K.DYDVEIR.L

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464. AT2B2_HUMAN **Score:** 23 **Queries matched:** 8
Plasma membrane calcium-transporting ATPase 2 OS=Homo sapiens GN=ATP2B2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
303	432.22	862.42	862.42	2.57	0	4	3.5	6	K.LPDESFR.M
2048	596.30	1190.58	1190.57	5.96	0	(0)	7.8	6	R.MVTGDNINTAR.A
2122	604.29	1206.57	1206.57	2.71	0	22	0.043	2	R.MVTGDNINTAR.A 2118 2119 2120 2121
3837	821.43	1640.85	1640.84	6.93	0	0	5.9	3	R.QVVAVTGDGTNDGPALK.K

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465. KANK1_HUMAN **Score:** 23 **Queries matched:** 1
KN motif and ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=KANK1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
82	408.25	814.49	814.49	-1.27	0	23	0.034	7	R.QLVSQLK.N

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466. RHG35_HUMAN **Score:** 23 **Queries matched:** 1
Rho GTPase-activating protein 35 OS=Homo sapiens GN=ARHGAP35 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
82	408.25	814.49	814.49	-1.27	0	23	0.034	7	K.QISQVLK.G

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467. RUFY3_HUMAN **Score:** 23 **Queries matched:** 4
Protein RUFY3 OS=Homo sapiens GN=RUFY3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1704	566.78	1131.54	1131.55	-8.86	0	23	0.039	3	R.TAEGQALSEAR.K 1703 1705 1706

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468. STK4_HUMAN **Score:** 22 **Queries matched:** 4
Serine/threonine-protein kinase 4 OS=Homo sapiens GN=STK4 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1161	517.75	1033.49	1033.49	6.78	0	22	0.038	2	R.AVGDEMGTVR.V 1157 1158 1160

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469. CCD41_HUMAN **Score:** 22 **Queries matched:** 4
Coiled-coil domain-containing protein 41 OS=Homo sapiens GN=CCDC41 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
498	452.26	902.51	902.51	0.50	1	7	2	8	R.GELVEKTK.D
819	486.30	970.58	970.58	-0.34	1	22	0.034	2	K.VLLVEKDR.E 820
2771	666.35	1330.68	1330.67	2.68	1	5	3	7	R.SQAEKAQLEAEK.T

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470. TXLNB_HUMAN **Score:** 22 **Queries matched:** 4
Beta-taxilin OS=Homo sapiens GN=TXLNB PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1649	562.26	1122.50	1122.50	-0.58	0	(18)	0.07	2	K.LEQAQEMMK.E 1648 1651
1650	562.26	1122.50	1122.50	-0.04	0	22	0.027	2	K.LEQAQEMMK.E

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471. DYST_HUMAN **Mass:** 865259 **Score:** 22 **Queries matched:** 9 **emPAI:** 0.00
Dystonin OS=Homo sapiens GN=DST PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
232	**423.24**	**844.47**	**844.47**	**4.22**	**1**	**10**	**1.4**	**3**	**K.SPASKLDK.S**
389	442.72	883.42	883.41	7.50	0	21	0.048	3	K.CSFLETK.L 387 388
594	460.75	919.49	919.48	9.98	0	6	2.5	6	K.LMSLGDIR.L
1948	585.29	1168.57	1168.57	-0.66	0	5	2.3	3	K.EISSHGLPSDK.A 1946
2704	**659.33**	**1316.64**	**1316.65**	**-7.08**	**1**	**11**	**0.53**	**1**	**R.LENCEDRLIR.Q** 2705

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472. F117B_HUMAN **Score:** 22 **Queries matched:** 1
Protein FAM117B OS=Homo sapiens GN=FAM117B PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide

767	480.29	958.56	958.56	1.84	1	22	0.038	2	K.NKVNFIPK.S

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473. MA1B1_HUMAN **Mass:** 79815 **Score:** 22 **Queries matched:** 8 **emPAI:** 0.05
Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens GN=MAN1B1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
99	**410.20**	**818.39**	**818.38**	**6.33**	**1**	**22**	**0.039**	**1**	**M.AACEGRR.S**
1721	567.78	1133.54	1133.53	5.13	1	5	2.4	5	K.DGTQEEATKR.Q 1722 1724 1725
2445	632.81	1263.61	1263.60	8.59	0	15	0.24	2	R.ADSYYEYLLK.Q 2443 2444

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474. TRY3_HUMAN **Score:** 22 **Queries matched:** 1
Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
45	405.73	809.44	809.44	1.99	0	22	0.028	2	R.LGEHNIK.V

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475. WDR67_HUMAN **Score:** 22 **Queries matched:** 3
WD repeat-containing protein 67 OS=Homo sapiens GN=WDR67 PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
89	409.21	816.40	816.40	-2.54	0	6	1.6	5	R.LDDEIGR.K
431	445.26	888.51	888.52	-7.93	1	22	0.052	2	K.MQTRILK.Q
2107	602.31	1202.61	1202.61	-1.95	0	0	9.4	9	K.LIEAGETQSQK.T

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476. INP4B_HUMAN **Score:** 22 **Queries matched:** 1
Type II inositol 3,4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=2 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
4234	887.89	1773.77	1773.78	-8.14	0	22	0.018	2	K.SSTEESSPQDQPPVMR.G

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477. M3K9_HUMAN **Score:** 21 **Queries matched:** 1
Mitogen-activated protein kinase kinase kinase 9 OS=Homo sapiens GN=MAP3K9 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
96	409.25	816.48	816.48	0.46	1	21	0.036	2	R.KSLINSR.S

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478. PD2R2_HUMAN **Score:** 21 **Queries matched:** 1
Prostaglandin D2 receptor 2 OS=Homo sapiens GN=PTGDR2 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
82	408.25	814.49	814.49	-1.27	0	21	0.044	9	R.QVALAVSK.F

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479. K1671_HUMAN **Mass:** 197617 **Score:** 21 **Queries matched:** 10 **emPAI:** 0.02
Uncharacterized protein KIAA1671 OS=Homo sapiens GN=KIAA1671 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
77	407.71	813.40	813.40	-2.41	0	7	1.1	6	K.AAESPSPR.L 78
206	421.22	840.43	840.43	-6.26	0	5	1.1	2	K.QGSPVEPK.A
924	495.76	989.51	989.52	-7.63	0	11	0.75	2	R.SGPFVDQLK.Q
1260	524.75	1047.48	1047.48	-5.82	1	11	0.34	2	K.DSTEEKSPR.K 1259
3099	**704.86**	**1407.70**	**1407.69**	**8.48**	**0**	**19**	**0.088**	**1**	**K.QLAETLETAMGTK.S** 3096 3097 3100

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480. DPYD_HUMAN **Score:** 21 **Queries matched:** 1
Dihydropyrimidine dehydrogenase [NADP(+)] OS=Homo sapiens GN=DPYD PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
82	408.25	814.49	814.49	-1.23	1	21	0.045	10	K.KIIAENK.I

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481. PADI6_HUMAN **Score:** 21 **Queries matched:** 1
Protein-arginine deiminase type-6 OS=Homo sapiens GN=PADI6 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
32	403.73	805.45	805.45	-2.74	1	21	0.045	2	R.AMSKTLR.D

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482. RRP36_HUMAN **Score:** 21 **Queries matched:** 2
Ribosomal RNA processing protein 36 homolog OS=Homo sapiens GN=RRP36 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
574	457.26	912.51	912.50	2.58	0	21	0.053	3	K.QLVAGNSPK.K 573

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483. UBP54_HUMAN **Mass:** 189609 **Score:** 21 **Queries matched:** 4 **emPAI:** 0.02
Inactive ubiquitin carboxyl-terminal hydrolase 54 OS=Homo sapiens GN=USP54 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
612	463.22	924.43	924.43	0.17	1	21	0.043	2	R.DSTGFKDR.S 613
1129	515.28	1028.54	1028.54	8.27	1	5	2.8	5	R.AQEQELRR.K
4258	**892.43**	**1782.84**	**1782.85**	**-3.19**	**1**	**2**	**3.7**	**1**	**R.SLAEQFQRMQGVSMR.D**

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484. NEBL_HUMAN **Score:** 21 **Queries matched:** 4
Nebulette OS=Homo sapiens GN=NEBL PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
226	423.20	844.39	844.39	-1.33	0	21	0.027	2	K.DSPEIER.V 225 227 228

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485. TIM21_HUMAN **Score:** 21 **Queries matched:** 3
Mitochondrial import inner membrane translocase subunit Tim21 OS=Homo sapiens GN=TIMM21 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
462	448.72	895.43	895.42	3.18	0	21	0.057	3	R.CGLQYQK.K 461 463

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486. LINES_HUMAN **Mass:** 87512 **Score:** 21 **Queries matched:** 3 **emPAI:** 0.04
Protein Lines homolog OS=Homo sapiens GN=LINS PE=2 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
244	424.70	847.39	847.39	-0.82	0	21	0.051	1	K.VGEDLCR.G 245 246

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487. POP1_HUMAN **Score:** 21 **Queries matched:** 1
Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
538	454.27	906.53	906.52	8.49	1	21	0.046	2	K.NLLEKYK.R

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488. PEG3_HUMAN **Score:** 21 **Queries matched:** 5
Paternally-expressed gene 3 protein OS=Homo sapiens GN=PEG3 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
785	482.73	963.44	963.44	6.86	1	21	0.043	2	R.ESSDRSQR.F 786
882	491.72	981.42	981.42	5.17	0	2	2.2	3	R.YHFDTDGK.G 878 879

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489. DJB14_HUMAN **Score:** 21 **Queries matched:** 3
DnaJ homolog subfamily B member 14 OS=Homo sapiens GN=DNAJB14 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
617	464.21	926.42	926.42	-1.54	0	21	0.024	2	K.TDMQYAAK.V
1016	503.73	1005.44	1005.45	-1.44	1	5	0.98	4	R.NNCWKER.Q 1017

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490. PITM2_HUMAN **Mass:** 149980 **Score:** 21 **Queries matched:** 2 **emPAI:** 0.02

Membrane-associated phosphatidylinositol transfer protein 2 OS=Homo sapiens GN=PITPNM2 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
330	435.25	868.49	868.50	-9.82	0	21	0.032	1	R.LEPLLER.R
5946	1603.71	4808.11	4808.10	1.46	1	4	0.37	1	R.RGSVVSMQDNDLLSPGILMNAAHCCGGGGGGGGGGGSSGGGGSSGGSSLESSR.H

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491. CMBL_HUMAN **Mass:** 28372 **Score:** 21 **Queries matched:** 2 **emPAI:** 0.13

Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
309	432.73	863.45	863.45	-3.81	0	5	4	7	R.LEYGGLGR.E
875	491.27	980.53	980.53	4.80	0	21	0.046	1	R.EVQVEHIK.A

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492. KDM2A_HUMAN **Mass:** 135159 **Score:** 21 **Queries matched:** 3 **emPAI:** 0.03

Lysine-specific demethylase 2A OS=Homo sapiens GN=KDM2A PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
110	411.73	821.45	821.45	4.71	1	21	0.041	2	R.YSQRLR.G
3879	826.85	1651.68	1651.67	4.68	0	3	0.56	1	R.GSWAQDGDESWMQR.E 3880

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493. ZCHC4_HUMAN **Score:** 20 **Queries matched:** 4

Zinc finger CCHC domain-containing protein 4 OS=Homo sapiens GN=ZCCHC4 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
389	442.72	883.42	883.41	3.70	1	20	0.059	4	K.MKMETTK.G 387 388
3857	823.36	1644.70	1644.69	6.30	1	0	0.92	2	R.KDCNFFQWEDEK.L

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494. EXD2_HUMAN **Mass:** 71221 **Score:** 20 **Queries matched:** 2 **emPAI:** 0.05

Exonuclease 3'-5' domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
338	436.23	870.44	870.44	-3.57	0	20	0.052	1	R.LLEDPER.R 337

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495. TILB_HUMAN **Score:** 20 **Queries matched:** 2

Protein TILB homolog OS=Homo sapiens GN=LRRC6 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
612	463.22	924.43	924.43	-3.46	1	20	0.05	3	K.SMKTTSDR.S 613

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496. I22R1_HUMAN **Score:** 20 **Queries matched:** 2

Interleukin-22 receptor subunit alpha-1 OS=Homo sapiens GN=IL22RA1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
612	463.22	924.43	924.43	-3.46	1	20	0.05	3	R.SATKMTDR.F 613

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497. ANKH1_HUMAN **Score:** 20 **Queries matched:** 5

Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
151	415.23	828.45	828.45	0.38	0	3	3.1	3	K.LNELGQR.I
839	487.73	973.45	973.45	7.76	0	20	0.052	2	K.DQQAAEANK.N 837 838
2002	590.33	1178.65	1178.65	5.20	1	3	2.6	9	R.KITPLMSAFR.K

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498. LRC45_HUMAN **Score:** 20 **Queries matched:** 5

Leucine-rich repeat-containing protein 45 OS=Homo sapiens GN=LRRC45 PE=2 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
83	408.71	815.41	815.41	-1.23	0	20	0.061	2	R.AIQAEER.L 84 85 86
2039	595.34	1188.67	1188.66	7.28	1	4	1.5	2	R.FLDLKGNNLR.A

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499. ACOC_HUMAN **Mass:** 98850 **Score:** 20 **Queries matched:** 2 **emPAI:** 0.04

Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
1555	**552.76**	**1103.50**	**1103.51**	**-5.55**	**0**	**20**	**0.051**	**1**	**K.TVVPCCSGPK.R** 1556

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500. PARI_HUMAN **Score:** 19 **Queries matched:** 3

PCNA-interacting partner OS=Homo sapiens GN=PARPBP PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
684	469.72	937.42	937.43	-7.03	1	19	0.045	3	K.YNRDNEK.V 683
1951	585.30	1168.58	1168.59	-7.35	0	0	7.3	4	K.GYAPPPSDPLR.T

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