SUPPLEMENTAL MATERIAL

Supplemental Figures

Supplemental Figure 1. Analysis of purified BCG phagosomes and sham BCG phagosome prepared from J774 cells 1 day post-infection.

Supplemental Figure 2. Iodixanol density gradient sedimentation of BCG phagosomes 3 h post-infection of THP-1 cells and analysis of purified 3 h BCG and latex bead phagosomes by Western immunoblotting.

Supplemental Figure 3. Analysis of 3-day post nuclear supernate of BCG infected THP-1 cells, purified BCG phagosomes, and purified latex bead phagosomes by Western immunoblotting for IQGAP1 and LAMP2.

Supplemental Figure 4. Immunofluorescence of FAM3C and beta-galactosidase in THP-1 cells 3 days after uptake of BCG and latex beads.

Supplemental Tables of HPLC-MS/MS Based Protein Identifications

Supplemental Table 1. Summary of proteins identified on BCG and latex bead phagosomes from human THP-1 cells at 3 hours, 1 day, 3 days, and 5 days after uptake.

Supplemental Table 2. Proteins identified on a 1-D gel of BCG phagosome from mouse J774 macrophages 1-day post-infection.

Supplemental Table 3. Proteins identified on a 2-D gel of BCG phagosome isolated from mouse J774 macrophages 1 day post-infection.

Supplemental Table 4. Proteins identified in 3-hour BCG infected human THP-1 phagosome preparation.

Supplemental Table 5. Proteins identified in 1-day BCG infected human THP-1 phagosome preparation.

Supplemental Table 6. Proteins identified in 3-day BCG infected human THP-1 phagosome preparation (a).

Supplemental Table 7. Proteins identified in 3-day BCG infected human THP-1 phagosome preparation (b).

Supplemental Table 8. Proteins identified in 5-day BCG infected human THP-1 phagosome preparation.

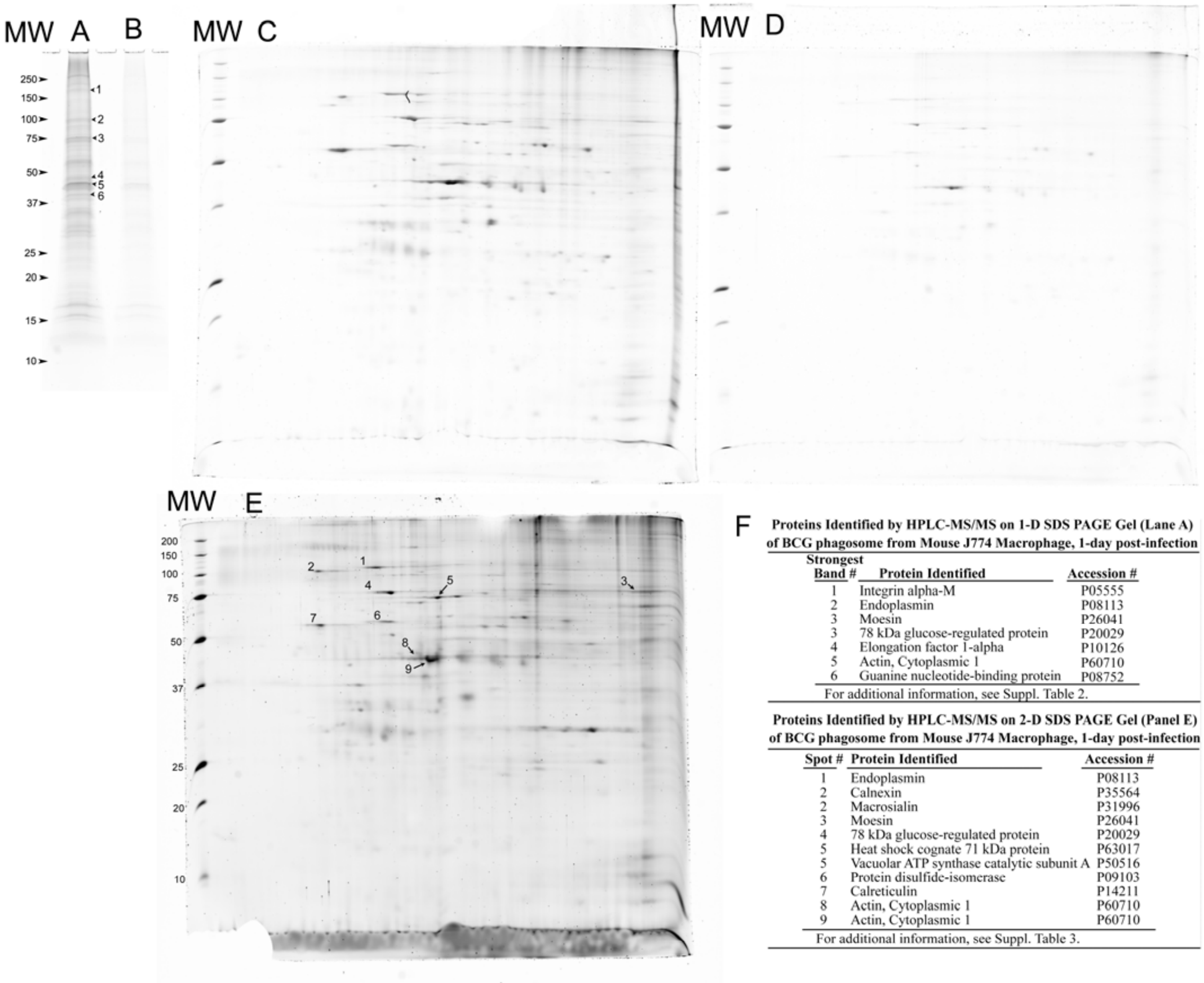
Supplemental Table 9. Proteins identified in 3-hour latex bead human THP-1 phagosome preparation.

Supplemental Table 10. Proteins identified in 3-day latex bead human THP-1 phagosome preparation.

Supplemental Table 11. Proteins identified in 5-day latex bead human THP-1 phagosome preparation.

Supplemental Table 12. Proteins identified by single-peptide based assignments by HPLC-MS/MS in various BCG phagosome preparations and latex bead phagosome preparations from human THP-1 macrophages.

Supplemental Document of Single Peptide Based Protein Identifications



Proteins Identified by HPLC-MS/MS on 1-D SDS PAGE Gel (Lane A) of BCG phagosome from Mouse J774 Macrophage, 1-day post-infection

Strongest Band #	Protein Identified	Accession #
1	Integrin alpha-M	P05555
2	Endoplasmin	P08113
3	Moesin	P26041
3	78 kDa glucose-regulated protein	P20029
4	Elongation factor 1-alpha	P10126
5	Actin, Cytoplasmic 1	P60710
6	Guanine nucleotide-binding protein	P08752

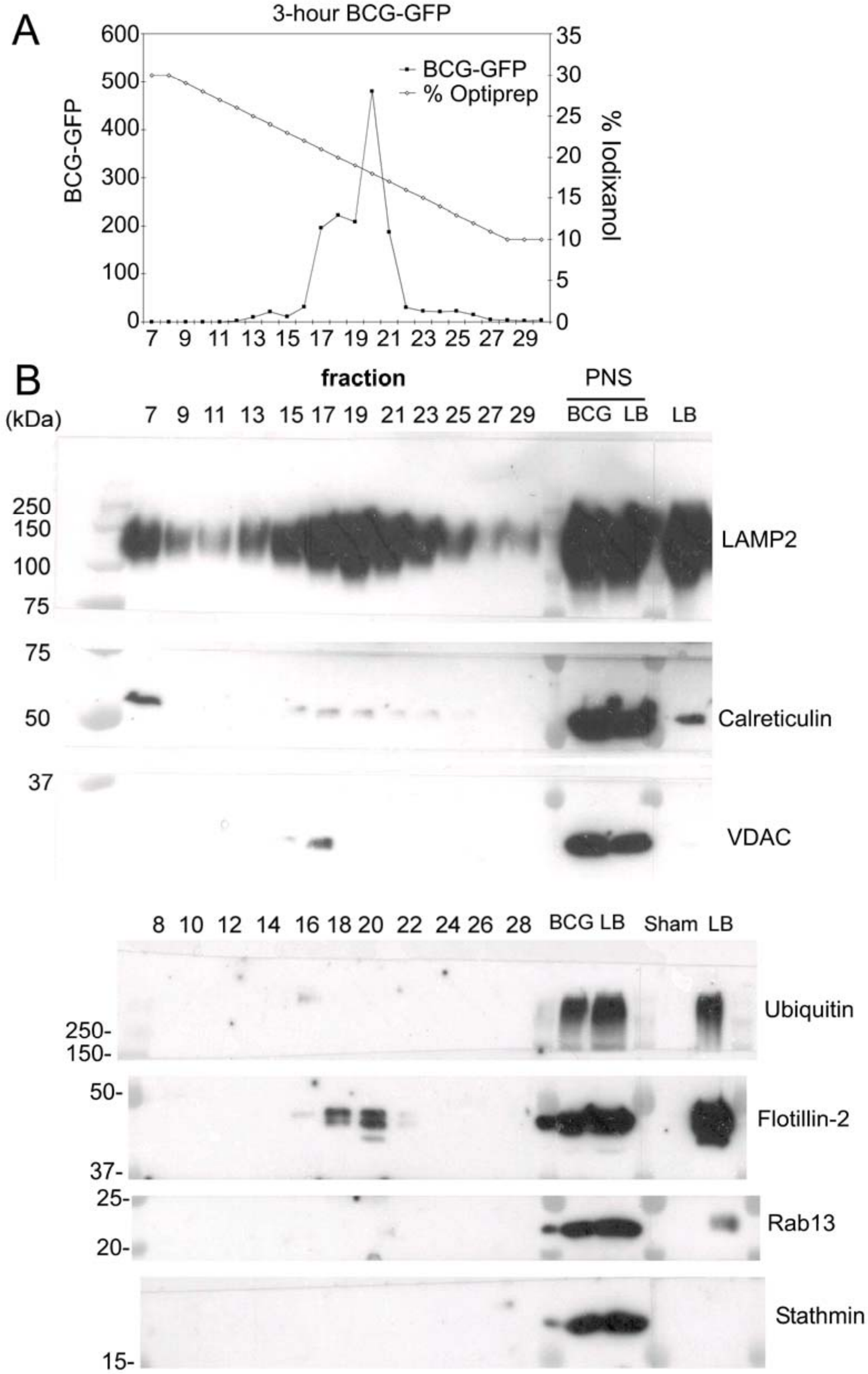
For additional information, see Suppl. Table 2.

Proteins Identified by HPLC-MS/MS on 2-D SDS PAGE Gel (Panel E) of BCG phagosome from Mouse J774 Macrophage, 1-day post-infection

Spot #	Protein Identified	Accession #
1	Endoplasmin	P08113
2	Calnexin	P35564
2	Macrosialin	P31996
3	Moesin	P26041
4	78 kDa glucose-regulated protein	P20029
5	Heat shock cognate 71 kDa protein	P63017
5	Vacuolar ATP synthase catalytic subunit A	P50516
6	Protein disulfide-isomerase	P09103
7	Calreticulin	P14211
8	Actin, Cytoplasmic 1	P60710
9	Actin, Cytoplasmic 1	P60710

For additional information, see Suppl. Table 3.

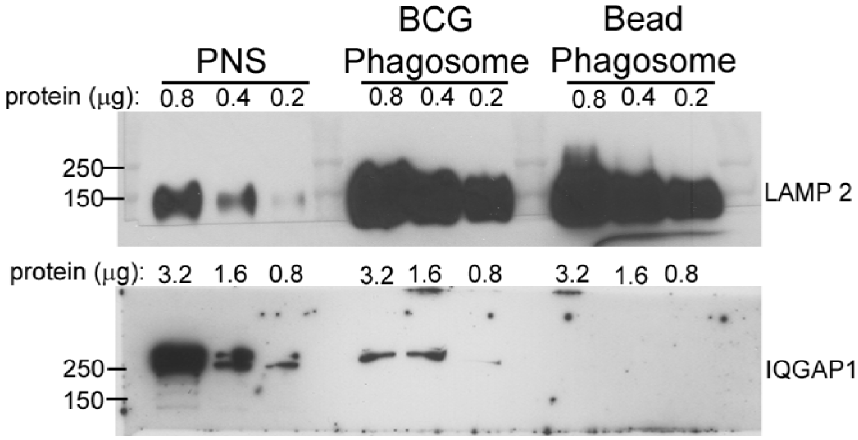
Supplemental Figure 1. Analysis of purified BCG phagosomes (A, C, E) and sham BCG phagosome (B, D) prepared from J774 cells 1 day post-infection. Mouse J774 macrophages were infected with *M. bovis* BCG (A, C, E) or left uninfected (B, D), and a phagosomal fraction isolated 1 day post-infection was resolved by 1-D (A, B) and 2-D (C, D, E) polyacrylamide gel electrophoresis and stained for protein by SYPRO ruby. The “sham phagosome” preparation (B, D) was processed identically to the infected phagosome preparation (A, C), except that the *M. bovis* BCG were added to the macrophages after culture and immediately prior to homogenization. The infected phagosome preparations (A, C) have more than 10-fold the protein content of the sham phagosome preparation (B, D), indicating that relatively little extraneous material from the J774 macrophages co-purifies with the BCG phagosomes. The relative positions of standard molecular weight markers are indicated in lanes marked “MW”. Protein bands and spots in the 1-D gel lane (A) and in the 2-D gel (E) were subjected to in-gel tryptic digestion and analyzed by HPLC-MS/MS. Proteins (and their Swiss-Prot accession numbers) identified by ESI-MS/MS in protein bands and spots indicated by numbered arrows in the 1-D gel lane (A) and in the 2-D gel (E), respectively, are listed in the Table (F). Additional details regarding protein identification in the 1-D and 2-D gel are provided in Supplemental Tables 2 and 3, respectively.



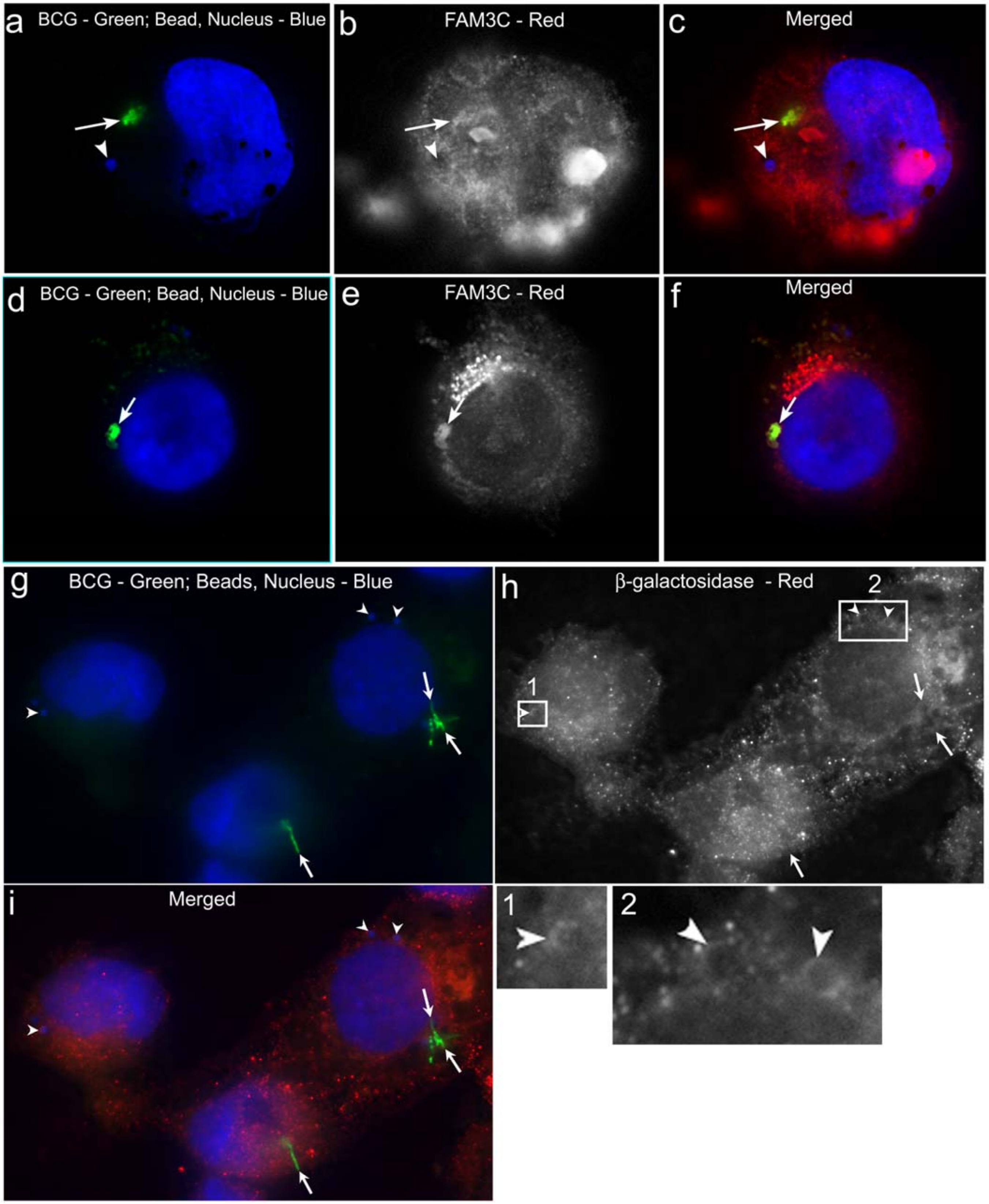
Supplemental Figure 2. Iodixanol density gradient sedimentation of BCG phagosomes 3 h post-infection of THP-1 cells (A) and analysis of purified 3 h BCG and latex bead phagosomes by Western immunoblotting (B). Equal numbers of human THP-1 macrophages were allowed to phagocytose live *M. bovis* BCG-GFP or latex beads, or left untreated ("sham") and a phagosomal

Supplemental Figure 2 (continued):

fraction purified 3 h post-infection. The “sham phagosome” preparation was processed identically to the BCG phagosome preparations except that BCG was added to the macrophages after culture and immediately prior to homogenization. Macrophages from all preparations were homogenized; post-nuclear supernatant (PNS) fractions obtained by low speed centrifugation; and a phagosomal fraction obtained by centrifugation through 15% sucrose onto 30% iodixanol. The latex bead phagosomes were purified by flotation on a sucrose step gradient (not shown) and the BCG phagosomes were centrifuged through a 15% sucrose cushion, followed by density gradient centrifugation on a linear 10-30% iodixanol gradient (A). The relative number of BCG-GFP per gradient fraction was determined by mixing equal aliquots of each fraction with formaldehyde and counting the number of green fluorescent bacteria per 400 x field by fluorescence microscopy. Gradient fractions were collected from the bottom and aliquots representing equal fractions of the iodixanol gradient or the PNS (0.06% of the entire gradient or 0.06% of the total PNS, respectively) were analyzed by 1-D SDS PAGE and Western immunoblotting (B). The majority of BCG phagosomes eluted in fractions 19-21, together with a strong band of LAMP2 immunostaining. In contrast, as can be seen by comparing the intensity of immunostaining of the PNS with the intensity of immunostaining of fractions from the iodixanol gradient, the majority of ER (represented by calreticulin immunostaining) and mitochondria (represented by VDAC immunostaining) were removed at the 15% sucrose gradient step and were not applied to the iodixanol gradient. Some remaining ER and mitochondria eluted on the iodixanol gradient in denser fractions (fraction 7 and 15 – 17, respectively), and a relatively weak band of calreticulin staining co-eluted with the BCG phagosomes. Whereas a high molecular weight form of ubiquitin is present in abundance in the latex bead phagosome and PNS, it is relatively depleted on the 3 h BCG phagosome. Flotillin-2 is highly enriched on the latex bead phagosome, but less abundant on the BCG phagosome. Rab13 is detected on the latex bead phagosome but not the BCG phagosome gradient. The cytoskeletal protein, stathmin, is detected in the PNS but not in the BCG gradient or in the latex bead phagosome pellet.



Supplemental Figure 3. Analysis of 3 day purified BCG phagosomes, latex bead phagosomes, and PNS by Western immunoblotting. Samples containing 0.8 µg – 3.2 µg of protein of purified BCG phagosomes, purified latex bead phagosomes, or the PNS, prepared from THP-1 cells 3 days post infection were separated by SDS-PAGE and electrophoretically transferred to a nitrocellulose membrane. The membrane was incubated with mouse monoclonal antibodies specific for LAMP2 and IQGAP1 followed by HRP-conjugated goat anti-mouse IgG secondary antibody, and developed with SuperSignal West Femto Maximum Sensitivity chemiluminescent substrate (Pierce), and the signal from immunoreactive protein bands detected by exposing the membrane to X-ray film. LAMP2 is enriched on both the BCG phagosomes and the latex bead phagosomes relative to the levels observed in the PNS. In contrast, IQGAP1 is more abundant in the PNS than in the purified phagosomes. Whereas IQGAP1 is detected on the purified BCG phagosomes, it is not detected on the purified latex bead phagosomes with comparable amounts of protein loading.



Supplemental Figure 4. Immunofluorescence of FAM3C and beta-galactosidase in THP-1 cells 3 days after uptake of BCG and latex beads. THP-1 cells, 3 days after uptake of BCG and latex beads, were fixed in 4% paraformaldehyde, heated to 95°C for 20 min in antigen retrieval buffer (5% urea, 100

Supplemental Figure 4 (continued):

mM Tris-HCl, pH 9.5), permeabilized with 0.1% saponin, and evaluated by immunofluorescence for FAM3C (a – f) and beta-galactosidase (g – i) using monoclonal antibodies specific for these proteins. Bacteria (arrows) were visualized by green fluorescence with an Oregon green-labeled rabbit anti-LAM antibody (a, d, g). Host nuclei [stained by DAPI (a, d, g)] and latex beads (arrowheads, a, g) were identified by blue fluorescence. FAM3C (b, e) and beta-galactosidase distribution (h) was visualized by staining with Texas red conjugated antibodies (red channel shown in black and white in panels b, e, h). The merged color images are shown on the right (c, f, i). FAM3C colocalizes with the BCG phagosomes (arrows, b, e) but not with the latex bead phagosomes (arrowhead, b). In contrast, beta-galactosidase colocalizes with the latex bead phagosomes (arrowheads, h and insets shown below at higher magnification for areas 1 and 2) but not with the BCG phagosomes (arrows, h). Quantitative analysis of the immunofluorescence revealed that FAM3C colocalized with 96% ± 4% of BCG and 17% ± 1% of latex bead phagosomes, and that beta-galactosidase colocalized with 4% ± 4% of the BCG and 69% ± 2% of the latex bead phagosomes (mean ± standard error).

Supplemental Table 1. Proteins identified on BCG and latex bead phagosomes from human THP-1 cells at 3 hours, 1 day, 3 days, and 5 days after uptake.

For each of the individual phagosome experiments listed below the number of unique peptides identified for each protein are indicated. The summary columns ("total # BCG" and "total # beads") lists the number of preparations in which the protein was identified. "[1]" indicates that the identification of the protein was based on a single peptide assignment. For details see Supplemental Tables 4-12.

Spectral and Peptide Counts are listed: Spectral counts refer to all acquired precursor ions for a particular protein while peptide counts only list the number of unique peptide sequences observed per protein. (*)

#	Protein Identified**	SwissProt Accession #	BCG (Spectral/Peptide Count)					beads (Spectral/Peptide Count)			total #	total #		
			3 h	1 day	3 days (a)	3 days (b)	5 days	3 h	3 days	5 days				
			Suppl T. 4	Suppl T. 5	Suppl T. 6	Suppl T. 7	Suppl T. 8	Suppl T. 9	Suppl T. 10	Suppl T. 11	BCG	beads	Reported location	Physiological Function
1	60 kDa heat shock protein, mitochondrial	P10809	9/9	19/19	15/14	2/2	18/18	12/12	16/16	5/5	5	3	Mitochondrion, Secretory granules	Chaperone. Extra-mitochondrial localization reported (Brudzynski et al. 1992a,b; Cechetto et al. 2000).
2	78 kDa glucose-regulated protein	P11021	5/5	16/16	6/6	8/8	13/13	5/5	8/8	16/16	5	3	Endoplasmic reticulum (ER), Melanosome	Chaperone. Member of heat shock protein 70 family.
3	Aminopeptidase N	P15144	13/13	8/8	31/20	20/20	21/21	9/9	17/12	9/9	5	3	Plasma membrane (PM)	Protein degradation.
4	ATP synthase subunit alpha, mitochondrial	P25705	13/13	12/12	2/2	4/4	6/6	9/9	7/7	2/2	5	3	Mitochondrion inner membrane	Ion transport. Generation of ATP.
5	Calnexin	P27824	[1]/[1]	2/2	2/2	[1]/[1]	2/2	[1]/[1]	[1]/[1]	3/3	5	3	ER	Chaperone. Protein folding.
6	Endoplasmin	P14625	4/4	11/11	10/10	14/14	13/13	9/8	10/9	14/13	5	3	ER	Chaperone. Protein folding.
7	Integrin beta-2	P05107	5/5	7/7	8/8	6/6	12/12	3/3	2/2	2/2	5	3	PM	Cell surface adhesion glycoprotein.
8	Lysosome membrane protein 2	Q14108	15/13	3/3	9/9	12/12	3/3	12/11	5/5	2/2	5	3	Lysosome	Lysosomal receptor. Scavenger receptor class B member 2.
9	Lysosome-associated membrane glycoprotein 1	P11279	4/4	2/2	4/3	6/6	3/3	4/4	3/3	2/2	5	3	Lysosome, Endosome, PM	Present carbohydrate ligands to selectins.
10	Lysosome-associated membrane glycoprotein 2	P13473	3/3	[1]/[1]	4/3	2/2	2/2	3/2	5/3	[1]/[1]	5	3	Lysosome, Endosome, PM	Protect lysosomal membrane from autodigestion.
11	Moesin	P26038	3/3	8/8	3/3	9/9	12/12	4/4	7/7	14/14	5	3	Cytoplasm	Connections of membrane to cytoskeleton.
12	Peroxiredoxin-1	Q06830	[1]/[1]	2/2	2/2	6/5	8/7	2/2	[1]/[1]	11/10	5	3	Cytoplasm, Melanosome	Redox regulation. Detoxification.
13	Protein disulfide-isomerase	P07237	3/3	2/2	5/5	9/9	7/7	2/2	7/7	11/11	5	3	ER	Disulfide bond rearrangement.
14	Protein disulfide-isomerase A3	P30101	[1]/[1]	2/2	10/10	9/9	10/10	2/2	7/6	7/7	5	3	ER	Disulfide bond rearrangement.
15	Putative elongation factor 1-alpha-like 3	Q5VTE0	2/2	5/5	4/4	3/3	5/5	4/4	8/7	7/5	5	3	Cytoplasm	Promotes GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis (by similarity).
16	Ras-related protein Rab-5C	P51148	4/4	4/4	5/5	8/7	3/3	4/4	6/5	[1]/[1]	5	3	Early endosome	Vesicular trafficking.
17	Acid ceramidase	Q13510	2/2	[1]/[1]	2/2	2/2	2/2	2/2	2/2	0	5	2	Lysosome	Hydrolyzes the sphingolipid ceramide into sphingosine and free fatty acid.
18	CD63 antigen	P08962	2/2	4/4	2/2	3/3	2/2	3/3	4/3	0	5	2	Late endosome-Lysosome	Unknown. May regulate transport of other proteins.
19	Coronin-1A	P31146	2/2	[1]/[1]	3/3	3/3	2/2	0	4/3	4/4	5	2	Cytoplasm	Cytoskeleton component. Important in membrane invaginations, protrusions, and cell locomotion.
20	Erythrocyte band 7 integral membrane protein (Stomatin)	P27105	[1]/[1]	2/2	2/2	3/3	4/4	6/6	6/6	0	5	2	PM, Melanosome	Regulate cation conductance. Associates with actin and lipid rafts.
21	Flotillin-1	O75955	3/3	[1]/[1]	7/7	[1]/[1]	[1]/[1]	4/3	9/9	0	5	2	PM, Phagosomal membrane	Lipid rafts. Clathrin independent endocytosis. Formation of caveolae or caveolae-like vesicles.
22	Fructose-bisphosphate aldolase A	P04075	3/3	8/8	5/5	14/12	15/15	4/4	0	14/13	5	2	Cytoplasm	Metabolism. Interacts with cytoskeleton (Schindler et al., 2001).
23	Heat shock protein HSP 90-beta	P08238	5/5	10/10	16/14	22/22	10/10	3/3	0	18/17	5	2	Cytoplasm, Melanosome	Chaperone.
24	Proactivator polypeptide (Prosaposin)	P07602	4/4	[1]/[1]	2/2	4/4	[1]/[1]	3/3	3/3	0	5	2	Lysosome	Sphingolipid degradation.
25	Ras-related protein Rab-11B*	Q15907*	[1]/[1]	2/2	2/2	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	0	5	2	Recycling endosome, PM	Regulation of endosomal recycling.
26	Stress-70 protein, mitochondrial	P38646	12/12	3/3	8/8	5/5	4/4	2/2	6/6	0	5	2	Mitochondrion, Cell surface	Chaperone. Control of cell proliferation and cellular aging.
27	Thioredoxin-dependent peroxide reductase, mitochondrial	P30048	2/1	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	0	5	2	Mitochondrion, Early endosome	Redox regulation.Presence in endosomes described by Liu et al., 2005.
28	Vacuolar ATP synthase subunit B	P21281	10/10	2/2	3/3	7/7	2/2	8/8	15/11	0	5	2	Endosome-Lysosome	Compartment acidification.
29	Actin-related protein 2	P61160	2/2	[1]/[1]	2/2	2/2	[1]/[1]	0	[1]/[1]	0	5	1	Cytoplasm	Cytoskeleton.
30	ATP synthase subunit beta, mitochondrial	P06576	6/6	9/9	14/14	3/3	10/9	0	0	2/2	5	1	Mitochondrion, PM	Generation of ATP. Reported in lipid rafts of PM (Bae et al. 2004) and to function on PM as enterostatin receptor (Park et al., 2004).
31	Heat shock protein beta-1	P04792	3/3	5/5	[1]/[1]	4/4	6/5	0	0	5/3	5	1	Cytoplasm	Cytoskeleton. Stress resistance and actin organization.
32	Integrin beta-1	P05556	2/2	2/2	3/3	5/5	[1]/[1]	2/2	0	0	5	1	PM	Receptor for fibronectin.
33	Actin, cytoplasmic 1	P60709	5/5	0	16/12	16/13	49/16	3/3	2/2	18/13	4	3	Cytoplasm	Cytoskeleton.
34	Annexin A2	P07355	5/5	0	4/4	9/9	9/9	15/13	8/6	5/5	4	3	Secreted, Extracellular Matrix, Basement Membrane	May cross-link plasma membrane phospholipids with actin cytoskeleton and be involved with exocytosis.
35	Brain acid soluble protein 1	P80723	4/4	0	6/5	3/3	4/4	3/3	5/5	[1]/[1]	4	3	Membrane	Signaling. Has calmodulin binding site. Is substrate for PKC. Present in lipid rafts. Regulation of actin dynamics.
36	Cathepsin D	P07339	6/5	0	5/5	8/8	9/8	9/8	15/11	5/5	4	3	Lysosome	Protein degradation.

37	Glyceraldehyde-3-phosphate dehydrogenase	P04406	2/2	0	3/3	3/3	7/7	3/3	3/3	5/5	4	3	Cytoplasm, membrane associated	Glycolysis. Membrane fusion. Microtubule bundling. Phosphotransferase activity. Nuclear RNA export. DNA replication and DNA repair (Sirover, 1999).
38	Heat shock cognate 71 kDa protein	P11142	6/6	0	9/9	22/22	8/8	3/3	5/5	11/11	4	3	Cytoplasm, Melanosome	Chaperone.
39	Palmitoyl-protein thioesterase 1	P50897	3/3	0	3/3	3/3	4/4	4/4	6/5	[1]/[1]	4	3	Lysosome	Lipoprotein degradation.
40	Plastin-2	P13796	0	10/10	2/2	12/12	14/14	2/2	3/3	11/11	4	3	Cytoplasm	Cytoskeleton.
41	Ras-related protein Rab-7A	P51149	2/2	0	5/5	4/4	7/7	3/3	3/3	2/2	4	3	Late endosome	Late endosomal transport, phagosome maturation.
42	Vacuolar ATP synthase catalytic subunit A	P38606	3/3	0	[1]/[1]	7/7	4/4	4/4	12/10	[1]/[1]	4	3	Endosome-Lysosome	Compartment acidification.
43	Vimentin	P08670	0	5/5	9/9	2/2	5/5	7/7	8/8	[1]/[1]	4	3	Cytoplasm	Cytoskeleton. Intermediate filament.
44	Voltage-dependent anion-selective channel protein 1	P21796	4/4	0	2/[1]	5/5	7/7	2/2	3/3	5/5	4	3	Mitochondrion, PM	Channel for small hydrophilic molecules, present in secretory pathway and PM (Buettner et al. 2000).
45	Voltage-dependent anion-selective channel protein 2	P45880	2/2	0	3/3	2/2	5/5	2/2	[1]/[1]	2/2	4	3	Mitochondrion	Channel for small hydrophilic molecules.
46	10 kDa heat shock protein, mitochondrial	P61604	6/6	6/5	4/4	4/4	0	3/3	5/5	0	4	2	Mitochondrion, and non-mitochondrial sites	Co-chaperone for Hsp60 in the protein folding process. Also identified in non-mitochondrial sites, including secretory granules (Sadacharan et al., 2001).
47	40S ribosomal protein SA (laminin receptor-1)	P08865	0	[1]/[1]	2/[1]	3/3	5/5	0	[1]/[1]	3/3	4	2	Cytoplasm	Protein synthesis. Cell adhesion (Nelson et al. 2008).
48	ADP-ribosylation factor-like protein 8B*	Q9NVJ2*	3/3	[1]/[1]	[1]/[1]	[1]/[1]	0	2/2	[1]/[1]	0	4	2	Late endosome-Lysosome	Endosome and lysosome motility.
49	Alpha-enolase	P06733	0	[1]/[1]	2/2	6/6	7/7	[1]/[1]	0	3/3	4	2	Cytoplasm, PM, Myofibril, Sarcomere	Carbohydrate degradation. Glycolysis. Promotes vacuole fusion in yeast. May also function as a plasminogen receptor and activator on the cell surface.
50	Cathepsin Z	Q9UBR2	3/3	0	[1]/[1]	3/3	2/2	2/2	2/2	0	4	2	Lysosome	Carboxy-dipeptidase.
51	Cofilin-1	P23528	[1]/[1]	2/2	0	2/2	[1]/[1]	[1]/[1]	0	2/2	4	2	Cytoplasm	Controls actin polymerization.
52	Gelsolin	P06396	0	[1]/[1]	2/2	8/8	5/5	[1]/[1]	0	7/7	4	2	Cytoplasm	Cytoskeleton.
53	Hypoxia up-regulated protein 1	Q9Y4L1	0	2/1	[1]/[1]	2/2	7/7	[1]/[1]	0	3/3	4	2	ER lumen	Chaperone, induced by hypoxia.
54	Lysosomal acid phosphatase	P11117	0	[1]/[1]	2/2	[1]/[1]	3/3	3/3	5/5	0	4	2	Lysosome	Phosphate monoester hydrolysis.
55	Lysosomal alpha-glucosidase	P10253	2/2	0	2/2	[1]/[1]	[1]/[1]	3/3	2/2	0	4	2	Lysosome	Glycogen degradation.
56	Malate dehydrogenase, mitochondrial	P40926	11/11	0	6/5	2/2	8/8	5/5	5/5	0	4	2	Mitochondrion	Glycolysis. Tricarboxylic acid cycle.
57	Myosin-9	P35579	0	14/14	5/5	29	15	0	7/7	34/34	4	2	Cytoplasm	Cytoskeleton.
58	N-acetylglucosamine-6-sulfatase	P15586	8/8	[1]/[1]	[1]/[1]	3/3	0	3/3	2/2	0	4	2	Lysosome	Heparan sulfate/keratan sulfate hydrolysis.
59	Nicastrin	Q92542	2/2	[1]/[1]	2/2	2/2	0	4/4	3/3	0	4	2	Golgi, ER, PM, Melanosome	Component of the gamma-secretase complex.
60	Protein disulfide-isomerase A6	Q15084	0	3/3	[1]/[1]	4/4	6/6	[1]/[1]	0	2/2	4	2	ER, ER-Golgi intermediate compartment, Melanosome	Disulfide bond rearrangement.
61	Ras-related protein Rab-21	Q9UL25	[1]/[1]	0	2/2	2/2	[1]/[1]	[1]/[1]	2/2	0	4	2	Endosomes	Controls traffic of beta-1 integrins.
62	Sulfide:quinone oxidoreductase, mitochondrial	Q9Y6N5	2/2	0	6/6	4/4	6/6	2/2	2/2	0	4	2	Mitochondrion	Hydrogen sulfide oxidation.
63	Vacuolar proton pump subunit d 1	P61421	3/3	0	6/5	5/5	[1]/[1]	4/4	5/4	0	4	2	Intracellular compartments, Endosome-Lysosome	Compartment acidification.
64	Citrate synthase, mitochondrial	O75390	[1]/[1]	0	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	0	4	2	Mitochondrion	Carbohydrate metabolism, tricarboxylic acid cycle.
65	Interferon-induced transmembrane protein 3*	Q01628*	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	0	[1]/[1]	[1]/[1]	0	4	2	PM, Golgi, integral membrane protein	Cell differentiation and homing, immune response.
66	2,4-dienoyl-CoA reductase, mitochondrial	Q16698	5/4	0	4/4	[1]/[1]	4/4	0	2/2	0	4	1	Mitochondrion	Beta-oxidation of unsaturated fatty acids.
67	Adenylyl cyclase-associated protein 1	Q01518	0	4/4	13/13	13/13	21/16	0	0	23/22	4	1	Membrane, PM	Signaling. Binds actin monomers and directly regulates filament dynamics.
68	Alpha-actinin-1	P12814	0	4/4	4/4	11/11	5/5	0	0	6/6	4	1	Cytoplasm	Cross links actin. F-actin assembly.
69	Alpha-actinin-4	O43707	0	5/5	3/3	7/7	3/3	0	0	4/4	4	1	Cytoplasm	Cross links actin. F-actin assembly.
70	Annexin A5	P08758	[1]/[1]	0	2/[1]	2/2	6/6	0	0	[1]/[1]	4	1	Cytoplasm	Calcium-dependent phospholipid binding.
71	Basigin	P35613	0	[1]/[1]	2/2	[1]/[1]	2/2	0	0	[1]/[1]	4	1	PM, Melanosome	May be a receptor for oligomannosidic glycans. May be associated with a monocarboxylate transporter.
72	D-3-phosphoglycerate dehydrogenase	O43175	0	4/4	3/3	5/5	6/6	0	0	8/8	4	1	Cytoplasm	Metabolism. Amino acid biosynthesis.
73	Dipeptidyl-peptidase 2	Q9UHL4	5/5	4/4	[1]/[1]	[1]/[1]	0	3/3	0	0	4	1	Cytoplasmic vesicles, Lysosome	N-terminal dipeptidase.
74	Ezrin	P15311	[1]/[1]	2/2	3/3	6/6	0	0	3/3	0	4	1	Membrane	Interaction of cytoskeleton with membrane.
75	Heat shock protein HSP 90-alpha	P07900	0	6/6	14/12	16/16	7/7	0	0	13/13	4	1	Cytoplasm	Chaperone.
76	Leucine-rich PPR motif-containing protein, mitochondrial	P42704	12/12	4/4	4/4	0	2/2	4/4	0	0	4	1	Mitochondrion, Nucleus	May play a role in RNA metabolism in both nuclei and mitochondria. Binds RNA, DNA, and beta-tubulin.

77	Macrophage-capping protein	P40121	0	2/2	[1]/[1]	6/6	9/8	0	0	6/5	4	1	Cytoplasm, Nucleus, Melanosome	Cytoskeleton. Actin capping.
78	Mannose-6-phosphate receptor-binding protein 1	O60664	0	2/2	2/2	2/2	3/3	0	0	2/2	4	1	Endosome, Golgi	Transport M6PR from endosomes to the TGN.
79	Platelet glycoprotein 4 (CD36)	P16671	[1]/[1]	0	2/2	[1]/[1]	3/3	[1]/[1]	0	0	4	1	Membrane, PM, Golgi	LDL receptor activity. Scavenger receptor. Phagocytic receptor (Baranova et al. 2008)
80	Protein disulfide-isomerase A4	P13667	0	[1]/[1]	3/3	2/2	4/4	0	[1]/[1]	0	4	1	ER	Disulfide bond rearrangement.
81	Ras-related protein Rab-1A	P62820	2/2	0	2/2	4/4	4/4	0	2/2	0	4	1	ER, Golgi	ER to Golgi traffic.
82	Sodium/potassium-transporting ATPase subunit alpha-1	P05023	0	5/5	6/6	9/9	7/7	0	2/2	0	4	1	Membrane	Ion transport. Generation of ATP.
83	Talin-1	Q9Y490	0	14/14	3/3	11/11	18/18	0	0	20/20	4	1	Cytoplasm	Cytoskeleton.
84	Glucosidase 2 subunit beta	P14314	0	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	0	0	[1]/[1]	4	1	ER, Golgi	N-linked oligosaccharide processing.
85	Phosphate carrier protein, mitochondrial	Q00325	0	[1]/[1]	[1]/[1]	[1]/[1]	[1]/[1]	0	[1]/[1]	0	4	1	Mitochondrion	Transport of phosphate groups.
86	CD44 antigen	P16070	0	[1]/[1]	[1]/[1]	[1]/[1]	2/2	0	0	0	4	0	PM	Hyaluronic acid (HA) receptor.
87	Erlin-2 (SPFH domain containing protein 2)	O94905	3/3	0	5/5	[1]/[1]	3/3	0	0	0	4	0	ER membrane, PM	Lipid raft associated.
88	Golgi apparatus protein 1 (E-selectin ligand 1)	Q92896	0	2/2	4/4	24/24	11/11	0	0	0	4	0	Golgi, PM	Binds fibroblast growth factor and E-selectin.
89	Intercellular adhesion molecule 1	P05362	0	[1]/[1]	2/2	3/3	[1]/[1]	0	0	0	4	0	PM	Ligand for LFA-1protein.
90	Protein FAM3C	Q92520	0	4/4	2/2	4/4	4/4	0	0	0	4	0	Putative secreted protein	Unknown. Member of cytokine-like gene family. May be involved in cell differentiation and proliferation during embryogenesis
91	Ras GTPase-activating-like protein IQGAP1	P46940	0	3/3	5/4	9/9	14/14	0	0	0	4	0	Membrane	Integrates Ca2+/calmodulin and Cdc42 signaling.
92	Ras-related protein Rab-6A	P20340	0	2/2	2/2	7/7	6/6	0	0	0	4	0	Golgi	Golgi to ER traffic.
93	Stress-induced-phosphoprotein 1	P31948	0	6/6	2/2	5/5	8/8	0	0	0	4	0	Cytoplasm, Nucleus	Mediate the association of chaperones HSC70 and HSC90.
94	Transmembrane emp24 domain-containing protein 9	Q9BVK6	0	[1]/[1]	[1]/[1]	2/2	[1]/[1]	0	0	0	4	0	ER membrane	Unkown.
95	Tubulin alpha-1C chain	Q9BQE3	0	7/7	3/3	7/7	2/2	0	0	0	4	0	Cytoplasm	Cytoskeleton.
96	Tubulin beta chain	P07437	0	13/12	12/11	12/12	4/4	0	0	0	4	0	Cytoplasm	Cytoskeleton.
97	Tumor protein D54	O43399	0	[1]/[1]	2/2	3/3	[1]/[1]	0	0	0	4	0	Unknown	Unknown.
98	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	P49748	0	4/4	4/4	[1]/[1]	2/2	0	0	0	4	0	Mitochondrion	Fatty acid beta-oxidation system.
99	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	P39656	0	0	2/2	4/4	2/2	2/2	[1]/[1]	[1]/[1]	3	3	ER membrane	Glycosylation.
100	Peptidyl-prolyl cis-trans isomerase B (Cyclophilin B)	P23284	3/3	0	3/3	3/3	0	6/6	2/2	4/4	3	3	ER, Melanosome, Synaptic vesicle, Secreted protein	Protein folding. Chaperone.
101	Vacuolar proton pump subunit E 1	P36543	4/4	0	5/5	4/4	0	3/3	5/5	2/2	3	3	Intracellular compartments, Endosome-Lysosome	Compartment acidification.
102	Ras-related protein Rap-1b*	P61224*	[1]/[1]	0	[1]/[1]	[1]/[1]	0	[1]/[1]	[1]/[1]	[1]/[1]	3	3	Late endosome, Lysosome, Phagosome, Exosome	Regulation of integrin signaling.
103	Apolipoprotein E	P02649	2/2	0	0	5/5	7/7	[1]/[1]	0	[1]/[1]	3	2	Secreted protein	Lipoprotein internalization/catabolism.
104	ATP synthase subunit gamma, mitochondrial	P36542	[1]/[1]	0	2/2	[1]/[1]	0	[1]/[1]	[1]/[1]	0	3	2	Mitochondrion	ATP synthesis. Ion transport.
105	Beta-hexosaminidase subunit beta	P07686	2/2	0	0	2/2	2/2	2/2	0	[1]/[1]	3	2	Lysosome	Degradation of terminal N-acetyl hexosamines.
106	Cathepsin S	P25774	0	0	[1]/[1]	2/2	[1]/[1]	[1]/[1]	2/2	0	3	2	Lysosome	Key protease for the removal of invariant chain from MHC class II molecules.
107	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	Q9NX63	[1]/[1]	0	2/2	0	[1]/[1]	2/2	[1]/[1]	0	3	2	Mitochondrion (by similarity)	Unkown.
108	Cytochrome c oxidase subunit 2	P00403	[1]/[1]	2/2	[1]/[1]	0	0	[1]/[1]	[1]/[1]	0	3	2	Mitochondrion	Respiratory Chain. Electron transport.
109	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	P04843	0	0	2/2	2/2	8/8	4/4	0	2/2	3	2	ER membrane, Melanosome	Glycosylation.
110	Endoplasmic reticulum protein ERp29	P30040	0	0	[1]/[1]	2/2	2/2	0	[1]/[1]	4/4	3	2	ER lumen, Melanosome	Protein synthesis and folding.
111	F-actin-capping protein subunit beta	P47756	0	0	[1]/[1]	[1]/[1]	[1]/[1]	0	[1]/[1]	2/2	3	2	Cytoplasm	Cytoskeleton.
112	Galectin-9B*	Q3B8N2*	0	0	[1]/[1]	[1]/[1]	[1]/[1]	2/2	[1]/[1]	0	3	2	Unknown	Binds galactosides.
113	L-lactate dehydrogenase A chain	P00338	0	0	3/3	5/5	5/5	0	[1]/[1]	5/5	3	2	Cytoplasm	Anaerobic glycolysis.
114	Neutral alpha-glucosidase AB	Q14697	0	5/5	3/3	[1]/[1]	0	0	2/2	2/2	3	2	ER, Golgi, Melanosome	N-linked oligosaccharide processing.
115	Peroxisomal multifunctional enzyme type 2	P51659	0	0	3/3	3/3	2/2	2/2	2/2	0	3	2	Peroxisome	Fatty acid beta-oxidation cycle.

116	Ras-related protein Rab-13	P51153	0	0	3/3	2/2	2/2	2/2	3/3	0	3	2	Cell junction	Polarized transport of vesicles.
117	Serpin H1	P50454	0	0	2/2	2/2	[1]/[1]	0	[1]/[1]	2/2	3	2	ER lumen	Binds collagen.
118	Synaptogyrin-2	O43760	0	0	[1]/[1]	2/2	2/2	[1]/[1]	[1]/[1]	0	3	2	Membrane	Unknown.
119	Syntaxin-12	Q86Y82	2/2	0	[1]/[1]	0	3/3	2/2	[1]/[1]	0	3	2	Membrane	Regulate protein transport between late endos
osomes and the TGN.
120	Tripeptidyl-peptidase 1	O14773	3/3	2/2	0	2/2	0	4/4	4/4	0	3	2	Lysosome	Serine protease.
121	14-3-3 protein beta/alpha	P31946	0	0	3/3	5/5	5/5	0	0	6/6	3	1	Cytoplasm, Melanosome	Regulates signal transduction pathways.
122	14-3-3 protein gamma	P61981	0	0	4/4	6/6	5/5	0	0	6/6	3	1	Cytoplasm	Regulates signal transduction pathways.
123	14-3-3 protein zeta/delta	P63104	0	0	4/3	5/5	5/5	0	0	7/6	3	1	Cytoplasm, Melanosome	Regulates signal transduction pathways.
124	6-phosphogluconate dehydrogenase, decarboxylating	P52209	0	0	2/2	3/3	6/6	0	0	4/4	3	1	Cytoplasm	Metabolism. Pentose phosphate pathway. May form supramolecular complex that can associate with cytoskeleton (Kindzelskii et al., 2004).
125	60S ribosomal protein L7	P18124	0	0	2/2	2/2	[1]/[1]	0	0	[1]/[1]	3	1	Cytoplasm	Protein synthesis.
126	Actin-related protein 2/3 complex subunit 5	O15511	0	0	2/2	2/2	[1]/[1]	0	0	[1]/[1]	3	1	Cytoplasm	F-actin assembly.
127	Annexin A4	P09525	0	0	2/2	2/2	3/3	0	0	5/5	3	1	Cytoplasm, Cytoskeleton	Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis.
128	Apolipoprotein D	P05090	2/2	0	[1]/[1]	2/2	0	0	4/4	0	3	1	Secreted protein	Lipid binding and transport.
129	ATP synthase subunit delta, mitochondrial	P30049	[1]/[1]	0	2/2	[1]/[1]	0	0	[1]/[1]	0	3	1	Mitochondrion	ATP synthesis. Ion transport.
130	ATP synthase subunit O, mitochondrial	P48047	2/2	0	2/2	0	5/5	[1]/[1]	0	0	3	1	Mitochondrion	ATP synthesis. Ion transport.
131	Calreticulin	P27797	0	3/3	0	3/3	2/2	0	0	[1]/[1]	3	1	ER lumen. Cytosol. Secreted. Also found on cell surface (T cells), cytosol and extracellular matrix. Associated with the lytic granules in the cytolytic T-lymphocytes.	Calcium-binding chaperone protein. Involved in protein synthesis and folding.
132	Carbonic anhydrase 2	P00918	0	[1]/[1]	0	[1]/[1]	[1]/[1]	0	0	2/2	3	1	Cytoplasm	Hydration of carbon dioxide.
133	Carnitine O-palmitoyltransferase 2, mitochondrial	P23786	0	[1]/[1]	3/3	0	2/2	[1]/[1]	0	0	3	1	Mitochondrion	Fatty acid beta-oxidation cycle.
134	Cathepsin B	P07858	2/2	0	0	4/3	[1]/[1]	2/2	0	0	3	1	Lysosome	Protein degradation. Thiol protease.
135	Chloride intracellular channel protein 1	O00299	0	0	2/[1]	4/4	7/6	0	0	3/3	3	1	Nucleus, Cytoplasm, PM, Cytosol	Chloride ion channel. Can insert into membranes from aqueous phase.
136	Cytochrome b-c1 complex subunit 2, mitochondrial	P22695	3/2	0	[1]/[1]	0	[1]/[1]	0	[1]/[1]	0	3	1	Mitochondrion	Respiratory Chain. Electron transport.
137	Elongation factor 2	P13639	0	8/8	0	6/6	4/4	0	0	3/3	3	1	Cytoplasm	Translation elongation factor activity. GTPase.
138	Elongation factor Tu, mitochondrial	P49411	5/5	0	[1]/[1]	0	4/4	2/2	0	0	3	1	Mitochondrion	Translation elongation factor activity. GTPase.
139	Monocarboxylate transporter 4	O15427	0	0	[1]/[1]	[1]/[1]	3/3	0	[1]/[1]	0	3	1	PM, Membrane	Monocarboxylic acid transport.
140	Myosin light polypeptide 6	P60660	0	0	3/3	5/4	3/3	0	0	2/2	3	1	Cytoplasm	Cytoskeleton.
141	Phosphoglycerate kinase 1	P00558	0	0	[1]/[1]	4/4	8/8	0	0	3/3	3	1	Cytoplasm	Carbohydrate degradation. Glycolysis.
142	Prohibitin-2	Q99623	4/4	0	2/2	0	[1]/[1]	0	3/3	0	3	1	Mitochondrion, Cytoplasm, Nucleus	Transcriptional repression.
143	Pyruvate kinase isozymes M1/M2	P14618	0	9/9	0	8/8	10/10	0	0	7/7	3	1	Cytoplasm	Carbohydrate degradation. Glycolysis.
144	Ras-related protein Rab-1B	Q9H0U4	0	0	2/2	3/3	4/4	0	0	2/2	3	1	ER, Golgi, Cytoplasm	Regulates vesicular transport between the ER and successive Golgi compartments.
145	Ras-related protein Rab-5A	P20339	0	0	2/2	4/3	2/2	0	3/3	0	3	1	Endosome, Melanosome	Fusion of PM and early endosomes.
146	Ras-related protein Rab-8B	Q92930	0	0	2/2	2/2	3/3	0	2/2	0	3	1	Membrane	Vesicular trafficking.
147	Serine hydroxymethyltransferase, mitochondrial	P34897	5/5	2/2	0	0	[1]/[1]	3/3	0	0	3	1	Mitochondrion	Interconversion of serine and glycine.
148	Sideroflexin-1	Q9H9B4	2/2	0	[1]/[1]	0	3/3	[1]/[1]	0	0	3	1	Mitochondrion	May be involved in transport of a component required for iron utilization.
149	Superoxide dismutase [Mn], mitochondrial	P04179	0	0	3/3	[1]/[1]	6/6	0	2/2	0	3	1	Mitochondrion	Detoxification of superoxide radicals.
150	T-complex protein 1 subunit beta	P78371	0	2/2	0	2/2	2/2	0	0	6/6	3	1	Cytoplasm	Molecular chaperone. Assist the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.
151	T-complex protein 1 subunit epsilon	P48643	0	4/4	2/2	0	3/3	0	0	6/6	3	1	Cytoplasm	Molecular chaperone. Assist the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.
152	T-complex protein 1 subunit theta	P50990	0	9/9	0	11/11	3/3	0	0	11/11	3	1	Cytoplasm	Molecular chaperone; assist the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.

153	Transgelin-2	P37802	0	0	3/3	2/2	4/4	0	0	2/2	3	1	Cytoplasm	Cytoskeleton. Probable actin cross-linking.
154	Trifunctional enzyme subunit beta, mitochondrial	P55084	3/3	0	3/3	0	5/5	0	[1]/[1]	0	3	1	Mitochondrion	Fatty acid beta-oxidation cycle.
155	UPF0550 protein C7orf28	O95766	4/4	[1]/[1]	0	[1]/[1]	0	2/2	0	0	3	1	Unknown	Unknown.
156	ATP synthase subunit g, mitochondrial	O75964	[1]/[1]	0	[1]/[1]	[1]/[1]	0	[1]/[1]	0	0	3	1	Mitochondrion	ATP synthesis. Ion transport.
157	Catalase	P04040	0	0	[1]/[1]	[1]/[1]	[1]/[1]	0	0	[1]/[1]	3	1	Peroxisome	Oxido-reductase.
158	Retinoid-inducible serine carboxypeptidase	Q9HB40	[1]/[1]	0	0	[1]/[1]	[1]/[1]	[1]/[1]	0	0	3	1	Secreted protein, Lysosome	Carboxypeptidase. Colocalizes with LAMP2 (Lee, et al. 2006).
159	Vacuolar ATP synthase 16 kDa proteolipid subunit	P27449	[1]/[1]	[1]/[1]	0	0	[1]/[1]	[1]/[1]	0	0	3	1	Vacuole membrane	Acidification of intracellular compartments.
160	ADP/ATP translocase 2	P05141	4/4	3/3	[1]/[1]	0	0	0	0	0	3	0	Mitochondrial Membrane, PM	ATP/ADP translocation.
161	Alpha-mannosidase 2	Q16706	0	2/2	0	6/6	12/12	0	0	0	3	0	Golgi	N-glycosylation.
162	Band 4.1-like protein 3	Q9Y2J2	0	0	[1]/[1]	[1]/[1]	2/2	0	0	0	3	0	Cytoplasm	Links membrane to cytoskeleton.
163	Charged multivesicular body protein 4b	Q9H444	0	0	5/3	2/2	[1]/[1]	0	0	0	3	0	Cytoplasm; Endosome	MVB formation & sorting of endosomal cargo proteins into MVBs.
164	Glutamate dehydrogenase 1, mitochondrial	P00367	4/3	2/2	2/2	0	0	0	0	0	3	0	Mitochondrion	Oxidative deamination of glutamate to alpha-ketoglutarate.
165	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	P62873	3/3	0	0	2/2	2/2	0	0	0	3	0	Membrane	Transmembrane signaling.
166	Integrin alpha-5	P08648	[1]/[1]	3/3	[1]/[1]	0	0	0	0	0	3	0	PM	Receptor for fibronectin and fibrinogen, present in endocytic pathway (Shakibaei et al., 1993).
167	Nucleobindin-1	Q02818	0	3/3	0	6/6	8/8	0	0	0	3	0	Golgi, Cytoplasm, Membrane	Calcium homeostasis.
168	Platelet endothelial cell adhesion molecule	P16284	0	0	5/5	4/4	5/5	0	0	0	3	0	PM	Cell adhesion. Signal transduction.
169	Ras-related protein Rab-14	P61106	0	[1]/[1]	[1]/[1]	2/2	0	0	0	0	3	0	Membrane	Vesicular trafficking.
170	Septin-7	Q16181	0	0	2/2	2/2	4/4	0	0	0	3	0	Cytoplasm	Associates with actin stress fibers. GTPase. Cytokinesis and exocytosis.
171	Synaptic vesicle membrane protein VAT-1 homolog	Q99536	2/2	0	0	[1]/[1]	2/2	0	0	0	3	0	Membrane	Unknown. Has ATPase activity and sequence homology to alcohol dehydrogenase and ξ-crystallin.
172	Vacuolar proton pump subunit C 1	P21283	6/6	0	0	[1]/[1]	[1]/[1]	0	0	0	3	0	Intracellular compartments, Endosome-Lysosome	Compartment acidification.
173	Vesicle-trafficking protein SEC22b	O75396	0	0	2/2	2/2	3/3	0	0	0	3	0	ER-Golgi intermediate compartment, Melanosome	ER to Golgi targeting and fusion.
174	60S ribosomal protein L35	P42766	0	[1]/[1]	0	[1]/[1]	[1]/[1]	0	0	0	3	0	Cytoplasm	Protein synthesis.
175	60S ribosomal protein L8	P62917	0	0	[1]/[1]	[1]/[1]	[1]/[1]	0	0	0	3	0	Cytoplasm	Protein synthesis.
176	Macrophage migration inhibitory factor	P14174	0	[1]/[1]	[1]/[1]	[1]/[1]	0	0	0	0	3	0	Secreted protein	Pro-inflammatory immune modulator.
177	Ras-related protein Ral-B*	P11234*	[1]/[1]	0	0	[1]/[1]	[1]/[1]	0	0	0	3	0	Membrane	Signal transduction. Regulation of exocytosis. Activation of IkappaB kinase TBK1.
178	Translocon-associated protein subunit alpha	P43307	[1]/[1]	0	[1]/[1]	0	[1]/[1]	0	0	0	3	0	ER	Bind calcium to the ER membrane. Regulate retention of ER resident proteins.
179	60S ribosomal protein L22	P35268	0	0	[1]/[1]	[1]/[1]	0	[1]/[1]	[1]/[1]	[1]/[1]	2	3	Cytoplasm	Protein synthesis.
180	B-cell receptor-associated protein 31	P51572	0	0	0	2/2	2/2	3/3	2/2	0	2	2	ER, Golgi	Putative cargo receptor for ER to Golgi anterograde transport of membrane proteins. CASP8-mediated apoptosis. Interacts with VAMP3, VAMP1 and membrane IgD immunoglobulins. May interact with ACTG1 and non-muscle myosin II.
181	Flotillin-2	Q14254	3/3	0	4/4	0	0	3/3	7/7	0	2	2	PM, Phagosomal membrane	Lipid rafts. Clathrin independent endocytosis. Formation of caveolae or caveolae-like vesicles.
182	Guanine nucleotide-binding protein G(i), alpha-2 subunit	P04899	2/2	0	0	0	8/7	3/3	0	2/2	2	2	Membrane	Transmembrane signaling.
183	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5	P63218	[1]/[1]	0	0	2/2	0	2/2	2/2	0	2	2	Membrane	Transmembrane signaling.
184	Guanine nucleotide-binding protein G(k) subunit alpha	P08754	0	0	5/5	0	5/4	3/3	0	2/2	2	2	Membrane	Transmembrane signaling.
185	Heat shock 70 kDa protein 1	P08107	0	0	0	5/5	5/5	0	3/3	6/6	2	2	Cytoplasm	Chaperone involved in protein stablizing and folding.
186	Phospholipase D3	Q8IV08	4/4	0	0	0	2/2	4/4	2/2	0	2	2	ER membrane	Lipid degradation.
187	Ras-related C3 botulinum toxin substrate 1	P63000	2/2	0	2/2	0	0	5/5	3/3	0	2	2	Membrane, Melanosome	Cellular response regulator.
188	Sugar phosphate exchanger 2	Q8TED4	0	0	[1]/[1]	[1]/[1]	0	[1]/[1]	2/2	0	2	2	Membrane	Sugar transport.
189	Trifunctional enzyme subunit alpha, mitochondrial	P40939	6/6	0	0	0	3/3	[1]/[1]	[1]/[1]	0	2	2	Mitochondrion	Fatty acid beta-oxidation cycle.
190	V-type proton ATPase subunit G 1	O75348	2/2	0	0	4/4	0	3/3	3/3	0	2	2	Membrane	Compartment acidification.

191	V-type proton ATPase 116 kDa subunit a isoform 3	Q13488	6/6	0	0	4/4	0	4/4	4/4	0	2	2	Membrane	Compartment acidification.
192	Vesicle transport through interaction with t-SNAREs homolog 1B	Q9UEU0	[1]/[1]	0	0	[1]/[1]	0	[1]/[1]	[1]/[1]	0	2	2	Cytoplasmic vesicles	Late endosome fusion. Forms SNARE complex with VAMP8, STX7, and STX8.
193	14-3-3 protein theta	P27348	0	0	0	3/3	3/3	0	0	4/4	2	1	Cytoplasm	Regulates signal transduction pathways.
194	40S ribosomal protein S19	P39019	0	0	0	[1]/[1]	3/3	0	0	[1]/[1]	2	1	Cytoplasm	Protein synthesis.
195	40S ribosomal protein S25	P62851	0	0	[1]/[1]	3/3	0	0	0	3/3	2	1	Cytoplasm	Protein synthesis.
196	40S ribosomal protein S3	P23396	0	0	0	2/2	3/3	0	0	2/2	2	1	Cytoplasm	Protein synthesis.
197	40S ribosomal protein S4, X isoform	P62701	0	0	0	2/2	[1]/[1]	0	0	3/3	2	1	Cytoplasm	Protein synthesis.
198	60S acidic ribosomal protein P0	P05388	[1]/[1]	0	0	0	3/3	0	0	2/2	2	1	Cytoplasm	Protein synthesis.
199	60S ribosomal protein L13	P26373	0	0	[1]/[1]	[1]/[1]	0	0	0	2/2	2	1	Cytoplasm	Protein synthesis.
200	Actin-related protein 2/3 complex subunit 4	P59998	0	2/2	[1]/[1]	0	0	0	0	[1]/[1]	2	1	Cytoplasm	Cytoskeleton. F-actin assembly.
201	Annexin A1	P04083	0	0	0	3/3	7/7	0	0	4/4	2	1	Membrane, Cytoplasm	Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis.
202	Cytochrome b-c1 complex subunit 1, mitochondrial	P31930	4/3	0	2/2	0	0	0	[1]/[1]	0	2	1	Mitochondrion	Respiratory Chain. Electron transport.
203	F-actin-capping protein subunit alpha-1	P52907	0	0	0	3/3	2/2	0	0	2/2	2	1	Cytoplasm	Cytoskeleton. Actin capping.
204	GTP-binding nuclear protein Ran	P62826	0	2/2	0	[1]/[1]	0	0	0	[1]/[1]	2	1	Nucleus, Cytoplasm, Melanosome	GTPase. Regulates protein transport into nucleus.
205	Importin subunit beta-1	Q14974	0	[1]/[1]	0	4/4	0	0	0	3/3	2	1	Nucleus, Cytoplasm	Nuclear protein import.
206	Isocitrate dehydrogenase [NADP], mitochondrial	P48735	7/7	0	2/2	0	0	0	3/3	0	2	1	Mitochondrion	Metabolism and energy production.
207	L-lactate dehydrogenase B chain	P07195	0	0	0	6/6	5/5	0	0	6/6	2	1	Cytoplasm	Anaerobic glycolysis.
208	LIM and SH3 domain protein 1	Q14847	0	0	0	3/3	2/2	0	0	3/3	2	1	Cytoplasm	Cytoskeleton. Regulation of dynamic actin-based, cytoskeletal activities.
209	Leukocyte common antigen (CD45)	P08575	0	0	0	3/3	3/3	0	0	[1]/[1]	2	1	PM	Receptor-linked protein tyrosine phosphatase involved in signal transduction.
210	Long-chain-fatty-acid--CoA ligase 4	O60488	0	0	5/5	2/2	0	0	[1]/[1]	0	2	1	Mitochondrion, Microsome, Peroxisome	Lipid metabolism.
211	Malate dehydrogenase, cytoplasmic	P40925	0	0	0	[1]/[1]	2/2	0	0	2/2	2	1	Cytoplasm	Metabolism.
212	Niemann-Pick C1 protein	O15118	0	2/2	0	3/3	0	0	2/2	0	2	1	Endosome-Lysosome	Intracellular trafficking of cholesterol.
213	Phosphoserine aminotransferase	Q9Y617	0	0	0	2/2	2/2	0	0	2/2	2	1	Cytoplasm	Amino acid biosynthesis.
214	Poly(rC)-binding protein 1	Q15365	0	0	0	2/2	4/4	0	0	3/3	2	1	Nucleus, Cytoplasm	Binds single-stranded nucleic acid.
215	Programmed cell death 6-interacting protein	Q8WUM4	0	0	2/2	0	[1]/[1]	0	0	3/3	2	1	Cytoplasm, Endosome, MVB, Melanosome	Cargo protein sorting. Membrane traffic.
216	Protein DJ-1	Q99497	0	[1]/[1]	0	[1]/[1]	0	0	0	2/2	2	1	Nucleus, Cytoplasm	May function as a redox-sensitive chaperone and sensor for oxidative stress.
217	Rho GDP-dissociation inhibitor 2	P52566	0	0	[1]/[1]	[1]/[1]	0	0	0	2/2	2	1	Cytoplasm	Regulator for Rho GTP/GDP exchange.
218	Stathmin*	P16949*	0	[1]/[1]	0	0	[1]/[1]	0	0	2/2	2	1	Cytoplasm	Microtubule regulator.
219	T-complex protein 1 subunit eta	Q99832	0	0	0	3/3	4/4	0	0	6/6	2	1	Cytoplasm	Molecular chaperone. Assist the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.
220	T-complex protein 1 subunit gamma	P49368	0	6/6	0	5/5	0	0	0	6/6	2	1	Cytoplasm	Molecular chaperone. Assist the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.
221	T-complex protein 1 subunit zeta	P40227	0	4/4	0	0	2/2	0	0	7/7	2	1	Cytoplasm	Molecular chaperone. Assist the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.
222	Vesicle-associated membrane protein 8	Q9BV40	0	0	[1]/[1]	3/3	0	4/4	0	0	2	1	Vesicle membrane	Homotypic fusion of early and late endosomes.
223	Zyxin	Q15942	0	0	0	2/2	[1]/[1]	0	0	3/3	2	1	Cytoplasm	Associates with actinin and sites of actin-membrane interaction.
224	40S ribosomal protein S21	P63220	0	[1]/[1]	0	[1]/[1]	0	0	[1]/[1]	0	2	1	Cytoplasm	Protein synthesis.
225	Eukaryotic translation initiation factor 3 subunit H	O15372	0	0	0	[1]/[1]	[1]/[1]	0	0	[1]/[1]	2	1	Cytoplasm	Protein synthesis and folding.
226	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Q16718	[1]/[1]	0	[1]/[1]	0	0	0	[1]/[1]	0	2	1	Mitochondrion	Respiratory Chain. Electron transport.
227	Proteasome subunit alpha type-3	P25788	0	0	0	[1]/[1]	[1]/[1]	0	0	[1]/[1]	2	1	Cytoplasm	Part of ATP-dependent multicatalytic proteinase complex.

228	Proteasome subunit beta type-6	P28072	0	0	0	[1]/[1]	[1]/[1]	0	0	[1]/[1]	2	1	Cytoplasm	Part of ATP-dependent multicatalytic proteinase complex.
229	Single-stranded DNA-binding protein, mitochondrial	Q04837	[1]/[1]	0	0	[1]/[1]	0	[1]/[1]	0	0	2	1	Mitochondrion	DNA replication.
230	Thioredoxin domain-containing protein 1	Q9H3N1	0	0	[1]/[1]	0	[1]/[1]	0	[1]/[1]	0	2	1	Membrane, ER	Redox reactions.
231	Tryptophanyl-tRNA synthetase, cytoplasmic	P23381	0	0	0	[1]/[1]	[1]/[1]	0	0	[1]/[1]	2	1	Cytoplasm	Protein synthesis.
232	Voltage-dependent anion-selective channel protein 3	Q9Y277	[1]/[1]	0	0	[1]/[1]	0	0	0	[1]/[1]	2	1	Mitochondrion	Channel for small hydrophilic molecules.
233	14-3-3 protein epsilon	P62258	0	0	0	5/4	4/4	0	0	0	2	0	Cytoplasm	Regulates signal transduction pathways.
234	3-hydroxyacyl-CoA dehydrogenase type-2	Q99714	2/2	0	0	0	[1]/[1]	0	0	0	2	0	PM	Lipid metabolism. Oxidation reduction.
235	40S ribosomal protein S18	P62269	0	0	0	2/2	2/2	0	0	0	2	0	Cytoplasm	Protein synthesis.
236	40S ribosomal protein S3a	P61247	0	0	0	2/2	3/3	0	0	0	2	0	Cytoplasm	Protein synthesis.
237	4F2 cell-surface antigen heavy chain	P08195	0	0	6/5	3/3	0	0	0	0	2	0	PM, Melanosome	Amino acid transport.
238	Actin-related protein 3	P61158	0	0	2/2	4/4	0	0	0	0	2	0	Cytoplasm	Cytoskeleton.
239	Adipophilin	Q99541	0	10/10	0	0	4/4	0	0	0	2	0	Membrane (lipid droplet and raft)	Serves as scaffolding during lipid droplet formation.
240	ADP-ribosylation factor 3	P61204	0	4/4	0	2/2	0	0	0	0	2	0	Golgi, Cytoplasmic vesicles	Regulation of membrane traffic and cytoskeleton.
241	Annexin A11	P50995	0	4/4	0	0	[1]/[1]	0	0	0	2	0	Cytoplasm, Nucleus, Melanosome	Calcium-dependent phospholipid binding.
242	Aspartyl-tRNA synthetase, cytoplasmic	P14868	0	2/2	0	[1]/[1]	0	0	0	0	2	0	Cytoplasm	Protein synthesis.
243	ATP synthase subunit e, mitochondrial	P56385	2/2	0	0	[1]/[1]	0	0	0	0	2	0	Mitochondrion	ATP synthesis. Ion transport.
244	ATP-citrate synthase	P53396	0	4/4	0	5/5	0	0	0	0	2	0	Cytosol	Synthesis of cytosolic acetyl-CoA .
245	Beta-1-syntrophin	Q13884	0	0	[1]/[1]	0	3/3	0	0	0	2	0	PM, Cytoplasm	Cytoskeleton. Adaptor protein. Links membrane receptors to actin cytoskeleton.
246	Carboxypeptidase D	O75976	0	0	0	7/7	3/3	0	0	0	2	0	Membrane	Metallocarboxypeptidase.
247	Cation-independent mannose-6-phosphate receptor	P11717	0	0	0	14/14	5/5	0	0	0	2	0	Late endosome, Trans-Golgi network	Transport of phosphorylated lysosomal enzymes from the Golgi complex and the cell surface to lysosomes.
248	CD166 antigen	Q13740	0	0	2/2	4/4	0	0	0	0	2	0	PM	Cell-cell interaction.
249	Dihydropyrimidinase-related protein 2	Q16555	0	[1]/[1]	0	3/3	0	0	0	0	2	0	Cytoplasm	Necessary for signaling by class 3 semaphorins and subsequent remodeling of the cytoskeleton.
250	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3	O94766	0	0	0	2/2	2/2	0	0	0	2	0	Golgi	Protein modification. Protein glycosylation.
251	Galectin-1	P09382	0	0	[1]/[1]	4/4	0	0	0	0	2	0	PM, Golgi	Beta-galactoside-binding lectin. Has a prominent role in regulating cell adhesion, cell growth and immune responses.
252	Glutathione transferase omega-1	P78417	0	0	0	2/2	[1]/[1]	0	0	0	2	0	Cytoplasm	Detoxification of electrophilic compounds, including drugs, toxins, and products of oxidative stress.
253	Golgi integral membrane protein 4	O00461	0	0	0	2/2	[1]/[1]	0	0	0	2	0	Golgi, Endosome	Plays a role in endosome to Golgi protein trafficking. Mediates protein transport along the late endosome-bypass pathway from the early endosome to the Golgi.
254	Golgin subfamily B member 1	Q14789	0	0	0	[1]/[1]	2/2	0	0	0	2	0	Golgi, ER-Golgi intermediate compartment	Forms intercisternal cross-bridges of the Golgi complex.
255	Heparan sulfate 2-O-sulfotransferase 1	Q7LGA3	0	0	0	[1]/[1]	2/2	0	0	0	2	0	Golgi	Heparan sulfate biosynthesis.
256	Histone H4	P62805	0	0	3/3	2/2	0	0	0	0	2	0	Nucleus	Component of nucleosome.
257	Mitochondrial inner membrane protein	Q16891	[1]/[1]	0	0	0	5/5	0	0	0	2	0	Mitochondrion inner membrane	Unknown. May be involved in protein import.
258	Monocyte differentiation antigen CD14	P08571	0	0	2/2	0	2/2	0	0	0	2	0	PM	Interacts with MD-2 and TLR4 to mediate innate immune response to bacterial lipopolysaccharide.
259	Polypeptide N-acetylgalactosaminyltransferase 2	Q10471	0	0	0	5/5	5/5	0	0	0	2	0	Golgi, Secreted protein	Protein glycosylation.
260	Prohibitin	P35232	3/3	0	0	[1]/[1]	0	0	0	0	2	0	Mitochondrion, PM, Nucleoplasm, Lipid rafts	Inhibit DNA synthesis. Modulate gene expression. Chaperones for imported proteins in mitochondria (reviewed by Mishra et al., 2006).
261	Proteasome subunit alpha type-6	P60900	0	0	0	2/2	3/3	0	0	0	2	0	Cytoplasm	Part of ATP-dependent multicatalytic proteinase complex.
262	Protein S100-A11	P31949	0	3/3	0	5/5	0	0	0	0	2	0	Cytoplasm, PM, Sarcoplasmic reticulum of muscle	Calcium-dependent actin binding protein involved in the regulation of actin filaments (Zhao et al., 2000).

263	Putative annexin A2-like protein	A6NMY6	2/2	0	2/2	0	0	0	0	0	2	0	Secreted protein, Melanosome	Calcium-regulated membrane-binding protein whose affinity for calcium is greatly enhanced by anionic phospholipids (By similarity). May be involved in heat-stress response (By similarity).
264	Rab GDP dissociation inhibitor beta	P50395	0	0	0	3/3	4/4	0	0	0	2	0	Cytoplasm	Regulator/Rab GTP/GDP exchange.
265	Ras-related protein Rab-2A	P61019	0	0	0	2/2	[1]/[1]	0	0	0	2	0	Golgi	Golgi to ER traffic.
266	Ras-related protein Rab-5B	P61020	0	0	0	2/2	3/3	0	0	0	2	0	Endosome	Vesicular trafficking.
267	Ras-related protein Rab-10	P61026	2/2	0	0	0	2/2	0	0	0	2	0	Endosome	Vesicular trafficking.
268	Septin-11	Q9NVA2	0	0	2/2	0	4/4	0	0	0	2	0	Cytoplasm	GTPase. Cytokinesis. Exocytosis. Colocalizes with sub-membrane actin during the early stages of FcgammaR-mediated phagocytosis. Required for phagosome formation (Huang et al., 2008).
269	Serine/threonine-protein kinase 10	O94804	0	0	0	2/2	2/2	0	0	0	2	0	Cytoplasm	Protein phosphorylation. Signal transduction.
270	Sideroflexin-3	Q9BWM7	2/2	0	0	0	3/3	0	0	0	2	0	Mitochondrial Membrane	Potential iron transporter.
271	Stomatin-like protein 2	Q9UJZ1	3/3	0	[1]/[1]	0	0	0	0	0	2	0	Membrane, Cytoplasm, Cytoskeleton	Unknown. Partitions into lipid rafts and contributes to T-cell receptor signaling (Kirchof et al., 2008).
272	Thioredoxin domain-containing protein 4	Q9BS26	0	0	0	3/3	5/5	0	0	0	2	0	ER	Chaperone. May have a role in the control of oxidative protein folding in the endoplasmic reticulum.
273	Transmembrane 9 superfamily member 1	O15321	0	0	0	2/2	3/3	0	0	0	2	0	Membrane	Unknown.
274	Transmembrane 9 superfamily member 2	Q99805	0	0	0	2/2	3/3	0	0	0	2	0	Endosome	May function as a channel or small molecule transporter.
275	Transmembrane 9 superfamily member 3	Q9HD45	0	0	0	4/4	3/3	0	0	0	2	0	Membrane	Unknown.
276	Transmembrane 9 superfamily member 4	Q92544	0	0	0	2/2	3/3	0	0	0	2	0	Membrane	Unknown.
277	Transmembrane protein 165	Q9HC07	0	0	0	2/2	2/2	0	0	0	2	0	Membrane	Unknown.
278	Tubulin beta-2C chain	P68371	0	13/12	9/0	11/11	0	0	0	0	2	0	Cytoplasm	Cytoskeleton.
279	Uncharacterized protein KIAA2013	Q8IYS2	0	[1]/[1]	0	2/2	1/0	0	0	0	2	0	Membrane	Unknown.
280	UPF0404 protein C11orf59	Q6IAA8	[1]/[1]	0	0	2/2	0	0	0	0	2	0	Unknown	Unknown.
281	Vesicle-fusing ATPase (NEM-sensitive fusion protein, NSF)	P46459	0	0	2/2	4/4	0	0	0	0	2	0	Cytoplasm	Required for vesicle-mediated transport.
282	Vinculin	P18206	0	3/3	0	2/2	0	0	0	0	2	0	Cytoplasm	Cytoskeleton. May be involved in attachment of the actin microfilaments to PM.
283	60S ribosomal protein L12	P30050	0	0	[1]/[1]	[1]/[1]	0	0	0	0	2	0	Cytoplasm	Protein synthesis.
284	60S ribosomal protein L15	P61313	0	[1]/[1]	0	0	[1]/[1]	0	0	0	2	0	Cytoplasm	Protein synthesis.
285	60S ribosomal protein L27a	P46776	0	[1]/[1]	0	0	[1]/[1]	0	0	0	2	0	Cytoplasm	Protein synthesis.
286	AP-2 complex subunit beta-1	P63010	0	0	[1]/[1]	0	[1]/[1]	0	0	0	2	0	Membrane, Cytoplasmic vesicles	Component of the adaptor complexes which link clathrin to receptors in coated vesicles.
287	ATP synthase subunit b, mitochondrial	P24539	0	[1]/[1]	[1]/[1]	0	0	0	0	0	2	0	Mitochondrion	ATP synthesis. Ion transport.
288	Beta-2-microglobulin	P61769	0	0	[1]/[1]	[1]/[1]	0	0	0	0	2	0	PM, early Endosome membrane, Golgi, Secreted Protein	Antigen processing and presentation via MHC class I.
289	Bone marrow stromal antigen 2	Q10589	0	0	[1]/[1]	0	[1]/[1]	0	0	0	2	0	Golgi, PM	May be involved in the sorting of secreted proteins (By similarity).
290	Coatomer subunit gamma	Q9Y678	0	[1]/[1]	0	0	[1]/[1]	0	0	0	2	0	Cytoplasm, Cytoplasmic vesicle, Golgi	Coat protein.
291	Cytochrome c oxidase subunit 5B, mitochondrial	P10606	[1]/[1]	0	[1]/[1]	0	0	0	0	0	2	0	Mitochondrion	Electron transport. Respiratory chain. Apoptosis. Caspase activation.
292	Cytosol aminopeptidase	P28838	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Cytoplasm	Processing and turnover of intracellular proteins.
293	EF-hand domain-containing protein D2	Q96C19	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Unknown	Unknown.
294	ERO1-like protein alpha	Q96HE7	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	ER	Disulfide bond formation.
295	Fumarate hydratase, mitochondrial	P07954	[1]/[1]	0	0	0	[1]/[1]	0	0	0	2	0	Mitochondrion, Cytoplasm	Carbohydrate metabolism.
296	Golgi-associated plant pathogenesis-related protein 1	Q9H4G4	[1]/[1]	0	0	[1]/[1]	0	0	0	0	2	0	Golgi	Unknown.
297	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Q16836	[1]/[1]	0	[1]/[1]	0	0	0	0	0	2	0	Mitochondrion	Lipid metabolism. Fatty acid beta-oxidation.
298	LETM1 and EF-hand domain-containing protein 1, mitochondrial	O95202	[1]/[1]	0	[1]/[1]	0	0	0	0	0	2	0	Mitochondrion	May play a role in mitochondrial morphology.

299	Lon protease homolog, mitochondrial	P36776	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Mitochondrion	ATP-dependent proteolysis.
300	Major facilitator superfamily domain-containing protein 1	Q9H3U5	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Membrane	Unknown.
301	Minor histocompatibility antigen H13	Q8TCT9	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	ER membrane	Catalyzes intramembrane proteolysis of some signal peptides after they have been cleaved from a preprotein.
302	Mitochondrial import receptor subunit TOM22 homolog	Q9NS69	[1]/[1]	0	[1]/[1]	0	0	0	0	0	2	0	Mitochondrion	Receptor component of mitochondria outer membrane translocase.
303	Protein CASC4	Q6P4E1	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Membrane	Unknown.
304	Protein transport protein Sec61 subunit gamma	P60059	0	0	[1]/[1]	[1]/[1]	0	0	0	0	2	0	ER	Protein translocation.
305	Proto-oncogene vav	P15498	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Cytoplasm, Cytoplasmic vesicles	Regulation of Rho-signal transduction.
306	SH3 domain-binding glutamic acid-rich-like protein 3	Q9H299	0	[1]/[1]	0	[1]/[1]	0	0	0	0	2	0	Nucleus, Cytoplasm	May act as modulator of glutaredoxin activity.
307	Syntaxin-3	Q13277	[1]/[1]	0	0	0	[1]/[1]	0	0	0	2	0	Membrane, Vacuole, Golgi	Docking of synaptic vesicles at presynaptic active zones.
308	Transaldolase	P37837	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Cytoplasm	Carbohydrate degradation. Pentose-phosphate pathway.
309	Transforming growth factor-beta-induced protein ig-h3	Q15582	0	0	0	[1]/[1]	[1]/[1]	0	0	0	2	0	Secreted protein	Binds collagen type I, II, IV.
310	Translocon-associated protein subunit delta	P51571	0	0	[1]/[1]	[1]/[1]	0	0	0	0	2	0	ER	Binds calcium to the ER membrane. Regulates the retention of ER resident proteins.
311	UPF0539 protein C7orf59	Q0VGL1	0	0	[1]/[1]	[1]/[1]	0	0	0	0	2	0	Unknown	Unknown.
312	Vacuolar proton pump subunit D	Q9Y5K8	[1]/[1]	0	0	[1]/[1]	0	0	0	0	2	0	Intracellular compartments, Endosome-Lysosome	Compartment acidification.
313	40S ribosomal protein S14	P62263	0	0	0	2/2	0	[1]/[1]	[1]/[1]	0	1	2	Cytoplasm	Protein synthesis.
314	Dihydrolipoyl dehydrogenase, mitochondrial	P09622	2/2	0	0	0	0	2/2	[1]/[1]	0	1	2	Mitochondrion	Component of the glycine cleavage system and the alpha-ketoacid dehydrogenase complex.
315	Glucosylceramidase	P04062	2/2	0	0	0	0	4/4	0	2/2	1	2	Lysosome	Remove D-glucose from D-glucosyl-N-acylsphingosine.
316	Ubiquitin	P62988	0	0	0	2/2	0	2/2	2/2	0	1	2	Cytoplasm, Nucleus, Endosome-Lysosome	Modify proteins for degradation by proteasome. Regulation of cell signaling and intra-endosomal membrane traffic (Haglund and Dikic, 2005; Goot and Gruenberg, 2006).
317	Mitogen-activated protein-binding protein-interacting protein	Q9Y2Q5	[1]/[1]	0	0	0	0	[1]/[1]	[1]/[1]	0	1	2	Late endosome, Lysosome	Facilitates the activation of MAPK2.
318	40S ribosomal protein S8	P62241	0	0	0	2/2	0	0	0	[1]/[1]	1	1	Cytoplasm	Protein synthesis.
319	40S ribosomal protein S9	P46781	0	0	0	0	2/2	0	0	[1]/[1]	1	1	Cytoplasm	Protein synthesis.
320	60S ribosomal protein L11	P62913	0	0	0	3/3	0	2	0	0	1	1	Cytoplasm	Protein synthesis.
321	Actin-related protein 2/3 complex subunit 2	O15144	0	0	0	3/3	0	0	0	2/2	1	1	Cytoplasm	Cytoskeleton. F-actin assembly.
322	Annexin A6	P08133	0	0	0	3/3	0	0	0	6/6	1	1	Cytoplasm, Melanosome	May associate with CD21. May regulate the release of Ca(2+) from intracellular stores.
323	Band 4.1-like protein 2	O43491	0	0	0	0	3/3	0	0	2/2	1	1	Membrane	Links membrane to cytoskeleton.
324	Bifunctional aminoacyl-tRNA synthetase	P07814	0	0	0	0	2/2	0	0	6/6	1	1	Cytoplasm	Protein synthesis.
325	CAAX prenyl protease 1 homolog	O75844	0	0	0	0	2/2	0	2/2	0	1	1	ER, Golgi	Removes the C-terminal 3 residues of farnesylated proteins.
326	Clathrin heavy chain 1	Q00610	0	12/12	0	0	0	0	0	3/3	1	1	Membrane, Cytoplasmic vesicles	Major protein of the polyhedral coat of coated pits and vesicles.
327	Elongation factor 1-delta	P29692	0	0	0	0	2/2	0	0	2/2	1	1	Cytoplasm	Protein synthesis and folding.
328	Epididymal secretory protein E1 (NPC2)	P61916	3/3	0	0	0	0	2/2	0	0	1	1	Lysosome, Secreted protein	Lipid transport.
329	Fatty acid synthase	P49327	0	12/12	0	0	0	0	0	[1]/[1]	1	1	Cytoplasm, Melanosome	Lipid synthesis.
330	Fatty acid-binding protein, epidermal	Q01469	0	0	2/2	0	0	0	0	2/2	1	1	Cytoplasm	Lipid chaperone. Expressed in adipocytes and macrophages.
331	Gamma-glutamyl hydrolase	Q92820	5/5	0	0	0	0	2/2	0	0	1	1	Lysosome, Secreted protein, Melanosome	Hydrolyze pteroylpolyglutamate.
332	Heat shock 70 kDa protein 4	P34932	0	0	0	[1]/[1]	0	0	0	4/4	1	1	Cytoplasm	Chaperone.
333	Heat shock 70 kDa protein 6	P17066	0	0	0	6/6	0	0	0	4/4	1	1	Cytoplasm	Chaperone. Stablize and fold proteins.
334	Isoleucyl-tRNA synthetase, cytoplasmic	P41252	0	2/2	0	0	0	0	0	3/3	1	1	Cytoplasm	Protein synthesis.
335	Liver carboxylesterase 1 (Monocyte/macrophage serine esterase)	P23141	0	0	0	0	4/4	0	0	2/2	1	1	ER	Detoxification. Hydrolyzes aromatic and aliphatic esters.
336	Lysozyme C	P61626	0	0	0	2/2	0	0	0	[1]/[1]	1	1	Lysosome	Carbohydrate degradation.
337	Myosin regulatory light chain MRLC2	O14950	0	0	2/2	0	0	0	0	2/2	1	1	Cytoplasm, Myosin complex	Myosin regulatory subunit. Implicated in cytokinesis, receptor capping, and cell locomotion.

338	Myristoylated alanine-rich C-kinase substrate	P29966	0	0	0	0	3/3	0	0	2/2	1	1	Cytoplasm, Cytoskeleton, Membrane	Protein kinase C substrate. Binds calmodulin, actin, and synapsin. F-actin cross-linking protein.
339	Non-specific lipid-transfer protein	P22307	0	0	3/3	0	0	[1]/[1]	0	0	1	1	Cytoplasm, Mitochondrion, Peroxisome	Transfer phospholipids, cholesterol and gangliosides between membranes.
340	P2X purinoceptor 4	Q99571	0	0	0	2/2	0	0	[1]/[1]	0	1	1	Membrane, PM	Receptor for ATP that acts as a ligand gated ion channel.
341	Peptidyl-prolyl cis-trans isomerase A	P62937	0	0	0	8/8	0	0	0	4/4	1	1	Cytoplasm	Chaperone. Protein folding.
342	Phosphatidylinositol 4-kinase type 2 alpha	Q9BTU6	3/3	0	0	0	0	4/4	0	0	1	1	Cytoplasm, Membrane (non-caveolar membrane rafts)	1-Phosphatidylinositol 4-kinase activity. Contributes to the production of inositol 1,4,5-trisphosphate in stimulated cells (By similarity).
343	Profilin-1	P07737	0	0	0	4/4	0	0	0	2/2	1	1	Cytoplasm	Cytoskeleton. Binds actin and affects the structure of the cytoskeleton.
344	Proteasome subunit beta type-4	P28070	0	0	0	2/2	0	0	0	[1]/[1]	1	1	Cytoplasm	Part of ATP-dependent multicatalytic proteinase complex.
345	Ras-related protein Rab-8A	P61006	0	0	3/3	0	0	0	4/4	0	1	1	Membrane	Vesicular trafficking.
346	T-complex protein 1 subunit alpha	P17987	0	6/6	0	0	0	0	0	3/3	1	1	Cytoplasm	Molecular chaperone. Assists the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.
347	T-complex protein 1 subunit delta	P50991	0	0	0	2/2	0	0	0	9/9	1	1	Cytoplasm, Melanosome	Molecular chaperone. Assists the folding of proteins upon ATP hydrolysis. Known to play a role, in vitro, in the folding of actin and tubulin.
348	Tropomyosin alpha-3 chain	P06753	0	0	0	[1]/[1]	0	0	0	5/5	1	1	Cytoplasm	Cytoskeleton. Binds to actin filaments in muscle and non-muscle cells.
349	Tyrosyl-tRNA synthetase, cytoplasmic	P54577	0	0	0	0	[1]/[1]	0	0	4/4	1	1	Cytoplasm	Protein synthesis.
350	Ubiquitin-conjugating enzyme E2 variant 2	Q15819	0	0	0	2/2	0	0	0	2/2	1	1	Cytoplasm	Poly-ubiquitination.
351	Ubiquitin-like modifier-activating enzyme 1	P22314	0	0	0	2/2	0	0	0	2/2	1	1	Cytoplasm	Ubiquitin conjugation pathway.
352	Uncharacterized protein KIAA0174	P53990	0	0	0	0	[1]/[1]	0	3/3	0	1	1	ER-Golgi intermediate compartment	Unknown.
353	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1	Q93050	0	0	0	2/2	0	0	2/2	0	1	1	Cytoplasmic vesicle membrane	Required for assembly and activity of the vacuolar ATPase.
354	WD repeat-containing protein 1	O75083	0	0	0	[1]/[1]	0	0	0	4/4	1	1	Cytoplasm	Cytoskeleton. Induces disassembly of actin filaments in conjunction with ADF/cofilin family proteins.
355	ATP synthase subunit d, mitochondrial	O75947	[1]/[1]	0	0	0	0	[1]/[1]	0	0	1	1	Mitochondrion	ATP synthesis. Ion transport.
356	Clathrin light chain A	P09496	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasmic vesicles	Major protein of the polyhedral coat of coated pits and vesicles.
357	Cytochrome b-245 heavy chain	P04839	0	0	0	0	[1]/[1]	0	[1]/[1]	0	1	1	Membrane	Critical component of the membrane-bound oxidase of phagocytes that generates superoxide.
358	Cytochrome c	P99999	[1]/[1]	0	0	0	0	0	[1]/[1]	0	1	1	Mitochondrion	Electron transport. Respiratory chain. Apoptosis. Caspase activation.
359	Cytoplasmic dynein 1 heavy chain 1	Q14204	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasm	ATPase motor. Drives vesicles and organelles to minus end of microtubules.
360	Dolichol-phosphate mannosyltransferase subunit 3	Q9P2X0	0	0	0	[1]/[1]	0	0	[1]/[1]	0	1	1	ER membrane	Stabilizer subunit of the dolichol-phosphate-mannose synthase complex.
361	Electron transfer flavoprotein subunit alpha, mitochondrial	P13804	[1]/[1]	0	0	0	0	0	[1]/[1]	0	1	1	Mitochondrion	Transfers electrons to the main mitochondrial respiratory chain.
362	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12	Q9UBI6	0	0	0	[1]/[1]	0	0	[1]/[1]	0	1	1	Membrane	Transmembrane signaling.
363	Heat shock protein 105 kDa	Q92598	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasm	Prevents the aggregation of denatured proteins in cells under severe stress.
364	Hsp90 co-chaperone Cdc37	Q16543	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasm	Co-chaperone that binds to numerous kinases and promotes their interaction with the Hsp90 complex, resulting in stabilization and promotion of their activity.
365	Lactoylglutathione lyase	Q04760	0	0	0	0	[1]/[1]	0	0	[1]/[1]	1	1	Cytoplasm	Methylglyoxal degradation. Defence against glycation reactions.
366	Plasminogen activator inhibitor 1 RNA-binding protein	Q8NC51	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasm, Nucleus	May play a role in mRNA stability.
367	Proteasome activator complex subunit 1	Q06323	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasm	Implicated in immunoproteasome assembly and required for efficient antigen processing.
368	Proteasome subunit alpha type-4	P25789	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasm	Part of ATP-dependent multicatalytic proteinase complex.
369	Proteasome subunit beta type-2	P49721	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Cytoplasm	Part of ATP-dependent multicatalytic proteinase complex.
370	Transmembrane glycoprotein NMB	Q14956	[1]/[1]	0	0	0	0	[1]/[1]	0	0	1	1	Membrane, Melanosome	Possible melanogenic enzyme (by similarity).

371	Tripeptidyl-peptidase 2	P29144	0	[1]/[1]	0	0	0	0	0	[1]/[1]	1	1	Cytoplasm	Component of the proteolytic cascade acting downstream of the 26S proteasome in the ubiquitin-proteasome pathway.
372	Xaa-Pro dipeptidase	P12955	0	0	0	[1]/[1]	0	0	0	[1]/[1]	1	1	Unknown	Splits dipeptides with a prolyl or hydroxyprolyl residue in the C-terminal position.
373	14-3-3 protein eta	Q04917	0	0	0	3/3	0	0	0	0	1	0	Cytoplasm	Regulates signal transduction pathways.
374	2'-5'-oligoadenylate synthetase 2	P29728	0	0	0	3/3	0	0	0	0	1	0	Mitochondrion, Nucleus, Microsome, ER	RNA degradation, IFN inducible. May play a role in mediating resistance to virus infection, control of cell growth, differentiation, and apoptosis.
375	6-phosphofructokinase type C	Q01813	0	2/2	0	0	0	0	0	0	1	0	Cytoplasm	Glycolysis.
376	60S ribosomal protein L14	P50914	0	0	0	0	2/2	0	0	0	1	0	Cytoplasm	Translational elongation.
377	Acetyl-CoA acetyltransferase, mitochondrial	P24752	5/5	0	0	0	0	0	0	0	1	0	Mitochondrion	Ketone body metabolism.
378	Actin, cytoplasmic 2	P63261	0	0	0	0	40/16	0	0	0	1	0	Cytoplasm	Cytoskeleton.
379	Adipocyte plasma membrane-associated protein	Q9HDC9	0	0	2/2	0	0	0	0	0	1	0	Membrane	May play a role in adipocyte differentiation.
380	ADP/ATP translocase 3	P12236	0	2/2	0	0	0	0	0	0	1	0	Mitochondrion	ATP/ADP translocation.
381	ADP-ribosylation factor 1	P84077	0	0	0	2/2	0	0	0	0	1	0	Golgi, Cytosol, PM	Involved in protein trafficking among different compartments. Modulates vesicle budding and uncoating within the Golgi complex.
382	Aldehyde dehydrogenase, mitochondrial	P05091	0	0	0	0	2/2	0	0	0	1	0	Mitochondrion	Alcohol metabolism. Ethanol degradation.
383	Alpha-(1,6)-fucosyltransferase	Q9BYC5	0	0	0	2/2	0	0	0	0	1	0	Golgi	Glycosylation.
384	Alpha-N-acetylgalactosaminidase	P17050	2/2	0	0	0	0	0	0	0	1	0	Lysosome	Carbohydrate degradation.
385	Alpha-soluble NSF attachment protein	P54920	0	0	0	0	2/2	0	0	0	1	0	Membrane, Cytoplasmic vesicles	Vesicular transport.
386	Alpha-synuclein	P37840	0	0	0	0	2/2	0	0	0	1	0	Cytoplasm, Membrane, Nucleus	Soluble protein present in presynaptic nerve terminals. In neuronal cells, regulates dopamine metabolism; associates with phospholipid vesicles, actin cytoskeleton, exhibits chaperone activity and interacts with tau.
387	ANKRD26-like family C member 1A	Q6S8J3	0	0	5/3	0	0	0	0	0	1	0	Unknown	Unknown.
388	Arylsulfatase A	P15289	3/3	0	0	0	0	0	0	0	1	0	Lysosome	Hydrolyzes cerebroside sulfate.
389	Aspartate aminotransferase, mitochondrial (Fatty acid-binding protein)	P00505	5/5	0	0	0	0	0	0	0	1	0	Mitochondrion, PM	Aspartate catabolism. Lipid binding and transport (Isola et al., 1995; Zhou et al., 1995).
390	Chitinase-3-like protein 1	P36222	0	0	0	2/2	0	0	0	0	1	0	Secreted protein	May play a role in tissue remodeling & defense against pathogens.
391	Complement component C9	P02748	2/2	0	0	0	0	0	0	0	1	0	Secreted protein	Complement pathway.
392	Cullin-associated NEDD8-dissociated protein 1	Q86VP6	0	0	0	0	2/2	0	0	0	1	0	Nucleus, Ubiquitin ligase complex	Down-regulate ubiquination of target proteins. Transcription enhancer.
393	Cytoskeleton-associated protein 4	Q07065	0	0	0	0	2/2	0	0	0	1	0	PM, ER, Golgi	Cytoskeletal binding. CKAP4/p63 Is a plasma membrane receptor for the frizzled-8 protein-related antiproliferative factor (Conrads et al., 2006).
394	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	P36957	2/2	0	0	0	0	0	0	0	1	0	Mitochondrion	Tricarboxylic acid cycle. Amino acid degradation.
395	EH domain-containing protein 1	Q9H4M9	0	0	3/3	0	0	0	0	0	1	0	PM, Early endosome, Recycling endosome	Acts in early endocytic membrane fusion and membrane trafficking of recycling endosomes.
396	EH domain-containing protein 4	Q9H223	0	0	0	0	4/4	0	0	0	1	0	Endosome	Plays a role in early endosomal transport. Functions in Arf6 regulated membrane recycling.
397	Electron transfer flavoprotein subunit beta	P38117	0	3/3	0	0	0	0	0	0	1	0	Mitochondrion	Electron transport chain.
398	Eukaryotic translation initiation factor 2 subunit 1	P05198	0	0	0	0	3/3	0	0	0	1	0	Cytoplasm	Protein biosynthesis. Translation regulation.
399	Golgin subfamily A member 3	Q08378	0	0	0	0	5/5	0	0	0	1	0	Golgi, Cytoplasm	Probably involved in maintaining Golgi structure. Intra-Golgi vesicle mediated transport.
400	Golgin subfamily A member 5	Q8TBA6	0	0	0	0	4/4	0	0	0	1	0	Golgi, Cytoplasm	Involved in maintaining Golgi structure. Golgi retrograde transport. Interacts with Rab1A.
401	Guanine nucleotide-binding protein alpha-13 subunit	Q14344	0	0	2/2	0	0	0	0	0	1	0	Membrane, Melanosome	Modulator or transducer in transmembrane signaling.
402	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	P62879	0	0	3/3	0	0	0	0	0	1	0	Membrane	Modulator or transducer in transmembrane signaling.

403	Guanine nucleotide-binding protein subunit beta-2-like 1	P63244	0	0	0	2/2	0	0	0	0	1	0	Membrane	Intracellular receptor to anchor activated PKC to the cytoskeleton.
404	Heat shock 70 kDa protein 1L	P34931	0	0	0	5/5	0	0	0	0	1	0	Cytoplasm	Chaperone. Stablize and fold proteins.
405	Heat shock protein 75 kDa, mitochondrial (Tumor necrosis factor type 1 receptor-associated protein)	Q12931	3/3	0	0	0	0	0	0	0	1	0	Mitochondrion	Chaperone. Binds to the intracellular domain of tumor necrosis factor type 1 receptor.
406	High affinity immunoglobulin epsilon receptor subunit gamma	P30273	0	0	0	2/2	0	0	0	0	1	0	Membrane	Associates with a variety of FcR alpha chains to form a functional signaling complex. Regulates several aspects of the immune response. Has a critical role in allowing the IgE Fc receptor to reach the cell surface.
407	Histone H2B type 2-F	Q5QNW6	0	0	2/2	0	0	0	0	0	1	0	Nucleus	Component of nucleosome.
408	HLA class I histocompatibility antigen, A-34 alpha chain	P30453	0	0	0	0	8/7	0	0	0	1	0	PM	Antigen presentation.
409	HLA class I histocompatibility antigen, A-68 alpha chain	P01891	0	0	0	0	4/4	0	0	0	1	0	PM	Antigen presentation.
410	HLA class I histocompatibility antigen, B-27 alpha chain	P03989	0	0	2/2	0	0	0	0	0	1	0	PM	Antigen presentation.
411	HLA class I histocompatibility antigen, B-58 alpha chain	P10319	2/2	0	0	0	0	0	0	0	1	0	PM	Antigen presentation.
412	HLA class I histocompatibility antigen, B-67 alpha chain	Q29836	0	0	3/3	0	0	0	0	0	1	0	PM	Antigen presentation.
413	HLA class I histocompatibility antigen, Cw-16 alpha chain	Q29960	0	0	0	0	5/4	0	0	0	1	0	PM	Antigen presentation.
414	Ig gamma-1 chain C region	P01857	0	2/2	0	0	0	0	0	0	1	0	Secreted protein	Immunoglobulin.
415	Ig mu chain C region	P01871	0	2/2	0	0	0	0	0	0	1	0	Secreted protein	Immunoglobulin.
416	Integrin alpha-V	P06756	0	0	3/3	0	0	0	0	0	1	0	Membrane	Alpha-V integrins are receptors for vitronectin, cytotactin, fibronectin, fibrinogen, laminin, matrix metalloproteinase-2, osteopontin, osteomodulin, prothrombin, thrombospondin and vWF. Recognizes R-G-D sequence in a variety of ligands.
417	Integrin alpha-X	P20702	0	0	2/2	0	0	0	0	0	1	0	Membrane	Receptor for fibrinogen.
418	Lamin-A/C	P02545	0	0	2/2	0	0	0	0	0	1	0	Nucleus	Component of the nuclear lamina.
419	Long-chain-fatty-acid--CoA ligase 1	P33121	0	0	0	0	3/3	0	0	0	1	0	Mitochondrion, ER, Peroxisome	Lipid metabolism.
420	Lysosomal alpha-mannosidase	O00754	2/2	0	0	0	0	0	0	0	1	0	Lysosome	Hydrolyses terminal alpha-D-mannose residues in alpha-D-mannosides.
421	Matrix metalloproteinase-9	P14780	0	0	0	2/2	0	0	0	0	1	0	Secreted protein	Proteolysis of extracellular matrix.
422	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	P11310	2/2	0	0	0	0	0	0	0	1	0	Mitochondrion	Fatty acid beta-oxidation cycle.
423	Multifunctional protein ADE2	P22234	0	0	0	0	2/2	0	0	0	1	0	Unknown	Purine biosynthesis.
424	Neuroblast differentiation-associated protein AHNAK (Desmoyokin)	Q09666	0	4/3	0	0	0	0	0	0	1	0	Nucleus, Cytoplasm, Enlargeosome	May be involved in neuronal differentiation. Colocalizes with VAMP-4 in cytoplasmic vesicles called "enlargeosomes" (Cocucci et al., 2008).
425	Peptidyl-prolyl cis-trans isomerase, mitochondrial	P30405	2/2	0	0	0	0	0	0	0	1	0	Mitochondrion	Protein folding.
426	Peroxiredoxin-6	P30041	0	0	0	0	2/2	0	0	0	1	0	Cytoplasm, Lysosome, Cytoplasmic vesicle	Redox regulation, detoxification, phospholipid turnover. Can reduce H(2)O(2) and short chain organic, fatty acid, and phospholipid hydroperoxides.
427	Platelet factor 4	P02776	4/3	0	0	0	0	0	0	0	1	0	Secreted protein	Chemotactic for neutrophils and monocytes. Stored in secretory granules of platelets and released during platelet aggregation and in response to protein kinase C activation.
428	Plectin-1	Q15149	0	0	0	0	2/2	0	0	0	1	0	Cytoplasm, Cytoskeleton, PM	Interlinks intermediate filaments with microtubules and microfilaments and anchors intermediate filaments to desmosomes or hemidesmosomes. May also bind muscle proteins such as actin to membrane complexes in muscle.
429	Probable ATP-dependent RNA helicase DHX40	Q8IX18	2/2	0	0	0	0	0	0	0	1	0	Unknown	Possible RNA helicase
430	Protein CASP	Q13948	0	0	0	0	2/2	0	0	0	1	0	Golgi	May be involved in intra-Golgi retrograde transport.
431	Protein S100-A4	P26447	0	0	0	2/2	0	0	0	0	1	0	Cytoplasm, Cytoskeleton	Ca(2+) dependent interaction with liprin-beta1, methionine aminopeptidase, p53 tumor suppressor protein, and proteins involved in cytoskeletal rearrangement and cell motility such as F-actin, tropomyosin, and nonmuscle myosin II.
432	Protein YIPF4	Q9BSR8	0	0	0	0	2/2	0	0	0	1	0	Membrane	Unknown.

433	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	P11177	2/2	0	0	0	0	0	0	0	1	0	Mitochondrion	Glycolysis.
434	Ras-related protein Rab-35	Q15286	3/3	0	0	0	0	0	0	0	1	0	Endosome, PM, Melanosome	Endocytic recycling. Cytokinesis.
435	Receptor-type tyrosine-protein phosphatase eta	Q12913	0	0	2/2	0	0	0	0	0	1	0	Membrane, PM, Nucleus	Receptor protein tyrosine phosphatase. May contribute to contact inhibition of cell growth.
436	Ribonuclease inhibitor	P13489	0	0	0	2/2	0	0	0	0	1	0	Cytoplasm	RNase inhibitor.
437	Septin-2	Q15019	0	0	0	0	4/4	0	0	0	1	0	Cytoplasm	Associates with actin stress fibers. Colocalizes with submembrane actin. Required for phagosome formation (Huang et al., 2008).
438	Signal transducer and activator of transcription 1-alpha/beta	P42224	0	0	0	0	4/4	0	0	0	1	0	Cytoplasm, Nucleus	Signal transducer in repsonse to interferons.
439	Syntaxin-binding protein 2	Q15833	0	0	2/2	0	0	0	0	0	1	0	Post-Golgi vesicles	Post-Golgi transport to PM.
440	Trans-Golgi network integral membrane protein 2	O43493	0	0	0	0	2/2	0	0	0	1	0	Trans-Golgi network, PM, Transport vesicle, Membrane	Regulates membrane traffick to and from TGN.
441	Transketolase	P29401	0	0	0	0	2/2	0	0	0	1	0	Cytosol	Pentose phosphate pathway.
442	Transmembrane emp24 domain-containing protein 10	P49755	0	0	0	2/2	0	0	0	0	1	0	ER-Golgi intermediate compartment, Zymogen granule membrane, Melanosome	Vesicular protein trafficking.
443	Transmembrane emp24 domain-containing protein 4	Q7Z7H5	0	0	0	2/2	0	0	0	0	1	0	ER membrane	Involved in endoplasmic reticulum stress response. May play a role in the regulation of heat-shock response and apoptosis (By similarity).
444	Triosephosphate isomerase	P60174	0	0	0	0	3/3	0	0	0	1	0	Cytoplasm	Carbohydrate metabolism. Gluconeogenesis.
445	Vacuolar proton pump subunit H	Q9UI12	3/3	0	0	0	0	0	0	0	1	0	Intracellular compartments, Endosome-Lysosome	Compartment acidification.
446	Vasodilator-stimulated phosphoprotein	P50552	0	0	0	0	2/2	0	0	0	1	0	Cytoplasm	Associates with cytoskeleton, membrane focal adhesions, and lamellipodia. Involved in remodeling of actin cytoskeleton.
447	Vesicular integral-membrane protein VIP36	Q12907	0	0	0	0	3/3	0	0	0	1	0	ER-Golgi intermediate compartment, Golgi	Secretory pathway. Transport and sorting of high mannose glycans.
448	Beta-galactosidase	P16278	0	0	0	0	0	[1]/[1]	[1]/[1]	0	0	2	Lysosome	Carbohydrate degradation.
449	Sialate O-acetylesterase	Q9HAT2	0	0	0	0	0	[1]/[1]	[1]/[1]	0	0	2	Lysosome	Removal of O-acetyl ester groups from sialic acid, N-acetylneuraminic acid.
450	60S ribosomal protein L30	P62888	0	0	0	0	0	2/2	0	0	0	1	Cytoplasm	Protein synthesis.
451	Arylsulfatase B	P15848	0	0	0	0	0	2/2	0	0	0	1	Lysosome	Hydrolyzes chondroitin sulfate and dermatan sulfate.
452	ATP-dependent RNA helicase DDX3X	O00571	0	0	0	0	0	0	2/2	0	0	1	Nucleus, Cytoplasm	ATP-dependent RNA helicase.
453	C-1-tetrahydrofolate synthase, cytoplasmic	P11586	0	0	0	0	0	0	0	2/2	0	1	Cytoplasm	Metabolism. Tetrahydrofolate pathway.
454	C-C motif chemokine 20	P78556	0	0	0	0	0	0	2/2	0	0	1	Monocyte secreted protein	Chemotactic factor that attracts lymphocytes and, slightly, neutrophils, but not monocytes. Possesses antibacterial activity.
455	Cell division control protein 42 homolog	P60953	0	0	0	0	0	0	2/2	0	0	1	PM	Rho family small GTPase. Cellular response regulator. Actin cytoskeleton organization.
456	Complement C3	P01024	0	0	0	0	0	5/4	0	0	0	1	Secreted protein	Complement pathway.
457	COX assembly mitochondrial protein homolog	Q7Z7K0	0	0	0	0	0	2/2	0	0	0	1	Mitochondrion	Required for mitochondrial cytochrome c oxidase (COX) assembly and respiration. May be involved in copper trafficking and distribution to COX and SOD1 (By similarity).
458	Developmentally-regulated GTP-binding protein 1	Q9Y295	0	0	0	0	0	0	2/2	0	0	1	Cytoplasm, Cytoskeleton	May play a role in cell proliferation, differentiation and death.
459	Epithelial cadherin	P12830	0	0	0	0	0	2/2	0	0	0	1	PM, Cell junction	Cell adhesion. Cytoplasmic domain interacts directly with CTNNB1 or JUP to form the PSEN1/cadherin/catenin adhesion complex which connects to the actin skeleton through the actin binding of alpha-catenin.
460	Glucose-6-phosphate isomerase	P06744	0	0	0	0	0	0	0	3/3	0	1	Cytoplasm	Gluconeogenesis. Glycolysis.
461	Guanine nucleotide-binding protein subunit beta-4	Q9HAV0	0	0	0	0	0	0	2/2	0	0	1	Membrane	Modulator or transducer in transmembrane signaling systems.
462	Hsc70-interacting protein	P50502	0	0	0	0	0	0	0	3/3	0	1	Cytoplasm	Stabilizes ADP state of HSC70 that has a high affinity for substrate protein. Through its own chaperone activity, it may contribute to the interaction of HSC70 with various target proteins.
463	Ig alpha-1 chain C region	P01876	0	0	0	0	0	0	0	3/3	0	1	Secreted protein	Immunoglobulin.

464	Leucine-rich repeat flightless-interacting protein 1	Q32MZ4	0	0	0	0	0	0	0	2/2	0	1	Nucleus, Cytoplasm, Cytoskeleton	Transcriptional repressor.
465	Nuclear protein Hcc-1	P82979	0	0	0	0	0	0	3/3	0	0	1	Nucleus	May have nucleic acid binding capability that may participate in transcriptional or translational control of cell growth, metabolism and carcinogenesis.
466	Peroxiredoxin-2	P32119	0	0	0	0	0	0	0	3/2	0	1	Cytoplasm	Redox regulation, detoxification.
467	Peroxiredoxin-5, mitochondrial	P30044	0	0	0	0	0	0	0	2/2	0	1	Mitochondrion, Cytoplasm, Peroxisome	Reduces hydrogen peroxide and alkyl hydroperoxides. Involved in intracellular redox signaling.
468	Polyadenylate-binding protein 4	Q13310	0	0	0	0	0	0	0	2/2	0	1	Cytoplasm	mRNA stability.
469	Putative neutrophil cytosol factor 1B	A6NI72	0	0	0	0	0	3/3	0	0	0	1	Cytoplasm	May be required for activation of the latent NADPH oxidase (necessary for superoxide production) (By similarity).
470	Putative tropomyosin alpha-3 chain-like protein	A6NL28	0	0	0	0	0	0	0	2/2	0	1	Cytoplasm, Cytoskeleton	Binds to actin filaments in muscle and non-muscle cells (By similarity).
471	Ras-related C3 botulinum toxin substrate 2	P15153	0	0	0	0	0	0	2/2	0	0	1	Membrane	Cellular response regulator.
472	Ras-related protein Rap-2b	P61225	0	0	0	0	0	2/2	0	0	0	1	Membrane	Small GTPase mediated signal transduction.
473	Serum amyloid P-component	P02743	0	0	0	0	0	3/3	0	0	0	1	Secreted protein	May scavenge nuclear material released from damaged circulating cells. May also function as a calcium-dependent lectin.
474	Sorting nexin-6	Q9UNH7	0	0	0	0	0	0	0	2/2	0	1	Cytoplasm	Intracellular trafficking.
475	Tropomyosin alpha-4 chain	P67936	0	0	0	0	0	0	0	4/4	0	1	Cytoplasm	Cytoskeleton. Binds actin filaments.
476	U2 small nuclear ribonucleoprotein B''	P08579	0	0	0	0	0	0	2/2	0	0	1	Nucleus	Pre-mRNA splicing.

The number of distinct proteolytic peptides (in some cases in parenthesis the number of observed redundant peptide sequences) is shown for protein observed in each experiment with multiple peptide assignments per protein
"[1]": protein identified in this preparation by a single peptide assignment

* Single peptide assignments that map to more than one protein sequence:
Protein #25. Ras-related protein Rab-11B (Q15907): single peptide assignments indicated as [1] could possibly also be assigned to:
RB11A_HUMAN Ras-related protein Rab-11A (Rab-11) (P62491)

Protein #48. ADP-ribosylation factor-like protein 8B (Q9NVJ2): single peptide assignments indicated as [1] could possibly also be assigned to:
ARL8A_HUMAN ADP-ribosylation factor-like protein 8A (Q96BM9)

Protein #65. Interferon-induced transmembrane protein 3 (Q01628): single peptide assignments indicated as [1] could possibly also be:
IFM1_HUMAN Interferon-induced transmembrane protein 1 (P13164) or
IFM2_HUMAN Interferon-induced transmembrane protein 2 (Q01629)

Protein #102. Ras-related protein Rap-1b (P61224): single peptide assignments indicated as [1] could possibly also be assigned to:
RAP1A_HUMAN Ras-related protein Rap-1A precursor (P62834)

Protein #112. Galectin-9B (Q3B8N2): single peptide assignments indicated as [1] could possibly also be assigned to:
LEG9C_HUMAN Galectin-9C (Galectin-9-like protein B) (Q6DKI2)

Protein #177. Ras-related protein Ral-B (P11234): single peptide assignments indicated as [1] could possibly also be assigned to:
RALA_HUMAN Ras-related protein Ral-A precursor (P11233)

Protein #218. Stathmin (P16949): single peptide assignments indicated as [1] could possibly also be assigned to:
STMN2_HUMAN Stathmin-2 (Q93045)

(*) For correlation of spectral counts to the relative protein concentration see Liu et al. [Liu, H., Sadygov, R. G., and Yates, J. R., III (2004) Anal. Chem. 76, 4193–4201].
** Proteins identified exclusively by single peptide assignments in each of the phagosomal preparations are indicated in blue font
Except where indicated by referenced citation, "Reported location" and "Physiological function" are abstracted from the Swiss-Prot database.

REFERENCES

Arnold, H., and Pette, D. (1970) Binding of aldolase and triosephosphate dehydrogenase to F-actin and modification of catalytic properties of aldolase. *Eur J Biochem* **15**, 360-366

Bae, T. J., Kim, M. S., Kim, J. W., Kim, B. W., Choo, H. J., Lee, J. W., Kim, K. B., Lee, C. S., Kim, J. H., Chang, S. Y., Kang, C. Y., Lee, S. W., and Ko, Y. G. (2004) Lipid raft proteome reveals ATP synthase complex in the cell surface. *Proteomics* **4**, 3536-3548

Baranova, I. N., Kurlander, R., Bocharov, A. V., Vishnyakova, T. G., Chen, Z., Remaley, A. T., Csako, G., Patterson, A. P., and Eggerman, T. L. (2008) Role of human CD36 in bacterial recognition, phagocytosis, and pathogen-induced JNK-mediated signaling. *J Immunol* **181**, 7147-7156

Brudzynski, K., Martinez, V., and Gupta, R. S. (1992) Immunocytochemical localization of heat-shock protein 60-related protein in beta-cell secretory granules and its altered distribution in non-obese diabetic mice. *Diabetologia* **35**, 316-324

Brudzynski, K., Martinez, V., and Gupta, R. S. (1992) Secretory granule autoantigen in insulin-dependent diabetes mellitus is related to 62 kDa heat-shock protein (hsp60). *J Autoimmun* **5**, 453-463

Buettner, R., Papoutsoglou, G., Scemes, E., Spray, D. C., and Dermietzel, R. (2000) Evidence for secretory pathway localization of a voltage-dependent anion channel isoform. *Proc Natl Acad Sci U S A* **97**, 3201-

Cechetto, J. D., Soltys, B. J., and Gupta, R. S. (2000) Localization of mitochondrial 60-kD heat shock chaperonin protein (Hsp60) in pituitary growth hormone secretory granules and pancreatic zymogen granules. *J Histochem Cytochem* **48**, 45-56

Cocucci, E., Racchetti, G., Rupnik, M., and Meldolesi, J. (2008) The regulated exocytosis of enlargeosomes is mediated by a SNARE machinery that includes VAMP4. *J Cell Sci* **121**, 2983-2991

Conrads, T. P., Tocci, G. M., Hood, B. L., Zhang, C. O., Guo, L., Koch, K. R., Michejda, C. J., Veenstra, T. D., and Keay, S. K. (2006) CKAP4/p63 is a receptor for the frizzled-8 protein-related antiproliferative factor from interstitial cystitis patients. *J Biol Chem* **281**, 37836-37843

Das, S., Laxminarayana, S. V., Chandra, N., Ravi, V., and Desai, A. (2008) Heat shock protein 70 on Neuro2a cells is a putative receptor for Japanese encephalitis virus. *Virology*

Furuhashi, M., Fucho, R., Gorgun, C. Z., Tuncman, G., Cao, H., and Hotamisligil, G. S. (2008) Adipocyte/macrophage fatty acid-binding proteins contribute to metabolic deterioration through actions in both macrophages and adipocytes in mice. *J Clin Invest* **118**, 2640-2650

Garrett, S. C., Varney, K. M., Weber, D. J., and Bresnick, A. R. (2006) S100A4, a mediator of metastasis. **181**, 7147-7156

Haglund, K., and Dikic, I. (2005) Ubiquitylation and cell signaling. *EMBO J* **24**, 3353-3359

Huang, Y. W., Yan, M., Collins, R. F., Diciccio, J. E., Grinstein, S., and Trimble, W. S. (2008) Mammalian septins are required for phagosome formation. *Mol Biol Cell* **19**, 1717-1726

Isola, L. M., Zhou, S. L., Kiang, C. L., Stump, D. D., Bradbury, M. W., and Berk, P. D. (1995) 3T3 fibroblasts transfected with a cDNA for mitochondrial aspartate aminotransferase express plasma membrane fatty acid-binding protein and saturable fatty acid uptake. *Proc Natl Acad Sci U S A* **92**, 9866-9870

Kindzelskii, A. L., Ueki, T., Michibata, H., Chaiworapongsa, T., Romero, R., and Petty, H. R. (2004) 6-phosphogluconate dehydrogenase and glucose-6-phosphate dehydrogenase form a supramolecular complex in human neutrophils that undergoes retrograde trafficking during pregnancy. *J Immunol* **172**, 6373-6381

Kirchhof, M. G., Chau, L. A., Lemke, C. D., Vardhana, S., Darlington, P. J., Marquez, M. E., Taylor, R., Rizkalla, K., Blanca, I., Dustin, M. L., and Madrenas, J. (2008) Modulation of T cell activation by stomatin-like protein 2. *J Immunol* **181**, 1927-1936

Lee, T. H., Streb, J. W., Georger, M. A., and Miano, J. M. (2006) Tissue expression of the novel serine carboxypeptidase Scpep1. *J Histochem Cytochem* **54**, 701-711

Liu, L., Yang, C., Yuan, J., Chen, X., Xu, J., Wei, Y., Yang, J., Lin, G., and Yu, L. (2005) RPK118, a PX domain-containing protein, interacts with peroxiredoxin-3 through pseudo-kinase domains. *Mol Cells* **19**, 39-

Mishra, S., Murphy, L. C., and Murphy, L. J. (2006) The Prohibitins: emerging roles in diverse functions. *J Cell Mol Med* **10**, 353-363

Nelson, J., McFerran, N. V., Pivato, G., Chambers, E., Doherty, C., Steele, D., and Timson, D. J. (2008) The 67 kDa laminin receptor: structure, function and role in disease. *Biosci Rep* **28**, 33-48

Park, M., Lin, L., Thomas, S., Braymer, H. D., Smith, P. M., Harrison, D. H., and York, D. A. (2004) The F1-ATPase beta-subunit is the putative enterostatin receptor *Peptides* **25**, 2127-2133

Sadacharan, S. K., Cavanagh, A. C., and Gupta, R. S. (2001) Immunoelectron microscopy provides evidence for the presence of mitochondrial heat shock 10-kDa protein (chaperonin 10) in red blood cells and a variety of secretory granules. *Histochem Cell Biol* **116**, 507-517

Schindler, R., Weichselsdorfer, E., Wagner, O., and Bereiter-Hahn, J. (2001) Aldolase-localization in cultured cells: cell-type and substrate-specific regulation of cytoskeletal associations. *Biochem Cell Biol* **79**, 719-

Shakibaei, M., Zimmermann, B., and Scheller, M. (1993) Endocytosis of integrin alpha 5 beta 1 (fibronectin receptor) of mouse peritoneal macrophages in vitro: an immunoelectron microscopic study. *J Struct Biol* **111**, 180-189

Sirover, M. A. (1999) New insights into an old protein: the functional diversity of mammalian glyceraldehyde-3-phosphate dehydrogenase. *Biochim Biophys Acta* **1432**, 159-184

van der Goot, F. G., and Gruenberg, J. (2006) Intra-endosomal membrane traffic. *Trends Cell Biol* **16**, 514-521

Zhao, X. Q., Naka, M., Muneyuki, M., and Tanaka, T. (2000) Ca(2+)-dependent inhibition of actin-activated myosin ATPase activity by S100C (S100A11), a novel member of the S100 protein family. *Biochem Biophys Res Commun* **267**, 77-79

Zhou, S. L., Stump, D., Kiang, C. L., Isola, L. M., and Berk, P. D. (1995) Mitochondrial aspartate aminotransferase expressed on the surface of 3T3-L1 adipocytes mediates saturable fatty acid uptake *Proc Soc Exp Biol Med* **208**, 263-270

Supplemental Table 2. Proteins Identified by HPLC-MS/MS separated on a 1-D SDS PAGE Gel of BCG phagosome from Mouse J774 Macrophage, 1-day post-infection.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest Band	# gel bands found
P05555	3%	122	3	128541	6.9	P05555|ITAM_MOUSE Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2												1	1
						252	261	543.73	1085.45	1085.63	-0.18	0	45	0.0019876	K.ILVVITDGEK.F		19.57		
						416	425	520.24	1038.46	1038.62	-0.15	0	43	0.0023791	R.VQSLVLGAPR.Y		19.13		
						634	644	654.74	1307.46	1307.65	-0.19	0	35	0.0170556	R.SVFACQEQVLK.N		19.36		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest Band	# gel bands found
P08113	4%	143	3	92703	4.7	P08113|ENPL_MOUSE Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2												2	1
						76	84	541.21	1080.4	1080.54	-0.13	0	52	0.0003168	K.FAFQAEVNR.M		19.34		
						103	114	638.24	1274.46	1274.64	-0.17	0	47	0.0009991	R.ELISNASDALDK.I		19.2		
						169	177	491.69	981.36	981.48	-0.12	0	45	0.0013053	K.SGTSEFLNK.M		14.49		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest Band	# gel bands found
P26041	7%	225	4	67839	6.2	P26041|MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3												3	2
						144	151	405.62	809.23	809.39	-0.16	0	34	0.0110695	K.SGYLAGDK.L		12.95		
						413	427	847.3	1692.58	1692.8	-0.22	0	36	0.0108905	K.TQEQLASEMAELTAR.I	Oxidation (M)	18.95		
						428	435	482.19	962.37	962.49	-0.11	0	39	0.0072	R.ISQLEMAR.K	Oxidation (M)	12.84		
						449	458	603.69	1205.37	1205.56	-0.19	0	53	0.0002538	K.AQMVQEDLEK.T	Oxidation (M)	13.13		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest Band	# gel bands found
P20029	5%	204	3	72492	5.1	P20029|GRP78_MOUSE 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3												3	2
						51	61	614.73	1227.45	1227.62	-0.17	0	69	6.65E-06	R.VEIIANDQGNR.I		13.92		
						83	97	839.31	1676.6	1676.8	-0.2	0	42	0.002846	K.NQLTSNPENTVFDAK.R		19.37		
						525	533	537.71	1073.41	1073.55	-0.14	0	61	4.50E-05	K.ITITNDQNR.L		12.9		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest Band	# gel bands found
P10126	4%	109	2	50424	9.1	P10126|EF1A1_MOUSE Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3												5	1
						256	266	513.25	1024.48	1024.6	-0.13	0	50	0.0005008	K.IGGIGTVPVGR.V		18.56		
						431	439	457.7	913.38	913.56	-0.18	0	59	8.00E-05	R.QTVAVGVIK.A		14.91		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest Band	# gel bands found
P60710	10%	160	3	42052	5.3	P60710|ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1												6	1
						19	28	488.66	975.31	975.44	-0.13	0	73	2.83E-06	K.AGFAGDDAPR.A		13.14		
						96	113	651.94	1952.8	1953.06	-0.26	0	41	0.003268	R.VAPEEHPVLLTEAPLNPK.A		19.34		
						316	326	589.19	1176.37	1176.61	-0.24	0	46	0.0011395	K.EITALAPSTMK.I	Oxidation (M)	14.53		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest Band	# gel bands found
P08752	9%	185	3	41015	5.3	P08752|GNAI2_MOUSE Guanine nucleotide-binding protein G(i), alpha-2 subunit OS=Mus musculus GN=Gnai2 PE=1 SV=4												7	2
						36	46	529.24	1056.46	1056.62	-0.16	0	48	0.0010277	K.LLLLGAGESGK.S		19.72		
						87	100	796.27	1590.53	1590.75	-0.22	0	66	1.22E-05	K.AMGNLQIDFADPQR.A	Oxidation (M)	19.76		
						199	206	463.14	924.27	924.41	-0.14	0	37	0.0055751	K.MFDVGGQR.S	Oxidation (M)	13.59		

***Footnotes to Supplemental Table 2:**

Data sets were searched with the Mascot search engine (see Perkins et al. (1999) *Electrophoresis* **20**, 3551-3567).
Detailed are the SwissProt accession number, the number of distinct proteolytic peptides and the sequence coverage of the protein (%).
Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.
Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (Strongest Band in which the protein was identified, and the total # of gel bands in which the protein was identified.)

Supplemental Table 3. Proteins Identified by HPLC-MS/MS separated on a 2-D SDS PAGE gel of BCG phagosome isolated from mouse J774 macrophages 1 day post-infection.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 2D-SDS PAGE gel.

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P08113	2%	155	2	92703	4.7	P08113|ENPL_MOUSE Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2												1
						169	177	491.69	981.36	981.48	-0.12	0	52	0.0002539	K.SGTSEFLNK.M		19.89	
						725	733	497.2	992.38	992.52	-0.14	0	40	0.0058666	R.SGYLLPDTK.A		23.92	
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P35564	5%	143	3	67635	4.5	P35564|CALX_MOUSE Calnexin OS=Mus musculus GN=Canx PE=1 SV=1												2
						49	58	493.67	985.33	985.47	-0.14	0	57	0.0001159	K.SDASTPPSPK.V		14.73	
						172	183	468.49	1402.46	1402.67	-0.22	0	55	0.0001681	K.TAELSLDQFHDK.T		23.8	
						518	526	485.67	969.32	969.48	-0.15	0	35	0.0138969	K.TDAPQPDVK.D		15.28	
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P31996	6%	74	2	35309	9.1	P31996|CD68_MOUSE Macrosialin OS=Mus musculus GN=Cd68 PE=2 SV=1												2
						150	158	508.71	1015.41	1015.58	-0.17	0	38	0.0105789	R.ILYPIQGGR.K		23.55	
						269	277	492.2	982.39	982.54	-0.16	0	36	0.0121194	R.LQAAQLPDK.G		17.39	
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P26041	5%	137	3	67839	6.2	P26041|MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3												3
						401	408	444.17	886.33	886.49	-0.16	0	41	0.0062448	K.EALLQASR.D		18.61	
						428	435	482.14	962.26	962.49	-0.22	0	50	0.0002921	R.ISQLEMAR.K	Oxidation (M)	16.32	
						449	458	603.66	1205.3	1205.56	-0.26	0	46	0.0005636	K.AQMVQEDLEK.T	Oxidation (M)	16.82	
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P20029	15%	580	10	72492	5.1	P20029|GRP78_MOUSE 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3												4
						51	61	614.7	1227.38	1227.62	-0.24	0	70	4.34E-06	R.VEIIANDQGNR.I		18.36	
						83	97	839.26	1676.51	1676.8	-0.29	0	76	1.05E-06	K.NQLTSNPENTVFDAK.R		24.06	
						187	198	617.2	1232.39	1232.62	-0.22	0	66	1.36E-05	K.DAGTIAGLNVMR.I	Oxidation (M)	23.98	
						346	353	459.8	917.59	917.47	0.11	0	42	0.0038346	K.VLEDSDLK.K		19.16	
						346	354	523.69	1045.37	1045.57	-0.19	1	48	0.0009637	K.VLEDSDLKK.S		16	
						354	368	530.19	1587.54	1587.85	-0.31	1	40	0.0058173	K.KSDIDEIVLVGGSTR.I		24.75	
						372	377	364.67	727.32	727.46	-0.14	0	37	0.0104021	K.IQQLVK.E		16.77	
						525	533	537.69	1073.37	1073.55	-0.17	0	63	3.28E-05	K.ITITNDQNR.L		16.39	
						534	541	493.8	985.59	985.51	0.08	0	40	0.0065388	R.LTPEEIER.M		21.11	
						623	634	699.27	1396.53	1396.78	-0.25	0	38	0.0083054	K.ELEEIVQPIISK.L		25.75	
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P63017	14%	542	9	71055	5.4	P63017|HSP7C_MOUSE Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1												5
						26	36	614.7	1227.39	1227.62	-0.23	0	62	3.07E-05	K.VEIIANDQGNR.T		18.4	
						57	71	833.23	1664.45	1664.78	-0.33	0	84	1.21E-07	K.NQVAMNPTNTVFDAK.R	Oxidation (M)	23.1	
						129	137	497.2	992.39	992.52	-0.13	0	38	0.0095933	K.EIAEAYLGK.T		23.3	
						160	171	600.22	1198.43	1198.67	-0.23	0	41	0.0050851	K.DAGTIAGLNVLR.I		25.71	
						312	319	429.65	857.28	857.45	-0.17	0	42	0.0030528	R.GTLDPVEK.A		17.16	
						349	357	541.2	1080.38	1080.56	-0.18	0	57	0.0001023	K.LLQDFFNGK.E		25.95	
						459	469	599.22	1196.42	1196.66	-0.23	0	35	0.0158424	K.FELTGIPPAPR.G		25	
						501	507	402.64	803.27	803.44	-0.17	0	39	0.0079294	K.ITITNDK.G		16.03	
						510	517	495.17	988.33	988.52	-0.19	1	53	0.0003001	R.LSKEDIER.M		15.8	
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P50516	7%	186	4	68625	5.4	P50516|VATA_MOUSE Vacuolar ATP synthase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2												5
						121	129	451.66	901.31	901.5	-0.18	0	50	0.0006435	R.GVNVSALSR.D		20.72	
						257	265	481.69	961.36	961.54	-0.18	0	43	0.0029643	K.TVISQSLSK.Y		18.67	
						281	289	525.65	1049.28	1049.48	-0.2	0	48	0.0004702	R.GNEMSEVLR.D	Oxidation (M)	16.42	
						309	323	766.25	1530.49	1530.78	-0.3	0	45	0.0015725	R.TALVANTSNMPVAAR.E	Oxidation (M)	17.95	
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P09103	15%	461	8	57507	4.8	P09103|PDIA1_MOUSE Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1												6
						72	80	501.69	1001.36	1001.55	-0.19	1	49	0.0008361	K.LKAEGSEIR.L		15.02	
						198	209	475.51	1423.5	1423.77	-0.28	1	35	0.0175043	K.YQLDKDGVVLFK.K		24.48	
						203	209	389.16	776.3	776.44	-0.14	0	55	0.0002102	K.DGVVLFK.K		24.56	

						216	224	526.35	1050.69	1050.5	0.19	0	51	0.0004	R.NNFEGEITK.E		20.15	
						233	249	655.56	1963.67	1964.04	-0.37	0	45	0.0012741	K.HNQLPLVIEFTEQTAPK.I		25.77	
						303	310	483.69	965.37	965.56	-0.19	0	45	0.0015807	R.ILEFFGLK.K		27.09	
						319	328	611.71	1221.41	1221.62	-0.2	0	52	0.0003243	R.LITLEEEMTK.Y	Oxidation (M)	22.89	
						427	438	655.3	1308.59	1308.59	0	0	88	8.11E-08	K.MDSTANEVEAVK.V	Oxidation (M)	17.01	

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P14211	12%	289	6	48136	4.3	P14211|CALR_MOUSE Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1												7
						49	55	369.3	736.59	736.41	0.17	0	52	0.0001036	K.FVLSSGK.F		18.47	
						65	73	488.16	974.3	974.48	-0.18	0	35	0.01766	K.GLQTSQDAR.F		14.76	
						74	80	400.16	798.3	798.43	-0.13	0	44	0.0017505	R.FYALSAK.F		22.32	
						88	98	610.26	1218.51	1218.7	-0.19	0	49	0.0007019	K.GQTLVVQFTVK.H		24.98	
						112	120	502.69	1003.36	1003.53	-0.18	0	44	0.0025679	K.LFPSGLDQK.D		23.54	
						279	286	496.65	991.29	991.46	-0.18	0	35	0.0116452	R.QIDNPDYK.G		15.78	

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P60710	14%	246	5	42052	5.3	P60710|ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1												8
						19	28	488.64	975.26	975.44	-0.18	0	84	1.35E-07	K.AGFAGDDAPR.A		17.22	
						184	191	507.64	1013.27	1013.47	-0.2	0	30	0.0195421	R.DLTDYLMK.I	Oxidation (M)	25.38	
						285	290	389.11	776.2	776.35	-0.15	0	47	0.0005796	K.CDVDIR.K		16.91	
						316	326	589.3	1176.59	1176.61	-0.02	0	49	0.0006773	K.EITALAPSTMK.I	Oxidation (M)	20.75	
						329	335	398.17	794.33	794.47	-0.13	0	35	0.0139125	K.IIAPPER.K		17.17	

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Gel Spot
P60710	19%	346	7	42052	5.3	P60710|ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1												9
						19	28	488.63	975.25	975.44	-0.19	0	73	1.38E-06	K.AGFAGDDAPR.A		17.13	
						96	113	651.9	1952.69	1953.06	-0.37	0	42	0.0029628	R.VAPEEHPVLLTEAPLNPK.A		24.52	
						184	191	507.65	1013.28	1013.47	-0.2	0	42	0.0014487	R.DLTDYLMK.I	Oxidation (M)	25.48	
						197	206	566.66	1131.31	1131.52	-0.21	0	54	0.0001484	R.GYSFTTTAER.E		22.91	
						285	290	389.11	776.21	776.35	-0.14	0	44	0.0013253	K.CDVDIR.K		16.82	
						316	326	589.3	1176.59	1176.61	-0.02	0	51	0.0005009	K.EITALAPSTMK.I	Oxidation (M)	20.97	
						329	335	398.16	794.3	794.47	-0.16	0	41	0.0039222	K.IIAPPER.K		17.17	

***Footnotes to Supplemental Table 3:**

Data sets were searched with the Mascot search engine (see Perkins et al. (1999)*Electrophoresis* **20**, 3551-3567).
Detailed are the SwissProt accession number, the number of distinct proteolytic peptides, and the sequence coverage of the protein (%).
Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.

Supplemental Table 4. Proteins identified by HPLC-MS/MS in 3-hour BCG infected human THP-1 phagosome preparation.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1.

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13473	6%	150	3	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												2	4
						145	152	494.29	986.57	986.55	0.01	0	57	0.0001593	R.IPLNDLFR.C		22.08		
						153	161	526.28	1050.54	1050.5	0.03	0	60	7.18E-05	R.CNSLSTLEK.N		15.92		
						281	289	551.31	1100.61	1100.59	0.02	0	33	0.0431522	K.YLDFVFAVK.N		23.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92542	3%	85	2	79103	5.7	Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2												2	2
						315	323	485.29	968.56	968.53	0.03	0	32	0.0436944	K.APDVTTLPR.N		18.72		
						486	496	543.33	1084.64	1084.62	0.01	0	53	0.0004197	K.ALADVATVLGR.A		21.61		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08238	8%	232	5	83554	5	P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4												3	1
						42	53	638.33	1274.64	1274.64	0	0	38	0.0118205	R.ELISNASDALDK.I		20.26		
						73	82	597.84	1193.67	1193.64	0.03	0	38	0.0110154	K.IDIIPNPQER.T		20.82		
						96	107	621.85	1241.69	1241.7	-0.01	0	73	3.94E-06	K.ADLINNLGTIAK.S		21.43		
						482	491	580.8	1159.59	1159.58	0.01	0	36	0.0205253	K.SIYYITGESK.E		20.34		
						492	502	625.31	1248.61	1248.61	0	0	47	0.0014854	K.EQVANSAFVER.V		17.61		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	7%	239	5	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												3	2
						156	165	545.29	1088.57	1088.55	0.02	0	47	0.0015904	R.ALNEITESGR.I		15.46		
						166	174	485.27	968.52	968.5	0.02	0	44	0.0029677	R.IGFGSFVDK.T		21.47		
						275	285	563.82	1125.63	1125.61	0.01	0	56	0.000175	K.LGAILTPNDGR.C		20.04		
						544	554	582.79	1163.57	1163.51	0.05	0	44	0.0027135	R.YNGQVCGGPGR.G		13.32		
						578	586	524.26	1046.5	1046.48	0.02	0	48	0.0013416	R.TTEGCLNPR.R		13.53		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	5%	157	4	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												3	1
						76	84	541.34	1080.66	1080.54	0.12	0	45	0.0020299	K.FAFQAEVNR.M		20.6		
						103	114	638.33	1274.64	1274.64	0	0	38	0.0118205	R.ELISNASDALDK.I		20.26		
						548	557	575.79	1149.58	1149.53	0.05	0	38	0.009999	K.EAESSPFVER.L		17.71		
						725	733	497.27	992.52	992.52	0.01	0	38	0.0107979	R.SGYLLPDTK.A		20.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	24%	675	13 (14)	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												4	6
						78	92	584.96	1751.85	1751.85	0	1	54	0.0002627	R.GETPRVEEVGPYTYR.E		19.91		
						83	92	606.81	1211.61	1211.58	0.03	0	59	7.77E-05	R.VEEVGPYTYR.E		19.87		
						116	121	392.7	783.39	783.39	0	0	38	0.0090756	K.AYVFER.D		19.22		
						116	129	537.6	1609.78	1609.77	0.01	1	38	0.0108273	K.AYVFERDQSVGDPK.I		19.35		
						154	161	481.77	961.52	961.52	0.01	0	44	0.0035188	R.EIIEAMLK.A	Oxidation (M)	19.74		
						228	234	423.23	844.45	844.44	0	0	45	0.0034974	K.IVEWNGK.T		17.68		
						235	244	632.81	1263.61	1263.61	0	0	55	0.000207	K.TSLDWWITDK.C		22.71		
						263	275	823.89	1645.76	1645.74	0.01	0	38	0.0111444	K.DEVLYVFPSDFCR.S		23.03		
						331	348	703.67	2107.98	2107.98	0	0	50	0.0005306	K.NGAPIIMSFPHFYQADER.F	Oxidation (M)	21.57		
						391	402	469.91	1406.72	1406.7	0.02	1	50	0.0006465	K.KLDDFVETGDIR.T		20.69		
						392	402	640.32	1278.63	1278.61	0.02	0	66	1.67E-05	K.LDDFVETGDIR.T		20.91		
						460	472	676.75	1351.49	1351.53	-0.04	0	44	0.0025322	K.GQGSMDEGTADER.A		13.2		
						460	472	684.78	1367.55	1367.53	0.03	0	64	2.62E-05	K.GQGSMDEGTADER.A	Oxidation (M)	12.54		
						460	477	640.31	1917.91	1917.89	0.03	1	76	1.39E-06	K.GQGSMDEGTADERAPLIR.T	Oxidation (M)	16.28		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38646	21%	794	12	73920	5.9	P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2												5	1
						77	85	479.75	957.49	957.49	0	0	60	8.63E-05	K.VLENAEGAR.T		13.31		
						86	99	725.87	1449.72	1449.71	0.01	0	74	2.72E-06	R.TTPSVVAFTADGER.L		20.67		
						108	121	784.88	1567.75	1567.76	-0.01	0	87	1.41E-07	R.QAVTNPNNTFYATK.R		18.98		
						108	122	575.62	1723.85	1723.86	-0.01	1	49	0.000829	R.QAVTNPNNTFYATKR.L		15.97		
						174	187	536.91	1607.72	1607.76	-0.04	1	50	0.0006465	K.MKETAENYLGHTAK.N	Oxidation (M)	13.87		
						188	202	847.93	1693.85	1693.84	0.01	0	60	6.65E-05	K.NAVITVPAYFNDSQR.Q		21.58		
						207	218	621.84	1241.67	1241.67	0	0	81	6.04E-07	K.DAGQISGLNVLR.V		21.32		
						219	234	823.44	1644.87	1644.87	0	0	81	5.17E-07	R.VINEPTAAALAYGLDK.S		21.63		
						293	307	569.61	1705.81	1705.83	-0.02	1	39	0.0074801	R.ETGVDLTKDNMALQR.V	Oxidation (M)	19.11		
						349	360	681.3	1360.59	1360.74	-0.15	0	53	0.0003801	R.AQFEGIVTDLIR.R		22.93		
						395	405	645.85	1289.69	1289.67	0.02	0	72	4.03E-06	K.VQQTVQDLFGR.A		21.19		
						635	646	616.33	1230.64	1230.66	-0.01	0	89	9.81E-08	R.QAASSLQQASLK.L		15.02		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15586	16%	427	8	62840	8.6	P15586|GNS_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3												5	2
						126	137	699.89	1397.78	1397.77	0.01	0	36	0.0191088	K.IQEPNTFPAILR.S		21.71		
						138	149	706.8	1411.59	1411.59	0	0	52	0.0004139	R.SMCGYQTFFAGK.Y	Oxidation (M)	21.02		
						247	255	525.28	1048.54	1048.55	0	0	42	0.0046808	K.AFQNVFAPR.N		20.97		
						342	349	528.26	1054.51	1054.53	-0.02	0	45	0.0020994	R.QLYEFDIK.V		21.28		
						389	401	753.89	1505.76	1505.76	0	0	92	4.37E-08	K.TQMDGMSLLPILR.G	2 Oxidation (M)	22.1		
						410	421	676.33	1350.65	1350.64	0.01	0	68	9.96E-06	R.SDVLVEYQGEGR.N		20.15		
						494	502	493.28	984.54	984.55	0	0	40	0.0083771	K.TIDPELLGK.M		20.58		
						507	519	786.83	1571.64	1571.66	-0.01	0	53	0.0004205	R.LMMLQSCSGPTCR.T	2 Oxidation (M)	14.79		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11142	12%	311	6	71082	5.4	P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1												5	1
						26	36	614.81	1227.6	1227.62	-0.02	0	48	0.0014589	K.VEIIANDQGNR.T		15.53		
						37	49	744.36	1486.71	1486.69	0.02	0	47	0.0014842	R.TTPSYVAFTDTER.L		20.8		
						57	71	833.4	1664.78	1664.78	0	0	76	1.72E-06	K.NQVAMNPTNTVFDAK.R	Oxidation (M)	19.93		
						103	112	394.21	1179.6	1179.61	-0.01	1	32	0.0442088	K.VQVEYKGETK.S		13.4		
						160	171	600.34	1198.66	1198.67	0	0	70	8.52E-06	K.DAGTIAGLNVLR.I		21.76		
						221	236	564.58	1690.72	1690.72	0	0	40	0.0063713	K.STAGDTHLGGEDFDNR.M		17.01		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	8%	246	5	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												5	1
						50	60	614.81	1227.6	1227.62	-0.02	0	48	0.0014589	R.VEIIANDQGNR.I		15.53		
						82	96	839.4	1676.78	1676.8	-0.02	0	73	3.40E-06	K.NQLTSNPENTVFDAK.R		20.45		
						186	197	617.32	1232.62	1232.62	0	0	46	0.0016972	K.DAGTIAGLNVMR.I	Oxidation (M)	20.41		
						345	352	459.74	917.47	917.47	0	0	45	0.0029008	K.VLEDSDLK.K		15.4		
						524	532	537.77	1073.53	1073.55	-0.01	0	35	0.0247056	K.ITITNDQNR.L		14.05		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40939	8%	262	6	83688	9.2	P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2												5	1
						520	531	559.8	1117.59	1117.6	-0.01	0	58	0.0001337	K.DTSASAVAVGLK.Q		19.76		
						541	549	507.25	1012.49	1012.46	0.02	0	41	0.0057684	K.DGPGFYTTR.C		19.37		
						561	569	499.79	997.56	997.54	0.01	0	44	0.0029887	R.ILQEGVDPK.K		14.75		
						611	625	797.41	1592.81	1592.79	0.02	0	38	0.0122168	R.FGGGNPELLTQMVSK.G	Oxidation (M)	20.63		
						635	644	602.32	1202.62	1202.6	0.02	0	35	0.0266288	K.GFYIYQEGVK.R		21.06		
						720	728	520.78	1039.54	1039.53	0	0	49	0.000881	R.FVDLYGAQK.I		20.37		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08962	8%	106	2	26474	8.1	P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2												5	12
						111	120	637.29	1272.56	1272.56	0	0	72	4.87E-06	K.VMSEFNNNFR.Q	Oxidation (M)	19.59		
						121	128	527.2	1052.39	1052.46	-0.07	0	34	0.0242779	R.QQMENYPK.N	Oxidation (M)	13.1		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38606	5%	159	3	68660	5.3	P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2												5	3
						121	129	451.75	901.49	901.5	-0.01	0	42	0.006011	R.GVNVSALSR.D		17.87		
						281	289	525.74	1049.47	1049.48	-0.01	0	37	0.0156175	R.GNEMSEVLR.D	Oxidation (M)	14.13		
						309	323	766.4	1530.78	1530.78	0	0	80	6.51E-07	R.TALVANTSNMPVAAR.E	Oxidation (M)	15.58		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	5%	129	3	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												5	1
						428	435	482.23	962.45	962.49	-0.03	0	43	0.0042405	R.ISQLEMAR.Q	Oxidation (M)	13.92		
						449	458	603.8	1205.59	1205.56	0.03	0	46	0.0018111	K.AQMVQEDLEK.T	Oxidation (M)	14.31		
						569	577	585.76	1169.5	1169.5	0	1	40	0.0061499	K.QRIDEFESM.-	Oxidation (M)	19.02		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q12931	4%	125	3	80345	8.3	Q12931|TRAP1_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3												5	1
						115	126	645.35	1288.68	1288.65	0.03	0	49	0.000963	R.ELISNASDALEK.L		20.23		
						358	368	591.31	1180.6	1180.61	-0.01	0	41	0.005405	R.ELGSSVALYSR.K		20.32		
						693	699	414.76	827.5	827.51	-0.01	0	36	0.0193684	R.LNELLVK.A		20.02		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04062	3%	77	2	60134	7.3	P04062|GLCM_HUMAN Glucosylceramidase OS=Homo sapiens GN=GBA PE=1 SV=3												5	2
						317	324	510.27	1018.53	1018.51	0.01	0	37	0.0166117	R.LLMLDDQR.L	Oxidation (M)	20.06		
						333	342	521.8	1041.58	1041.57	0.01	0	40	0.0084364	K.VVLTDPEAAK.Y		17.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10809	18%	512	9	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												7	2
						97	121	854.07	2559.2	2559.24	-0.04	0	85	1.55E-07	K.LVQDVANNTNEEAGDGTTTATVLAR.S		20.25		
						222	233	695.34	1388.66	1388.7	-0.04	0	44	0.0030869	R.GYISPYFINTSK.G		21.33		
						293	301	456.79	911.57	911.58	-0.01	0	70	5.84E-06	K.VGLQVVAVK.A		20.08		
						302	309	417.2	832.39	832.38	0	0	34	0.0396432	K.APGFGDNR.K		13.93		
						345	352	422.76	843.5	843.51	-0.01	0	41	0.0081928	K.VGEVIVTK.D		14.85		
						345	359	549.63	1645.87	1645.9	-0.03	1	46	0.0019013	K.VGEVIVTKDDAMLLK.G	Oxidation (M)	20.34		
						406	417	617.3	1232.59	1232.59	0	0	75	2.63E-06	K.VGGTSDVEVNEK.K		13.71		
						471	481	401.58	1201.71	1201.71	0	1	59	0.0001083	R.TLKIPAMTIAK.N	Oxidation (M)	18.94		
						482	493	608.33	1214.64	1214.65	-0.01	0	64	3.72E-05	K.NAGVEGSLIVEK.I		19.95		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15289	7%	109	3	54409	5.7	P15289|ARSA_HUMAN Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3												7	1
						85	97	713.34	1424.67	1424.68	-0.01	0	35	0.0227724	R.MGMYPGVLVPSSR.G	2 Oxidation (M)	20.42		
						303	311	470.23	938.45	938.45	0	0	33	0.0274773	K.GTTYEGGVR.E		13.4		
						464	479	815.92	1629.83	1629.85	-0.02	0	41	0.0053385	K.AQLDAAVTFGPSQVAR.G		20.99		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	7%	172	3	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												7	1
						317	326	611.82	1221.63	1221.62	0.01	0	50	0.0006901	R.LITLEEEMTK.Y	Oxidation (M)	19.9		
						327	338	484.56	1450.67	1450.69	-0.03	0	54	0.0002432	K.YKPESEELTAER.I		14.68		
						425	436	655.29	1308.56	1308.59	-0.02	0	68	1.24E-05	K.MDSTANEVEAVK.V	Oxidation (M)	14.59		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31146	6%	81	2	51678	6.3	P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4												7	1
						384	393	513.82	1025.63	1025.61	0.01	0	39	0.0075784	R.DAGPLLISLK.D		22.12		
						417	432	751.82	1501.62	1501.7	-0.08	0	42	0.0046312	R.AAPEASGTPSSDAVSR.L		13.79		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	26%	820	13	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												8	1
						46	58	720.33	1438.65	1438.66	-0.01	0	82	4.34E-07	K.TGTAEMSSILEER.I	Oxidation (M)	19.17		
						59	73	788.4	1574.79	1574.78	0.01	0	98	1.05E-08	R.ILGADTSVDLEETGR.V		20.69		
						74	83	500.78	999.55	999.57	-0.02	0	54	0.0003151	R.VLSIGDGIAR.V		20.43		
						134	149	812.94	1623.87	1623.88	-0.02	0	55	0.000229	R.TGAIVDVPVGEELLGR.V		22.18		
						150	161	586.31	1170.61	1170.62	-0.01	0	90	8.54E-08	R.VVDALGNAIDGK.G		20.3		
						150	167	570.97	1709.89	1709.93	-0.04	1	54	0.0002649	R.VVDALGNAIDGKGPIGSK.T		20.35		
						172	182	374.24	1119.69	1119.71	-0.02	1	59	8.82E-05	R.VGLKAPGIIPR.I		20.04		
						183	194	458.91	1373.71	1373.73	-0.03	1	41	0.0060141	R.ISVREPMQTGIK.A	Oxidation (M)	14.52		
						195	204	513.79	1025.57	1025.59	-0.02	0	54	0.0002539	K.AVDSLVPIGR.G		20.74		
						219	230	658.86	1315.71	1315.73	-0.03	0	77	1.76E-06	K.TSIAIDTIINQK.R		21.26		
						254	261	423.25	844.49	844.5	-0.01	0	47	0.0019398	R.STVAQLVK.R		16.38		
						335	347	518.58	1552.71	1552.73	-0.02	0	33	0.0319685	R.EAYPGDVFYLHSR.L		21.13		
						435	441	446.74	891.47	891.48	-0.02	0	47	0.0016589	K.LELAQYR.E		19.82		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21281	25%	568	10	56807	5.6	P21281|VATB2_HUMAN Vacuolar ATP synthase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3												8	1
						30	37	437.23	872.45	872.47	-0.02	0	48	0.0014662	R.EQALAVSR.N		13.96		
						83	93	545.79	1089.56	1089.57	-0.01	0	72	4.68E-06	R.SGQVLEVSGSK.A		14.65		
						94	108	760.89	1519.76	1519.79	-0.02	0	83	3.95E-07	K.AVVQVFEGTSGIDAK.K		20.91		
						121	130	560.77	1119.52	1119.52	-0.01	0	44	0.0032377	R.TPVSEDMLGR.V	Oxidation (M)	14.74		
						131	141	397.2	1188.59	1188.63	-0.03	0	36	0.0201029	R.VFNGSGKPIDR.G		13.6		
						164	185	814.37	2440.09	2440.16	-0.07	0	44	0.0021521	R.IYPEEMIQTGISAIDGMNSIAR.G	2 Oxidation (M)	22.05		
						322	337	956.97	1911.93	1911.87	0.06	0	44	0.0026051	R.GFPGYMYTDLATIYER.A	Oxidation (M)	22.48		
						387	400	798.97	1595.92	1595.9	0.02	0	39	0.0089158	R.QIYPPINVLPSLSR.L		22.35		
						461	471	654.81	1307.61	1307.63	-0.01	0	46	0.0018394	R.NFIAQGPYENR.T		20.08		
						495	506	719.36	1436.7	1436.73	-0.03	0	83	3.07E-07	R.IPQSTLSEFYPR.D		21.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06576	15%	292	6	56525	5.3	P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3												8	3
						110	121	639.81	1277.61	1277.63	-0.02	0	53	0.0003423	R.TIAMDGTEGLVR.G	Oxidation (M)	19.43		
						144	155	701.35	1400.68	1400.7	-0.02	0	40	0.0079282	R.IMNVIGEPIDER.G	Oxidation (M)	20.39		
						189	198	544.81	1087.6	1087.63	-0.02	0	40	0.0092199	K.VVDLLAPYAK.G		21.57		
						202	212	488.28	974.55	974.55	-0.01	0	55	0.0002825	K.IGLFGGAGVGK.T		21.22		
						282	294	720.38	1438.74	1438.78	-0.05	0	55	0.0002049	R.VALTGLTVAEYFR.D		22.91		
						388	406	994.51	1987.01	1987.03	-0.02	0	50	0.0005802	R.AIAELGIYPAVDPLDSTSR.I		22.52		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UHL4	12%	264	5	54749	5.9	Q9UHL4|DPP2_HUMAN Dipeptidyl-peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=2												8	1
						26	34	508.74	1015.47	1015.47	0	0	39	0.0110548	R.APDPGFQER.F		14.57		
						113	123	596.3	1190.59	1190.6	-0.01	0	51	0.0005441	K.SLPFGAQSTQR.G		19.91		
						204	215	647.3	1292.59	1292.59	0	0	59	9.93E-05	R.DVTADFEGQSPK.C		19.95		
						229	240	699.33	1396.64	1396.7	-0.06	0	54	0.0002658	K.DLFLQGAYDTVR.W		22.26		
						449	462	488.89	1463.64	1463.7	-0.06	0	60	6.01E-05	R.ASHPEDPASVVEAR.K		15.92		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P34897	10%	241	5	56414	8.8	P34897|GLYM_HUMAN Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3												8	1
						201	214	774.91	1547.8	1547.83	-0.03	0	86	1.71E-07	K.TGLIDYNQLALTAR.L		21.87		
						220	230	568.31	1134.61	1134.64	-0.03	0	48	0.001069	R.LIIAGTSAYAR.L		20.22		
						349	356	490.27	978.52	978.54	-0.02	0	38	0.0108776	R.EYSLQVLK.N		20.78		
						360	368	503.24	1004.47	1004.5	-0.03	0	36	0.021457	R.AMADALLER.G	Oxidation (M)	19.13		
						426	434	443.25	884.49	884.51	-0.02	0	33	0.0411395	R.LGAPALTSR.Q		16.47		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O95766	9%	230	4	56286	6.1	O95766|CG028_HUMAN UPF0550 protein C7orf28 OS=Homo sapiens GN=C7orf28A PE=1 SV=1												8	1
						213	221	539.78	1077.55	1077.54	0.01	0	42	0.0049385	R.MEESLNIVK.Y	Oxidation (M)	19.09		
						247	255	549.29	1096.57	1096.59	-0.02	0	43	0.0033952	K.YLTTSLFPR.H		21.65		
						282	295	757.88	1513.75	1513.78	-0.03	0	76	1.49E-06	R.FLTGPLNLNDPDAK.C		21.61		
						448	456	560.32	1118.62	1118.63	-0.02	0	68	1.18E-05	R.ELYVILNQK.N		21.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8IV08	8%	188	4	55127	6	Q8IV08|PLD3_HUMAN Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1												8	4
						150	157	449.77	897.53	897.53	0	0	52	0.0003694	R.QLQTLAPK.G		14.82		
						310	319	542.81	1083.6	1083.6	-0.01	0	47	0.0014244	K.ALLNVVDNAR.S		20.56		
						397	408	658.35	1314.68	1314.69	-0.01	0	52	0.0005311	K.LFVVPADEAQAR.I		20.61		
						458	466	538.81	1075.6	1075.6	0	0	36	0.0172679	R.SQLEAIFLR.D		22		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00367	8%	181	3	61701	7.7	P00367|DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2												8	1
						152	162	621.29	1240.56	1240.58	-0.02	0	59	9.23E-05	R.YSTDVSVDEVK.A		19.26		
						400	420	748.04	2241.1	2241.16	-0.07	1	64	2.06E-05	K.IIAEGANGPTTPEADKIFLER.N		21.09		
						536	545	540.4	1078.79	1078.57	0.22	0	59	6.56E-05	R.TAAYVNAIEK.V		18.02		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UI12	6%	135	3	56417	6.1	Q9UI12|VATH_HUMAN Vacuolar proton pump subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1												8	1
						284	290	402.26	802.5	802.51	0	0	38	0.0146311	R.IILAAFR.N		21.39		
						450	458	510.29	1018.56	1018.58	-0.02	0	52	0.0005962	R.YNALLAVQK.L		20.26		
						470	482	714.33	1426.65	1426.72	-0.07	0	45	0.002091	K.QLQSEQPQTAAAR.S		13.36		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P09622	5%	123	2	54686	7.6	P09622|DLDH_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=1												8	1
						167	177	552.78	1103.54	1103.55	0	0	84	3.23E-07	K.ADGGTQVIDTK.N		13.87		

						405	417	527.92	1580.75	1580.76	-0.01	1	39	0.0083686	K.SEEQLKEEGIEYK.V		17.02		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75955	9%	186	3	47554	7.1	O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3												9	2
						41	51	608.41	1214.8	1214.72	0.07	0	55	0.0002572	R.ISLNTLTLNVK.S		20.99		
						262	274	735.36	1468.71	1468.76	-0.05	0	62	4.71E-05	R.AQQVAVQEQEIAR.R		13.81		
						378	392	698.36	1394.7	1394.71	-0.01	0	73	3.18E-06	K.ITLVSSGSGTMGAAK.V	Oxidation (M)	13.89		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14254	9%	143	3	41830	5.2	Q14254|FLOT2_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=1												9	2
						175	184	562.32	1122.63	1122.56	0.07	0	33	0.0317557	K.SAFSEEVNIK.T		16.44		
						259	269	600.35	1198.68	1198.66	0.03	0	56	0.0002087	K.QVLLAQAEAEK.I		15.11		
						329	341	687.86	1373.7	1373.7	0	0	55	0.0002613	K.VDEIVVLSGDNSK.V		19.21		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31930	8%	133	3	53297	5.9	P31930|QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3												9	1
						112	126	560.96	1679.86	1679.76	0.1	0	47	0.0012356	K.EVESMGAHLNAYSTR.E	Oxidation (M)	13.36		
						379	390	662.3	1322.58	1322.61	-0.03	0	45	0.0022467	R.LCTSATESEVAR.G		13.3		
						433	442	529.78	1057.55	1057.58	-0.03	0	42	0.0065379	R.IAEVDASVVR.E		14.51		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P55084	6%	130	3	51547	9.4	P55084|ECHB_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3												9	1
						53	61	478.77	955.52	955.55	-0.02	0	33	0.0336992	R.NVVVVDGVR.T		14.55		
						230	238	453.25	904.49	904.51	-0.03	0	55	0.0002616	R.LAAAFAVSR.L		15.54		
						239	247	568.78	1135.54	1135.55	-0.01	0	42	0.0045322	R.LEQDEYALR.S		14.68		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36957	5%	95	2	49041	9.1	P36957|ODO2_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=3												9	1
						278	286	508.27	1014.54	1014.52	0.01	0	34	0.0333236	K.LGFMSAFVK.A	Oxidation (M)	20.2		
						334	345	712.81	1423.61	1423.64	-0.03	0	61	5.97E-05	R.NVEAMNFADIER.T	Oxidation (M)	17.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	4%	90	2	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												9	2
						256	266	513.31	1024.6	1024.6	0	0	47	0.0012998	K.IGGIGTVPVGR.V		15.59		
						431	439	457.77	913.52	913.56	-0.04	0	43	0.0035303	R.QTVAVGVIK.A		14.38		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P80723	32%	176	4	22680	4.6	P80723|BASP_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2												10	1
						98	121	766.72	2297.13	2297.13	0	1	33	0.0257004	K.AEPPKAPEQEQAAPGPAAGGEAPK.A		13.88		
						150	163	471.58	1411.73	1411.73	0	1	34	0.0287671	K.KTEAPAAPAAQETK.S		12.69		
						164	184	644.98	1931.91	1931.87	0.03	0	60	6.62E-05	K.SDGAPASDSKPGSSEAAPSSK.E		12.63		
						185	198	693.83	1385.65	1385.67	-0.01	0	49	0.0008146	K.ETPAATEAPSSTPK.A		13.36		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48735	17%	301	7	51333	8.9	P48735|IDHP_HUMAN Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2												10	1
						46	60	570.26	1707.77	1707.78	-0.01	0	40	0.0064747	K.VAKPVVEMDGDEMTR.I	2 Oxidation (M)	13.32		
						113	122	567.26	1132.51	1132.52	-0.01	0	37	0.014259	K.CATITPDEAR.V		14.05		
						181	188	447.73	893.44	893.42	0.02	0	39	0.0075661	K.ATDFVADR.A		15		
						289	299	630.84	1259.66	1259.68	-0.01	0	61	6.39E-05	R.LIDDMVAQVLK.S	Oxidation (M)	21.05		
						341	353	452.56	1354.67	1354.68	-0.01	0	40	0.0064935	K.TIEAEAAHGTVTR.H		13.75		
						385	393	522.27	1042.53	1042.54	-0.01	0	38	0.0120191	K.LDGNQDLIR.F		18.11		
						401	413	713.82	1425.63	1425.65	-0.01	0	45	0.0021614	K.VCVETVESGAMTK.D	Oxidation (M)	15.31		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60709	16%	252	5	42052	5.3	P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1												10	11
						19	28	488.73	975.45	975.44	0.01	0	59	0.000113	K.AGFAGDDAPR.A		14.27		
						197	206	566.8	1131.58	1131.52	0.06	0	33	0.0412456	R.GYSFTTTAER.E		19.04		
						239	254	895.96	1789.9	1789.88	0.01	0	61	5.75E-05	K.SYELPDGQVITIGNER.F		21.87		
						316	326	589.31	1176.6	1176.61	0	0	47	0.0017115	K.EITALAPSTMK.I	Oxidation (M)	16.88		
						360	372	506.24	1515.71	1515.7	0.01	0	53	0.0003305	K.QEYDESGPSIVHR.K		15.54		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49411	11%	290	5	49852	7.3	P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2												10	1
						80	88	408.24	814.46	814.45	0	0	34	0.0385596	K.ILAEGGGAK.F		13.14		
						239	252	771.96	1541.91	1541.85	0.06	0	81	5.05E-07	K.LLDAVDTYIPVPAR.D		21.96		
						316	327	593.32	1184.63	1184.61	0.02	0	78	1.20E-06	R.AEAGDNLGALVR.G		20.43		
						352	361	575.33	1148.65	1148.64	0	0	56	0.0001839	K.VEAQVYILSK.E		20.57		
						406	411	388.25	774.48	774.48	0.01	0	42	0.0065122	K.FNLILR.Q		21.39		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99536	8%	112	2	42122	5.9	Q99536|VAT1_HUMAN Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2												10	1
						256	271	795.9	1589.79	1589.76	0.03	0	62	3.77E-05	K.GVDIVMDPLGGSDTAK.G	Oxidation (M)	20.74		
						282	295	740.41	1478.81	1478.78	0.03	0	49	0.0007636	K.VVTYGMANLLTGPK.R	Oxidation (M)	20.7		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11310	6%	80	2	47015	8.6	P11310|ACADM_HUMAN Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1												10	1
						260	271	610.32	1218.63	1218.62	0.01	0	47	0.0013702	K.ENVLIGDGAGFK.V		20.83		
						280	294	489.28	1464.83	1464.85	-0.03	0	33	0.0347364	K.TRPVVAAGAVGLAQR.A		18.96		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y6N5	6%	166	2	50214	9.2	Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1												10	3
						66	79	735.39	1468.77	1468.75	0.02	0	82	4.85E-07	K.VGAENVAIVEPSER.H		19.82		
						345	358	672.39	1342.76	1342.72	0.04	0	85	2.32E-07	K.TAAAVAAQSGILDR.T		20.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O14773	6%	162	3	61723	6	O14773|TPP1_HUMAN Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2												10	2
						246	259	492.26	1473.75	1473.75	0	0	52	0.0004402	R.LFGGNFAHQASVAR.V		19.87		
						340	346	425.72	849.43	849.43	0	0	44	0.0029614	R.VNTELMK.A	Oxidation (M)	13.1		
						507	520	535.61	1603.81	1603.81	0	0	66	1.74E-05	R.LYQQHGAGLFDVTR.G		20.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P22695	6%	169	2	48584	8.7	P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3												10	1
						232	241	626.32	1250.62	1250.61	0.02	0	59	9.05E-05	K.QVAEQFLNMR.G	Oxidation (M)	20.09		
						360	375	815.94	1629.87	1629.83	0.04	0	110	6.60E-10	K.TIAQGNLSNTDVQAAK.N		16.41		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BTU6	5%	135	3	54388	8.5	Q9BTU6|P4K2A_HUMAN Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1												10	2
						116	123	465.27	928.52	928.5	0.02	0	56	0.000246	R.QAELAIER.C		16.46		
						203	210	477.3	952.59	952.57	0.02	0	47	0.0012929	K.LELNIVPR.T		21.09		
						297	305	552.36	1102.71	1102.68	0.03	0	33	0.047918	R.LVVLDYIIR.N		23.09		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P17050	5%	93	2	47047	5	P17050|NAGAB_HUMAN Alpha-N-acetylgalactosaminidase OS=Homo sapiens GN=NAGA PE=1 SV=2												10	1
						305	315	605.84	1209.66	1209.65	0.01	0	45	0.0019822	K.INQDPLGIQGR.R		20		
						335	344	579.29	1156.56	1156.57	-0.01	0	48	0.0012994	K.ASALVFFSCR.T		22		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P24752	14%	264	5	45456	9	P24752|THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1												11	1
						41	49	487.3	972.58	972.56	0.02	0	35	0.0296821	K.EVVIVSATR.T		17.07		
						67	78	600.36	1198.7	1198.69	0.01	0	80	8.34E-07	K.LGSIAIQGAIEK.A		20.41		
						88	105	947.47	1892.93	1892.87	0.06	0	51	0.0004948	K.EAYMGNVLQGGEGQAPTR.Q	Oxidation (M)	19.37		
						209	221	772.84	1543.67	1543.69	-0.02	0	67	1.47E-05	R.NEQDAYAINSYTR.S		19.84		
						366	373	495.25	988.48	988.49	-0.01	0	37	0.0154078	K.MLEIDPQK.V	Oxidation (M)	16.45		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00505	14%	251	5	47844	9.1	P00505|AATM_HUMAN Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=2												11	1
						108	122	765.91	1529.8	1529.79	0.01	0	43	0.0029888	K.ASAELALGENSEVLK.S		20.63		
						126	139	725.42	1448.82	1448.8	0.02	0	38	0.0106478	R.FVTVQTISGTGALR.I		20.97		
						140	147	446.27	890.52	890.5	0.02	0	73	4.94E-06	R.IGASFLQR.F		20.28		
						171	180	577.77	1153.52	1153.52	0	0	50	0.0006541	R.DAGMQLQGYR.Y	Oxidation (M)	15.73		
						326	337	634.4	1266.78	1266.73	0.05	0	46	0.0015061	R.IAAAILNTPDLR.K		21.02		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21283	13%	238	6	44085	7	P21283|VATC1_HUMAN Vacuolar proton pump subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4												11	1
						29	37	480.77	959.52	959.5	0.01	0	39	0.0115622	K.NNNLAVTSK.F		13.37		
						38	44	423.75	845.48	845.46	0.01	0	51	0.0007999	K.FNIPDLK.V		21.1		
						128	137	551.8	1101.59	1101.57	0.02	0	36	0.0215224	K.GVTQIDNDLK.S		18.44		
						148	155	472.25	942.49	942.49	0	0	47	0.0017348	K.GNLQNLER.K		15.08		
						302	309	474.79	947.56	947.54	0.02	0	33	0.0425155	R.VFVESVLR.Y		20.84		
						374	382	576.31	1150.61	1150.57	0.04	0	33	0.0360602	K.IDCNLLEFK.-		21.58		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O94905	12%	148	3	38044	5.5	O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1												11	1
						61	72	674.9	1347.79	1347.69	0.1	0	45	0.0024829	K.SVQTTLQTDEVK.N		17.34		
						221	232	653.86	1305.7	1305.69	0.01	0	71	5.73E-06	K.VAQVAEITYGQK.V		19.5		
						300	314	815.86	1629.71	1629.7	0.01	0	32	0.0420166	K.DIPNMFMDSAGSVSK.Q	2 Oxidation (M)	20.15		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UJZ1	10%	149	3	38624	6.9	Q9UJZ1|STML2_HUMAN Stomatin-like protein 2 OS=Homo sapiens GN=STOML2 PE=1 SV=1												11	1
						202	211	531.79	1061.56	1061.54	0.02	0	39	0.0117811	R.ATVLESEGTR.E		14.3		
						212	221	509.28	1016.54	1016.51	0.03	0	45	0.0026962	R.ESAINVAEGK.K		15.78		
						322	337	758	1513.99	1513.74	0.25	0	66	1.77E-05	K.APVPGTPDSLSSGSSR.D		17.24		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10319	6%	89	2	40597	5.9	P10319|1B58_HUMAN HLA class I histocompatibility antigen, B-58 alpha chain OS=Homo sapiens GN=HLA-B PE=2 SV=1												11	1
						46	59	815.45	1628.89	1628.82	0.07	0	48	0.0011831	R.FIAVGYVDDTQFVR.F		21.8		
						60	68	483.23	964.45	964.43	0.02	0	42	0.005244	R.FDSDAASPR.T		13.47		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61160	6%	92	2	45017	6.3	P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1												11	1
						54	65	675.82	1349.62	1349.61	0.01	0	53	0.0003347	K.DLMVGDEASELR.S	Oxidation (M)	20.45		
						107	118	685.39	1368.76	1368.73	0.02	0	38	0.0098785	K.ILLTEPPMNPTK.N	Oxidation (M)	19.97		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04075	9%	187	3	39851	8.3	P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2												12	2
						29	42	666.88	1331.74	1331.69	0.04	0	63	4.18E-05	K.GILAADESTGSIAK.R		19.7		
						61	69	522.8	1043.59	1043.56	0.02	0	51	0.0006809	R.QLLLTADDR.V		20.09		
						332	342	566.8	1131.59	1131.57	0.02	0	74	3.05E-06	R.ALANSLACQGK.Y		14.57		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61421	8%	151	3	40759	4.9	P61421|VA0D1_HUMAN Vacuolar proton pump subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1												12	2
						121	128	428.77	855.53	855.51	0.03	0	40	0.0078098	R.SIAELVPK.C		20.43		
						188	195	510.76	1019.5	1019.5	0.01	0	34	0.0348471	K.AYLESFYK.F		20.78		
						276	288	652.85	1303.69	1303.64	0.05	0	77	1.51E-06	K.LLFEGAGSNPGDK.T		20.3		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P04899	7%	112	2	40995	5.3	P04899|GNAI2_HUMAN Guanine nucleotide-binding protein G(i), alpha-2 subunit OS=Homo sapiens GN=GNAI2 PE=1 SV=3												12	2
						36	46	529.33	1056.65	1056.62	0.04	0	71	6.27E-06	K.LLLLGAGESGK.S		20.82		
						87	100	775.88	1549.74	1549.72	0.02	0	41	0.0055328	K.AMGNLQIDFADPSR.A	Oxidation (M)	21		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07355	16%	259	5	38808	7.6	P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2												13	2
						11	28	615.65	1843.94	1843.9	0.04	0	50	0.0006327	K.LSLEGDHSTPPSAYGSVK.A		19.59		
						69	77	556.3	1110.59	1110.55	0.04	0	39	0.0082955	R.QDIAFAYQR.R		20.21		
						105	115	611.82	1221.63	1221.59	0.04	0	72	4.82E-06	K.TPAQYDASELK.A		16.12		
						136	145	622.83	1243.65	1243.62	0.03	0	64	3.35E-05	R.TNQELQEINR.V		15.21		
						170	176	381.24	760.47	760.45	0.01	0	36	0.0249144	K.LMVALAK.G	Oxidation (M)	16.68		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	15%	737	13	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												13	2
						87	98	482.28	1443.81	1443.78	0.03	0	35	0.0201706	R.VTLRPYLTPNDR.G		19.9		
						205	219	545.31	1632.92	1632.86	0.05	2	37	0.0138328	R.KVVATTQMQAADARK.S	Oxidation (M)	12.47		
						206	218	689.36	1376.7	1376.67	0.03	0	94	2.81E-08	K.VVATTQMQAADAR.K	Oxidation (M)	12.99		
						242	252	609.86	1217.7	1217.63	0.07	0	39	0.0093703	K.DLTALSNMLPK.G	Oxidation (M)	21.15		
						293	301	479.29	956.56	956.54	0.02	0	62	4.93E-05	K.QASNGVLIR.I		15.07		
						364	379	862.95	1723.89	1723.83	0.06	0	82	4.05E-07	R.ENSLLFDPLSSSSSNK.E		21.9		
						433	442	627.33	1252.64	1252.61	0.03	0	44	0.0028284	K.DLMVLNDVYR.V	Oxidation (M)	21.37		
						486	497	709.86	1417.71	1417.68	0.03	0	61	6.39E-05	R.MLSSFLSEDVFK.Q	Oxidation (M)	22.33		
						659	673	538.3	1611.89	1611.84	0.05	0	59	8.47E-05	R.AQIINDAFNLASAHK.V		21.06		
						778	793	663.99	1988.95	1988.93	0.03	0	43	0.0030742	K.QWMENPNNNPIHPNLR.S	Oxidation (M)	19.72		
						837	843	472.28	942.55	942.53	0.02	0	32	0.0456773	K.ELWILNR.Y		21.98		
						844	855	734.41	1466.81	1466.78	0.04	0	81	5.18E-07	R.YLSYTLNPDLIR.K		21.68		
						936	943	451.27	900.52	900.49	0.03	0	38	0.0139374	R.ALEQALEK.T		15.29		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P42704	10%	597	12	159003	5.8	P42704|LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3												13	1
						115	128	450.94	1349.81	1349.78	0.03	0	45	0.0025565	R.SGGLGGSHALLLLR.S		20.97		
						129	138	552.31	1102.6	1102.57	0.03	0	36	0.0197934	R.SCGSLLPELK.L		21.01		
						179	187	513.28	1024.55	1024.52	0.03	0	39	0.0078023	K.FSPTDFLAK.M		21.85		
						188	197	609.3	1216.58	1216.55	0.03	0	71	5.74E-06	K.MEEANIQPNR.V	Oxidation (M)	13.34		
						454	463	563.87	1125.74	1125.68	0.06	0	44	0.0025533	K.NVQGIIEILK.G		22.03		
						542	549	446.77	891.53	891.52	0.01	0	42	0.005544	R.SSLLLGFR.R		21.72		
						865	876	458.26	1371.77	1371.76	0.01	1	42	0.0043726	K.LVEKGETDLIQK.A		15.25		
						930	941	702.85	1403.69	1403.67	0.02	0	72	4.49E-06	R.CVANNQVETLEK.L		15.68		
						1129	1139	636.84	1271.66	1271.65	0.02	0	60	7.81E-05	K.TVLDQQQTPSR.L		14.03		
						1164	1176	696.88	1391.75	1391.7	0.06	0	76	1.51E-06	K.MLNGLEDSIGLSK.M	Oxidation (M)	20.88		
						1177	1189	745.94	1489.87	1489.83	0.04	0	39	0.0090244	K.MVFINNIALAQIK.N	Oxidation (M)	21.76		
						1327	1338	438.57	1312.69	1312.65	0.04	1	33	0.0341764	K.SYVSEKDVTSAK.A		13.86		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04406	9%	129	2	36201	8.6	P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3												13	1
						201	215	706.42	1410.83	1410.78	0.04	0	49	0.0007569	R.GALQNIIPASTGAAK.A		20.61		
						235	248	765.92	1529.82	1529.79	0.04	0	80	6.72E-07	R.VPTANVSVVDLTCR.L		20.75		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11279	9%	183	4	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												13	10
						138	146	517.29	1032.57	1032.55	0.03	0	63	4.55E-05	K.TVESITDIR.A		19.85		
						327	337	576.32	1150.63	1150.6	0.04	0	44	0.0026609	R.ALQATVGNSYK.C		16.03		
						349	356	463.27	924.53	924.51	0.03	0	37	0.0116462	K.AFSVNIFK.V		21.54		
						410	417	438.73	875.44	875.41	0.03	0	40	0.0083375	R.SHAGYQTI.-		14.47		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05556	3%	86	2	91714	5.3	P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=1												13	2
						191	202	662.86	1323.71	1323.67	0.03	0	52	0.0004445	K.TVMPYISTTPAK.L	Oxidation (M)	17.68		
						785	794	508.3	1014.58	1014.57	0.01	0	34	0.0337095	K.SAVTTVVNPK.Y		14.55		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40926	40%	713	11	35965	8.9	P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=2												14	3
						27	45	897.06	1792.11	1792.08	0.03	0	68	1.01E-05	K.VAVLGASGGIGQPLSLLLK.N		23.35		
						92	104	669.86	1337.7	1337.71	-0.01	0	38	0.0107128	K.GCDVVVIPAGVPR.K		20.79		
						166	176	617.38	1232.74	1232.71	0.03	0	73	3.99E-06	K.IFGVTTLDIVR.A		22.36		
						177	185	496.79	991.56	991.53	0.03	0	72	5.20E-06	R.ANTFVAELK.G		20.27		
						204	215	685.9	1369.79	1369.76	0.03	0	49	0.0008737	K.TIIPLISQCTPK.V		21.32		
						216	229	780.93	1559.85	1559.79	0.05	0	70	6.30E-06	K.VDFPQDQLTALTGR.I		21.71		
						230	239	537.3	1072.59	1072.58	0.02	0	68	1.56E-05	R.IQEAGTEVVK.A		13.76		
						242	257	735.86	1469.71	1469.69	0.02	0	92	4.47E-08	K.AGAGSATLSMAYAGAR.F	Oxidation (M)	18.8		
						258	269	672.36	1342.71	1342.66	0.05	0	68	1.19E-05	R.FVFSLVDAMNGK.E	Oxidation (M)	21.88		
						270	279	577.29	1152.56	1152.55	0.01	0	60	6.85E-05	K.EGVVECSFVK.S		19.93		
						315	324	566.82	1131.63	1131.58	0.04	0	56	0.0002039	K.MISDAIPELK.A	Oxidation (M)	20.66		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92820	17%	185	5	36340	6.7	Q92820|GGH_HUMAN Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2												14	1
						33	42	386.25	1155.72	1155.7	0.01	0	33	0.0422318	K.KPIIGILMQK.C	Oxidation (M)	20.14		
						54	62	539.29	1076.56	1076.55	0.01	0	36	0.0188963	R.YYIAASYVK.Y		20.19		
						63	70	433.72	865.43	865.43	0	0	40	0.0065774	K.YLESAGAR.V		13.38		
						89	103	772.94	1543.87	1543.84	0.03	0	41	0.0053167	K.SINGILFPGGSVDLR.R		22.4		
						254	266	445.91	1334.7	1334.69	0.01	0	35	0.0227237	K.NLDGISHAPNAVK.T		15.28		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P62873	10%	115	3	38151	5.6	P62873|GBB1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3												14	1
						2	15	864.97	1727.92	1727.87	0.05	1	43	0.0029985	M.SELDQLRQEAEQLK.N	Acetyl (Protein N-term)	22.23		
						69	78	509.4	1016.79	1016.55	0.24	0	36	0.0107638	R.LLVSASQDGK.L		15.15		
						305	314	505.25	1008.49	1008.51	-0.02	0	35	0.0190476	R.AGVLAGHDNR.V		12.79		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P02649	8%	83	2	36246	5.7	P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1												14	1
						199	207	484.81	967.61	967.55	0.06	0	50	0.0007102	R.LGPLVEQGR.V		18.05		
						301	317	810.93	1619.85	1619.79	0.06	0	33	0.0322664	K.VQAAVGTSAAPVPSDNH.-		15.36		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P45880	7%	114	2	32060	7.5	P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2												14	3
						236	247	647.37	1292.72	1292.66	0.06	0	61	5.82E-05	K.YQLDPTASISAK.V		20.23		
						268	277	508.82	1015.62	1015.59	0.02	0	53	0.0004284	K.LTLSALVDGK.S		21.49		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q86Y82	7%	74	2	31736	5.5	Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1												14	2
						11	20	511.78	1021.55	1021.53	0.02	0	41	0.0056241	R.NPGPSGPQLR.D		14.02		
						36	44	480.29	958.56	958.54	0.02	0	33	0.0466647	R.ISQATAQIK.N		13.42		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11177	6%	96	2	39550	6.2	P11177|ODPB_HUMAN Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3												14	1
						325	336	632.85	1263.69	1263.62	0.07	0	46	0.0018793	R.VTGADVPMPYAK.I	Oxidation (M)	17.85		
						337	347	628.36	1254.7	1254.68	0.02	0	51	0.0005925	K.ILEDNSIPQVK.D		20.01		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
A6NMY6	6%	81	2	38806	6.5	A6NMY6|AXA2L_HUMAN Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2												14	1
						105	115	611.82	1221.63	1221.59	0.04	0	36	0.0191828	K.TPAQYDASELK.A		16.45		
						136	145	622.83	1243.65	1243.62	0.03	0	45	0.0023443	R.TNQELQEINR.V		15.5		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BWM7	6%	121	2	35823	9.3	Q9BWM7|SFXN3_HUMAN Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=2 SV=1												14	1
						136	144	473.26	944.51	944.49	0.02	0	69	1.15E-05	R.SGDTPITVR.Q		14.72		
						214	222	455.27	908.53	908.5	0.03	0	52	0.0004401	R.LGYSVTAAK.Q		15.63		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50897	14%	230	3	34627	6.1	P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1												15	5
						105	122	1009.48	2016.96	2016.95	0.01	0	107	1.19E-09	K.LQQGYNAMGFSQGGQFLR.A	Oxidation (M)	20.76		
						165	174	526.79	1051.56	1051.57	-0.01	1	37	0.0133102	R.KTLNAGAYSK.V		12.9		
						254	268	897.48	1792.94	1792.88	0.06	0	86	1.70E-07	K.ETIPLQETSLYTQDR.L		20.81		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99623	13%	220	4	33276	9.8	Q99623|PHB2_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2												15	1
						98	107	602.83	1203.65	1203.63	0.02	0	33	0.0432001	K.DLQMVNISLR.V	Oxidation (M)	20.89		
						148	157	589.35	1176.68	1176.63	0.05	0	62	5.28E-05	K.FNASQLITQR.A		20.68		
						158	165	450.28	898.55	898.56	-0.01	0	42	0.0044137	R.AQVSLLIR.R		20.59		
						225	236	608.33	1214.64	1214.61	0.03	0	84	3.53E-07	K.IVQAEGEAEAAK.M		13.47		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UBR2	11%	141	3	34530	6.7	Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1												15	2
						70	81	654.84	1307.67	1307.65	0.02	0	47	0.0013142	R.NVDGVNYASITR.N		19.98		
						190	199	505.75	1009.49	1009.48	0.01	0	56	0.000165	R.VGDYGSLSGR.E		15.85		
						275	284	371.22	1110.62	1110.59	0.03	1	38	0.0104194	R.IVTSTYKDGK.G		12.84		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H9B4	7%	88	2	35881	9.2	Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4												15	1
						203	214	635.82	1269.62	1269.63	-0.01	0	48	0.0011554	K.VGIPVTDENGNR.L		17.02		
						224	233	550.84	1099.67	1099.63	0.04	0	40	0.0092409	K.QAITQVVVSR.I		18.9		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36543	18%	184	4	26186	7.7	P36543|VATE1_HUMAN Vacuolar proton pump subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1												16	1
						34	42	554.77	1107.52	1107.51	0.02	0	43	0.0033961	K.AEEEFNIEK.G		19.49		
						70	80	669.32	1336.63	1336.62	0.01	0	64	2.55E-05	K.IQMSNLMNQAR.L	2 Oxidation (M)	13.33		
						138	145	487.78	973.54	973.56	-0.02	1	37	0.0175302	R.KQDFPLVK.A		17.74		
						200	212	788.42	1574.83	1574.78	0.05	0	39	0.0085972	R.LDLIAQQMMPEVR.G	2 Oxidation (M)	20.4		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16698	14%	249	4	36330	9.3	Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1												16	1
						50	60	603.31	1204.6	1204.59	0.01	0	54	0.0003123	K.AMLPPNSFQGK.V	Oxidation (M)	16.77		
						61	73	589.34	1176.67	1176.65	0.02	0	57	0.0001565	K.VAFITGGGTGLGK.G		20.45		
						98	110	667.83	1333.65	1333.65	0	0	95	2.11E-08	K.ATAEQISSQTGNK.V		13.16		
						235	244	556.83	1111.65	1111.64	0.02	0	43	0.0030331	R.FNVIQPGPIK.T		20.49		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21796	13%	247	4	30868	8.6	P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2												16	5
						2	12	587.31	1172.61	1172.61	0.01	0	61	6.30E-05	M.AVPPTYADLGK.S	Acetyl (Protein N-term)	21.1		
						97	109	700.83	1399.66	1399.66	-0.01	0	74	2.73E-06	K.LTFDSSFSPNTGK.K		20.75		
						97	110	510.27	1527.77	1527.76	0.02	1	56	0.0001881	K.LTFDSSFSPNTGKK.N		20.06		
						164	174	607.32	1212.62	1212.61	0.01	0	56	0.0001914	R.VTQSNFAVGYK.T		19.28		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05141	13%	177	4	33102	9.8	P05141|ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=6												17	1
						2	10	476.25	950.48	950.47	0.01	0	58	0.0001128	M.TDAAVSFAK.D	Acetyl (Protein N-term)	20.45		

						11	23	610.34	1218.66	1218.66	0	0	42	0.0041955	K.DFLAGGVAAAISK.T		21.71		
						24	31	428.75	855.49	855.48	0.01	0	38	0.0107068	K.TAVAPIER.V		13.98		
						97	105	488.78	975.54	975.54	0	0	42	0.0050695	K.QIFLGGVDK.R		20.5		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35232	11%	143	3	29843	5.6	P35232|PHB_HUMAN Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1												17	1
						134	143	575.29	1148.57	1148.58	-0.02	0	63	3.33E-05	R.FDAGELITQR.E		20.98		
						178	186	512.23	1022.45	1022.49	-0.04	0	37	0.0125422	K.EFTEAVEAK.Q		15.5		
						209	219	531.27	1060.53	1060.54	-0.01	0	43	0.0036911	K.AAIISAEGDSK.A		14.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07858	6%	78	2	38766	5.9	P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3												17	4
						210	220	657.78	1313.55	1313.6	-0.04	0	38	0.0107862	K.ICEPGYSPTYK.Q		17.55		
						238	245	499.74	997.48	997.48	0	0	41	0.0054135	K.DIMAEIYK.N	Oxidation (M)	19.8		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07339	13%	225	5	45037	6.1	P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1												18	8
						177	184	440.23	878.45	878.45	0	0	34	0.0289497	R.QVFGEATK.Q		14.15		
						185	194	523.31	1044.6	1044.6	0	0	66	2.04E-05	K.QPGITFIAAK.F		20.44		
						236	253	902.47	1802.93	1802.8	0.14	0	36	0.0163537	R.DPDAQPGGELMLGGTDSK.Y	Oxidation (M)	19.92		
						349	357	533.28	1064.56	1064.54	0.02	0	52	0.0004309	K.LSPEDYTLK.V		20.05		
						404	411	410.71	819.4	819.42	-0.03	0	36	0.019251	R.VGFAEAAR.L		14.99		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07686	4%	105	2	63527	6.3	P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3												18	3
						426	435	583.77	1165.52	1165.53	-0.01	0	55	0.0002214	K.DSAYPEELSR.V		18.95		
						466	476	595.82	1189.63	1189.6	0.03	0	51	0.0005744	K.VEPLDFGGTQK.Q		20.35		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04792	15%	158	3	22826	6	P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2												19	1
						28	37	582.31	1162.6	1162.61	-0.01	0	54	0.0003169	R.LFDQAFGLPR.L		21.83		
						80	89	538.27	1074.52	1074.57	-0.04	0	70	8.49E-06	R.QLSSGVSEIR.H		15.99		
						189	198	471.25	940.48	940.5	-0.01	0	36	0.0168065	R.AQLGGPEAAK.S		13.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99714	11%	112	2	27134	7.7	Q99714|HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3												19	1
						131	147	901.4	1800.79	1800.81	-0.02	0	68	1.01E-05	R.LVAGEMGQNEPDQGGQR.G	Oxidation (M)	13.43		
						173	184	600.86	1199.71	1199.67	0.04	0	43	0.0035429	K.GGIVGMTLPIAR.D	Oxidation (M)	20.61		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51148	23%	254	4	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												20	1
						24	34	543.31	1084.61	1084.65	-0.04	0	61	6.98E-05	K.LVLLGESAVGK.S		20.68		
						122	135	698.42	1394.82	1394.79	0.04	0	71	4.71E-06	R.QASPNIVIALAGNK.A		21.16		
						185	196	606.29	1210.56	1210.57	-0.01	0	58	0.0001026	K.NEPQNATGAPGR.N		12.66		
						199	210	650.31	1298.6	1298.62	-0.03	0	64	2.62E-05	R.GVDLQENNPASR.S		14.93		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05090	13%	111	2	21547	5.1	P05090|APOD_HUMAN Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1												20	1
						152	164	712.34	1422.66	1422.74	-0.08	0	35	0.0222882	R.NPNLPPETVDSLK.N		19.99		
						177	187	654.79	1307.57	1307.58	-0.02	0	51	0.0005938	K.MTVTDQVNCPK.L	Oxidation (M)	13.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15286	15%	139	3	23296	8.5	Q15286|RAB35_HUMAN Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1												21	2
						11	21	536.28	1070.55	1070.63	-0.09	0	39	0.0108233	K.LLIIGDSGVGK.S		22.04		
						49	56	445.21	888.41	888.46	-0.05	0	36	0.0250418	R.TVEINGEK.V		13.99		
						179	189	671.81	1341.6	1341.66	-0.07	0	65	2.27E-05	K.QQQQQQNDVVK.L		13.22		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51149	11%	81	2	23760	6.4	P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1												21	2
						11	21	529.27	1056.53	1056.62	-0.09	0	49	0.0009742	K.VIILGDSGVGK.T		21.34		
						147	157	642.28	1282.54	1282.62	-0.08	0	32	0.0431424	K.NNIPYFETSAK.E		21.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48047	9%	78	2	23377	10	P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1												21	1
						91	98	431.2	860.38	860.46	-0.08	0	35	0.0306123	K.SLNDITAK.E		15.73		
						177	188	637.79	1273.56	1273.67	-0.11	0	43	0.0038488	K.TDPSILGGMIVR.I	Oxidation (M)	21.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61026	9%	84	2	22755	8.6	P61026|RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1												21	1
						12	22	536.28	1070.55	1070.63	-0.09	0	39	0.0108233	K.LLLIGDSGVGK.T		22.04		
						155	161	401.26	800.51	800.44	0.07	0	45	0.0031616	K.ANINIEK.A		14.78		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62820	9%	73	2	22891	5.9	P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3												21	1
						14	24	536.28	1070.55	1070.63	-0.09	0	39	0.0108233	K.LLLIGDSGVGK.S		22.04		
						52	58	388.17	774.32	774.41	-0.09	0	34	0.0392401	R.TIELDGK.T		16.41		
						or P61006|RAB8A_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1													
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30048	7%	86	2	28017	7.7	P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3												21	2
						74	83	511.23	1020.45	1020.52	-0.07	0	36	0.0185379	K.GTAVVNGEFK.D		17.15		
						208	214	417.21	832.4	832.43	-0.03	0	50	0.0008169	R.SVEETLR.L		14.85		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63000	10%	118	2	21835	8.8	P63000|RAC1_HUMAN Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1												22	1
						6	16	530.73	1059.44	1059.54	-0.1	0	54	0.0003733	K.CVVVGDGAVGK.T		16.08		
						167	174	475.72	949.43	949.49	-0.05	0	51	0.0005795	K.TVFDEAIR.A		21.34		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9NVJ2	13%	159	3	21753	8.7	Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1												23	3
						1	7	431.21	860.4	860.48	-0.08	0	33	0.0499914	-.MLALISR.L	Acetyl (Protein N-term); Oxidation (M)	23.17		
						133	141	507.72	1013.42	1013.5	-0.08	0	48	0.0012279	R.DLPNALDEK.Q		20.88		
						147	155	532.23	1062.44	1062.51	-0.07	0	79	1.07E-06	K.MNLSAIQDR.E	Oxidation (M)	16.11		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23284	16%	136	3	22785	9.3	P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=1												24	1
						44	51	430.67	859.34	859.4	-0.07	0	35	0.0308716	R.IGDEDVGR.V		14.18		
						64	76	682.77	1363.52	1363.7	-0.18	0	68	1.12E-05	K.TVDNFVALATGEK.G		22.85		
						138	150	729.31	1456.61	1456.72	-0.11	0	35	0.025653	K.DTNGSQFFITTVK.T		22.65		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30405	8%	81	2	22368	9.5	P30405|PPIF_HUMAN Peptidyl-prolyl cis-trans isomerase, mitochondrial OS=Homo sapiens GN=PPIF PE=1 SV=1												24	1
						125	133	555.73	1109.44	1109.54	-0.1	0	40	0.0070804	R.FPDENFTLK.H		21.92		
						183	190	448.2	894.39	894.48	-0.09	1	41	0.0049812	K.KIESFGSK.S		14.05		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61916	17%	119	3	16902	7.6	P61916|NPC2_HUMAN Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1												25	2
						26	35	525.19	1048.37	1048.49	-0.12	0	36	0.0207675	K.DCGSVDGVIK.E		18.41		
						95	103	508.71	1015.4	1015.51	-0.11	0	48	0.0012975	K.SGINCPIQK.D		14.71		
						117	123	412.3	822.59	822.41	0.17	0	35	0.0161095	K.SEYPSIK.L		16.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13488	8%	337	6	93680	6.6	Q13488|VPP3_HUMAN Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 OS=Homo sapiens GN=TCIRG1 PE=1 SV=2												26	3
						29	38	566.77	1131.52	1131.63	-0.11	0	67	1.62E-05	R.LGELGLVEFR.D		23.32		
						39	49	604.25	1206.48	1206.6	-0.12	0	66	1.66E-05	R.DLNASVSAFQR.R		21.54		
						64	73	635.25	1268.49	1268.64	-0.15	0	32	0.0416855	K.TFTFLQEEVR.R		22.85		
						75	83	446.24	890.47	890.56	-0.08	0	66	2.32E-05	R.AGLVLPPPK.G		20.49		
						104	109	365.18	728.34	728.42	-0.08	0	40	0.0083247	R.LAQELR.D		14.16		
						134	151	625.57	1873.68	1873.87	-0.19	0	33	0.026909	R.QGHEPQLAAAHTDGASER.T		13.78		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10253	3%	126	2	106126	5.6	P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=2												26	5
						838	849	643.82	1285.62	1285.71	-0.09	0	57	0.0001472	R.QQPMALAVALTK.G	Oxidation (M)	21.36		
						892	903	615.78	1229.55	1229.66	-0.11	0	69	8.97E-06	R.VTSEGAGLQLQK.V		17.63		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75348	21%	159	2	13863	8.9	O75348|VATG1_HUMAN Vacuolar proton pump subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3												29	1
						2	17	913.89	1825.76	1825.96	-0.21	1	84	2.33E-07	M.ASQSQGIQQLLQAEKR.A	Acetyl (Protein N-term)	22.38		
						81	89	594.74	1187.47	1187.6	-0.13	0	76	2.21E-06	K.MTILQTYFR.Q	Oxidation (M)	22.92		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O00754	2%	84	2	114357	6.8	O00754|MA2B1_HUMAN Lysosomal alpha-mannosidase OS=Homo sapiens GN=MAN2B1 PE=1 SV=3												30	2
						941	950	600.74	1199.47	1199.62	-0.14	0	51	0.0005849	R.DLFSTFTITR.L		24.37		
						951	962	693.3	1384.59	1384.77	-0.17	0	34	0.0267691	R.LQETTLVANQLR.E		21.08		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13510	5%	88	2	45077	7.5	Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4												31	1
						82	92	612.23	1222.45	1222.6	-0.15	0	32	0.0454359	K.NMINTFVPSGK.V	Oxidation (M)	20.59		
						93	100	482.18	962.34	962.47	-0.13	0	56	0.0001762	K.VMQVVDEK.L	Oxidation (M)	13.61		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P02776	36%	234	3 (4)	11123	8.9	P02776|PLF4_HUMAN Platelet factor 4 OS=Homo sapiens GN=PF4 PE=1 SV=2												32	2
						54	62	520.26	1038.5	1038.61	-0.11	0	54	0.0002956	R.HITSLEVIK.A		19.39		
						63	77	526.55	1576.62	1576.84	-0.22	0	72	4.00E-06	K.AGPHCPTAQLIATLK.N		21.4		
						82	92	667.27	1332.52	1332.71	-0.19	0	68	1.27E-05	K.ICLDLQAPLYK.K		22.7		
						82	93	487.87	1460.6	1460.81	-0.21	1	42	0.0044321	K.ICLDLQAPLYKK.I		21.83		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P56385	30%	92	2	7928	9.3	P56385|ATP5I_HUMAN ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=2 SV=2												32	1
						2	12	588.79	1175.56	1175.73	-0.16	0	51	0.0006969	M.VPPVQVSPLIK.L		21.53		
						60	69	566.72	1131.43	1131.57	-0.14	0	41	0.0057141	R.ELAEDDSILK.-		21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61604	60%	333	6	10925	8.9	P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2												33	2
						29	36	430.67	859.33	859.45	-0.12	0	64	3.55E-05	K.GGIMLPEK.S	Oxidation (M)	18.99		
						41	54	658.28	1314.55	1314.75	-0.21	0	77	1.41E-06	K.VLQATVVAVGSGSK.G		20.18		
						57	66	507.22	1012.43	1012.56	-0.12	0	42	0.0039916	K.GGEIQPVSVK.V		15.69		
						71	80	538.74	1075.46	1075.59	-0.13	0	51	0.0005838	K.VLLPEYGGTK.V		20.87		
						81	92	510.54	1528.59	1528.79	-0.2	1	44	0.0025444	K.VVLDDKDYFLFR.D		22.91		
						93	99	359.14	716.27	716.37	-0.1	0	55	0.0003644	R.DGDILGK.Y		16.17		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07602	7%	221	4	59899	5.1	P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2												33	2
						233	242	539.19	1076.37	1076.5	-0.13	0	60	8.11E-05	R.LGPGMADICK.N	Oxidation (M)	16.04		
						405	413	536.15	1070.29	1070.42	-0.13	0	34	0.0122264	K.DGGFCEVCK.K		17.27		
						430	438	507.73	1013.44	1013.58	-0.13	0	76	2.22E-06	K.QEILAALEK.G		21.74		

						439	449	656.23	1310.44	1310.6	-0.16	0	52	0.000356	K.GCSFLPDPYQK.Q		21.91		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P02748	4%	108	2	64615	5.4	P02748|CO9_HUMAN Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2												33	2
						473	483	621.8	1241.58	1241.74	-0.16	0	41	0.0066978	K.LSPIYNLVPVK.M		22.82		
						497	508	728.25	1454.49	1454.7	-0.22	0	67	1.29E-05	R.AIEDYINEFSVR.K		23.52		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8IX18	1%	75	2	89815	8.9	Q8IX18|DHX40_HUMAN Probable ATP-dependent RNA helicase DHX40 OS=Homo sapiens GN=DHX40 PE=2 SV=2												33	1
						108	117	521.73	1041.45	1041.63	-0.18	1	40	0.0073478	R.KVAAISVAQR.V		13.58		
						109	117	457.69	913.37	913.53	-0.17	0	35	0.0242364	K.VAAISVAQR.V		14.18		

***Footnotes to Supplemental Table 4:**

Data sets were searched with the Mascot search engine (see Perkins et al. (1999)*Electrophoresis* **20**, 3551-3567).

Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).

Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.

Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest gel slice in which the protein was identified, and the total # of adjacent gel slices in which the protein was found).

Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 5. Proteins identified by HPLC-MS/MS in 1-day BCG infected human THP-1 phagosome preparation.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05141	10%	117	3	33102	9.8	P05141|ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=6												1	3
						2	10	476.16	950.31	950.47	-0.16	0	31	0.0432418	M.TDAAVSFAK.D	Acetyl (Protein N-term)	19.5		
						11	23	610.23	1218.45	1218.66	-0.21	0	53	0.0003347	K.DFLAGGVAAAISK.T		20.67		
						73	80	428.86	855.7	855.49	0.21	0	34	0.0134017	R.GNLANVIR.Y		16.42		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P12236	7%	84	2	33073	9.8	P12236|ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4												1	1
						11	23	617.25	1232.49	1232.68	-0.19	0	50	0.0007489	K.DFLAGGIAAAISK.T		21.29		
						73	80	428.86	855.7	855.49	0.21	0	34	0.0134017	R.GNLANVIR.Y		16.42		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27105	7%	105	2	31882	7.7	P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3												2	3
						145	152	458.2	914.39	914.55	-0.17	0	48	0.0013803	R.LLAQTTLR.N		14.68		
						221	232	632.21	1262.41	1262.59	-0.18	0	57	0.0001439	K.VIAAEGEMNASR.A	Oxidation (M)	12.36		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q09666	1%	140	3 (4)	629213	5.8	Q09666|AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2												2	1
						764	775	634.24	1266.47	1266.65	-0.18	0	48	0.0010333	K.AEGPEVDVNLPK.A		19.19		
						1141	1152	627.23	1252.45	1252.63	-0.18	0	32	0.0390033	K.GEGPEVDVNLPK.A		19.27		
						1281	1289	451.17	900.33	900.46	-0.13	0	40	0.0091561	K.ADIDVSGPK.V		13.23		
						1409	1417	444.16	886.3	886.44	-0.14	0	38	0.0119581	K.ADVDVSGPK.M		12.66		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08962	11%	166	4	26474	8.1	P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2												4	12
						109	120	506.17	1515.5	1515.68	-0.18	1	50	0.0006939	R.DKVMSEFNNNFR.Q	Oxidation (M)	16.74		
						111	120	637.19	1272.36	1272.56	-0.2	0	57	8.85E-05	K.VMSEFNNNFR.Q	Oxidation (M)	16.47		
						121	128	527.17	1052.32	1052.46	-0.14	0	31	0.0418269	R.QQMENYPK.N	Oxidation (M)	12.03		
						139	144	378.11	754.2	754.33	-0.13	0	28	0.0329329	R.MQADFK.C	Oxidation (M)	12.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05023	6%	227	5	114135	5.3	P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1												4	4
						228	240	760.25	1518.48	1518.7	-0.22	0	67	1.24E-05	R.SPDFTNENPLETR.N		19.57		
						446	458	616.24	1230.47	1230.65	-0.18	0	46	0.001905	R.AVAGDASESALLK.C		17.72		
						648	658	618.74	1235.47	1235.7	-0.23	0	33	0.0306012	R.LNIPVSQVNPR.D		19.09		
						699	707	544.2	1086.39	1086.59	-0.2	0	37	0.0153683	K.LIIVEGCQR.Q		17.43		
						728	743	753.76	1505.51	1505.74	-0.23	0	43	0.0036887	K.ADIGVAMGIAGSDVSK.Q	Oxidation (M)	18.88		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15118	2%	116	2	144868	5.2	O15118|NPC1_HUMAN Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=1 SV=2												4	3
						715	726	679.26	1356.5	1356.7	-0.2	0	58	0.0001278	R.LQGETLDQQLGR.V		18.49		
						998	1010	768.3	1534.59	1534.75	-0.16	0	58	0.0001063	R.FLPMFLSDNPNPK.C	Oxidation (M)	20.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y490	6%	664	14	271766	5.8	Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3												6	3
						285	295	641.71	1281.4	1281.53	-0.13	0	51	0.0003869	K.NCGQMSEIEAK.V	Oxidation (M)	12.21		
						625	634	507.16	1012.31	1012.49	-0.18	0	32	0.0271973	R.SAQPASAEPR.Q		11.85		
						899	910	610.2	1218.39	1218.6	-0.21	0	62	3.69E-05	R.MATNAAAQNAIK.K	Oxidation (M)	12.34		
						1026	1035	529.21	1056.41	1056.59	-0.18	0	57	0.0001743	K.NLGTALAELR.T		20.07		
						1199	1207	538.67	1075.32	1075.49	-0.17	0	35	0.0195351	R.CVSCLPGQR.D		13.25		
						1321	1332	599.24	1196.47	1196.64	-0.17	0	44	0.0025813	K.ALSTDPAAPNLK.S		15.29		
						1402	1415	717.74	1433.47	1433.72	-0.25	0	66	1.86E-05	K.VLGEAMTGISQNAK.N	Oxidation (M)	13.78		
						1531	1541	573.23	1144.44	1144.61	-0.17	0	46	0.0019678	K.EVANSTANLVK.T		13.49		
						1594	1604	573.24	1144.47	1144.62	-0.15	0	33	0.0383389	R.AAMEPIVISAK.T	Oxidation (M)	16.13		
						1605	1618	732.26	1462.5	1462.74	-0.24	0	47	0.0013658	K.TMLESAGGLIQTAR.A	Oxidation (M)	19.14		
						1752	1766	576.21	1725.61	1725.87	-0.26	0	36	0.0168654	K.TLSHPQQMALLDQTK.T	Oxidation (M)	13.92		
						2032	2043	622.22	1242.43	1242.66	-0.23	0	60	6.29E-05	K.VLVQNAAGSQEK.L		12.51		
						2090	2099	494.71	987.41	987.56	-0.15	0	44	0.0039767	K.ALGDLISATK.A		19.66		
						2120	2130	610.74	1219.46	1219.68	-0.22	0	55	0.0002635	K.VMVTNVTSLLK.T	Oxidation (M)	19.94		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49327	5%	554	12	275850	6	P49327|FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=2												7	1
						203	213	604.68	1207.34	1207.56	-0.22	0	57	9.21E-05	R.LGMLSPEGTCK.A	Oxidation (M)	13.58		
						225	235	558.25	1114.48	1114.66	-0.18	0	32	0.0491068	R.SEGVVAVLLTK.K		20.51		
						299	310	649.72	1297.42	1297.66	-0.24	0	47	0.0011141	K.VGDPQELNGITR.A		17.59		
						317	326	543.22	1084.42	1084.61	-0.19	0	42	0.0054987	R.QEPLLIGSTK.S		18.94		
						374	384	632.27	1262.52	1262.73	-0.22	0	56	0.0002089	R.LQVVDQPLPVR.G		19.37		

						469	477	461.15	920.29	920.47	-0.18	0	39	0.0071226	R.GYAVLGGER.G		15.84		
						928	936	481.19	960.36	960.52	-0.16	0	63	4.18E-05	K.TGTVSLEVR.L		15.21		
						1073	1082	522.22	1042.42	1042.58	-0.16	0	51	0.0006189	K.AQVADVVVSR.W		14.7		
						1132	1142	651.73	1301.45	1301.66	-0.21	0	53	0.0003299	R.AALQEELQLCK.G		19.5		
						1172	1180	535.19	1068.36	1068.52	-0.16	0	38	0.0096678	R.DPSQQELPR.L		13.41		
						1712	1724	735.25	1468.49	1468.69	-0.2	0	41	0.0052672	R.FPQLDSTSFANSR.D		19.85		
						2221	2233	721.76	1441.5	1441.76	-0.26	0	36	0.0162755	R.SLLVNPEGPTLMR.L	Oxidation (M)	19.63		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35579	7%	631	14	227646	5.5	P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4												8	5
						359	373	804.2	1606.39	1606.69	-0.3	0	40	0.0024401	R.NTDQASMPDNTAAQK.V	Oxidation (M)	11.87		
						663	670	481.17	960.32	960.48	-0.16	0	42	0.0049998	R.NTNPNFVR.C		13.2		
						694	702	509.17	1016.33	1016.51	-0.17	0	56	0.0002007	R.CNGVLEGIR.I		18.72		
						712	718	462.67	923.33	923.49	-0.16	0	46	0.0015421	R.VVFQEFR.Q		19.57		
						738	745	489.68	977.34	977.5	-0.17	0	40	0.008276	K.QACVLMIK.A	Oxidation (M)	17.63		
						746	755	597.22	1192.42	1192.61	-0.19	0	56	0.000155	K.ALELDSNLYR.I		19.88		
						803	810	482.16	962.31	962.49	-0.17	0	46	0.0018348	R.QQQLTAMK.V	Oxidation (M)	12.04		
						815	821	420.14	838.27	838.4	-0.14	0	39	0.0053581	R.NCAAYLK.L		13.15		
						1250	1260	642.76	1283.5	1283.71	-0.21	0	35	0.0237286	K.VEAQLQELQVK.F		19.28		
						1484	1492	532.67	1063.32	1063.49	-0.17	0	45	0.0017857	R.ALEEAMEQK.A	Oxidation (M)	12.22		
						1529	1538	610.73	1219.44	1219.58	-0.14	0	45	0.0023058	R.ALEQQVEEMK.T	Oxidation (M)	13.27		
						1558	1566	531.2	1060.39	1060.56	-0.17	0	60	8.43E-05	R.LEVNLQAMK.A	Oxidation (M)	16.81		
						1794	1802	525.67	1049.32	1049.51	-0.18	0	33	0.0292385	K.LQEMEGTVK.S	Oxidation (M)	12.26		
						1807	1815	452.19	902.36	902.51	-0.15	0	58	0.0001395	K.ASITALEAK.I		15.6		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P46940	2%	160	3	189761	6.1	P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1												10	1
						327	336	513.23	1024.44	1024.6	-0.17	0	49	0.0009083	R.ALQSPALGLR.G		19.27		
						1028	1035	466.18	930.34	930.5	-0.16	0	48	0.0013964	K.TALQEEIK.S		14.18		
						1506	1516	618.72	1235.42	1235.65	-0.23	0	64	2.87E-05	K.LQQTYAALNSK.A		14.57		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q00610	7%	598	12	193260	5.5	Q00610|CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5												11	1
						87	96	626.72	1251.42	1251.65	-0.24	0	44	0.0025334	K.TLQIFNIEMK.S	Oxidation (M)	20.51		
						177	188	677.23	1352.45	1352.68	-0.23	0	72	4.31E-06	R.VVGAMQLYSVDR.K	Oxidation (M)	19.09		
						355	366	652.7	1303.38	1303.65	-0.27	0	73	2.71E-06	R.NNLAGAEELFAR.K		20.29		
						488	500	754.25	1506.48	1506.75	-0.27	0	46	0.001583	K.VIQCFAETGQVQK.I		16.6		
						799	806	528.19	1054.37	1054.57	-0.2	0	47	0.0010639	K.YIEIYVQK.V		19.39		
						882	892	667.68	1333.35	1333.63	-0.28	0	61	2.77E-05	K.IYIDSNNNPER.F		14.07		
						1040	1046	470.64	939.26	939.45	-0.19	0	29	0.0413766	R.VMEYINR.L	Oxidation (M)	13.1		
						1123	1130	469.66	937.31	937.48	-0.17	0	39	0.0069501	K.EAIDSYIK.A		18.93		
						1156	1161	399.13	796.24	796.39	-0.15	0	39	0.0046585	K.YLQMAR.K	Oxidation (M)	12.31		
						1216	1226	648.73	1295.44	1295.66	-0.22	0	58	9.43E-05	K.LLYNNVSNFGR.L		19.71		
						1398	1406	563.7	1125.39	1125.58	-0.2	0	54	0.0002512	K.VANVELYYR.A		19.29		
						1510	1516	413.17	824.32	824.48	-0.16	0	40	0.0053702	R.IAAYLFK.G		19.8		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	8%	457	8	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												12	3
						196	204	550.64	1099.27	1099.46	-0.19	0	41	0.0013927	R.SEYMEGNVR.K	Oxidation (M)	12.36		
						205	218	502.51	1504.5	1504.77	-0.27	1	47	0.0011943	R.KVVATTQMQAADAR.K	Oxidation (M)	11.9		
						206	218	689.23	1376.45	1376.67	-0.22	0	92	4.13E-08	K.VVATTQMQAADAR.K	Oxidation (M)	12.15		
						242	252	609.71	1217.41	1217.63	-0.22	0	58	0.0001177	K.DLTALSNMLPK.G	Oxidation (M)	20.08		
						293	301	479.19	956.37	956.54	-0.17	0	61	6.41E-05	K.QASNGVLIR.I		13.57		
						364	379	862.8	1723.58	1723.83	-0.25	0	62	4.33E-05	R.ENSLLFDPLSSSSSNK.E		20.69		
						433	442	627.21	1252.41	1252.61	-0.21	0	51	0.0004572	K.DLMVLNDVYR.V	Oxidation (M)	20.27		
						642	648	443.67	885.33	885.5	-0.17	0	46	0.0019302	K.IQTQLQR.D		12.66		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05556	2%	72	2	91714	5.3	P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=1												12	2
						182	190	492.18	982.34	982.51	-0.17	0	39	0.0082196	R.IGFGSFVEK.T		20.03		
						785	794	508.21	1014.4	1014.57	-0.17	0	33	0.0442603	K.SAVTTVVNPK.Y		13.33		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P41252	2%	74	2	146178	5.9	P41252|SYIC_HUMAN Isoleucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1												12	1
						629	638	587.25	1172.48	1172.69	-0.21	0	33	0.0445403	R.LYLINSPVVR.A		19.99		
						922	933	733.24	1464.46	1464.71	-0.25	0	42	0.0040301	K.QLSSEELEQFQK.T		19.32		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92896	2%	68	2	138382	6.5	Q92896|GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=1												12	1
						385	392	501.15	1000.29	1000.48	-0.18	0	39	0.0062307	R.CNVENLPR.S		13.48		
						1089	1100	743.69	1485.37	1485.61	-0.24	0	29	0.0349375	R.QMSCLMEALEDK.R	2 Oxidation (M)	19.11		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P08648	4%	166	3	115605	5.5	P08648|ITA5_HUMAN Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2												13	2
						567	581	814.33	1626.65	1626.91	-0.25	0	75	1.98E-06	R.QATLTQTLLIQNGAR.E		20.08		
						695	708	744.78	1487.55	1487.76	-0.21	0	58	0.0001118	R.VTAPPEAEYSGLVR.H		19.48		
						728	738	638.23	1274.45	1274.64	-0.18	0	32	0.0409138	R.LLVCDLGNPMK.A	Oxidation (M)	19.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P42704	3%	199	4	159003	5.8	P42704|LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3												13	1
						188	197	609.19	1216.37	1216.55	-0.18	0	51	0.0004712	K.MEEANIQPNR.V	Oxidation (M)	12.55		
						740	750	553.18	1104.34	1104.57	-0.23	0	47	0.0012093	R.LDSSAVLDTGK.Y		17.37		
						1099	1109	583.19	1164.37	1164.55	-0.19	0	39	0.0079013	K.GFTLNDAANSR.L		18.74		
						1129	1139	636.73	1271.44	1271.65	-0.21	0	62	4.27E-05	K.TVLDQQQTPSR.L		13.24		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16706	2%	109	2	131742	7.2	Q16706|MA2A1_HUMAN Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2												13	1
						61	73	749.81	1497.61	1497.82	-0.2	0	77	1.43E-06	R.LLAENNEIISNIR.D		20		
						965	974	551.19	1100.37	1100.55	-0.17	0	32	0.0445163	R.GLEQGIQDNK.I		13.37		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y4L1	2%	83	2	111494	5.2	Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1												13	1
						269	278	567.71	1133.4	1133.58	-0.17	0	39	0.0090581	R.TLGGLEMELR.L	Oxidation (M)	19.69		
						283	291	524.2	1046.39	1046.55	-0.16	0	44	0.003162	R.LAGLFNEQR.K		19.56		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11279	5%	133	2	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												16	5
						138	146	517.2	1032.38	1032.55	-0.16	0	62	5.08E-05	K.TVESITDIR.A		18.97		
						327	337	576.21	1150.41	1150.6	-0.19	0	67	1.24E-05	R.ALQATVGNSYK.C		13.66		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P53396	4%	228	4	121674	7	P53396|ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3												16	1
						89	97	451.69	901.36	901.49	-0.13	0	49	0.0013049	R.LGQEATVGK.A		12.45		
						636	650	760.26	1518.5	1518.77	-0.27	0	48	0.0010557	K.IGNTGGMLDNILASK.L	Oxidation (M)	19.89		
						663	676	754.26	1506.5	1506.71	-0.21	0	72	4.35E-06	R.SGGMSNELNNIISR.T	Oxidation (M)	19.5		
						935	944	460.68	919.34	919.48	-0.14	0	61	5.36E-05	R.FGGALDAAAK.M		15.01		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P18206	3%	142	3	124292	5.5	P18206|VINC_HUMAN Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4												16	1
						327	339	755.23	1508.45	1508.7	-0.25	0	56	0.0001503	K.MLGQMTDQVADLR.A	2 Oxidation (M)	18.58		
						670	680	585.73	1169.44	1169.64	-0.2	0	32	0.040223	R.ELTPQVVSAAR.I		17.9		
						803	815	635.25	1268.49	1268.67	-0.18	0	55	0.0002438	K.AVAGNISDPGLQK.S		14.87		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	14%	610	11	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												18	3
						76	84	541.19	1080.37	1080.54	-0.17	0	46	0.0014833	K.FAFQAEVNR.M		19.41		
						103	114	638.23	1274.45	1274.64	-0.19	0	68	1.13E-05	R.ELISNASDALDK.I		19.23		
						103	116	515.53	1543.58	1543.82	-0.24	1	65	2.41E-05	R.ELISNASDALDKIR.L		19.84		
						143	156	510.52	1528.53	1528.77	-0.24	0	61	4.80E-05	K.NLLHVTDTGVGMTR.E	Oxidation (M)	18.56		
						169	177	491.66	981.32	981.48	-0.16	0	68	8.20E-06	K.SGTSEFLNK.M		14.45		
						385	395	594.26	1186.5	1186.67	-0.17	0	40	0.0080672	K.SILFVPTSAPR.G		20.32		
						435	448	743.28	1484.54	1484.75	-0.21	0	88	1.04E-07	K.GVVDSDDLPLNVSR.E		20.02		
						494	503	380.47	1138.38	1138.57	-0.19	0	41	0.0043179	K.LGVIEDHSNR.T		12.94		
						548	557	575.68	1149.35	1149.53	-0.18	0	47	0.0011711	K.EAESSPFVER.L		15.39		
						672	682	645.21	1288.4	1288.59	-0.19	0	35	0.0192079	K.DISTNYYASQK.K		16.05		
						725	733	497.2	992.38	992.52	-0.14	0	55	0.0002196	R.SGYLLPDTK.A		19.06		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13639	9%	365	8	96246	6.4	P13639|EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4												18	2
						2	10	546.21	1090.41	1090.58	-0.17	0	62	4.42E-05	M.VNFTVDQIR.A		19.62		
						43	50	379.67	757.32	757.44	-0.13	0	34	0.0429473	K.AGIIASAR.A		13.16		
						227	235	551.68	1101.34	1101.52	-0.17	0	53	0.0002816	K.QFAEMYVAK.F	Oxidation (M)	15.35		
						240	249	507.17	1012.33	1012.49	-0.16	0	40	0.0054586	K.GEGQLGPAER.A		12.72		
						416	426	554.24	1106.47	1106.63	-0.16	0	62	4.43E-05	R.VFSGLVSTGLK.V		19.93		
						429	438	547.19	1092.37	1092.53	-0.16	0	41	0.0052447	R.IMGPNYTPGK.K	Oxidation (M)	13.46		
						499	506	445.69	889.36	889.5	-0.14	0	34	0.0312078	K.FSVSPVVR.V		18.97		
						573	580	461.67	921.32	921.46	-0.14	0	38	0.009693	K.SDPVVSYR.E		13.76		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43707	6%	298	5	105245	5.3	O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2												18	1
						115	122	432.68	863.34	863.48	-0.13	0	47	0.0015034	K.ALDFIASK.G		19.67		
						153	166	769.29	1536.56	1536.77	-0.21	0	75	1.95E-06	R.FAIQDISVEETSAK.E		20.15		
						626	632	406.19	810.36	810.5	-0.13	0	32	0.0377586	K.VQQLVPK.R		13.29		
						746	757	715.28	1428.55	1428.76	-0.21	0	85	2.01E-07	R.TINEVENQILTR.D		19.88		
						761	771	684.72	1367.42	1367.61	-0.2	0	60	5.56E-05	K.GISQEQMQEFR.A	Oxidation (M)	13.89		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14697	5%	196	5	107263	5.7	Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3												18	1
						103	109	436.16	870.3	870.44	-0.15	0	41	0.0043268	R.IDELEPR.R		14.06		
						158	164	437.17	872.33	872.46	-0.13	0	37	0.0198549	R.LDLLEDR.S		19.8		
						165	173	486.72	971.43	971.58	-0.15	0	37	0.0194045	R.SLLLSVNAR.G		19.71		
						591	602	446	1334.98	1334.68	0.3	0	44	0.001989	R.SGGMERPFVLAR.A	Oxidation (M)	16.34		
						915	929	580.9	1739.68	1739.92	-0.24	0	39	0.0091113	R.LSFQHDPETSVLVLR.K		20.19		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P12814	5%	277	4	103563	5.3	P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2												18	1
						96	103	432.68	863.34	863.48	-0.13	0	47	0.0015034	K.ALDFIASK.G		19.67		
						134	147	769.29	1536.56	1536.77	-0.21	0	75	1.95E-06	R.FAIQDISVEETSAK.E		20.15		
						727	738	715.28	1428.55	1428.76	-0.21	0	85	2.01E-07	R.TINEVENQILTR.D		19.88		
						742	752	677.7	1353.39	1353.6	-0.2	0	71	4.08E-06	K.GISQEQMNEFR.A	Oxidation (M)	13.98		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08238	15%	555	10	83554	5	P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4												19	4
						42	53	638.23	1274.45	1274.64	-0.18	0	76	1.90E-06	R.ELISNASDALDK.I		19.23		
						73	82	597.73	1193.44	1193.64	-0.2	0	38	0.0105914	K.IDIIPNPQER.T		19.6		
						83	95	683.27	1364.52	1364.72	-0.2	0	81	5.40E-07	R.TLTLVDTGIGMTK.A	Oxidation (M)	19.68		
						96	107	621.76	1241.51	1241.7	-0.19	0	59	9.25E-05	K.ADLINNLGTIAK.S		20.2		
						276	284	576.19	1150.37	1150.55	-0.18	0	46	0.0015715	K.YIDQEELNK.T		14		
						379	392	757.27	1512.52	1512.78	-0.26	0	77	1.48E-06	R.GVVDSEDLPLNISR.E		20.25		
						429	435	446.14	890.26	890.42	-0.15	0	34	0.0231432	K.FYEAFSK.N		18.65		
						482	491	580.7	1159.39	1159.58	-0.19	0	45	0.0023784	K.SIYYITGESK.E		19.14		
						492	502	625.23	1248.45	1248.61	-0.16	0	70	7.86E-06	K.EQVANSAFVER.V		15.06		
						613	623	648.65	1295.29	1295.48	-0.19	0	29	0.0178197	R.DNSTMGYMMAK.K	3 Oxidation (M)	12.37		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	9%	300	7	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												19	3
						149	155	372.16	742.31	742.43	-0.13	0	33	0.0364554	K.LGGDLLR.A		18.32		
						166	174	485.18	968.35	968.5	-0.14	0	33	0.0293445	R.IGFGSFVDK.T		20.29		
						275	285	563.73	1125.44	1125.61	-0.18	0	50	0.0006888	K.LGAILTPNDGR.C		18.6		
						311	325	836.84	1671.67	1671.89	-0.22	0	59	8.04E-05	K.LAENNIQPIFAVTSR.M		20.55		
						489	498	576.66	1151.31	1151.49	-0.18	0	30	0.0364212	R.SSQELEGSCR.K		12.32		
						544	554	582.67	1163.33	1163.51	-0.19	0	41	0.0038255	R.YNGQVCGGPGR.G		12.57		
						578	586	524.19	1046.36	1046.48	-0.12	0	55	0.0002433	R.TTEGCLNPR.R		12.62		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07900	9%	363	6	85006	4.9	P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5												19	2
						88	100	683.27	1364.52	1364.72	-0.2	0	81	5.40E-07	R.TLTIVDTGIGMTK.A	Oxidation (M)	19.68		
						101	112	621.76	1241.51	1241.7	-0.19	0	59	9.25E-05	K.ADLINNLGTIAK.S		20.2		
						284	292	576.19	1150.37	1150.55	-0.18	0	46	0.0015715	K.YIDQEELNK.T		14		
						387	400	757.27	1512.52	1512.78	-0.26	0	77	1.48E-06	R.GVVDSEDLPLNISR.E		20.25		
						437	443	474.65	947.29	947.44	-0.15	0	34	0.0247872	K.FYEQFSK.N		16.57		
						500	510	618.21	1234.4	1234.59	-0.19	0	66	1.82E-05	K.DQVANSAFVER.L		16.16		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27824	3%	83	2	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												19	2
						211	217	420.15	838.28	838.41	-0.13	0	41	0.0041984	K.TGIYEEK.H		12.88		
						574	582	544.8	1087.59	1087.51	0.07	0	42	0.0050551	K.AEEDEILNR.S		15.76		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	6%	164	3	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												21	3
						83	92	606.71	1211.41	1211.58	-0.17	0	39	0.0069222	R.VEEVGPYTYR.E		17.86		
						116	121	392.63	783.25	783.39	-0.14	0	31	0.0268462	K.AYVFER.D		15.96		
						391	402	704.25	1406.48	1406.7	-0.23	1	94	2.68E-08	K.KLDDFVETGDIR.T		19.37		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P01871	5%	73	2	49960	6.3	P01871|IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3												21	1
						113	120	450.71	899.4	899.52	-0.12	0	35	0.028709	K.VSVFVPPR.D		18.85		
						154	169	809.27	1616.52	1616.8	-0.28	0	38	0.0094851	K.QVGSGVTTDQVQAEAK.E		13.59		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01813	4%	77	2	86454	7.5	Q01813|K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2												21	1
						26	44	902.33	1802.65	1802.89	-0.24	0	44	0.002365	K.AIGVLTSGGDAQGMNAAVR.A	Oxidation (M)	18.45		
						487	496	635.21	1268.41	1268.61	-0.2	0	33	0.0321958	K.YLEEIATQMR.T	Oxidation (M)	18.06		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15311	3%	103	2	69484	5.9	P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4												21	2
						364	371	501.67	1001.33	1001.51	-0.19	0	51	0.0005659	R.ELSEQIQR.A		13.08		
						372	379	494.18	986.35	986.5	-0.15	0	51	0.000616	R.ALQLEEER.K		14.61		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	28%	908	16	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												22	1
						47	60	519.18	1554.51	1554.79	-0.27	1	58	9.96E-05	K.NGRVEIIANDQGNR.I		13.2		
						50	60	614.73	1227.45	1227.62	-0.17	0	69	1.02E-05	R.VEIIANDQGNR.I		13.88		
						61	74	783.79	1565.56	1565.77	-0.22	0	61	5.10E-05	R.ITPSYVAFTPEGER.L		19.84		
						82	96	839.29	1676.58	1676.8	-0.23	0	95	2.09E-08	K.NQLTSNPENTVFDAK.R		19.36		
						82	97	611.87	1832.6	1832.9	-0.3	1	66	1.36E-05	K.NQLTSNPENTVFDAKR.L		18.97		
						124	138	802.84	1603.67	1603.86	-0.19	0	50	0.0006705	K.TKPYIQVDIGGGQTK.T		18.79		
						139	152	776.79	1551.56	1551.79	-0.22	0	41	0.0045086	K.TFAPEEISAMVLTK.M	Oxidation (M)	20.49		
						186	197	617.23	1232.44	1232.62	-0.18	0	49	0.0009927	K.DAGTIAGLNVMR.I	Oxidation (M)	19.27		
						198	214	605.92	1814.73	1814.99	-0.26	1	62	3.43E-05	R.IINEPTAAAIAYGLDKR.E		20.05		
						325	336	510.18	1527.53	1527.74	-0.21	1	49	0.0009472	R.AKFEELNMDLFR.S	Oxidation (M)	19.97		
						345	352	459.68	917.34	917.47	-0.13	0	36	0.0201278	K.VLEDSDLK.K		13.73		
						353	367	794.81	1587.61	1587.85	-0.23	1	85	2.45E-07	K.KSDIDEIVLVGGSTR.I		19.71		
						448	464	918.84	1835.66	1835.93	-0.27	0	31	0.0460498	K.SQIFSTASDNQPTVTIK.V		19.58		
						524	532	537.71	1073.4	1073.55	-0.15	0	60	8.62E-05	K.ITITNDQNR.L		12.9		
						563	573	658.73	1315.44	1315.63	-0.19	0	45	0.0023727	R.NELESYAYSLK.N		20.01		
						622	633	699.3	1396.58	1396.78	-0.2	0	55	0.0002369	K.ELEEIVQPIISK.L		20.36		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	12%	366	8	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												22	2
						28	35	488.7	975.39	975.54	-0.14	0	40	0.0084762	K.QLFDQVVK.T		19.53		
						264	273	591.72	1181.42	1181.59	-0.17	0	51	0.0004801	K.APDFVFYAPR.L		20.62		
						361	371	463.16	1386.47	1386.69	-0.22	1	43	0.0036346	K.AQQELEEQTRR.A		12.21		
						372	379	494.2	986.38	986.5	-0.13	0	38	0.0120838	R.ALELEQER.K		14.83		
						401	408	444.18	886.35	886.49	-0.14	0	53	0.0004478	K.EALLQASR.D		14.07		
						428	435	482.18	962.35	962.49	-0.14	0	44	0.0030542	R.ISQLEMAR.Q	Oxidation (M)	12.86		
						449	458	603.7	1205.39	1205.56	-0.17	0	56	0.0001639	K.AQMVQEDLEK.T	Oxidation (M)	13.07		
						569	577	585.67	1169.32	1169.5	-0.18	1	40	0.0031614	K.QRIDEFESM.-	Oxidation (M)	16.2		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38646	5%	178	3	73920	5.9	P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2												22	1
						207	218	621.77	1241.53	1241.67	-0.15	0	49	0.0010713	K.DAGQISGLNVLR.V		20.23		
						395	405	645.74	1289.47	1289.67	-0.2	0	36	0.0177157	K.VQQTVQDLFGR.A		20.1		
						635	646	616.24	1230.47	1230.66	-0.18	0	93	3.54E-08	R.QAASSLQQASLK.L		13.55		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13796	16%	535	10	70815	5.2	P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5												24	1
						4	15	707.68	1413.34	1413.58	-0.24	0	53	9.03E-05	R.GSVSDEEMMELR.E	2 Oxidation (M)	13.77		
						133	141	545.14	1088.27	1088.46	-0.18	0	49	0.0003166	K.ALENDPDCR.H		12.39		
						166	178	759.77	1517.53	1517.74	-0.21	0	70	6.63E-06	K.MINLSVPDTIDER.T	Oxidation (M)	19.96		
						286	294	497.68	993.35	993.51	-0.16	0	34	0.028326	K.IGNFSTDIK.D		18.69		
						286	297	442.16	1323.45	1323.67	-0.22	1	51	0.0004758	K.IGNFSTDIKDSK.A		14.9		
						334	343	626.18	1250.34	1250.54	-0.2	0	54	0.0001787	R.AECMLQQAER.L	Oxidation (M)	12.61		
						348	357	568.22	1134.43	1134.6	-0.17	0	53	0.0003351	R.QFVTATDVVR.G		19		
						473	488	838.3	1674.59	1674.83	-0.24	0	72	4.19E-06	K.FSLVGIGGQDLNEGNR.T		20.52		
						585	591	414.15	826.29	826.4	-0.11	0	31	0.0356227	K.YAISMAR.K	Oxidation (M)	12.91		
						597	610	793.32	1584.63	1584.84	-0.21	0	67	1.31E-05	R.VYALPEDLVEVNPK.M		20.57		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31948	11%	267	6	63227	6.4	P31948|STIP1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1												24	1
						1	10	653.22	1304.43	1304.63	-0.2	1	51	0.0004727	-.MEQVNELKEK.G	Acetyl (Protein N-term); Oxidation (M)	14.03		
						110	118	532.17	1062.33	1062.48	-0.15	0	45	0.0020984	K.EGLQNMEAR.L	Oxidation (M)	12.22		
						352	364	744.8	1487.58	1487.79	-0.21	0	44	0.0024959	R.LAYINPDLALEEK.N		20.35		
						454	462	504.65	1007.28	1007.46	-0.17	0	37	0.0088187	K.ALDLDSSCK.E		14.07		
						506	513	509.71	1017.41	1017.55	-0.14	0	39	0.0103335	R.LILEQMQK.D	Oxidation (M)	13.99		
						534	543	558.74	1115.47	1115.64	-0.17	0	52	0.0004907	K.LMDVGLIAIR.-	Oxidation (M)	20.26		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49368	11%	285	6	61066	6.1	P49368|TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4												24	1
						238	248	640.27	1278.53	1278.71	-0.18	0	35	0.0225139	R.IVLLDSSLEYK.K		20.48		
						307	313	379.67	757.33	757.44	-0.11	0	36	0.0261137	R.ANITAIR.R		13.43		
						371	377	423.7	845.38	845.48	-0.1	0	43	0.0057683	K.ACTILLR.G		17.77		
						439	449	583.77	1165.52	1165.68	-0.16	0	51	0.0005238	R.AVAQALEVIPR.T		19.79		
						450	461	667.24	1332.47	1332.68	-0.21	0	51	0.0005934	R.TLIQNCGASTIR.L		15.06		
						508	518	593.27	1184.53	1184.71	-0.19	0	70	8.87E-06	K.TAVETAVLLLR.I		21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49748	7%	200	4	70745	8.9	P49748|ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1												24	1
						342	353	614.69	1227.37	1227.57	-0.21	0	56	0.0001312	R.FGMAAALAGTMR.G	2 Oxidation (M)	14.78		
						460	469	589.23	1176.44	1176.61	-0.18	0	41	0.0055289	R.IFEGTNDILR.L		19.87		
						539	550	653.26	1304.51	1304.7	-0.19	0	37	0.0143915	R.ALEQFATVVEAK.L		20		

						557	567	658.78	1315.54	1315.72	-0.19	0	66	1.93E-05	K.GIVNEQFLLQR.L		20.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10809	35%	1027	19	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												25	1
						97	121	853.96	2558.85	2559.24	-0.39	0	85	2.43E-07	K.LVQDVANNTNEEAGDGTTTATVLAR.S		19.18		
						206	218	760.77	1519.54	1519.74	-0.21	0	66	1.93E-05	K.TLNDELEIIEGMK.F	Oxidation (M)	20.71		
						222	233	695.25	1388.49	1388.7	-0.21	0	58	0.0001107	R.GYISPYFINTSK.G		20.1		
						251	268	640.26	1917.75	1918.06	-0.32	0	52	0.0003533	K.ISSIQSIVPALEIANAHR.K		20.84		
						293	301	456.72	911.43	911.58	-0.15	0	61	5.20E-05	K.VGLQVVAVK.A		18.84		
						302	309	417.12	832.23	832.38	-0.15	0	34	0.0176663	K.APGFGDNR.K		12.79		
						345	359	549.55	1645.63	1645.9	-0.26	1	51	0.0004869	K.VGEVIVTKDDAMLLK.G	Oxidation (M)	19.23		
						353	359	411.14	820.26	820.4	-0.14	0	31	0.0490034	K.DDAMLLK.G	Oxidation (M)	14.48		
						397	405	451.2	900.39	900.53	-0.14	0	34	0.0375994	K.LSDGVAVLK.V		16.8		
						406	417	617.21	1232.4	1232.59	-0.19	0	92	4.07E-08	K.VGGTSDVEVNEK.K		12.66		
						421	429	480.68	959.34	959.5	-0.16	0	59	0.0001226	R.VTDALNATR.A		12.92		
						430	446	842.84	1683.67	1683.9	-0.23	0	52	0.0003988	R.AAVEEGIVLGGGCALLR.C		20.62		
						447	462	886.28	1770.54	1770.85	-0.31	0	70	5.73E-06	R.CIPALDSLTPANEDQK.I		20.01		
						463	469	393.19	784.37	784.51	-0.13	0	42	0.0047403	K.IGIEIIK.R		19.62		
						463	470	471.24	940.46	940.61	-0.15	1	36	0.0156848	K.IGIEIIKR.T		18.58		
						471	481	401.51	1201.51	1201.71	-0.2	1	57	0.0001618	R.TLKIPAMTIAK.N	Oxidation (M)	15.32		
						474	481	430.68	859.35	859.48	-0.14	0	56	0.0002317	K.IPAMTIAK.N	Oxidation (M)	12.62		
						482	493	608.24	1214.46	1214.65	-0.19	0	48	0.0012056	K.NAGVEGSLIVEK.I		18.49		
						517	523	372.16	742.3	742.42	-0.12	0	43	0.0040716	K.GIIDPTK.V		13.96		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14618	21%	523	9	58470	8	P14618|KPYM_HUMAN Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4												25	1
						33	43	599.24	1196.47	1196.64	-0.17	0	49	0.0008144	R.LDIDSPPITAR.N		19.32		
						44	56	680.25	1358.48	1358.7	-0.22	0	62	4.32E-05	R.NTGIICTIGPASR.S		19.1		
						126	135	495.68	989.34	989.5	-0.16	0	59	0.0001062	K.GSGTAEVELK.K		13.22		
						142	151	607.2	1212.38	1212.57	-0.19	0	45	0.001579	K.ITLDNAYMEK.C	Oxidation (M)	17.14		
						189	206	890.31	1778.61	1778.87	-0.26	0	82	3.31E-07	K.GADFLVTEVENGGSLGSK.K		20.67		
						208	224	818.83	1635.65	1635.88	-0.23	0	50	0.0007067	K.GVNLPGAAVDLPAVSEK.D		20.19		
						295	305	571.22	1140.42	1140.6	-0.18	0	48	0.0009847	R.GDLGIEIPAEK.V		19.66		
						423	433	611.23	1220.44	1220.63	-0.18	0	66	1.70E-05	K.CCSGAIIVLTK.S		19.36		
						490	498	498.17	994.32	994.49	-0.17	0	62	3.43E-05	R.VNFAMNVGK.A	Oxidation (M)	14.26		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50990	17%	538	9	60153	5.4	P50990|TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4												25	1
						2	7	353.65	705.29	705.42	-0.13	0	39	0.0094738	M.ALHVPK.A	Acetyl (Protein N-term)	14.61		
						63	74	667.28	1332.55	1332.74	-0.19	0	90	8.07E-08	K.LFVTNDAATILR.E		20.41		
						261	270	593.19	1184.37	1184.54	-0.16	0	61	5.35E-05	K.TAEELMNFSK.G	Oxidation (M)	16.01		
						282	296	686.78	1371.54	1371.74	-0.2	0	88	1.15E-07	K.AIADTGANVVVTGGK.V		16.58		
						327	335	443.19	884.36	884.51	-0.15	0	39	0.0088911	K.TVGATALPR.L		13.53		
						368	378	587.26	1172.51	1172.64	-0.13	0	44	0.0034734	K.EDGAISTIVLR.G		19.84		
						391	400	533.19	1064.37	1064.51	-0.15	0	39	0.008595	R.AVDDGVNTFK.V		14.93		
						441	450	575.71	1149.41	1149.58	-0.18	0	63	3.12E-05	K.FAEAFEAIPR.A		19.97		
						510	520	564.75	1127.48	1127.67	-0.18	0	77	1.67E-06	K.LATNAAVTVLR.V		18.97		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P17987	12%	243	6	60819	5.8	P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=CCT1 PE=1 SV=1												25	1
						1	11	633.19	1264.37	1264.58	-0.2	0	47	0.0011571	-.MEGPLSVFGDR.S	Acetyl (Protein N-term); Oxidation (M)	21.76		
						19	33	766.79	1531.57	1531.8	-0.23	0	59	7.68E-05	R.SQNVMAAASIANIVK.S	Oxidation (M)	19.71		
						190	199	573.74	1145.47	1145.64	-0.17	0	34	0.0302623	R.YPVNSVNILK.A		19.45		
						371	378	430.7	859.38	859.51	-0.14	0	33	0.0470952	R.TSASIILR.G		16.54		
						434	443	574.22	1146.43	1146.6	-0.18	0	33	0.0376584	R.EQLAIAEFAR.S		20.14		
						516	526	603.25	1204.48	1204.68	-0.2	0	37	0.015931	K.FATEAAITILR.I		20.27		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40227	7%	159	4	58444	6.2	P40227|TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3												25	1
						130	138	538.72	1075.42	1075.59	-0.17	0	43	0.0041505	K.ALQFLEEVK.V		20.36		
						200	208	511.19	1020.36	1020.51	-0.15	0	39	0.0085376	K.SETDTSLIR.G		14.39		
						296	307	631.74	1261.47	1261.66	-0.19	0	44	0.0029372	K.GIDPFSLDALSK.E		21.19		
						308	314	379.16	756.31	756.45	-0.14	0	33	0.037295	K.EGIVALR.R		16.76		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48643	7%	207	4	60089	5.5	P48643|TCPE_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1												25	1
						28	35	445.68	889.36	889.49	-0.14	0	40	0.0096886	R.LMGLEALK.S	Oxidation (M)	19.05		
						133	142	547.19	1092.36	1092.52	-0.16	0	76	1.71E-06	R.IADGYEQAAR.V		13.01		
						345	352	462.67	923.32	923.46	-0.14	0	52	0.0003424	R.FSELTAEK.L		13.91		
						515	525	645.74	1289.47	1289.68	-0.21	0	41	0.0058424	K.QQISLATQMVR.M	Oxidation (M)	15.84		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

Q02818	6%	137	3	53846	5.2	Q02818|NUCB1_HUMAN Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4												25	2
						72	81	536.7	1071.38	1071.56	-0.18	0	37	0.0179366	K.LQAANAEDIK.S		13.18		
						350	357	482.66	963.3	963.47	-0.17	0	35	0.0179011	R.FEEELAAR.E		14.82		
						368	377	552.2	1102.39	1102.56	-0.17	0	65	2.89E-05	R.LSQETEALGR.S		13.44		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27797	6%	119	3	48283	4.3	P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1												25	1
						49	55	369.14	736.27	736.41	-0.14	0	38	0.0109454	K.FVLSSGK.F		14.31		
						65	73	488.17	974.32	974.48	-0.16	0	39	0.008995	K.GLQTSQDAR.F		12.01		
						279	286	496.65	991.29	991.46	-0.17	0	44	0.0024942	R.QIDNPDYK.G		12.7		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	4%	116	2	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												25	1
						425	436	655.2	1308.39	1308.59	-0.19	0	81	4.38E-07	K.MDSTANEVEAVK.V	Oxidation (M)	13.27		
						453	461	533.67	1065.33	1065.51	-0.18	0	35	0.0170131	R.TVIDYNGER.T		14.13		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07437	30%	631	12	50095	4.8	P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2												27	2
						47	58	651.23	1300.45	1300.63	-0.18	0	66	1.58E-05	R.ISVYYNEATGGK.Y		17.3		
						63	77	816.3	1630.59	1630.82	-0.23	0	50	0.000641	R.AILVDLEPGTMDSVR.S	Oxidation (M)	20.09		
						163	174	668.25	1334.48	1334.69	-0.21	0	72	4.41E-06	R.IMNTFSVVPSPK.V	Oxidation (M)	19.39		
						242	251	565.71	1129.4	1129.59	-0.18	0	70	8.63E-06	R.FPGQLNADLR.K		19.35		
						263	276	546.19	1635.56	1635.82	-0.26	0	41	0.0046002	R.LHFFMPGFAPLTSR.G	Oxidation (M)	20.48		
						283	297	830.32	1658.63	1658.89	-0.26	0	37	0.0135492	R.ALTVPELTQQVFDAK.N		21.26		
						298	306	549.12	1096.22	1096.41	-0.19	0	48	0.0001393	K.NMMAACDPR.H	2 Oxidation (M)	11.79		
						310	318	520.21	1038.41	1038.59	-0.18	0	36	0.0166446	R.YLTVAAVFR.G		20.52		
						321	336	657.86	1970.56	1970.87	-0.31	1	40	0.0055821	R.MSMKEVDEQMLNVQNK.N	3 Oxidation (M)	12.88		
						325	336	731.74	1461.46	1461.68	-0.21	0	58	9.04E-05	K.EVDEQMLNVQNK.N	Oxidation (M)	13.45		
						351	359	514.71	1027.4	1027.51	-0.11	0	40	0.0073565	K.TAVCDIPPR.G		17.41		
						381	390	623.2	1244.39	1244.59	-0.2	0	52	0.000429	R.ISEQFTAMFR.R	Oxidation (M)	19.48		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P68371	29%	647	12	50255	4.8	P68371|TBB2C_HUMAN Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1												27	2
						47	58	664.74	1327.46	1327.64	-0.18	0	53	0.0003589	R.INVYYNEATGGK.Y		17.61		
						63	77	809.29	1616.57	1616.81	-0.23	0	44	0.0024483	R.AVLVDLEPGTMDSVR.S	Oxidation (M)	19.87		
						163	174	668.25	1334.48	1334.69	-0.21	0	72	4.41E-06	R.IMNTFSVVPSPK.V	Oxidation (M)	19.39		
						242	251	565.71	1129.4	1129.59	-0.18	0	70	8.63E-06	R.FPGQLNADLR.K		19.35		
						263	276	546.19	1635.56	1635.82	-0.26	0	41	0.0046002	R.LHFFMPGFAPLTSR.G	Oxidation (M)	20.48		
						283	297	854.31	1706.61	1706.85	-0.24	0	72	3.90E-06	R.ALTVPELTQQMFDAK.N	Oxidation (M)	20.18		
						298	306	549.12	1096.22	1096.41	-0.19	0	48	0.0001393	K.NMMAACDPR.H	2 Oxidation (M)	11.79		
						310	318	520.21	1038.41	1038.59	-0.18	0	36	0.0166446	R.YLTVAAVFR.G		20.52		
						321	336	657.86	1970.56	1970.87	-0.31	1	40	0.0055821	R.MSMKEVDEQMLNVQNK.N	3 Oxidation (M)	12.88		
						325	336	731.74	1461.46	1461.68	-0.21	0	58	9.04E-05	K.EVDEQMLNVQNK.N	Oxidation (M)	13.45		
						351	359	514.68	1027.34	1027.51	-0.18	0	61	4.37E-05	K.TAVCDIPPR.G		13.1		
						381	390	623.2	1244.39	1244.59	-0.2	0	52	0.000429	R.ISEQFTAMFR.R	Oxidation (M)	19.48		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	23%	644	12	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												27	2
						46	58	720.24	1438.47	1438.66	-0.2	0	80	6.31E-07	K.TGTAEMSSILEER.I	Oxidation (M)	15.87		
						59	73	788.28	1574.55	1574.78	-0.23	0	77	1.30E-06	R.ILGADTSVDLEETGR.V		19.57		
						74	83	500.71	999.41	999.57	-0.17	0	35	0.0260452	R.VLSIGDGIAR.V		19.31		
						134	149	812.84	1623.66	1623.88	-0.22	0	45	0.0021228	R.TGAIVDVPVGEELLGR.V		20.87		
						150	161	586.23	1170.44	1170.62	-0.18	0	73	3.68E-06	R.VVDALGNAIDGK.G		19.13		
						176	182	362.17	722.32	722.44	-0.13	0	49	0.0007644	K.APGIIPR.I		14.1		
						195	204	513.72	1025.42	1025.59	-0.17	0	59	7.29E-05	K.AVDSLVPIGR.G		19.52		
						219	230	658.79	1315.57	1315.73	-0.17	0	65	2.60E-05	K.TSIAIDTIINQK.R		20		
						323	329	438.68	875.34	875.49	-0.15	0	37	0.0171913	R.QMSLLLR.R	Oxidation (M)	17.51		
						435	441	446.68	891.35	891.48	-0.13	0	46	0.0021258	K.LELAQYR.E		17.79		
						467	472	358.67	715.32	715.45	-0.13	0	37	0.0187512	R.LTELLK.Q		16.13		
						494	503	575.22	1148.42	1148.61	-0.18	1	42	0.0045044	R.GYLDKLEPSK.I		18.87		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BQE3	17%	324	7	50548	5	Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1												27	1
						65	79	851.33	1700.64	1700.9	-0.26	0	55	0.0002093	R.AVFVDLEPTVIDEVR.T		21.22		
						85	96	470.85	1409.52	1409.77	-0.25	0	53	0.0003257	R.QLFHPEQLITGK.E		19.83		
						113	121	543.22	1084.42	1084.61	-0.19	0	38	0.0133432	K.EIIDLVLDR.I		21.18		
						157	163	391.14	780.27	780.4	-0.13	0	37	0.0119284	R.LSVDYGK.K		13.58		
						216	229	573.54	1717.6	1717.87	-0.27	0	55	0.0001846	R.NLDIERPTYTNLNR.L		19		
						327	336	508.21	1014.41	1014.57	-0.16	0	48	0.0013804	K.DVNAAIATIK.T		19.26		
						423	430	461.64	921.27	921.41	-0.14	0	38	0.0079531	R.EDMAALEK.D	Oxidation (M)	12.24		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08670	11%	288	5	53676	5.1	P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4												27	1

						51	64	714.76	1427.5	1427.7	-0.2	0	56	0.0001658	R.SLYASSPGGVYATR.S		18.7		
						130	139	585.27	1168.53	1168.71	-0.18	0	48	0.001109	K.ILLAELEQLK.G		20.96		
						208	217	544.68	1087.35	1087.53	-0.17	0	74	3.06E-06	R.QDVDNASLAR.L		12.8		
						274	282	512.17	1022.33	1022.5	-0.18	0	39	0.0074955	R.QQYESVAAK.N		12.32		
						295	304	547.19	1092.36	1092.52	-0.16	0	71	5.51E-06	K.FADLSEAANR.N		16.19		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01518	9%	215	4	52222	8.3	Q01518|CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4												27	1
						2	10	567.18	1132.34	1132.52	-0.18	0	41	0.0044919	M.ADMQNLVER.L	Acetyl (Protein N-term); Oxidation (M)	15.95		
						101	113	713.8	1425.59	1425.81	-0.22	0	53	0.0003826	K.LSDLLAPISEQIK.E		20.74		
						156	167	747.7	1493.38	1493.59	-0.21	0	72	1.95E-06	K.EMNDAAMFYTNR.V	2 Oxidation (M)	16.58		
						423	433	618.21	1234.41	1234.59	-0.17	0	49	0.0008975	K.NSLDCEIVSAK.S		18.13		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50995	9%	159	4	54697	7.5	P50995|ANX11_HUMAN Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1												27	1
						192	204	680.26	1358.5	1358.68	-0.19	0	39	0.0090585	R.GTITDAPGFDPLR.D		20.22		
						256	264	505.66	1009.31	1009.47	-0.16	0	31	0.0421491	K.SELSGNFEK.T		13.97		
						347	359	741.21	1480.41	1480.65	-0.24	0	50	0.000427	R.DESTNVDMSLAQR.D	Oxidation (M)	14.76		
						462	470	531.19	1060.37	1060.54	-0.17	0	42	0.0043862	R.SETDLLDIR.S		20.05		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43175	9%	208	4	57356	6.3	O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4												27	1
						59	69	565.72	1129.42	1129.6	-0.18	0	62	4.85E-05	K.VTADVINAAEK.L		14.81		
						76	90	744.76	1487.5	1487.72	-0.22	0	75	2.26E-06	R.AGTGVDNVDLEAATR.K		18.96		
						147	155	450.21	898.41	898.56	-0.15	0	36	0.0190221	K.TLGILGLGR.I		20.57		
						237	247	550.22	1098.43	1098.6	-0.17	0	35	0.0221602	R.GGIVDEGALLR.A		19.79		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UHL4	9%	192	4	54749	5.9	Q9UHL4|DPP2_HUMAN Dipeptidyl-peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=2												27	2
						113	123	596.25	1190.49	1190.6	-0.12	0	54	0.0002832	K.SLPFGAQSTQR.G		17.7		
						204	215	647.2	1292.38	1292.59	-0.2	0	63	2.83E-05	R.DVTADFEGQSPK.C		18.74		
						229	240	699.26	1396.51	1396.7	-0.19	0	34	0.03053	K.DLFLQGAYDTVR.W		20.92		
						296	302	408.66	815.31	815.45	-0.14	0	41	0.0076777	R.LLSEAQR.I		12.49		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P01857	6%	78	2	36596	8.5	P01857|IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1												27	2
						5	16	593.74	1185.47	1185.64	-0.17	0	46	0.0019723	K.GPSVFPLAPSSK.S		19.74		
						132	138	426.14	850.27	850.42	-0.15	0	32	0.0328346	K.DTLMISR.T	Oxidation (M)	14.01		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30101	5%	97	2	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												27	1
						63	73	596.22	1190.43	1190.59	-0.17	0	64	3.25E-05	R.LAPEYEAAATR.L		13.92		
						367	379	684.73	1367.44	1367.66	-0.22	0	33	0.0272507	K.SEPIPESNDGPVK.V		13.75		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21281	4%	91	2	56807	5.6	P21281|VATB2_HUMAN Vacuolar ATP synthase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3												27	1
						83	93	545.7	1089.39	1089.57	-0.17	0	44	0.0032995	R.SGQVLEVSGSK.A		13.23		
						121	130	560.68	1119.34	1119.52	-0.18	0	47	0.0012224	R.TPVSEDMLGR.V	Oxidation (M)	13.32		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14868	4%	99	2	57499	6.1	P14868|SYDC_HUMAN Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2												27	1
						189	197	498.67	995.32	995.5	-0.18	0	42	0.0030733	R.TSTSQAVFR.L		13.27		
						321	330	604.22	1206.43	1206.62	-0.19	0	57	0.0001411	R.FQTEIQTVNK.Q		14.63		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00367	4%	96	2	61701	7.7	P00367|DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2												27	2
						152	162	621.2	1240.39	1240.58	-0.19	0	49	0.0006272	R.YSTDVSVDEVK.A		16.28		
						536	545	540.21	1078.4	1078.57	-0.16	0	47	0.0015722	R.TAAYVNAIEK.V		14.92		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P34897	4%	80	2	56414	8.8	P34897|GLYM_HUMAN Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3												27	1
						417	425	436.18	870.35	870.49	-0.14	0	38	0.0140539	R.SAITPGGLR.L		13.88		
						426	434	443.19	884.36	884.51	-0.15	0	43	0.0039731	R.LGAPALTSR.Q		14.27		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P78371	3%	82	2	57794	6	P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4												27	1
						182	189	435.7	869.39	869.53	-0.14	0	48	0.001009	K.LAVEAVLR.L		19.44		
						224	230	378.15	754.29	754.43	-0.14	0	34	0.0205102	K.IGVNQPK.R		12.28		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99541	29%	582	10	48274	6.3	Q99541|ADFP_HUMAN Adipophilin OS=Homo sapiens GN=ADFP PE=1 SV=2												28	2
						2	15	734.28	1466.54	1466.77	-0.23	0	33	0.0357741	M.ASVAVDPQPSVVTR.V	Acetyl (Protein N-term)	19.36		

						56	71	845.35	1688.69	1688.94	-0.25	0	63	3.20E-05	K.TITSVAMTSALPIIQK.L	Oxidation (M)	19.84		
						94	109	853.87	1705.72	1705.97	-0.25	0	78	1.00E-06	R.LPILNQPSTQIVANAK.G		19.67		
						117	127	532.2	1062.39	1062.56	-0.17	0	67	1.51E-05	K.DAVTTTVTGAK.D		13.42		
						128	140	670.22	1338.42	1338.63	-0.22	0	60	5.46E-05	K.DSVASTITGVMDK.T	Oxidation (M)	19.02		
						143	151	424.15	846.29	846.44	-0.16	0	35	0.0271242	K.GAVTGSVEK.T		12.04		
						154	167	688.27	1374.53	1374.75	-0.21	0	94	3.25E-08	K.SVVSGSINTVLGSR.M		19.8		
						168	182	820.28	1638.56	1638.8	-0.24	0	65	2.09E-05	R.MMQLVSSGVENALTK.S	2 Oxidation (M)	19.23		
						231	238	468.67	935.33	935.48	-0.15	0	35	0.0184465	R.AYQQALSR.V		12.72		
						365	375	583.2	1164.39	1164.59	-0.19	0	54	0.0002872	K.EVSDSLLTSSK.G		17.31		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06576	21%	503	9	56525	5.3	P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3												28	1
						110	121	639.72	1277.43	1277.63	-0.2	0	52	0.0004508	R.TIAMDGTEGLVR.G	Oxidation (M)	16.56		
						125	133	450.2	898.38	898.51	-0.13	0	44	0.0028659	K.VLDSGAPIK.I		13.59		
						134	143	519.72	1037.42	1037.59	-0.17	0	38	0.0100936	K.IPVGPETLGR.I		18.72		
						144	155	701.26	1400.5	1400.7	-0.2	0	62	4.09E-05	R.IMNVIGEPIDER.G	Oxidation (M)	19.06		
						189	198	544.74	1087.47	1087.63	-0.16	0	45	0.002696	K.VVDLLAPYAK.G		20.23		
						213	225	737.32	1472.63	1472.83	-0.2	0	50	0.0006944	K.TVLIMELINNVAK.A	Oxidation (M)	21.61		
						265	279	809.27	1616.52	1616.8	-0.27	0	53	0.0003046	K.VALVYGQMNEPPGAR.A	Oxidation (M)	18.09		
						311	324	718.27	1434.52	1434.75	-0.23	0	98	1.18E-08	R.FTQAGSEVSALLGR.I		20.28		
						407	422	611.19	1830.55	1830.86	-0.31	0	61	4.11E-05	R.IMDPNIVGSEHYDVAR.G	Oxidation (M)	18.67		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15084	10%	178	3	48490	5	Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1												28	2
						217	231	764.32	1526.63	1526.84	-0.21	0	70	6.97E-06	K.LAAVDATVNQVLASR.Y		20.36		
						374	386	742.24	1482.47	1482.71	-0.24	0	50	0.0005397	K.GSFSEQGINEFLR.E		20.49		
						393	409	808.31	1614.6	1614.84	-0.24	0	58	0.000101	R.GSTAPVGGGAFPTIVER.E		19.71		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O14773	4%	71	2	61723	6	O14773|TPP1_HUMAN Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2												28	1
						246	259	492.17	1473.5	1473.75	-0.25	0	33	0.0355875	R.LFGGNFAHQASVAR.V		18.8		
						340	346	425.65	849.29	849.43	-0.13	0	39	0.0099073	R.VNTELMK.A	Oxidation (M)	12.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	8%	204	5	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												29	13
						38	44	447.68	893.34	893.49	-0.15	1	32	0.0403566	R.TIEKFEK.E		12.36		
						38	51	542.84	1625.51	1625.8	-0.29	2	46	0.0013026	R.TIEKFEKEAAEMGK.G	Oxidation (M)	13.39		
						147	154	435.7	869.38	869.53	-0.15	0	50	0.0005752	K.QLIVGVNK.M		14.83		
						167	172	390.64	779.27	779.41	-0.13	0	40	0.0052729	R.YEEIVK.E		13.18		
						173	179	420.16	838.3	838.44	-0.14	0	37	0.0100414	K.EVSTYIK.K		13.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O60664	6%	141	2	47189	5.3	O60664|M6PBP_HUMAN Mannose-6-phosphate receptor-binding protein 1 OS=Homo sapiens GN=M6PRBP1 PE=1 SV=2												29	1
						129	140	605.22	1208.42	1208.57	-0.15	0	67	1.21E-05	K.VSGAQEMVSSAK.D	Oxidation (M)	12.04		
						167	180	690.25	1378.48	1378.69	-0.2	0	74	2.79E-06	K.SVVTGGVQSVMGSR.L	Oxidation (M)	14		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04075	20%	478	8	39851	8.3	P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2												31	1
						15	22	470.67	939.33	939.48	-0.15	0	50	0.0006089	K.ELSDIAHR.I		12.96		
						29	42	666.76	1331.5	1331.69	-0.19	0	92	4.31E-08	K.GILAADESTGSIAK.R		18.48		
						29	43	496.85	1487.54	1487.79	-0.25	1	60	7.15E-05	K.GILAADESTGSIAKR.L		15.05		
						44	57	549.51	1645.51	1645.8	-0.29	1	47	0.0012614	R.LQSIGTENTEENRR.F		12.57		
						61	69	522.7	1043.39	1043.56	-0.17	0	69	9.38E-06	R.QLLLTADDR.V		19		
						305	312	401.17	800.33	800.48	-0.15	0	51	0.0008506	R.ALQASALK.A		13.05		
						323	331	547.2	1092.38	1092.56	-0.17	1	43	0.0030516	K.AAQEEYVKR.A		12.07		
						332	342	566.7	1131.38	1131.57	-0.19	0	67	1.32E-05	R.ALANSLACQGK.Y		13.53		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40121	7%	112	2	38779	5.9	P40121|CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=1												31	1
						254	265	640.71	1279.4	1279.61	-0.2	0	66	1.54E-05	K.VSDATGQMNLTK.V	Oxidation (M)	12.38		
						307	319	695.27	1388.52	1388.74	-0.22	0	46	0.0018754	R.QAALQVAEGFISR.M		20.48		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04792	26%	254	5	22826	6	P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2												35	1
						28	37	582.22	1162.42	1162.61	-0.2	0	51	0.00059	R.LFDQAFGLPR.L		20.68		
						80	89	538.2	1074.38	1074.57	-0.19	0	65	2.43E-05	R.QLSSGVSEIR.H		14.15		
						172	188	953.34	1904.66	1904.98	-0.32	0	32	0.0362179	K.LATQSNEITIPVTFESR.A		20.41		
						189	198	471.18	940.35	940.5	-0.15	0	47	0.001174	R.AQLGGPEAAK.S		12.43		
						189	205	548.53	1642.55	1642.82	-0.26	1	60	6.37E-05	R.AQLGGPEAAKSDETAAK.-		12.53		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38117	10%	127	3	28054	8.2	P38117|ETFB_HUMAN Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3												35	1
						27	35	438.17	874.32	874.48	-0.15	0	46	0.0025625	R.TGVVTDGVK.H		12.77		

						77	85	461.14	920.27	920.44	-0.17	0	48	0.0008035	R.TALAMGADR.G	Oxidation (M)	12.23		
						99	106	427.2	852.39	852.52	-0.13	0	33	0.0276667	R.LGPLQVAR.V		17.3		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51148	23%	226	4	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												37	1
						24	34	543.24	1084.47	1084.65	-0.18	0	40	0.0086731	K.LVLLGESAVGK.S		19.68		
						122	135	698.28	1394.54	1394.79	-0.25	0	53	0.0003245	R.QASPNIVIALAGNK.A		20.07		
						185	196	606.18	1210.35	1210.57	-0.22	0	65	1.36E-05	K.NEPQNATGAPGR.N		11.93		
						199	210	650.21	1298.4	1298.62	-0.22	0	68	7.73E-06	R.GVDLQENNPASR.S		13.51		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92520	17%	202	4	24950	8.5	Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1												37	1
						31	41	605.71	1209.4	1209.58	-0.18	0	61	4.44E-05	K.MDASLGNLFAR.S	Oxidation (M)	20.28		
						42	49	402.64	803.27	803.41	-0.14	0	35	0.0303576	R.SALDTAAR.S		12.61		
						73	84	559.19	1116.37	1116.56	-0.19	0	66	1.92E-05	K.MASGAANVVGPK.I	Oxidation (M)	12.52		
						113	120	431.65	861.29	861.44	-0.16	0	40	0.0070738	K.TGEVLDTK.Y		12.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20340	13%	95	2	23692	5.4	P20340|RAB6A_HUMAN Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3												37	1
						2	13	645.73	1289.45	1289.64	-0.18	1	61	5.90E-05	M.STGGDFGNPLRK.F	Acetyl (Protein N-term)	18.87		
						170	183	731.22	1460.43	1460.69	-0.27	0	35	0.0190628	R.VAAALPGMESTQDR.S	Oxidation (M)	13.91		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q06830	11%	90	2	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												37	1
						17	27	590.71	1179.4	1179.56	-0.16	0	43	0.0029224	K.ATAVMPDGQFK.D	Oxidation (M)	13.55		
						141	151	606.24	1210.47	1210.67	-0.2	0	47	0.0013007	R.QITVNDLPVGR.S		19.37		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62826	10%	74	2	24579	7	P62826|RAN_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3												37	1
						2	12	622.71	1243.4	1243.62	-0.22	0	33	0.0370374	M.AAQGEPQVQFK.L	Acetyl (Protein N-term)	19.16		
						13	23	508.21	1014.4	1014.57	-0.17	0	43	0.0046027	K.LVLVGDGGTGK.T		16.1		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15907	8%	81	2	24588	5.6	Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4												37	1
						42	51	540.69	1079.37	1079.56	-0.19	0	49	0.0007882	K.STIGVEFATR.S		19.2		
						75	82	472.66	943.31	943.48	-0.17	0	32	0.041477	R.AITSAYYR.G		14.37		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00403	6%	82	2	25719	4.7	P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1												39	1
						135	141	422.66	843.3	843.45	-0.15	0	47	0.0014348	R.LLDVDNR.V		14.16		
						172	178	365.14	728.26	728.38	-0.13	0	35	0.0182001	K.TDAIPGR.L		12.61		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61204	24%	213	4	20645	6.8	P61204|ARF3_HUMAN ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2												41	1
						20	30	552.24	1102.46	1102.61	-0.15	0	54	0.0003262	R.ILMVGLDAAGK.T	Oxidation (M)	19.19		
						110	117	496.65	991.29	991.46	-0.17	0	39	0.0078939	R.MLAEDELR.D	Oxidation (M)	14.11		
						118	127	545.28	1088.55	1088.62	-0.07	0	42	0.0049603	R.DAVLLVFANK.Q		20.93		
						128	142	823.74	1645.47	1645.76	-0.29	0	78	8.76E-07	K.QDLPNAMNAAEITDK.L	Oxidation (M)	18.58		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23528	14%	132	2	18719	8.2	P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3												41	1
						2	13	572.72	1143.42	1143.61	-0.19	0	86	1.90E-07	M.ASGVAVSDGVIK.V	Acetyl (Protein N-term)	19.49		
						82	92	669.19	1336.36	1336.62	-0.26	0	45	0.0012067	R.YALYDATYETK.E		19.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P59998	11%	113	2	19768	8.5	P59998|ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3												41	1
						61	71	593.75	1185.48	1185.67	-0.19	0	68	1.21E-05	K.VLIEGSINSVR.V		19.06		
						98	105	505.18	1008.35	1008.54	-0.19	0	45	0.0017958	R.AENFFILR.R		20.59		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61604	48%	283	5	10925	8.9	P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2												43	1
						29	36	430.66	859.3	859.45	-0.15	0	49	0.0010728	K.GGIMLPEK.S	Oxidation (M)	15.12		
						41	54	658.4	1314.79	1314.75	0.03	0	94	3.03E-08	K.VLQATVVAVGSGSK.G		17.21		
						57	66	507.19	1012.37	1012.56	-0.18	0	42	0.0041394	K.GGEIQPVSVK.V		13.4		
						71	80	538.71	1075.41	1075.59	-0.18	0	51	0.0005506	K.VLLPEYGGTK.V		19.01		
						93	99	359.15	716.28	716.37	-0.09	0	48	0.0017649	R.DGDILGK.Y		13.93		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31949	27%	173	3	11847	6.6	P31949|S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2												43	1
						4	12	510.17	1018.32	1018.49	-0.18	0	47	0.0015478	K.ISSPTETER.C		12.29		
						28	36	530.66	1059.31	1059.49	-0.18	0	39	0.0072227	K.DGYNYTLSK.T		16.35		
						53	62	381.14	1140.4	1140.59	-0.19	1	58	0.0001007	K.NQKDPGVLDR.M		12.38		

***Footnotes to Supplemental Table 5:**
Data sets were searched with the Mascot search engine (see Perkins et al. (1999) *Electrophoresis* **20**, 3551-3567).
Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).
Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.
Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest gel slice in which the protein was identified, and the total # of adjacent gel slices in which the protein was found).
Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 6. Proteins identified by HPLC-MS/MS in 3-day BCG human THP-1 phagosome preparation (a).*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05023	7%	291	6	114135	5.3	P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1												1	3
						68	74	372.24	742.46	742.43	0.02	0	52	0.0004802	R.AAEILAR.D		21.06		
						213	227	810.44	1618.86	1618.74	0.12	0	67	1.36E-05	K.VDNSSLTGESEPQTR.S		20.37		
						228	240	760.47	1518.92	1518.7	0.22	0	46	0.0015284	R.SPDFTNENPLETR.N		28.37		
						446	458	616.41	1230.8	1230.65	0.15	0	34	0.0343401	R.AVAGDASESALLK.C		26.88		
						477	487	631.42	1260.82	1260.67	0.15	0	47	0.0015501	K.IVEIPFNSTNK.Y		28.67		
						648	658	618.92	1235.83	1235.7	0.13	0	45	0.0022316	R.LNIPVSQVNPR.D		27.53		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q12913	2%	90	2	147048	5.4	Q12913|PTPRJ_HUMAN Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3												1	1
						113	126	716.97	1431.92	1431.72	0.2	0	44	0.0030437	K.TPSSTGPSPVFDIK.A		28.81		
						1246	1254	497.31	992.6	992.53	0.07	0	47	0.0015536	R.TGTFIAIDR.L		28.28		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35579	3%	176	5	227646	5.5	P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4												2	3
						290	299	603.34	1204.67	1204.63	0.04	0	35	0.025854	K.TDLLLEPYNK.Y		28.99		
						359	373	804.4	1606.79	1606.69	0.1	0	42	0.0037663	R.NTDQASMPDNTAAQK.V	Oxidation (M)	16.61		
						712	718	462.77	923.52	923.49	0.03	0	33	0.0298492	R.VVFQEFR.Q		27.96		
						738	745	489.78	977.55	977.5	0.05	0	35	0.0246192	K.QACVLMIK.A	Oxidation (M)	26.31		
						746	755	597.36	1192.7	1192.61	0.09	0	34	0.0303625	K.ALELDSNLYR.I		28.56		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P46940	3%	165	4	189761	6.1	P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1												2	2
						192	201	579.32	1156.63	1156.56	0.07	0	40	0.0085259	K.YGIQMPAFSK.I	Oxidation (M)	26.83		
						557	567	577.39	1152.77	1152.69	0.08	0	44	0.0023205	K.TLQALQIPAAK.L		28.04		
						1466	1475	536.82	1071.63	1071.58	0.05	0	37	0.0190157	K.LTELGTVDPK.N		25.66		
						1506	1516	618.95	1235.89	1235.65	0.23	0	41	0.0050676	K.LQQTYAALNSK.A		23.7		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y490	1%	134	3	271766	5.8	Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3												2	2
						899	910	610.35	1218.69	1218.6	0.09	0	49	0.0008725	R.MATNAAAQNAIK.K	Oxidation (M)	17.89		
						1321	1332	599.35	1196.69	1196.64	0.05	0	32	0.0381416	K.ALSTDPAAPNLK.S		25.4		
						2032	2043	622.37	1242.73	1242.66	0.08	0	53	0.0003849	K.VLVQNAAGSQEK.L		18.2		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	23%	1313	20 (23)	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												3	3
						2	9	457.29	912.56	912.51	0.05	1	33	0.0412821	M.AKGFYISK.S		20.34		
						141	152	585.36	1168.7	1168.57	0.13	0	41	0.0056576	R.GVGGSQPPDIDK.T		19.34		
						196	204	542.8	1083.58	1083.47	0.12	0	36	0.0165432	R.SEYMEGNVR.K		19.95		
						196	204	550.78	1099.55	1099.46	0.09	0	49	0.001099	R.SEYMEGNVR.K	Oxidation (M)	17.86		
						205	218	497.31	1488.91	1488.77	0.14	1	56	0.0001724	R.KVVATTQMQAADAR.K		18.21		
						205	218	753.5	1504.99	1504.77	0.22	1	66	1.60E-05	R.KVVATTQMQAADAR.K	Oxidation (M)	17.3		
						205	219	545.33	1632.97	1632.86	0.11	2	56	0.0001706	R.KVVATTQMQAADARK.S	Oxidation (M)	16.45		
						206	218	681.38	1360.76	1360.68	0.08	0	78	1.32E-06	K.VVATTQMQAADAR.K		19.64		
						206	218	689.38	1376.75	1376.67	0.08	0	91	5.31E-08	K.VVATTQMQAADAR.K	Oxidation (M)	17.35		
						206	219	502.63	1504.87	1504.77	0.1	1	35	0.0207021	K.VVATTQMQAADARK.S	Oxidation (M)	16.76		
						220	230	672.83	1343.65	1343.55	0.1	0	35	0.0224664	K.SFPCFDEPAMK.A	Oxidation (M)	28.3		
						242	252	609.89	1217.76	1217.63	0.13	0	56	0.0002199	K.DLTALSNMLPK.G	Oxidation (M)	29.34		
						293	301	479.33	956.64	956.54	0.1	0	71	6.23E-06	K.QASNGVLIR.I		20.94		
						364	379	863	1723.98	1723.83	0.16	0	79	8.62E-07	R.ENSLLFDPLSSSSSNK.E		30.86		
						364	381	670.72	2009.13	2008.97	0.16	1	39	0.0069173	R.ENSLLFDPLSSSSSNKER.V		29.42		
						433	442	627.36	1252.71	1252.61	0.1	0	43	0.0036944	K.DLMVLNDVYR.V	Oxidation (M)	29.77		
						486	497	709.92	1417.82	1417.68	0.14	0	68	1.02E-05	R.MLSSFLSEDVFK.Q	Oxidation (M)	31.7		
						596	606	732.42	1462.83	1462.72	0.11	0	33	0.0339383	R.QQQDYWLIDVR.A		31.34		
						632	640	612.84	1223.66	1223.52	0.14	0	47	0.0012505	R.VNYDEENWR.K		26.51		
						642	648	443.79	885.56	885.5	0.06	0	44	0.0031065	K.IQTQLQR.D		18.39		
						649	658	374.56	1120.67	1120.6	0.07	0	38	0.0117192	R.DHSAIPVINR.A		25.68		
						659	673	538.31	1611.89	1611.84	0.06	0	76	1.59E-06	R.AQIINDAFNLASAHK.V		28.95		
						778	793	664.03	1989.07	1988.93	0.14	0	32	0.0316756	K.QWMENPNNNPIHPNLR.S	Oxidation (M)	26.38		
						837	843	472.31	942.61	942.53	0.08	0	46	0.0018483	K.ELWILNR.Y		31.12		
						844	855	734.45	1466.89	1466.78	0.11	0	82	3.69E-07	R.YLSYTLNPDLIR.K		30.51		
						924	935	635.33	1268.65	1268.53	0.13	0	68	1.05E-05	K.DNEETGFGSGTR.A		19.82		
						936	943	451.28	900.55	900.49	0.06	0	57	0.0002074	R.ALEQALEK.T		21.5		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92896	3%	193	4	138382	6.5	Q92896|GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=1												3	1
						223	232	616.83	1231.64	1231.59	0.05	0	58	0.0001235	K.MTAIIFSDYR.L	Oxidation (M)	29.21		
						361	367	425.77	849.53	849.46	0.07	0	37	0.0172046	K.LIAQDYK.V		19.9		
						925	933	569.82	1137.63	1137.54	0.09	0	40	0.0059051	R.QITQNTDYR.L		18.43		
						980	989	611.81	1221.61	1221.53	0.08	0	58	0.0001208	R.LSSDCEDQIR.I		19.25		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20702	1%	67	2	128946	6.2	P20702|ITAX_HUMAN Integrin alpha-X OS=Homo sapiens GN=ITGAX PE=1 SV=3												3	1
						608	614	399.81	797.61	797.51	0.1	0	33	0.0184879	R.GQVLLLR.T		27.95		
						1091	1099	495.8	989.59	989.54	0.05	0	34	0.0362646	R.AQTTTVLEK.Y		18.73		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P16284	7%	288	5	83396	6.5	P16284|PECA1_HUMAN Platelet endothelial cell adhesion molecule OS=Homo sapiens GN=PECAM1 PE=1 SV=1												4	3
						90	100	664.41	1326.81	1326.65	0.17	0	55	0.0002465	K.STESYFIPEVR.I		30.03		
						141	149	471.8	941.59	941.53	0.06	0	57	0.000139	K.EAIQGGIVR.V		22.75		
						362	374	756.43	1510.85	1510.72	0.14	0	59	7.75E-05	K.EDTIVSQTQDFTK.I		28.16		
						457	465	496.28	990.55	990.48	0.07	0	48	0.001076	K.NSNDPAVFK.D		22.36		
						565	577	833.7	1665.39	1665.67	-0.29	0	69	2.60E-06	K.EQEGEYYCTAFNR.A		28.25		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11279	7%	168	3	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												4	11
						138	146	517.32	1032.63	1032.55	0.09	0	71	7.27E-06	K.TVESITDIR.A		27.46		
						327	337	576.35	1150.69	1150.6	0.09	0	58	0.0001135	R.ALQATVGNSYK.C		21.45		
						410	417	438.74	875.47	875.41	0.06	0	39	0.0103284	R.SHAGYQTI.-		20.67		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13473	6%	149	3	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												4	5
						145	152	494.3	986.59	986.55	0.03	0	47	0.0017389	R.IPLNDLFR.C		31.38		
						153	161	526.29	1050.57	1050.5	0.07	0	65	1.88E-05	R.CNSLSTLEK.N		23.09		
						267	273	399.27	796.53	796.46	0.08	0	36	0.013156	R.SHTALLR.L		18.24		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05556	4%	131	3	91714	5.3	P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=1												4	2
						191	202	662.9	1323.78	1323.67	0.1	0	51	0.0004829	K.TVMPYISTTPAK.L	Oxidation (M)	26.15		
						229	238	546.34	1090.67	1090.57	0.1	0	33	0.0419229	K.GEVFNELVGK.Q		29.38		
						785	794	508.34	1014.66	1014.57	0.09	0	48	0.0014102	K.SAVTTVVNPK.Y		20.41		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P42704	3%	202	4	159003	5.8	P42704|LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3												4	1
						171	178	528.86	1055.7	1055.53	0.17	0	34	0.0331924	K.VYLQNEYK.F		24.93		
						188	197	609.35	1216.68	1216.55	0.13	0	50	0.0007906	K.MEEANIQPNR.V	Oxidation (M)	18.59		
						930	941	702.92	1403.82	1403.67	0.15	0	56	0.0001677	R.CVANNQVETLEK.L		23.88		
						1129	1139	636.86	1271.71	1271.65	0.07	0	63	4.03E-05	K.TVLDQQQTPSR.L		19.76		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92542	3%	68	2	79103	5.7	Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2												4	3
						315	323	485.32	968.62	968.53	0.09	0	34	0.0259538	K.APDVTTLPR.N		26.24		
						404	414	520.37	1038.72	1038.62	0.1	0	34	0.0265156	K.SGAGVPAVILR.R		28.59		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06756	3%	142	3	117048	5.5	P06756|ITAV_HUMAN Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2												4	1
						234	241	490.31	978.6	978.49	0.11	0	53	0.0003875	K.YNNQLATR.T		18.72		
						708	718	638.86	1275.71	1275.6	0.12	0	59	9.94E-05	R.QVVCDLGNPMK.A	Oxidation (M)	22.88		
						814	822	469.24	936.46	936.43	0.03	0	32	0.043469	R.NNGPSSFSK.A		18.28		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	13%	545	10	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												5	3
						103	114	638.37	1274.73	1274.64	0.09	0	81	5.15E-07	R.ELISNASDALDK.I		27.74		
						169	177	491.77	981.52	981.48	0.05	0	73	2.94E-06	K.SGTSEFLNK.M		23.7		
						435	448	743.49	1484.97	1484.75	0.22	0	86	1.75E-07	K.GVVDSDDLPLNVSR.E		29.26		
						494	503	380.56	1138.66	1138.57	0.09	0	33	0.0310617	K.LGVIEDHSNR.T		19.57		
						538	546	524.29	1046.56	1046.49	0.08	0	36	0.0194808	K.IYFMAGSSR.K	Oxidation (M)	26.61		
						548	557	575.83	1149.64	1149.53	0.11	0	50	0.0007305	K.EAESSPFVER.L		25.64		
						672	682	645.33	1288.64	1288.59	0.05	0	61	5.68E-05	K.DISTNYYASQK.K		26.22		
						684	690	438.78	875.55	875.45	0.1	0	47	0.00193	K.TFEINPR.H		26.91		
						725	733	497.3	992.58	992.52	0.06	0	47	0.0014071	R.SGYLLPDTK.A		27.82		
						745	754	543.34	1084.67	1084.58	0.1	0	34	0.0310511	R.LSLNIDPDAK.V		28.95		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05362	6%	107	2	58587	8.3	P05362|ICAM1_HUMAN Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=1 SV=2												5	2
						41	56	848.45	1694.89	1694.76	0.13	0	45	0.0018112	R.GGSVLVTCSTSCDQPK.L		23.21		

						274	287	725.42	1448.83	1448.67	0.16	0	62	4.81E-05	K.ASVSVTAEDEGTQR.L		19.92		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P12814	5%	184	4	103563	5.3	P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2												5	1
						134	147	769.48	1536.95	1536.77	0.19	0	35	0.0188891	R.FAIQDISVEETSAK.E		29.78		
						727	738	715.44	1428.86	1428.76	0.1	0	58	0.0001062	R.TINEVENQILTR.D		29.22		
						742	752	677.83	1353.65	1353.6	0.05	0	56	0.0001654	K.GISQEQMNEFR.A	Oxidation (M)	22.57		
						795	803	530.83	1059.65	1059.54	0.11	0	36	0.0232168	R.IMSIVDPNR.L	Oxidation (M)	24.93		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13740	5%	123	2	65745	5.9	Q13740|CD166_HUMAN CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2												5	2
						294	304	628.88	1255.75	1255.6	0.14	0	53	0.0004017	R.SSNTYTLTDVR.R		27.48		
						345	360	838.03	1674.04	1673.84	0.2	0	40	0.0058689	R.QIGDALPVSCTISASR.N		29		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43707	4%	177	3	105245	5.3	O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2												5	1
						153	166	769.48	1536.95	1536.77	0.19	0	35	0.0188891	R.FAIQDISVEETSAK.E		29.78		
						746	757	715.44	1428.86	1428.76	0.1	0	58	0.0001062	R.TINEVENQILTR.D		29.22		
						761	771	684.93	1367.85	1367.61	0.23	0	55	0.0002186	K.GISQEQMQEFR.A	Oxidation (M)	22.35		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8WUM4	2%	74	2	96590	6.1	Q8WUM4|PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1												5	1
						291	298	515.32	1028.63	1028.48	0.15	0	38	0.0139643	R.YDEYVNVK.D		25.38		
						542	553	660.91	1319.81	1319.68	0.13	0	38	0.0123544	K.TMQGSEVVNVLK.S	Oxidation (M)	27.78		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14697	2%	133	3	107263	5.7	Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3												5	1
						158	164	437.27	872.53	872.46	0.07	0	38	0.017044	R.LDLLEDR.S		29.13		
						806	812	350.24	698.47	698.41	0.07	0	31	0.0484943	R.GGTIVPR.W		19.44		
						858	863	403.28	804.54	804.45	0.09	0	33	0.0409869	R.QEFLLR.R		28.78		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08238	22%	844	14	83554	5	P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4												6	4
						42	53	638.38	1274.74	1274.64	0.11	0	65	2.22E-05	R.ELISNASDALDK.I		27.72		
						56	69	513.97	1538.88	1538.75	0.13	1	67	1.39E-05	R.YESLTDPSKLDSGK.E		26.58		
						73	82	597.88	1193.74	1193.64	0.1	0	43	0.0035975	K.IDIIPNPQER.T		28.72		
						83	95	683.42	1364.82	1364.72	0.1	0	70	6.37E-06	R.TLTLVDTGIGMTK.A	Oxidation (M)	28.98		
						96	107	621.92	1241.82	1241.7	0.13	0	83	3.44E-07	K.ADLINNLGTIAK.S		29.98		
						276	284	576.31	1150.61	1150.55	0.06	0	54	0.0003076	K.YIDQEELNK.T		22.22		
						292	306	924.49	1846.96	1846.79	0.17	0	66	1.69E-05	R.NPDDITQEEYGEFYK.S		29.63		
						331	337	415.3	828.58	828.52	0.06	0	38	0.0150757	R.ALLFIPR.R		31.15		
						339	347	540.84	1079.66	1079.53	0.13	0	39	0.0087721	R.APFDLFENK.K		31.54		
						379	392	757.47	1512.92	1512.78	0.14	0	100	6.99E-09	R.GVVDSEDLPLNISR.E		30.11		
						439	448	381.21	1140.61	1140.55	0.06	0	49	0.0008973	K.LGIHEDSTNR.R		18.41		
						482	491	580.85	1159.69	1159.58	0.11	0	58	0.0001409	K.SIYYITGESK.E		28.02		
						492	502	625.36	1248.71	1248.61	0.1	0	66	1.88E-05	K.EQVANSAFVER.V		25.37		
						613	623	648.79	1295.57	1295.48	0.09	0	49	0.0008653	R.DNSTMGYMMAK.K	3 Oxidation (M)	17.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07900	17%	730	12	85006	4.9	P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5												6	2
						47	58	646.37	1290.72	1290.63	0.09	0	71	6.07E-06	R.ELISNSSDALDK.I		26.76		
						47	60	521	1559.98	1559.82	0.16	1	34	0.027932	R.ELISNSSDALDKIR.Y		28.11		
						61	74	513.97	1538.88	1538.75	0.13	1	67	1.39E-05	R.YESLTDPSKLDSGK.E		26.58		
						88	100	683.42	1364.82	1364.72	0.1	0	70	6.37E-06	R.TLTIVDTGIGMTK.A	Oxidation (M)	28.98		
						101	112	621.92	1241.82	1241.7	0.13	0	83	3.44E-07	K.ADLINNLGTIAK.S		29.98		
						284	292	576.31	1150.61	1150.55	0.06	0	54	0.0003076	K.YIDQEELNK.T		22.22		
						300	314	917.54	1833.07	1832.77	0.3	0	49	0.0007844	R.NPDDITNEEYGEFYK.S		29.55		
						347	355	554.84	1107.67	1107.53	0.14	0	52	0.000415	R.APFDLFENR.K		31.8		
						387	400	757.47	1512.92	1512.78	0.14	0	100	6.99E-09	R.GVVDSEDLPLNISR.E		30.11		
						437	443	474.78	947.55	947.44	0.11	0	36	0.0206323	K.FYEQFSK.N		27.02		
						490	499	612.88	1223.74	1223.62	0.12	0	35	0.0191025	K.HIYYITGETK.D		25.41		
						500	510	618.36	1234.71	1234.59	0.12	0	80	7.98E-07	K.DQVANSAFVER.L		26.45		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	11%	355	8	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												6	3
						156	165	545.32	1088.63	1088.55	0.08	0	44	0.0033075	R.ALNEITESGR.I		22.18		
						275	285	563.86	1125.7	1125.61	0.09	0	48	0.0011017	K.LGAILTPNDGR.C		27.58		
						311	325	837.01	1672	1671.89	0.11	0	58	9.47E-05	K.LAENNIQPIFAVTSR.M		30.81		
						489	498	576.81	1151.6	1151.49	0.12	0	39	0.0082076	R.SSQELEGSCR.K		18.07		
						544	554	582.82	1163.63	1163.51	0.12	0	51	0.0006117	R.YNGQVCGGPGR.G		18.45		
						578	586	524.32	1046.63	1046.48	0.14	0	47	0.0015122	R.TTEGCLNPR.R		18.67		
						625	633	572.3	1142.59	1142.51	0.08	0	33	0.0406917	K.YISCAECLK.F		24.81		

						685	693	579.35	1156.69	1156.58	0.11	0	37	0.0148409	R.YLIYVDESR.E		29.37		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08195	9%	311	5 (6)	58023	5.2	P08195|4F2_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=2												6	3
						45	59	496.31	1485.9	1485.77	0.14	1	63	3.85E-05	K.IKVAEDEAEAAAAAK.F		24.28		
						45	59	744.06	1486.1	1485.77	0.33	1	87	1.10E-07	K.IKVAEDEAEAAAAAK.F		24.57		
						47	59	623.36	1244.7	1244.59	0.11	0	88	1.16E-07	K.VAEDEAEAAAAAK.F		19.97		
						187	197	626.87	1251.72	1251.6	0.12	0	44	0.0024802	K.EDFDSLLQSAK.K		31.02		
						203	212	602.39	1202.77	1202.67	0.1	0	44	0.0028527	R.VILDLTPNYR.G		30.02		
						410	423	753.48	1504.95	1504.75	0.2	0	48	0.0011589	K.GQSEDPGSLLSLFR.R		33.98		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27824	4%	112	2	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												6	2
						62	77	886	1769.99	1769.83	0.16	0	49	0.0008788	K.APVPTGEVYFADSFDR.G		31.33		
						574	582	544.81	1087.6	1087.51	0.09	0	63	4.36E-05	K.AEEDEILNR.S		26.06		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P16671	3%	68	2	53589	8.2	P16671|CD36_HUMAN Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2												6	2
						167	173	435.76	869.5	869.41	0.1	0	32	0.0421573	K.SSMFQVR.T	Oxidation (M)	21.14		
						224	231	461.81	921.61	921.52	0.09	0	36	0.0153399	K.VAIIDTYK.G		27.67		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06396	3%	110	2	86043	5.9	P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1												6	1
						585	597	660.43	1318.85	1318.69	0.16	0	67	1.41E-05	K.AGALNSNDAFVLK.T		29.29		
						616	623	444.3	886.58	886.49	0.09	0	43	0.0052804	K.TGAQELLR.V		25.33		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	18%	440	9	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												7	4
						83	92	606.86	1211.7	1211.58	0.11	0	50	0.0007239	R.VEEVGPYTYR.E		27.37		
						116	121	392.75	783.48	783.39	0.09	0	33	0.0271798	K.AYVFER.D		26.94		
						154	161	481.81	961.61	961.52	0.09	0	41	0.0071056	R.EIIEAMLK.A	Oxidation (M)	27.2		
						263	275	823.95	1645.89	1645.74	0.14	0	40	0.0069993	K.DEVLYVFPSDFCR.S		33.05		
						331	348	703.76	2108.25	2107.98	0.27	0	64	2.31E-05	K.NGAPIIMSFPHFYQADER.F	Oxidation (M)	30.55		
						391	402	469.96	1406.85	1406.7	0.15	1	53	0.0003669	K.KLDDFVETGDIR.T		28.72		
						392	402	640.37	1278.73	1278.61	0.12	0	44	0.0025474	K.LDDFVETGDIR.T		29.33		
						460	472	684.78	1367.54	1367.53	0.01	0	63	3.04E-05	K.GQGSMDEGTADER.A	Oxidation (M)	17.13		
						460	477	640.41	1918.21	1917.89	0.32	1	52	0.0003529	K.GQGSMDEGTADERAPLIR.T	Oxidation (M)	23.13		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O60488	7%	213	5	80220	8.7	O60488|ACSL4_HUMAN Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2												7	1
						100	113	817.44	1632.86	1632.73	0.13	0	65	1.90E-05	R.EILSEENEMQPNGK.V	Oxidation (M)	21.27		
						214	223	560.34	1118.67	1118.6	0.07	0	35	0.0276012	K.TALLDISCVK.H		29.94		
						389	397	584.83	1167.64	1167.56	0.09	0	37	0.0143437	K.VQEMNYIQK.T	Oxidation (M)	19.8		
						488	498	630.41	1258.81	1258.64	0.16	0	35	0.0216815	R.VGAPLICCEIK.L		29.16		
						665	670	373.74	745.47	745.44	0.03	0	41	0.007575	R.FEIPIK.V		29.46		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51659	6%	132	3	80092	9	P51659|DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3												7	1
						11	23	585.4	1168.78	1168.69	0.09	0	49	0.0009527	R.VVLVTGAGAGLGR.A		28.46		
						302	315	477.27	1428.78	1428.66	0.12	0	34	0.0250161	K.IDSEGGVSANHTSR.A		17.61		
						316	331	734.45	1466.88	1466.74	0.15	0	50	0.0007304	R.ATSTATSGFAGAIGQK.L		27.55		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15311	5%	106	3	69484	5.9	P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4												7	2
						144	151	449.75	897.5	897.42	0.08	0	34	0.0241068	K.SGYLSSER.L		19.93		
						185	193	556.8	1111.59	1111.52	0.07	0	37	0.0143398	K.DNAMLEYLK.I	Oxidation (M)	28.5		
						295	306	496.96	1487.85	1487.78	0.07	1	35	0.0224321	R.RKPDTIEVQQMK.A	Oxidation (M)	17.68		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P46459	3%	84	2	83021	6.5	P46459|NSF_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=2												7	1
						188	198	573.37	1144.72	1144.61	0.11	0	37	0.016704	K.AENSSLNLIGK.A		27.98		
						284	293	541.85	1081.69	1081.61	0.08	0	47	0.0013082	K.VVNGPEILNK.Y		27.24		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11142	17%	531	9	71082	5.4	P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1												8	2
						26	36	614.86	1227.71	1227.62	0.09	0	64	3.18E-05	K.VEIIANDQGNR.T		21.65		
						37	49	744.42	1486.83	1486.69	0.13	0	73	3.42E-06	R.TTPSYVAFTDTER.L		28.91		
						57	71	833.51	1665	1664.78	0.21	0	106	1.60E-09	K.NQVAMNPTNTVFDAK.R	Oxidation (M)	27.56		
						129	137	497.31	992.61	992.52	0.09	0	33	0.0328654	K.EIAEAYLGK.T		27.87		
						160	171	600.36	1198.71	1198.67	0.04	0	43	0.0042405	K.DAGTIAGLNVLR.I		31.07		
						172	187	830.52	1659.02	1658.89	0.13	0	54	0.0002652	R.IINEPTAAAIAYGLDK.K		31.12		
						221	236	564.59	1690.76	1690.72	0.04	0	50	0.000655	K.STAGDTHLGGEDFDNR.M		23.7		

						349	357	541.35	1080.68	1080.56	0.12	0	33	0.033459	K.LLQDFFNGK.E		31.41		
						540	550	660.36	1318.71	1318.59	0.12	0	44	0.0032034	K.NSLESYAFNMK.A	Oxidation (M)	28.78		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38646	14%	436	8	73920	5.9	P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2												8	1
						77	85	479.78	957.55	957.49	0.06	0	44	0.0033033	K.VLENAEGAR.T		18.31		
						108	121	784.95	1567.88	1567.76	0.11	0	71	4.87E-06	R.QAVTNPNNTFYATK.R		26.65		
						127	135	575.31	1148.6	1148.55	0.05	1	42	0.0042427	R.RYDDPEVQK.D		18.27		
						207	218	621.95	1241.89	1241.67	0.21	0	67	1.30E-05	K.DAGQISGLNVLR.V		30.3		
						219	234	823.48	1644.94	1644.87	0.07	0	43	0.0035962	R.VINEPTAAALAYGLDK.S		31.03		
						349	360	681.41	1360.81	1360.74	0.08	0	41	0.0056221	R.AQFEGIVTDLIR.R		33.14		
						395	405	645.91	1289.81	1289.67	0.14	0	41	0.0051809	K.VQQTVQDLFGR.A		29.99		
						635	646	616.4	1230.79	1230.66	0.13	0	87	1.52E-07	R.QAASSLQQASLK.L		20.91		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	12%	316	6	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												8	2
						50	60	614.86	1227.71	1227.62	0.09	0	64	3.18E-05	R.VEIIANDQGNR.I		21.65		
						61	74	783.97	1565.93	1565.77	0.16	0	47	0.0013478	R.ITPSYVAFTPEGER.L		29.78		
						82	96	839.46	1676.9	1676.8	0.1	0	47	0.0014473	K.NQLTSNPENTVFDAK.R		28.56		
						186	197	617.35	1232.69	1232.62	0.07	0	55	0.0002581	K.DAGTIAGLNVMR.I	Oxidation (M)	28.43		
						198	213	830.52	1659.02	1658.89	0.13	0	54	0.0002652	R.IINEPTAAAIAYGLDK.R		31.12		
						524	532	537.81	1073.6	1073.55	0.06	0	50	0.0007741	K.ITITNDQNR.L		19.35		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13667	5%	150	3	73229	5	P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2												8	1
						235	245	567.32	1132.63	1132.56	0.07	0	47	0.0015139	K.VDATAETDLAK.R		21.74		
						350	362	729.92	1457.83	1457.75	0.08	0	53	0.00034	K.VSQGQLVVMQPEK.F	Oxidation (M)	23.61		
						534	543	584.81	1167.62	1167.55	0.07	0	49	0.0008407	K.TFDSIVMDPK.K	Oxidation (M)	28.22		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	5%	144	3	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												8	2
						28	35	488.79	975.57	975.54	0.03	0	41	0.0062082	K.QLFDQVVK.T		29.04		
						361	370	616.39	1230.76	1230.58	0.18	0	44	0.002881	K.AQQELEEQTR.R		18.62		
						449	458	603.81	1205.6	1205.56	0.04	0	58	0.0001066	K.AQMVQEDLEK.T	Oxidation (M)	19.7		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13796	3%	89	2	70815	5.2	P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5												8	3
						133	141	545.27	1088.53	1088.46	0.07	0	45	0.0028347	K.ALENDPDCR.H		18.44		
						348	357	568.35	1134.69	1134.6	0.09	0	44	0.0029979	R.QFVTATDVVR.G		28.09		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49748	6%	172	4	70745	8.9	P49748|ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1												9	1
						265	276	578.85	1155.69	1155.61	0.08	0	54	0.0002757	K.TPVTDPATGAVK.E		20.25		
						342	353	614.82	1227.62	1227.57	0.05	0	45	0.002339	R.FGMAAALAGTMR.G	2 Oxidation (M)	25.94		
						460	469	589.34	1176.66	1176.61	0.05	0	35	0.0242872	R.IFEGTNDILR.L		29.72		
						532	538	366.21	730.4	730.4	0.01	0	37	0.0204142	R.SGELAVR.A		19.52		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23786	5%	125	3	74244	8.4	P23786|CPT2_HUMAN Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2												9	1
						143	151	563.29	1124.56	1124.51	0.05	0	33	0.0307344	K.SEYNDQLTR.A		20.73		
						306	316	619.83	1237.64	1237.56	0.08	0	54	0.0002613	K.LMSSGNEESLR.K	Oxidation (M)	19.35		
						545	554	549.29	1096.56	1096.46	0.1	0	38	0.011611	K.EAAMGQGFDR.H	Oxidation (M)	19.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11117	4%	79	2	48713	6.3	P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3												9	2
						154	161	472.32	942.62	942.47	0.14	0	32	0.0447516	K.FPLGPCPR.Y		28.33		
						255	265	584.43	1166.85	1166.71	0.14	0	47	0.0009598	R.LQGGVLLAQIR.K		30.77		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15833	4%	120	2	66853	6.1	Q15833|STXB2_HUMAN Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=2 SV=1												9	1
						214	225	600.81	1199.62	1199.57	0.05	0	71	5.64E-06	K.ADTPSLGEGPEK.T		21.73		
						415	424	530.81	1059.61	1059.52	0.09	0	49	0.0012825	R.NGVSEENLAK.L		19.65		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04843	3%	86	2	68641	6	P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1												9	1
						117	126	490.81	979.61	979.57	0.04	0	38	0.0110959	K.LPVALDPGAK.I		28.25		
						194	204	656.33	1310.64	1310.61	0.03	0	48	0.000983	R.SEDLLDYGPFR.D		32.73		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31948	3%	70	2	63227	6.4	P31948|STIP1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1												9	1
						110	118	532.33	1062.64	1062.48	0.17	0	33	0.0396809	K.EGLQNMEAR.L	Oxidation (M)	18.3		
						145	153	533.32	1064.62	1064.55	0.07	0	38	0.010693	R.TLLSDPTYR.E		28.16		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P02545	3%	87	2	74380	6.6	P02545|LMNA_HUMAN Lamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1												9	1
						51	60	545.35	1088.68	1088.55	0.14	0	55	0.0002538	R.SLETENAGLR.L		22.12		
						124	133	522.3	1042.59	1042.54	0.05	0	32	0.0487385	K.EGDLIAAQAR.L		23.85		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10809	20%	751	14	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												10	2
						222	233	695.4	1388.78	1388.7	0.08	0	49	0.0009237	R.GYISPYFINTSK.G		30.77		
						293	301	456.81	911.61	911.58	0.03	0	68	1.01E-05	K.VGLQVVAVK.A		28.36		
						302	309	417.24	832.47	832.38	0.09	0	42	0.0050953	K.APGFGDNR.K		19.76		
						345	352	422.77	843.53	843.51	0.03	0	35	0.0287923	K.VGEVIVTK.D		21.21		
						397	405	451.31	900.6	900.53	0.07	0	65	2.87E-05	K.LSDGVAVLK.V		27.54		
						406	417	617.34	1232.67	1232.59	0.08	0	82	5.01E-07	K.VGGTSDVEVNEK.K		19.15		
						406	418	454.58	1360.72	1360.68	0.04	1	46	0.0018193	K.VGGTSDVEVNEKK.D		18.16		
						406	420	544.97	1631.89	1631.81	0.07	2	59	8.24E-05	K.VGGTSDVEVNEKKDR.V		17.88		
						421	429	480.84	959.66	959.5	0.15	0	59	0.0001092	R.VTDALNATR.A		21.08		
						447	462	886.52	1771.03	1770.85	0.19	0	56	0.0001569	R.CIPALDSLTPANEDQK.I		30.55		
						463	469	393.27	784.52	784.51	0.01	0	42	0.0044805	K.IGIEIIK.R		29.91		
						471	481	401.59	1201.73	1201.71	0.02	1	50	0.000779	R.TLKIPAMTIAK.N	Oxidation (M)	26.8		
						474	481	430.76	859.5	859.48	0.02	0	44	0.0042125	K.IPAMTIAK.N	Oxidation (M)	19.23		
						482	493	608.38	1214.75	1214.65	0.1	0	55	0.0002617	K.NAGVEGSLIVEK.I		28.1		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H4M9	6%	129	3	60646	6.3	Q9H4M9|EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2												10	1
						221	231	674.88	1347.75	1347.65	0.1	0	44	0.0030058	K.ADQIETQQLMR.V	Oxidation (M)	22.76		
						243	251	520.84	1039.66	1039.6	0.06	0	32	0.0458763	K.IINTPEVVR.V		27.37		
						399	410	695.92	1389.82	1389.68	0.14	0	54	0.0002981	R.QEESLMPSQVVK.G	Oxidation (M)	26.07		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48643	3%	101	2	60089	5.5	P48643|TCPE_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1												10	1
						133	142	547.33	1092.65	1092.52	0.13	0	53	0.0003268	R.IADGYEQAAR.V		20.32		
						345	352	462.77	923.53	923.46	0.07	0	49	0.000726	R.FSELTAEK.L		22.84		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01518	34%	700	13	52222	8.3	Q01518|CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4												11	3
						2	10	567.3	1132.59	1132.52	0.07	0	47	0.0015671	M.ADMQNLVER.L	Acetyl (Protein N-term); Oxidation (M)	27.07		
						18	29	466.91	1397.69	1397.64	0.06	0	43	0.0037003	R.LEAVSHTSDMHR.G	Oxidation (M)	17.5		
						85	100	879.49	1756.97	1756.88	0.1	0	33	0.0278254	R.ALLVTASQCQQPAENK.L		26.86		
						101	113	713.93	1425.84	1425.81	0.03	0	78	1.07E-06	K.LSDLLAPISEQIK.E		32.16		
						156	167	747.85	1493.68	1493.59	0.09	0	66	1.92E-05	K.EMNDAAMFYTNR.V	2 Oxidation (M)	27.46		
						295	312	460.26	1837.03	1836.97	0.05	0	38	0.0107744	R.SGPKPFSAPKPQTSPSPK.R		19.43		
						317	327	404.92	1211.73	1211.68	0.05	1	38	0.0105045	K.KEPAVLELEGK.K		27.99		
						331	348	1037.06	2072.1	2072.03	0.07	0	78	8.49E-07	R.VENQENVSNLVIEDTELK.Q		31.32		
						349	355	442.78	883.54	883.48	0.06	0	32	0.0467494	K.QVAYIYK.C		26.15		
						367	376	582.32	1162.62	1162.57	0.06	0	69	1.04E-05	K.INSITVDNCK.K		21.46		
						367	377	431.26	1290.75	1290.66	0.09	1	47	0.001393	K.INSITVDNCKK.L		19.22		
						423	433	618.33	1234.64	1234.59	0.06	0	70	7.47E-06	K.NSLDCEIVSAK.S		27.9		
						434	458	943.16	2826.46	2826.31	0.16	0	34	0.0193334	K.SSEMNVLIPTEGGDFNEFPVPE	Oxidation (M)	33.62		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30101	23%	501	10	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												11	2
						63	73	596.35	1190.68	1190.59	0.08	0	55	0.0002498	R.LAPEYEAAATR.L		23.48		
						95	104	542.8	1083.58	1083.56	0.02	0	41	0.0062033	K.YGVSGYPTLK.I		28.59		
						131	140	498.32	994.62	994.56	0.06	0	43	0.0034004	K.QAGPASVPLR.T		22.68		
						336	344	594.8	1187.58	1187.53	0.05	0	46	0.0020036	K.FVMQEEFSR.D	Oxidation (M)	26.73		
						367	379	684.89	1367.77	1367.66	0.12	0	53	0.0003589	K.SEPIPESNDGPVK.V		22.3		
						423	433	399.92	1196.73	1196.71	0.02	1	47	0.0013064	K.LSKDPNIVIAK.M		22.54		
						434	448	840.94	1679.87	1679.75	0.13	0	95	2.07E-08	K.MDATANDVPSPYEVR.G	Oxidation (M)	28.16		
						449	460	671.37	1340.72	1340.68	0.04	0	34	0.0260904	R.GFPTIYFSPANK.K		32.07		
						472	482	685.88	1369.74	1369.69	0.06	0	49	0.0009086	R.ELSDFISYLQR.E		34.28		
						483	496	527.3	1578.87	1578.83	0.04	0	39	0.0082772	R.EATNPPVIQEEKPK.K		20.04		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08670	23%	491	9	53676	5.1	P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4												11	4
						14	28	504.3	1509.88	1509.7	0.18	0	41	0.0045534	R.MFGGPGTASRPSSSR.S	Oxidation (M)	18.73		
						101	113	529.96	1586.86	1586.79	0.07	1	58	0.0001245	R.TNEKVELQELNDR.F		27.2		
						130	139	585.37	1168.73	1168.71	0.03	0	62	4.04E-05	K.ILLAELEQLK.G		32.91		
						197	207	662.37	1322.73	1322.61	0.12	0	43	0.0033539	R.EEAENTLQSFR.Q		28.51		
						208	217	544.8	1087.58	1087.53	0.05	0	74	3.40E-06	R.QDVDNASLAR.L		19.82		
						274	282	512.27	1022.52	1022.5	0.02	0	60	6.83E-05	R.QQYESVAAK.N		18.77		
						295	304	547.31	1092.6	1092.52	0.08	0	66	1.71E-05	K.FADLSEAANR.N		27.38		

						365	378	589.64	1765.9	1765.8	0.1	1	42	0.0035983	R.LQDEIQNMKEEMAR.H	2 Oxidation (M)	19.17		
						411	424	785.99	1569.97	1569.89	0.09	0	44	0.0029714	R.ISLPLPNFSSLNLR.E		34.63		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	10%	248	5	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												11	1
						223	230	496.29	990.57	990.54	0.04	0	52	0.0004465	K.ENLLDFIK.H		34.08		
						317	326	611.84	1221.66	1221.62	0.05	0	32	0.0463354	R.LITLEEEMTK.Y	Oxidation (M)	28.2		
						327	338	484.6	1450.77	1450.69	0.08	0	46	0.0016403	K.YKPESEELTAER.I		20.77		
						376	385	607.32	1212.63	1212.53	0.1	0	34	0.0267198	K.NFEDVAFDEK.K		29.98		
						425	436	655.37	1308.72	1308.59	0.13	0	83	3.34E-07	K.MDSTANEVEAVK.V	Oxidation (M)	20.6		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31146	8%	160	3	51678	6.3	P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4												11	1
						384	393	513.82	1025.63	1025.61	0.02	0	45	0.0018376	R.DAGPLLISLK.D		32.34		
						417	432	751.9	1501.79	1501.7	0.09	0	75	2.53E-06	R.AAPEASGTPSSDAVSR.L		19.13		
						440	449	579.36	1156.7	1156.65	0.05	0	40	0.0075589	K.LQATVQELQK.R		25.22		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21281	7%	116	3	56807	5.6	P21281|VATB2_HUMAN Vacuolar ATP synthase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3												11	2
						83	93	545.79	1089.56	1089.57	-0.01	0	32	0.0469359	R.SGQVLEVSGSK.A		21.03		
						94	108	760.94	1519.87	1519.79	0.08	0	52	0.000482	K.AVVQVFEGTSGIDAK.K		30.11		
						121	130	560.8	1119.59	1119.52	0.07	0	32	0.04878	R.TPVSEDMLGR.V	Oxidation (M)	21.59		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08571	7%	84	2	40678	5.8	P08571|CD14_HUMAN Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2												11	2
						94	111	889.13	1776.25	1776.06	0.19	0	46	0.0014038	R.LTVGAAQVPAQLLVGALR.V		34.19		
						301	308	488.78	975.54	975.48	0.06	0	38	0.0142222	R.VLDLSCNR.L		26.32		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43175	6%	149	3	57356	6.3	O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4												11	1
						59	69	565.86	1129.7	1129.6	0.1	0	55	0.0002332	K.VTADVINAAEK.L		26.05		
						237	247	550.33	1098.64	1098.6	0.04	0	35	0.0247702	R.GGIVDEGALLR.A		30.24		
						385	394	536.34	1070.66	1070.57	0.09	0	59	0.0001024	K.QADVNLVNAK.L		22.64		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	5%	87	2	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												11	2
						134	149	812.96	1623.91	1623.88	0.03	0	35	0.0189197	R.TGAIVDVPVGEELLGR.V		32.6		
						150	161	586.35	1170.69	1170.62	0.07	0	52	0.000488	R.VVDALGNAIDGK.G		28.85		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06576	29%	754	14	56525	5.3	P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3												12	1
						110	121	639.88	1277.74	1277.63	0.11	0	84	2.97E-07	R.TIAMDGTEGLVR.G	Oxidation (M)	27.45		
						125	133	450.28	898.54	898.51	0.03	0	40	0.0066074	K.VLDSGAPIK.I		21.75		
						125	143	640.4	1918.17	1918.09	0.08	1	36	0.014008	K.VLDSGAPIKIPVGPETLGR.I		30.81		
						134	143	519.81	1037.6	1037.59	0.01	0	36	0.0171992	K.IPVGPETLGR.I		28.45		
						144	155	701.42	1400.83	1400.7	0.14	0	54	0.0002587	R.IMNVIGEPIDER.G	Oxidation (M)	28.85		
						189	198	544.83	1087.65	1087.63	0.03	0	50	0.0008886	K.VVDLLAPYAK.G		31.55		
						202	212	488.31	974.61	974.55	0.05	0	44	0.0032518	K.IGLFGGAGVGK.T		30.85		
						213	225	737.45	1472.89	1472.83	0.06	0	68	1.30E-05	K.TVLIMELINNVAK.A	Oxidation (M)	34.4		
						213	225	737.51	1473.01	1472.83	0.18	0	61	5.00E-05	K.TVLIMELINNVAK.A	Oxidation (M)	34.97		
						265	279	809.48	1616.95	1616.8	0.15	0	84	2.39E-07	K.VALVYGQMNEPPGAR.A	Oxidation (M)	27.93		
						282	294	720.45	1438.89	1438.78	0.11	0	79	9.11E-07	R.VALTGLTVAEYFR.D		33.94		
						311	324	718.42	1434.82	1434.75	0.08	0	86	1.95E-07	R.FTQAGSEVSALLGR.I		31.59		
						388	406	994.57	1987.13	1987.03	0.1	0	60	6.16E-05	R.AIAELGIYPAVDPLDSTSR.I		33.24		
						463	480	680.38	2038.12	2038	0.12	0	34	0.0225927	R.FLSQPFQVAEVFTGHMGK.L	Oxidation (M)	33.11		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07437	27%	610	11	50095	4.8	P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2												12	1
						47	58	651.37	1300.73	1300.63	0.1	0	61	5.90E-05	R.ISVYYNEATGGK.Y		28.02		
						63	77	816.47	1630.93	1630.82	0.1	0	40	0.0074216	R.AILVDLEPGTMDSVR.S	Oxidation (M)	31.16		
						163	174	668.5	1334.99	1334.69	0.3	0	65	1.58E-05	R.IMNTFSVVPSPK.V	Oxidation (M)	29.41		
						242	251	565.84	1129.67	1129.59	0.08	0	75	2.56E-06	R.FPGQLNADLR.K		29.37		
						253	262	580.33	1158.65	1158.62	0.02	0	60	7.69E-05	K.LAVNMVPFPR.L	Oxidation (M)	30.11		
						283	297	830.48	1658.95	1658.89	0.06	0	36	0.0160785	R.ALTVPELTQQVFDAK.N		33.51		
						298	306	549.24	1096.46	1096.41	0.05	0	50	0.0007187	K.NMMAACDPR.H	2 Oxidation (M)	17.61		
						321	336	657.99	1970.95	1970.87	0.08	1	49	0.0006632	R.MSMKEVDEQMLNVQNK.N	3 Oxidation (M)	20.01		
						325	336	731.9	1461.78	1461.68	0.11	0	57	0.00012	K.EVDEQMLNVQNK.N	Oxidation (M)	21.88		
						351	359	514.78	1027.54	1027.51	0.03	0	70	7.31E-06	K.TAVCDIPPR.G		21.05		
						381	390	623.34	1244.66	1244.59	0.08	0	47	0.0015403	R.ISEQFTAMFR.R	Oxidation (M)	29.81		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BQE3	8%	204	3	50548	5	Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1												12	1

						65	79	851.48	1700.94	1700.9	0.04	0	57	0.0001293	R.AVFVDLEPTVIDEVR.T		33.77		
						312	320	633.34	1264.66	1264.54	0.12	0	35	0.0227101	K.YMACCLLYR.G	Oxidation (M)	29.63		
						327	336	508.33	1014.64	1014.57	0.07	0	50	0.0008468	K.DVNAAIATIK.T		29.2		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9NVA2	6%	73	2	49652	6.4	Q9NVA2|SEP11_HUMAN Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3												12	2
						66	79	519.24	1554.71	1554.71	0	0	34	0.0267763	K.FESDPATHNEPGVR.L		19.97		
						84	93	612.85	1223.69	1223.58	0.11	0	39	0.0079449	R.SYELQESNVR.L		24.5		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00367	4%	131	2	61701	7.7	P00367|DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2												12	1
						152	162	621.34	1240.66	1240.58	0.08	0	72	4.29E-06	R.YSTDVSVDEVK.A		27.36		
						536	545	540.34	1078.67	1078.57	0.1	0	60	6.48E-05	R.TAAYVNAIEK.V		26.75		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75955	21%	353	7	47554	7.1	O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3												13	1
						41	51	608.44	1214.87	1214.72	0.14	0	70	7.72E-06	R.ISLNTLTLNVK.S		32.1		
						79	91	751.42	1500.83	1500.68	0.16	0	33	0.0319823	K.EMLAAACQMFLGK.T	2 Oxidation (M)	30.36		
						199	211	742.9	1483.78	1483.72	0.05	0	39	0.0092382	K.VSAQYLSEIEMAK.A	Oxidation (M)	30.53		
						254	261	478.82	955.63	955.55	0.08	0	53	0.0003368	R.VQVQVVER.A		21.92		
						262	274	735.44	1468.87	1468.76	0.11	0	66	1.62E-05	R.AQQVAVQEQEIAR.R		24.05		
						303	317	810.45	1618.89	1618.8	0.09	0	48	0.0010951	K.SQLIMQAEAEAASVR.M	Oxidation (M)	31.45		
						378	392	698.38	1394.76	1394.71	0.05	0	47	0.0012422	K.ITLVSSGSGTMGAAK.V	Oxidation (M)	23.79		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04075	15%	217	5	39851	8.3	P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2												13	3
						15	22	470.78	939.55	939.48	0.07	0	34	0.0233451	K.ELSDIAHR.I		20.75		
						29	42	666.89	1331.76	1331.69	0.07	0	51	0.000537	K.GILAADESTGSIAK.R		28.56		
						44	57	549.63	1645.86	1645.8	0.06	1	42	0.004286	R.LQSIGTENTEENRR.F		19.71		
						61	69	522.82	1043.63	1043.56	0.07	0	47	0.0017877	R.QLLLTADDR.V		29.52		
						332	342	566.83	1131.65	1131.57	0.08	0	44	0.0029334	R.ALANSLACQGK.Y		22.27		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y6N5	15%	323	6	50214	9.2	Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1												13	2
						66	79	735.44	1468.87	1468.75	0.11	0	78	1.09E-06	K.VGAENVAIVEPSER.H		28.43		
						118	125	458.27	914.52	914.47	0.05	0	34	0.0367262	R.VTELNPDK.N		19.75		
						166	173	434.25	866.49	866.45	0.04	0	34	0.0245381	K.IGSNYSVK.T		20.14		
						187	200	767.93	1533.85	1533.78	0.06	0	59	7.78E-05	K.EGNAIFTFPNTPVK.C		32.41		
						388	396	549.33	1096.64	1096.58	0.06	0	33	0.034504	R.VILAEFDYK.A		31.71		
						397	409	754.93	1507.85	1507.72	0.13	0	52	0.0004643	K.AEPLETFPFDQSK.E		32.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14254	11%	198	4	41830	5.2	Q14254|FLOT2_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=1												13	1
						121	128	451.77	901.53	901.5	0.03	0	49	0.0013	K.TQTAVVQR.D		18.45		
						248	256	508.3	1014.58	1014.53	0.04	0	46	0.0020172	R.IQQIAEGEK.V		19.62		
						259	269	600.36	1198.7	1198.66	0.04	0	61	5.69E-05	K.QVLLAQAEAEK.I		28.3		
						308	321	742.48	1482.94	1482.85	0.1	0	42	0.0043276	K.MALVLEALPQIAAK.I	Oxidation (M)	33.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	8%	176	4	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												13	16
						173	179	420.24	838.47	838.44	0.03	0	33	0.0315409	K.EVSTYIK.K		23.22		
						248	255	488.28	974.55	974.54	0.01	0	41	0.0066849	R.LPLQDVYK.I		29.31		
						256	266	513.33	1024.64	1024.6	0.03	0	60	5.87E-05	K.IGGIGTVPVGR.V		28.69		
						431	439	457.8	913.59	913.56	0.03	0	41	0.0054014	R.QTVAVGVIK.A		26.86		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08962	8%	94	2	26474	8.1	P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2												13	13
						111	120	637.34	1272.67	1272.56	0.12	0	54	0.0002815	K.VMSEFNNNFR.Q	Oxidation (M)	28.08		
						121	128	527.29	1052.57	1052.46	0.11	0	40	0.0067617	R.QQMENYPK.N	Oxidation (M)	18.5		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P55084	6%	123	3	51547	9.4	P55084|ECHB_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3												13	1
						53	61	478.82	955.63	955.55	0.08	0	34	0.0274372	R.NVVVVDGVR.T		27.47		
						62	72	607.37	1212.72	1212.64	0.08	0	52	0.0004496	R.TPFLLSGTSYK.D		31.54		
						239	247	568.8	1135.58	1135.55	0.03	0	37	0.0157509	R.LEQDEYALR.S		28.12		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O60664	6%	150	2	47189	5.3	O60664|M6PBP_HUMAN Mannose-6-phosphate receptor-binding protein 1 OS=Homo sapiens GN=M6PRBP1 PE=1 SV=2												13	1
						129	140	605.32	1208.62	1208.57	0.05	0	75	2.21E-06	K.VSGAQEMVSSAK.D	Oxidation (M)	18.41		
						167	180	690.5	1378.99	1378.69	0.3	0	75	1.65E-06	K.SVVTGGVQSVMGSR.L	Oxidation (M)	24		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

Q9HDC9	5%	74	2	46622	5.8	Q9HDC9|APMAP_HUMAN Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2												13	1
						184	195	643.89	1285.77	1285.71	0.06	0	39	0.0092582	K.LLLSSETPIEGK.N		30.09		
						348	356	549.8	1097.58	1097.54	0.04	0	35	0.020787	K.LFSQETVMK.F	Oxidation (M)	24.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P39656	5%	71	2	48893	5.4	P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2												13	1
						61	71	580.36	1158.7	1158.61	0.09	0	35	0.0278083	K.TADDPSLSLIK.Y		30.27		
						223	233	585.39	1168.76	1168.69	0.07	0	37	0.0145866	K.NTLLIAGLQAR.N		31.62		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35613	5%	80	2	42573	5.4	P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2												13	5
						274	282	507.78	1013.55	1013.49	0.05	0	40	0.0085945	R.FFVSSSQGR.S		27.03		
						308	317	537.35	1072.69	1072.59	0.1	0	40	0.0087817	K.GSDQAIITLR.V		29.74		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50454	5%	93	2	46525	8.8	P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2												13	1
						301	308	399.79	797.56	797.5	0.05	0	35	0.0165269	K.AVAISLPK.G		29.39		
						394	405	647.36	1292.71	1292.67	0.04	0	57	0.0001306	R.DTQSGSLLFIGR.L		32.89		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31930	5%	121	2	53297	5.9	P31930|QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3												13	1
						379	390	662.4	1322.79	1322.61	0.17	0	72	3.86E-06	R.LCTSATESEVAR.G		20.93		
						433	442	529.81	1057.61	1057.58	0.03	0	49	0.0012689	R.IAEVDASVVR.E		27.6		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61158	5%	122	2	47797	5.6	P61158|ARP3_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3												13	1
						255	264	547.8	1093.6	1093.58	0.02	0	67	1.27E-05	K.QYTGINAISK.K		27.29		
						349	357	474.27	946.52	946.47	0.05	0	55	0.0002775	K.LSEELSGGR.L		20.97		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52209	4%	120	2	53619	6.8	P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3												13	1
						39	48	561.32	1120.63	1120.54	0.09	0	45	0.002422	K.VDDFLANEAK.G		29.57		
						77	87	596.84	1191.66	1191.58	0.08	0	75	2.40E-06	K.AGQAVDDFIEK.L		29.61		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16181	4%	131	2	50933	8.8	Q16181|SEPT7_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2												13	1
						138	147	622.33	1242.64	1242.55	0.09	0	46	0.0016593	K.FEDYLNAESR.V		29.83		
						417	425	537.8	1073.58	1073.55	0.04	0	54	0.0003205	R.ILEQQNSSR.T		18.76		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06733	4%	76	2	47481	7	P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2												13	1
						93	103	656.85	1311.68	1311.57	0.11	0	38	0.0114071	K.LMIEMDGTENK.S	2 Oxidation (M)	21.79		
						222	228	401.27	800.53	800.46	0.06	0	38	0.0162793	K.EGLELLK.T		30.7		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P80723	41%	296	5	22680	4.6	P80723|BASP_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2												14	1
						39	52	714.34	1426.67	1426.66	0.01	0	46	0.0017075	K.ESEPQAAAEPAEAK.E		19.51		
						150	163	471.61	1411.79	1411.73	0.06	1	58	0.0001096	K.KTEAPAAPAAQETK.S		18.33		
						164	184	644.96	1931.85	1931.87	-0.02	0	83	3.09E-07	K.SDGAPASDSKPGSSEAAPSSK.E		18.2		
						185	198	693.86	1385.7	1385.67	0.03	0	58	0.0001205	K.ETPAATEAPSSTPK.A		19.34		
						199	227	964.83	2891.47	2891.41	0.05	1	51	0.0003565	K.AQGPAASAEEPKPVEAPAANSDQTVTVKE.-		27.49		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48735	4%	99	2	51333	8.9	P48735|IDHP_HUMAN Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2												14	1
						113	122	567.31	1132.61	1132.52	0.09	0	45	0.0023393	K.CATITPDEAR.V		20.74		
						181	188	447.74	893.46	893.42	0.03	0	54	0.0002805	K.ATDFVADR.A		23.12		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60709	34%	663	12 (14)	42052	5.3	P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1												15	14
						2	18	919.46	1836.91	1836.79	0.13	0	57	0.0001131	M.DDDIAALVVDNGSGMCK.A	Acetyl (Protein N-term); Oxidation (M)	35.24		
						19	28	488.76	975.5	975.44	0.06	0	72	4.98E-06	K.AGFAGDDAPR.A		21.68		
						40	50	401.86	1202.57	1202.55	0.02	0	39	0.0102177	R.HQGVMVGMGQK.D	2 Oxidation (M)	18.23		
						40	50	602.35	1202.69	1202.55	0.14	0	42	0.0048457	R.HQGVMVGMGQK.D	2 Oxidation (M)	18.3		
						51	61	599.79	1197.56	1197.51	0.05	0	59	9.65E-05	K.DSYVGDEAQSK.R		20.55		
						51	62	452.23	1353.68	1353.62	0.06	1	48	0.0010367	K.DSYVGDEAQSKR.G		19.73		
						96	113	652.05	1953.13	1953.06	0.07	0	59	7.52E-05	R.VAPEEHPVLLTEAPLNPK.A		30.87		
						184	191	507.76	1013.51	1013.47	0.03	0	38	0.012509	R.DLTDYLMK.I	Oxidation (M)	32.34		
						239	254	895.9	1789.79	1789.88	-0.1	0	114	2.91E-10	K.SYELPDGQVITIGNER.F		33.47		
						285	290	389.26	776.5	776.35	0.15	0	38	0.0125681	K.CDVDIR.K		21.16		
						316	326	589.37	1176.72	1176.61	0.12	0	49	0.0010546	K.EITALAPSTMK.I	Oxidation (M)	26.46		
						329	335	398.26	794.5	794.47	0.03	0	36	0.0158689	K.IIAPPER.K		21.72		
						360	372	750.39	1498.76	1498.67	0.09	0	52	0.0003808	K.QEYDESGPSIVHR.K	Gln->pyro-Glu (N-term Q)	29.34		

						360	372	506.25	1515.73	1515.7	0.03	0	45	0.0025482	K.QEYDESGPSIVHR.K		23.93		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O94905	17%	238	5	38044	5.5	O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1												15	1
						61	72	674.85	1347.69	1347.69	0.01	0	64	3.31E-05	K.SVQTTLQTDEVK.N		27.29		
						214	220	387.25	772.48	772.43	0.04	0	35	0.0314884	K.ALIEAEK.V		21.76		
						221	232	653.92	1305.82	1305.69	0.13	0	65	2.24E-05	K.VAQVAEITYGQK.V		29.12		
						276	285	626.42	1250.82	1250.66	0.16	0	36	0.0176024	K.LTPEYLQLMK.Y	Oxidation (M)	31.3		
						300	314	815.89	1629.77	1629.7	0.07	0	38	0.0100328	K.DIPNMFMDSAGSVSK.Q	2 Oxidation (M)	30.08		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q29836	9%	153	3	40602	5.8	Q29836|1B67_HUMAN HLA class I histocompatibility antigen, B-67 alpha chain OS=Homo sapiens GN=HLA-B PE=2 SV=1												15	1
						60	68	483.25	964.49	964.43	0.07	0	56	0.0001895	R.FDSDAASPR.E		19.95		
						122	132	621.76	1241.51	1241.48	0.03	0	59	9.37E-05	R.MYGCDVGPDGR.L	Oxidation (M)	21.55		
						195	205	450.92	1349.74	1349.69	0.04	1	38	0.012124	R.YLENGKETLQR.A		20.9		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14344	6%	73	2	44364	8.1	Q14344|GNA13_HUMAN Guanine nucleotide-binding protein alpha-13 subunit OS=Homo sapiens GN=GNA13 PE=1 SV=2												15	1
						51	61	529.35	1056.68	1056.62	0.06	0	42	0.0047324	K.ILLLGAGESGK.S		31.78		
						129	140	647.31	1292.6	1292.59	0.01	0	59	9.75E-05	R.APMAAQGMVETR.V	2 Oxidation (M)	19.14		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61160	5%	115	2	45017	6.3	P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1												15	1
						47	53	386.77	771.53	771.45	0.08	0	63	4.84E-05	K.VGNIEIK.D		23.5		
						54	65	675.83	1349.65	1349.61	0.04	0	52	0.0004631	K.DLMVGDEASELR.S	Oxidation (M)	30.69		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q6S8J3	4%	209	3 (4)	122882	5.8	Q6S8J3|A26CA_HUMAN ANKRD26-like family C member 1A OS=Homo sapiens GN=A26C1A PE=1 SV=3												15	1
						719	728	488.76	975.5	975.44	0.06	0	72	4.98E-06	K.AGFAGDDAPR.A		21.68		
						939	954	895.9	1789.79	1789.88	-0.1	0	114	2.91E-10	K.SYELPDGQVITIGNER.F		33.47		
						1060	1072	750.39	1498.76	1498.67	0.09	0	52	0.0003808	K.QEYDESGPSIVHR.K	Gln->pyro-Glu (N-term Q)	29.34		
						1060	1072	506.25	1515.73	1515.7	0.03	0	45	0.0025482	K.QEYDESGPSIVHR.K		23.93		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08754	13%	212	5	41076	5.5	P08754|GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3												16	1
						36	46	529.35	1056.68	1056.62	0.06	0	64	2.88E-05	K.LLLLGAGESGK.S		32.02		
						93	100	439.77	877.53	877.43	0.1	0	35	0.0234475	K.IDFGEAAR.A		29.27		
						133	142	548.77	1095.53	1095.48	0.05	0	36	0.0184158	R.DGGVQACFSR.S		27.53		
						198	205	463.2	924.39	924.41	-0.02	0	36	0.0145108	K.MFDVGGQR.S	Oxidation (M)	24.34		
						249	257	555.77	1109.53	1109.52	0.01	0	42	0.0037516	K.LFDSICNNK.W		29.79		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P03989	6%	79	2	40802	5.5	P03989|1B27_HUMAN HLA class I histocompatibility antigen, B-27 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=2												16	1
						60	68	483.29	964.57	964.43	0.15	0	38	0.0133863	R.FDSDAASPR.E		20.1		
						195	205	450.93	1349.77	1349.69	0.07	1	41	0.0056708	R.YLENGKETLQR.A		21.08		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
A6NMY6	6%	97	2	38806	6.5	A6NMY6|AXA2L_HUMAN Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2												17	2
						105	115	611.84	1221.66	1221.59	0.07	0	49	0.0009245	K.TPAQYDASELK.A		25.6		
						136	145	622.84	1243.67	1243.62	0.06	0	48	0.0012107	R.TNQELQEINR.V		23.64		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61421	14%	217	5	40759	4.9	P61421|VA0D1_HUMAN Vacuolar proton pump subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1												18	4
						188	195	510.79	1019.56	1019.5	0.07	0	37	0.0167173	K.AYLESFYK.F		29.6		
						247	257	615.88	1229.75	1229.68	0.07	0	51	0.0006198	R.LYPEGLAQLAR.A		30.46		
						258	265	484.27	966.53	966.43	0.1	0	31	0.0481851	R.ADDYEQVK.N		18.95		
						266	275	631.34	1260.67	1260.57	0.11	0	32	0.0495961	K.NVADYYPEYK.L		28.13		
						276	288	652.89	1303.77	1303.64	0.13	0	66	1.82E-05	K.LLFEGAGSNPGDK.T		28.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04406	11%	133	3	36201	8.6	P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3												18	2
						201	215	706.46	1410.91	1410.78	0.13	0	39	0.0093778	R.GALQNIIPASTGAAK.A		29.17		
						235	248	766	1529.99	1529.79	0.2	0	52	0.0004287	R.VPTANVSVVDLTCR.L		29.69		
						264	271	415.27	828.52	828.43	0.09	0	43	0.0049157	K.QASEGPLK.G		18.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07355	11%	217	4	38808	7.6	P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2												18	1
						69	77	556.33	1110.65	1110.55	0.11	0	54	0.0002511	R.QDIAFAYQR.R		28.34		
						105	115	611.85	1221.7	1221.59	0.11	0	51	0.0005661	K.TPAQYDASELK.A		23.54		
						136	145	622.87	1243.73	1243.62	0.12	0	79	1.05E-06	R.TNQELQEINR.V		21.77		
						170	176	381.3	760.58	760.45	0.13	0	34	0.0262196	K.LMVALAK.G	Oxidation (M)	25.23		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40926	18%	288	5	35965	8.9	P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=2												19	2
						92	104	670	1337.98	1337.71	0.27	0	70	4.88E-06	K.GCDVVVIPAGVPR.K		29.82		
						230	239	537.31	1072.6	1072.58	0.03	0	67	1.65E-05	R.IQEAGTEVVK.A		19.53		
						242	257	736	1469.98	1469.69	0.29	0	73	3.08E-06	K.AGAGSATLSMAYAGAR.F	Oxidation (M)	26.58		
						258	269	672.4	1342.79	1342.66	0.13	0	42	0.0049224	R.FVFSLVDAMNGK.E	Oxidation (M)	32.01		
						270	279	577.34	1152.67	1152.55	0.12	0	36	0.0178069	K.EGVVECSFVK.S		28.09		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62879	9%	157	3	38048	5.6	P62879|GBB2_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3												19	1
						69	78	509.33	1016.65	1016.55	0.1	0	55	0.0002648	R.LLVSASQDGK.L		20.84		
						198	209	628.38	1254.75	1254.59	0.16	0	50	0.0007829	R.TFVSGACDASIK.L		26.97		
						305	314	505.29	1008.57	1008.51	0.06	0	53	0.0003411	R.AGVLAGHDNR.V		18.06		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00338	8%	167	3	36950	8.4	P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2												19	1
						107	112	371.78	741.54	741.45	0.09	0	41	0.0044581	R.LNLVQR.N		22.94		
						158	169	624.84	1247.67	1247.59	0.08	0	75	2.14E-06	R.VIGSGCNLDSAR.F		21.31		
						306	315	567.84	1133.67	1133.56	0.11	0	51	0.0006446	K.VTLTSEEEAR.L		20.79		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99623	7%	116	2	33276	9.8	Q99623|PHB2_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2												19	3
						148	157	589.37	1176.73	1176.63	0.11	0	44	0.003272	K.FNASQLITQR.A		29.56		
						225	236	608.38	1214.74	1214.61	0.12	0	72	5.33E-06	K.IVQAEGEAEAAK.M		19.01		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H444	16%	253	3 (4)	24935	4.8	Q9H444|CHM4B_HUMAN Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1												20	2
						18	28	577.38	1152.75	1152.59	0.16	0	54	0.000289	K.GGPTPQEAIQR.L		20.59		
						46	55	565.92	1129.82	1129.63	0.19	1	56	0.0001598	K.KIEQELTAAK.K		19.57		
						46	56	420.3	1257.87	1257.73	0.14	2	43	0.0035939	K.KIEQELTAAKK.H		18.53		
						94	107	773.48	1544.94	1544.77	0.17	0	102	4.29E-09	R.EALENANTNTEVLK.N		27.04		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P45880	12%	164	3	32060	7.5	P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2												20	3
						108	120	714.97	1427.92	1427.69	0.23	0	62	4.04E-05	K.LTFDTTFSPNTGK.K		30.47		
						236	247	647.39	1292.77	1292.66	0.11	0	39	0.0092247	K.YQLDPTASISAK.V		28.65		
						268	277	508.85	1015.68	1015.59	0.09	0	63	4.56E-05	K.LTLSALVDGK.S		31.56		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P09525	6%	103	2	36088	5.8	P09525|ANXA4_HUMAN Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4												20	1
						260	270	587.86	1173.7	1173.6	0.1	0	65	2.35E-05	K.GLGTDDNTLIR.V		28.48		
						276	284	546.31	1090.61	1090.53	0.07	0	37	0.0141816	R.AEIDMLDIR.A	Oxidation (M)	29.48		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36543	21%	217	5	26186	7.7	P36543|VATE1_HUMAN Vacuolar proton pump subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1												21	2
						34	42	554.81	1107.6	1107.51	0.09	0	50	0.0006516	K.AEEEFNIEK.G		27.83		
						53	59	496.31	990.61	990.44	0.17	0	35	0.0238757	K.IMEYYEK.K	Oxidation (M)	21.09		
						70	80	669.38	1336.74	1336.62	0.12	0	46	0.0016777	K.IQMSNLMNQAR.L	2 Oxidation (M)	19.02		
						192	199	453.26	904.51	904.46	0.05	0	40	0.0083506	K.VSNTLESR.L		18.72		
						200	212	788.46	1574.91	1574.78	0.13	0	46	0.0018809	R.LDLIAQQMMPEVR.G	2 Oxidation (M)	29.43		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16698	14%	217	4	36330	9.3	Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1												21	1
						50	60	603.33	1204.66	1204.59	0.06	0	34	0.0297528	K.AMLPPNSFQGK.V	Oxidation (M)	25.43		
						61	73	589.39	1176.77	1176.65	0.12	0	48	0.001101	K.VAFITGGGTGLGK.G		29.69		
						98	110	667.86	1333.71	1333.65	0.06	0	80	7.06E-07	K.ATAEQISSQTGNK.V		18.63		
						235	244	556.88	1111.75	1111.64	0.11	0	54	0.0002387	R.FNVIQPGPIK.T		29.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50897	14%	194	3	34627	6.1	P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1												21	4
						105	122	1009.56	2017.12	2016.95	0.17	0	66	1.58E-05	K.LQQGYNAMGFSQGGQFLR.A	Oxidation (M)	30.34		
						166	174	462.79	923.56	923.47	0.09	0	56	0.0001738	K.TLNAGAYSK.V		19.71		
						254	268	897.5	1792.99	1792.88	0.11	0	72	3.64E-06	K.ETIPLQETSLYTQDR.L		30.38		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27105	8%	89	2	31882	7.7	P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3												21	2
						221	232	632.36	1262.7	1262.59	0.11	0	32	0.0423856	K.VIAAEGEMNASR.A	Oxidation (M)	18.76		
						252	263	676.44	1350.86	1350.74	0.12	0	56	0.000155	R.YLQTLTTIAAEK.N		30.21		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P18124	8%	84	2	29264	10.7	P18124|RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1												21	1
						116	124	527.33	1052.64	1052.57	0.07	0	33	0.0346782	R.QIFNGTFVK.L		30.12		
						167	177	585.92	1169.82	1169.68	0.14	0	51	0.0004941	R.IALTDNALIAR.S		30.64		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36542	7%	84	2	33032	9.2	P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1												21	1
						116	126	524.32	1046.63	1046.56	0.07	0	42	0.005304	K.SEVATLTAAGK.E		23.31		
						127	136	538.83	1075.64	1075.56	0.09	0	42	0.0049572	K.EVMLVGIGDK.I	Oxidation (M)	29.3		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61981	17%	240	4	28456	4.8	P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2												23	1
						20	28	524.24	1046.46	1046.4	0.06	0	54	0.000367	R.YDDMAAAMK.N	2 Oxidation (M)	16.82		
						29	42	822.43	1642.85	1642.78	0.07	0	74	2.70E-06	K.NVTELNEPLSNEER.N		25.93		
						62	69	452.28	902.55	902.51	0.04	0	38	0.0147112	R.VISSIEQK.T		18.89		
						133	142	540.81	1079.61	1079.55	0.06	0	44	0.0027129	R.YLAEVATGEK.R		24.72		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63104	14%	180	3	27899	4.7	P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1												23	2
						1	9	581.82	1161.62	1161.57	0.05	1	65	2.48E-05	-.MDKNELVQK.A	Acetyl (Protein N-term); Oxidation (M)	18.67		
						28	41	774.89	1547.76	1547.71	0.05	0	78	1.07E-06	K.SVTEQGAELSNEER.N		22.14		
						104	115	652.88	1303.75	1303.68	0.07	0	37	0.016836	K.FLIPNASQAESK.V		26.76		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07339	13%	237	5	45037	6.1	P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1												23	4
						177	184	440.25	878.49	878.45	0.04	0	45	0.0023804	R.QVFGEATK.Q		19.97		
						195	205	628.34	1254.67	1254.61	0.06	0	46	0.001647	K.FDGILGMAYPR.I	Oxidation (M)	27.89		
						236	253	902.45	1802.89	1802.8	0.09	0	61	5.21E-05	R.DPDAQPGGELMLGGTDSK.Y	Oxidation (M)	26.15		
						349	357	533.31	1064.6	1064.54	0.06	0	45	0.0023303	K.LSPEDYTLK.V		26.41		
						404	411	410.74	819.47	819.42	0.04	0	40	0.0082881	R.VGFAEAAR.L		22.31		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43399	13%	141	2	22281	5.3	O43399|TPD54_HUMAN Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2												23	2
						1	15	831.41	1660.8	1660.74	0.06	0	70	5.79E-06	-.MDSAGQDINLNSPNK.G	Acetyl (Protein N-term); Oxidation (M)	25.84		
						129	139	595.83	1189.65	1189.59	0.05	0	71	6.67E-06	K.TQETLSQAGQK.T		17.42		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31946	11%	156	3	28179	4.8	P31946|1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3												23	1
						21	29	524.24	1046.46	1046.4	0.06	0	54	0.000367	R.YDDMAAAMK.A	2 Oxidation (M)	16.82		
						63	70	452.28	902.55	902.51	0.04	0	38	0.0147112	R.VISSIEQK.T		18.89		
						130	140	591.81	1181.61	1181.56	0.05	0	64	2.42E-05	R.YLSEVASGDNK.Q		20.7		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9NX63	7%	125	2	26421	8.5	Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1												23	1
						28	35	473.28	944.55	944.49	0.06	0	67	1.95E-05	R.LSENVIDR.M		24.2		
						96	104	487.28	972.55	972.5	0.05	0	59	0.0001215	R.AAANEQLTR.A		17.51		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UL25	11%	128	2	24731	8.1	Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3												25	3
						2	16	557.29	1112.58	1112.53	0.04	0	75	2.51E-06	M.AAAGGGGGGAAAAGR.A	Acetyl (Protein N-term)	17.63		
						180	189	604.31	1206.6	1206.56	0.04	0	54	0.0003149	R.MIETAQVDER.A	Oxidation (M)	19.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92520	9%	116	2	24950	8.5	Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1												25	3
						73	84	559.32	1116.63	1116.56	0.07	0	73	3.74E-06	K.MASGAANVVGPK.I	Oxidation (M)	18.15		
						113	120	431.75	861.49	861.44	0.04	0	43	0.0047891	K.TGEVLDTK.Y		18.71		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51148	29%	245	5	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												26	3
						5	18	413.24	1236.7	1236.63	0.06	0	43	0.0033003	R.GGAARPNGPAAGNK.I		15.89		
						24	34	543.34	1084.67	1084.65	0.02	0	39	0.0107239	K.LVLLGESAVGK.S		27.27		
						122	135	698.44	1394.86	1394.79	0.07	0	42	0.0037515	R.QASPNIVIALAGNK.A		28.1		
						185	196	606.32	1210.63	1210.57	0.06	0	58	0.0001183	K.NEPQNATGAPGR.N		16.59		
						199	210	650.34	1298.67	1298.62	0.05	0	63	3.47E-05	R.GVDLQENNPASR.S		21.75		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20340	13%	126	2	23692	5.4	P20340|RAB6A_HUMAN Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3												26	2
						2	13	645.85	1289.68	1289.64	0.05	1	73	3.14E-06	M.STGGDFGNPLRK.F	Acetyl (Protein N-term)	26.06		
						170	183	731.37	1460.73	1460.69	0.04	0	53	0.0003589	R.VAAALPGMESTQDR.S	Oxidation (M)	22.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

Q9H0U4	11%	73	2	22328	5.5	Q9H0U4|RAB1B_HUMAN Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1												26	2
						49	55	388.23	774.45	774.41	0.04	0	34	0.0403395	R.TIELDGK.T		22.07		
						173	187	486.6	1456.77	1456.71	0.06	0	39	0.0098659	R.MGPGAASGGERPNLK.I	Oxidation (M)	17.59		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20339	11%	84	2	23872	8.3	P20339|RAB5A_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2												26	2
						23	33	543.34	1084.67	1084.65	0.02	0	39	0.0107239	K.LVLLGESAVGK.S		27.27		
						184	195	627.84	1253.66	1253.57	0.09	0	46	0.001901	K.NEPQNPGANSAR.G		16.49		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61006	11%	156	3	23824	9.2	P61006|RAB8A_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1												26	2
						49	55	388.23	774.45	774.41	0.04	0	34	0.0403395	R.TIELDGK.R		22.07		
						176	190	514.96	1541.87	1541.78	0.09	1	59	8.39E-05	K.KLEGNSPQGSNQGVK.I		16.45		
						177	190	707.9	1413.78	1413.68	0.09	0	63	3.39E-05	K.LEGNSPQGSNQGVK.I		16.85		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q06830	11%	124	2	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												26	2
						111	120	554.34	1106.66	1106.6	0.06	0	35	0.0232287	R.TIAQDYGVLK.A		26.45		
						141	151	606.37	1210.73	1210.67	0.06	0	58	0.000101	R.QITVNDLPVGR.S		26.75		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92930	10%	113	2	23740	9.2	Q92930|RAB8B_HUMAN Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2												26	2
						49	55	388.23	774.45	774.41	0.04	0	34	0.0403395	R.TIELDGK.K		22.07		
						177	190	660.83	1319.65	1319.58	0.07	0	79	8.35E-07	K.MNDSNSAGAGGPVK.I	Oxidation (M)	16.63		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75396	9%	74	2	24896	8.7	O75396|SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=3												26	1
						29	38	604.82	1207.63	1207.58	0.04	0	42	0.0045775	R.DLQQYQSQAK.Q		20.8		
						170	178	467.27	932.53	932.49	0.04	0	33	0.0484457	K.ANNLSSLSK.K		20.09		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15907	9%	103	2	24588	5.6	Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4												26	1
						14	24	522.34	1042.66	1042.6	0.05	0	54	0.0003506	K.VVLIGDSGVGK.S		26.1		
						34	41	490.77	979.53	979.46	0.07	0	49	0.0008339	R.NEFNLESK.S		25.54		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51149	29%	235	5	23760	6.4	P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1												27	2
						11	21	529.34	1056.66	1056.62	0.04	0	40	0.0086389	K.VIILGDSGVGK.T		26.48		
						22	31	607.34	1212.67	1212.58	0.09	0	40	0.0066044	K.TSLMNQYVNK.K	Oxidation (M)	20.34		
						114	126	738.44	1474.86	1474.75	0.11	0	47	0.0014694	R.DPENFPFVVLGNK.I		30.23		
						147	157	642.35	1282.68	1282.62	0.06	0	36	0.0161029	K.NNIPYFETSAK.E		26.66		
						158	171	795.48	1588.94	1588.82	0.12	0	72	4.16E-06	K.EAINVEQAFQTIAR.N		29.45		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51153	18%	167	3	22988	9.3	P51153|RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=2 SV=1												27	2
						11	21	536.36	1070.71	1070.63	0.08	0	45	0.0025904	K.LLLIGDSGVGK.T		27.74		
						105	116	420.91	1259.71	1259.65	0.06	1	39	0.009008	K.SIKENASAGVER.L		17.02		

						154	167	765.37	1528.73	1528.68	0.05	0	83	3.57E-07	K.SSMNVDEAFSSLAR.D	Oxidation (M)	27.44		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P37802	17%	123	3	22548	8.4	P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3												27	2
						128	139	616.38	1230.75	1230.68	0.07	0	40	0.0080236	R.TLMNLGGLAVAR.D	Oxidation (M)	27.13		
						161	171	640.33	1278.64	1278.58	0.06	0	39	0.0078542	R.NFSDNQLQEGK.N		23.23		
						172	182	609.86	1217.7	1217.62	0.08	0	44	0.003538	K.NVIGLQMGTNR.G	Oxidation (M)	24.92		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04179	14%	146	3	24878	8.3	P04179|SODM_HUMAN Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2												27	1
						69	75	411.74	821.47	821.43	0.04	0	46	0.0018953	K.YQEALAK.G		17.94		
						76	89	712.94	1423.86	1423.8	0.06	0	62	3.97E-05	K.GDVTAQIALQPALK.F		27.05		
						115	123	514.84	1027.67	1027.6	0.07	1	38	0.0114649	K.GELLEAIKR.D		25.7		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62820	11%	96	2	22891	5.9	P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3												27	3
						14	24	536.36	1070.71	1070.63	0.08	0	45	0.0025904	K.LLLIGDSGVGK.S		27.74		
						176	187	531.78	1061.55	1061.48	0.07	0	51	0.0006889	R.MGPGATAGGAEK.S	Oxidation (M)	16.16		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48047	9%	113	2	23377	10	P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1												27	1
						65	73	513.34	1024.66	1024.63	0.03	1	55	0.0002038	R.VAQILKEPK.V		19.79		
						74	84	580.87	1159.73	1159.66	0.07	0	58	0.0001146	K.VAASVLNPYVK.R		26.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63000	9%	176	2	21835	8.8	P63000|RAC1_HUMAN Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1												28	1
						154	163	620.84	1239.66	1239.59	0.06	0	59	7.92E-05	K.YLECSALTQR.G		25.64		
			redundant			167	174	475.78	949.54	949.49	0.06	0	42	0.0043027	K.TVFDEAIR.A		26.56		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23284	16%	127	3	22785	9.3	P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=1												29	1
						44	51	430.74	859.47	859.4	0.06	0	51	0.0008317	R.IGDEDVGR.V		18.04		
						64	76	682.88	1363.76	1363.7	0.06	0	38	0.0118524	K.TVDNFVALATGEK.G		28.51		
						138	150	729.42	1456.82	1456.72	0.1	0	40	0.0077293	K.DTNGSQFFITTVK.T		28.34		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O14950	12%	114	2	19824	4.7	O14950|MRLC2_HUMAN Myosin regulatory light chain MRLC2 OS=Homo sapiens GN=MYLC2B PE=1 SV=2												30	1
						36	45	627.32	1252.62	1252.55	0.07	0	66	1.69E-05	K.EAFNMIDQNR.D	Oxidation (M)	24.58		
						94	104	614.84	1227.66	1227.61	0.05	0	48	0.0014159	K.LNGTDPEDVIR.N		25.84		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15511	17%	74	2	16367	5.5	O15511|ARPC5_HUMAN Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3												31	1
						48	60	666.86	1331.71	1331.69	0.02	0	37	0.0147893	R.QGNMTAALQAALK.N	Oxidation (M)	25.86		
						132	143	535.83	1069.66	1069.62	0.03	0	37	0.0170087	K.ALAAGGVGSIVR.V		25.95		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5QNW6	14%	78	2	13912	10.3	Q5QNW6|H2B2F_HUMAN Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3												32	1
						48	58	390.21	1167.62	1167.59	0.03	0	42	0.0040148	K.QVHPDTGISSK.A		16.9		
						94	100	408.74	815.47	815.45	0.02	0	36	0.0255012	R.EIQTAVR.L		17.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60660	26%	163	3	17090	4.6	P60660|MYL6_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2												33	1
						27	37	679.32	1356.62	1356.62	0	0	37	0.0158523	K.ILYSQCGDVMR.A	Oxidation (M)	24.57		
						38	50	677.88	1353.74	1353.73	0.02	0	70	6.63E-06	R.ALGQNPTNAEVLK.V		25.09		
						95	110	580.3	1737.86	1737.84	0.03	1	56	0.0001539	R.VFDKEGNGTVMGAEIR.H	Oxidation (M)	24.44		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30049	14%	104	2	17479	5.4	P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2												33	2
						137	150	716.37	1430.72	1430.7	0.02	0	72	4.72E-06	K.AQAELVGTADEATR.A		24.79		
						157	165	493.79	985.57	985.54	0.02	0	33	0.0412667	R.IEANEALVK.A		23.87		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10253	3%	117	2	106126	5.6	P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=2												33	4
						838	849	643.86	1285.71	1285.71	0	0	51	0.0005608	R.QQPMALAVALTK.G	Oxidation (M)	26.57		
						892	903	615.85	1229.69	1229.66	0.03	0	66	2.06E-05	R.VTSEGAGLQLQK.V		24.53		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62805	31%	116	3	11360	11.4	P62805|H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2												34	1
						25	36	442.59	1324.75	1324.75	0.01	0	34	0.0266516	R.DNIQGITKPAIR.R		24.75		
						47	56	590.83	1179.65	1179.61	0.03	0	49	0.0009237	R.ISGLIYEETR.G		26.49		

						69	78	567.78	1133.55	1133.54	0.01	0	33	0.0385099	R.DAVTYTEHAK.R		17.73		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01469	13%	83	2	15497	6.6	Q01469|FABP5_HUMAN Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3												34	1
						2	10	522.3	1042.58	1042.54	0.04	0	37	0.0156629	M.ATVQQLEGR.W	Acetyl (Protein N-term)	26.44		
						73	81	513.24	1024.47	1024.45	0.02	0	45	0.0018716	K.FEETTADGR.K		17.64		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P22307	6%	146	3	59640	6.4	P22307|NLTP_HUMAN Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2												35	1
						483	492	522.81	1043.6	1043.56	0.04	1	37	0.0166371	K.GSVLPNSDKK.A		16.92		
						512	522	635.81	1269.61	1269.58	0.03	0	66	1.93E-05	K.MNPQSAFFQGK.L	Oxidation (M)	25.98		
						525	534	534.28	1066.55	1066.52	0.04	0	45	0.0020174	K.ITGNMGLAMK.L	2 Oxidation (M)	17.38		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13510	5%	129	2	45077	7.5	Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4												35	5
						82	92	612.33	1222.64	1222.6	0.04	0	58	0.0001191	K.NMINTFVPSGK.V	Oxidation (M)	25.76		
						93	100	482.26	962.51	962.47	0.03	0	71	5.94E-06	K.VMQVVDEK.L	Oxidation (M)	17.16		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61604	41%	251	4	10925	8.9	P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2												36	1
						29	36	430.75	859.49	859.45	0.04	0	53	0.0004797	K.GGIMLPEK.S	Oxidation (M)	25		
						41	54	658.41	1314.81	1314.75	0.06	0	91	5.60E-08	K.VLQATVVAVGSGSK.G		25.3		
						57	66	507.4	1012.79	1012.56	0.23	0	56	9.45E-05	K.GGEIQPVSVK.V		22.59		
						71	80	538.82	1075.63	1075.59	0.03	0	52	0.00053	K.VLLPEYGGTK.V		26.13		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07602	4%	93	2	59899	5.1	P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2												36	2
						430	438	507.82	1013.62	1013.58	0.05	0	47	0.0018151	K.QEILAALEK.G		27.09		
						439	449	656.33	1310.64	1310.6	0.04	0	46	0.0016732	K.GCSFLPDPYQK.Q		27.26		

***Footnotes to Supplemental Table 6:**
Data sets were searched with the Mascot search engine (see Perkins et al. (1999) *Electrophoresis* **20**, 3551-3567).
Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).
Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.
Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest gel slice in which the protein was identified, and the total # of adjacent gel slices in which the protein was found).
Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 7. Proteins identified by HPLC-MS/MS in 3-day BCG infected human THP-1 phagosome preparation (b).*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1.

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05023	11%	462	9	114135	5.3	P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1												1	2
						68	74	372.21	742.41	742.43	-0.03	0	49	0.0011027	R.AAEILAR.D		14		
						213	227	810.37	1618.73	1618.74	-0.01	0	64	2.46E-05	K.VDNSSLTGESEPQTR.S		13.83		
						228	240	760.37	1518.72	1518.7	0.03	0	67	1.43E-05	R.SPDFTNENPLETR.N		20.38		
						446	458	616.32	1230.63	1230.65	-0.01	0	37	0.0161302	R.AVAGDASESALLK.C		19.29		
						477	487	631.35	1260.68	1260.67	0.01	0	51	0.0005339	K.IVEIPFNSTNK.Y		20.47		
						613	625	466.57	1396.68	1396.74	-0.06	0	32	0.0443235	K.VIMVTGDHPITAK.A	Oxidation (M)	14.78		
						648	658	618.84	1235.67	1235.7	-0.02	0	53	0.0003345	R.LNIPVSQVNPR.D		19.85		
						699	707	544.29	1086.57	1086.59	-0.02	0	39	0.010847	K.LIIVEGCQR.Q		19.16		
						728	743	753.87	1505.73	1505.74	-0.01	0	69	8.59E-06	K.ADIGVAMGIAGSDVSK.Q	Oxidation (M)	19.68		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9HD45	7%	161	4	68584	6.8	Q9HD45|TM9S3_HUMAN Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2												1	2
						60	70	652.82	1303.63	1303.63	0	0	43	0.0035014	K.YFSLPFCVGSK.K		22.6		
						118	125	463.75	925.48	925.49	-0.02	0	31	0.0477793	R.DAFVYAIK.N		20.73		
						419	429	645.28	1288.55	1288.6	-0.04	0	52	0.0005016	R.NLSGQPNFPCR.V		18.68		
						430	440	407.23	1218.66	1218.71	-0.05	0	35	0.0248762	R.VNAVPRPIPEK.K		13.65		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13488	6%	195	4	93680	6.6	Q13488|VPP3_HUMAN Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 OS=Homo sapiens GN=TCIRG1 PE=1 SV=2												1	4
						29	38	566.82	1131.63	1131.63	0	0	59	9.56E-05	R.LGELGLVEFR.D		22.17		
						152	166	533.95	1598.81	1598.85	-0.04	0	33	0.0348526	R.TPLLQAPGGPHQDLR.V		19.37		
						328	337	563.31	1124.61	1124.62	-0.01	0	46	0.0017973	R.DLPALQEALR.D		21.69		
						338	351	497.54	1489.59	1489.65	-0.05	0	58	0.0001156	R.DSSMEEGVSAVAHR.I	Oxidation (M)	13.48		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99805	4%	69	2	76809	7.2	Q99805|TM9S2_HUMAN Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1												1	1
						242	260	541.99	2163.92	2163.97	-0.05	0	33	0.025625	K.HTHIDKPDCSGPPMDISNK.A	Oxidation (M)	12.79		
						504	509	364.7	727.38	727.4	-0.02	0	36	0.0211395	R.TNQIPR.Q		12.57		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15321	4%	85	2	69330	6.7	O15321|TM9S1_HUMAN Transmembrane 9 superfamily member 1 OS=Homo sapiens GN=TM9SF1 PE=2 SV=2												1	1
						38	48	594.83	1187.65	1187.66	0	0	54	0.000345	K.AGDPVILYVNK.V		20.55		
						436	446	624.76	1247.51	1247.54	-0.03	0	32	0.0496245	K.NNASPFDAPCR.T		17.21		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92544	3%	94	2	75211	6.1	Q92544|TM9S4_HUMAN Transmembrane 9 superfamily member 4 OS=Homo sapiens GN=TM9SF4 PE=1 SV=2												1	2
						85	98	818.41	1634.81	1634.83	-0.03	0	59	9.11E-05	R.IVNTPFQVLMNSEK.K	Oxidation (M)	21.65		
						483	488	364.7	727.38	727.4	-0.02	0	36	0.0211395	R.TNQIPR.Q		12.57		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q93050	3%	69	2	97148	6	Q93050|VPP1_HUMAN Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3												1	1
						121	129	553.8	1105.58	1105.6	-0.02	0	37	0.0167574	R.NFLELTELK.F		22.25		
						242	254	774.35	1546.69	1546.71	-0.02	0	32	0.0378064	R.ASLYPCPETPQER.K		19.42		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15118	3%	164	3	144868	5.2	O15118|NPC1_HUMAN Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=1 SV=2												1	2
						608	615	488.24	974.46	974.47	0	0	37	0.0192459	R.SIEDELNR.E		19.11		
						715	726	679.35	1356.69	1356.7	-0.01	0	71	5.72E-06	R.LQGETLDQQLGR.V		19.46		
						998	1010	768.38	1534.75	1534.75	0	0	56	0.0001515	R.FLPMFLSDNPNPK.C	Oxidation (M)	21.6		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62988	29%	82	2	8560	6.6	P62988|UBIQ_HUMAN Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1												2	7
						1	6	391.21	780.4	780.42	-0.02	0	32	0.0452604	-.MQIFVK.T	Oxidation (M)	14.72		
						12	27	894.48	1786.94	1786.92	0.02	0	50	0.0005621	K.TITLEVEPSDTIENVK.A		20.34		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9HC07	11%	112	2	35055	6.5	Q9HC07|TM165_HUMAN Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=1 SV=1												2	2
						43	67	883.12	2646.33	2646.39	-0.05	1	58	7.89E-05	R.NKEPPAPAQQLQPQPVAVQGPEPAR.V		18.88		
						253	263	586.85	1171.68	1171.69	-0.01	0	54	0.0003011	R.SQLTTIVLAAR.E		20.43		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11717	6%	704	14	281056	5.6	P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=2												2	2
						126	136	605.32	1208.62	1208.62	0	0	41	0.0055221	R.VQSSIAFLCGK.T		20.29		
						227	238	636.82	1271.63	1271.61	0.02	0	47	0.0013165	R.ACPPGTAACLVR.G		16.15		
						530	542	696.29	1390.56	1390.59	-0.03	0	77	1.39E-06	R.GCPEDAAVCAVDK.N		16.84		
						1031	1039	475.26	948.5	948.5	0	0	36	0.0215592	K.GTADAFIVR.F		19.5		
						1040	1052	757.36	1512.7	1512.69	0.01	0	67	1.46E-05	R.FVCNDDVYSGPLK.F		19.63		
						1213	1221	515.76	1029.5	1029.53	-0.02	0	37	0.0160466	R.TVEACPVVR.V		13.42		
						1265	1275	604.78	1207.55	1207.54	0.01	0	50	0.0006755	K.LSSDVCPTSDK.S		12.98		
						1373	1386	713.32	1424.62	1424.65	-0.03	0	68	1.06E-05	K.DGAGNSFDLSSLSR.Y		20.69		

						1448	1454	379.23	756.45	756.47	-0.02	0	40	0.0085466	R.DGIIVLK.Y		20.03		
						1536	1545	522.75	1043.49	1043.49	0	0	43	0.0045298	R.AGFTAAYSEK.G		15.59		
						1715	1726	624.84	1247.67	1247.69	-0.02	0	48	0.0012379	K.VPIDGPPIDIGR.V		20.16		
						1852	1862	553.78	1105.55	1105.54	0	0	62	4.53E-05	K.DGGVCLLSGTK.G		19.54		
						2087	2098	655.33	1308.64	1308.66	-0.02	0	55	0.0002497	K.TASSVIELTCTK.T		19.41		
						2147	2156	588.79	1175.57	1175.59	-0.02	0	42	0.0055869	K.SFSLGDIYFK.L		21.87		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35579	17%	1297	29	227646	5.5	P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4												3	2
						126	139	872.42	1742.83	1742.84	-0.01	0	37	0.0118971	K.NLPIYSEEIVEMYK.G	Oxidation (M)	21.8		
						160	180	777.99	2330.96	2330.98	-0.01	1	36	0.0143381	R.SMMQDREDQSILCTGESGAGK.T	2 Oxidation (M)	16.45		
						290	299	603.31	1204.62	1204.63	-0.02	0	51	0.0005464	K.TDLLLEPYNK.Y		20.85		
						359	373	804.34	1606.68	1606.69	-0.01	0	77	1.29E-06	R.NTDQASMPDNTAAQK.V	Oxidation (M)	11.98		
						408	419	653.33	1304.65	1304.66	-0.01	0	65	2.28E-05	K.EQADFAIEALAK.A		21.41		
						645	656	459.92	1376.73	1376.77	-0.04	1	38	0.0114271	R.TVGQLYKEQLAK.L		16.75		
						694	702	509.26	1016.5	1016.51	-0.01	0	34	0.0352981	R.CNGVLEGIR.I		19.49		
						712	718	462.74	923.47	923.49	-0.02	0	38	0.0093096	R.VVFQEFR.Q		20.23		
						746	755	597.31	1192.61	1192.61	0	0	67	1.43E-05	K.ALELDSNLYR.I		20.58		
						803	810	482.24	962.47	962.49	-0.02	0	39	0.0092773	R.QQQLTAMK.V	Oxidation (M)	12.23		
						843	856	585.59	1753.73	1753.77	-0.04	1	37	0.0141847	R.QEEEMMAKEEELVK.V	2 Oxidation (M)	13.5		
						1001	1016	623.62	1867.85	1867.91	-0.06	1	64	2.11E-05	R.IAEFTTNLTEEEEKSK.S		19.75		
						1220	1234	577.3	1728.87	1728.86	0	1	34	0.0228497	K.QTLENERGELANEVK.V		18.84		
						1248	1260	514.3	1539.87	1539.9	-0.03	2	32	0.0402251	R.KKVEAQLQELQVK.F		15.36		
						1358	1370	481.24	1440.7	1440.74	-0.04	0	32	0.0417398	K.QIATLHAQVADMK.K	Oxidation (M)	13.89		
						1358	1371	393.2	1568.77	1568.83	-0.06	1	36	0.0182068	K.QIATLHAQVADMKK.K	Oxidation (M)	12.97		
						1393	1400	459.23	916.45	916.46	-0.01	0	34	0.0341302	K.DLEGLSQR.H		17.14		
						1405	1413	518.77	1035.53	1035.56	-0.03	1	33	0.0346467	K.VAAYDKLEK.T		13.28		
						1446	1454	546.77	1091.52	1091.55	-0.03	0	40	0.0069388	K.FDQLLAEEK.T		19.8		
						1484	1497	554.93	1661.76	1661.79	-0.03	1	58	0.0001038	R.ALEEAMEQKAELER.L	Oxidation (M)	14.06		
						1504	1518	572.91	1715.71	1715.72	-0.01	1	56	0.0001629	R.TEMEDLMSSKDDVGK.S	2 Oxidation (M)	12.8		
						1529	1538	610.78	1219.55	1219.58	-0.02	0	39	0.0096538	R.ALEQQVEEMK.T	Oxidation (M)	13.63		
						1659	1669	405.88	1214.62	1214.66	-0.04	1	35	0.0268154	R.ASREEILAQAK.E		13.45		
						1792	1802	426.55	1276.62	1276.67	-0.05	1	39	0.0084324	K.VKLQEMEGTVK.S	Oxidation (M)	12.71		
						1794	1802	525.75	1049.49	1049.51	-0.01	0	47	0.0015262	K.LQEMEGTVK.S	Oxidation (M)	12.41		
						1807	1815	452.25	902.5	902.51	-0.01	0	34	0.0330467	K.ASITALEAK.I		16.62		
						1816	1828	765.87	1529.73	1529.76	-0.03	0	38	0.0101507	K.IAQLEEQLDNETK.E		19.88		
						1878	1888	666.31	1330.6	1330.6	0	0	62	4.82E-05	R.QLEEAEEEAQR.A		13.58		
						1899	1912	791.33	1580.64	1580.66	-0.02	0	79	7.51E-07	R.ELEDATETADAMNR.E	Oxidation (M)	13.84		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75976	6%	329	7	153919	5.7	O75976|CBPD_HUMAN Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2												3	1
						70	81	548.8	1095.58	1095.6	-0.03	0	41	0.0055232	R.EAAAAGLPGLAR.L		19.84		
						559	571	487.89	1460.64	1460.68	-0.05	0	37	0.0135709	K.YIGNMHGNEVVGR.E	Oxidation (M)	13.02		
						614	625	624.31	1246.6	1246.62	-0.01	0	80	7.57E-07	K.SQEGDSISVIGR.N		19.23		
						784	790	441.73	881.45	881.47	-0.02	0	38	0.0096366	R.SLIQFMK.Q	Oxidation (M)	19.97		
						1018	1027	556.8	1111.59	1111.6	-0.01	0	63	3.41E-05	K.NPAVTQLVDR.T		19.45		
						1030	1041	640.36	1278.71	1278.73	-0.01	0	37	0.0140962	R.IVIVPSLNPDGR.E		21.07		
						1230	1239	528.31	1054.61	1054.64	-0.02	0	34	0.0304641	K.AVIVLNEGIK.V		20.19		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P46940	5%	374	9	189761	6.1	P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1												3	1
						81	88	455.24	908.46	908.48	-0.02	0	36	0.0165641	K.LGNFFSPK.V		20.63		
						192	201	579.29	1156.56	1156.56	0	0	53	0.0003826	K.YGIQMPAFSK.I	Oxidation (M)	19.58		
						557	567	577.34	1152.68	1152.69	-0.01	0	47	0.0013791	K.TLQALQIPAAK.L		20.28		
						941	953	543.89	1628.65	1628.72	-0.07	1	36	0.015171	K.NKEQLSDMMMINK.Q	3 Oxidation (M)	12.63		
						989	997	567.8	1133.58	1133.59	-0.01	0	37	0.0155444	K.LIFQMPQNK.S	Oxidation (M)	19.36		
						1018	1024	468.26	934.5	934.51	-0.02	0	35	0.0266803	R.EEYLLLR.L		21.11		
						1186	1194	562.81	1123.61	1123.64	-0.03	0	33	0.0342408	K.IIGNLLYYR.Y		21.5		
						1466	1475	536.79	1071.57	1071.58	-0.02	0	47	0.0018928	K.LTELGTVDPK.N		17.97		
						1506	1516	618.81	1235.61	1235.65	-0.04	0	51	0.0005253	K.LQQTYAALNSK.A		15.28		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y490	5%	600	11	271766	5.8	Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3												3	2
						625	634	507.24	1012.47	1012.49	-0.02	0	37	0.0151725	R.SAQPASAEPR.Q		12.06		
						899	910	610.3	1218.58	1218.6	-0.02	0	60	6.60E-05	R.MATNAAAQNAIK.K	Oxidation (M)	12.76		
						1026	1035	529.29	1056.57	1056.59	-0.02	0	59	9.99E-05	K.NLGTALAELR.T		21.24		
						1321	1332	599.32	1196.63	1196.64	-0.01	0	43	0.0035869	K.ALSTDPAAPNLK.S		17.49		
						1402	1415	717.85	1433.69	1433.72	-0.03	0	77	1.34E-06	K.VLGEAMTGISQNAK.N	Oxidation (M)	14.58		
						1531	1541	573.3	1144.59	1144.61	-0.02	0	53	0.0003821	K.EVANSTANLVK.T		14.19		
						2032	2043	622.33	1242.64	1242.66	-0.02	0	80	7.73E-07	K.VLVQNAAGSQEK.L		12.89		
						2044	2057	708.89	1415.76	1415.77	-0.02	0	70	7.28E-06	K.LAQAAQSSVATITR.L		17.66		
						2090	2099	494.78	987.55	987.56	-0.01	0	49	0.001137	K.ALGDLISATK.A		20.67		
						2169	2177	533.26	1064.5	1064.51	-0.02	0	42	0.0041534	K.TSTPEDFIR.M		20.02		
						2351	2361	516.3	1030.59	1030.6	-0.01	0	33	0.0425371	K.SIAAATSALVK.A		19.71		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08575	2%	131	3	148644	5.8	P08575|CD45_HUMAN Leukocyte common antigen OS=Homo sapiens GN=PTPRC PE=1 SV=2												3	1
						315	322	461.22	920.43	920.46	-0.03	0	39	0.0091323	K.ADTTICLK.W		15.67		
						1055	1063	531.31	1060.6	1060.62	-0.02	0	47	0.001456	K.VIVMLTELK.H	Oxidation (M)	20.8		

						1134	1143	588.33	1174.65	1174.66	-0.01	0	45	0.0025735	K.ELISMIQVVK.Q	Oxidation (M)	20.5		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	21%	1099	20	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												4	3
						76	86	435.22	1302.65	1302.69	-0.04	0	33	0.0361554	R.LPNTLKPDSYR.V		16.09		
						87	98	482.26	1443.75	1443.78	-0.04	0	39	0.0089273	R.VTLRPYLTPNDR.G		19.65		
						205	218	502.58	1504.72	1504.77	-0.05	1	52	0.0003909	R.KVVATTQMQAADAR.K	Oxidation (M)	12.1		
						205	219	545.27	1632.79	1632.86	-0.07	2	66	1.54E-05	R.KVVATTQMQAADARK.S	Oxidation (M)	11.92		
						206	218	689.33	1376.65	1376.67	-0.02	0	112	4.22E-10	K.VVATTQMQAADAR.K	Oxidation (M)	12.44		
						220	230	672.77	1343.53	1343.55	-0.02	0	44	0.0026887	K.SFPCFDEPAMK.A	Oxidation (M)	20.65		
						242	252	609.81	1217.6	1217.63	-0.03	0	38	0.0129724	K.DLTALSNMLPK.G	Oxidation (M)	21.18		
						293	301	479.27	956.53	956.54	-0.01	0	65	2.32E-05	K.QASNGVLIR.I		14.44		
						364	379	862.91	1723.81	1723.83	-0.02	0	84	2.39E-07	R.ENSLLFDPLSSSSSNK.E		22.09		
						364	381	670.64	2008.9	2008.97	-0.07	1	53	0.000263	R.ENSLLFDPLSSSSSNKER.V		21.31		
						433	442	627.31	1252.6	1252.61	-0.01	0	42	0.0043405	K.DLMVLNDVYR.V	Oxidation (M)	21.48		
						486	497	709.83	1417.65	1417.68	-0.03	0	61	5.93E-05	R.MLSSFLSEDVFK.Q	Oxidation (M)	22.7		
						596	606	732.37	1462.73	1462.72	0.01	0	44	0.0030039	R.QQQDYWLIDVR.A		22.27		
						659	673	538.26	1611.75	1611.84	-0.09	0	55	0.0002009	R.AQIINDAFNLASAHK.V		21.05		
						778	793	663.97	1988.89	1988.93	-0.03	0	38	0.0083893	K.QWMENPNNNPIHPNLR.S	Oxidation (M)	19.47		
						837	843	472.27	942.53	942.53	0	0	43	0.0039926	K.ELWILNR.Y		22.18		
						844	855	734.38	1466.75	1466.78	-0.03	0	65	2.16E-05	R.YLSYTLNPDLIR.K		21.92		
						924	935	635.26	1268.51	1268.53	-0.02	0	73	3.52E-06	K.DNEETGFGSGTR.A		13.96		
						936	943	451.24	900.46	900.49	-0.03	0	51	0.0007131	R.ALEQALEK.T		14.83		
						956	967	740.43	1478.85	1478.74	0.11	0	42	0.004676	K.EVVLQWFTENSK.-		22.92		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92896	20%	1252	24	138382	6.5	Q92896|GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=1												4	2
						112	124	531.9	1592.67	1592.71	-0.04	1	45	0.0019677	K.LAEEESCREDVTR.V		12.83		
						182	197	592.95	1775.83	1775.86	-0.03	1	52	0.0004165	K.STITEIKECADEPVGK.G		19.34		
						198	208	451.53	1351.58	1351.6	-0.02	0	37	0.0129894	K.GYMVSCLVDHR.G	Oxidation (M)	19.51		
						223	232	616.79	1231.57	1231.59	-0.03	0	70	8.53E-06	K.MTAIIFSDYR.L	Oxidation (M)	20.96		
						298	310	501.89	1502.65	1502.7	-0.05	0	42	0.0039018	R.VAELSSDDFHLDR.H		20.26		
						323	333	634.77	1267.52	1267.53	0	0	69	8.85E-06	R.FCENTQAGEGR.V		12.66		
						359	367	369.54	1105.59	1105.61	-0.03	1	41	0.0057837	R.QKLIAQDYK.V		13.31		
						361	367	425.73	849.44	849.46	-0.02	0	34	0.0333036	K.LIAQDYK.V		13.83		
						385	392	501.24	1000.46	1000.48	-0.02	0	39	0.0110718	R.CNVENLPR.S		14.31		
						414	427	859.35	1716.68	1716.71	-0.02	0	48	0.0009477	R.QVSSECQGEMLDYR.R	Oxidation (M)	16		
						414	428	625.29	1872.84	1872.81	0.03	1	37	0.0139598	R.QVSSECQGEMLDYRR.M	Oxidation (M)	14.01		
						502	516	847.37	1692.73	1692.78	-0.05	0	88	1.01E-07	R.ALNEACESVIQTACK.H		19.73		
						546	555	641.34	1280.67	1280.71	-0.05	0	39	0.0090137	R.LLELQYFISR.D		23.45		
						631	638	450.23	898.45	898.48	-0.03	0	32	0.0400183	K.LDPALQDK.C		13.79		
						639	645	409.72	817.42	817.44	-0.02	0	39	0.0113474	K.CLIDLGK.W		20.48		
						734	747	549.94	1646.79	1646.83	-0.04	0	36	0.0152457	K.CAIGVTHFQLVQMK.D	Oxidation (M)	20.17		
						807	817	690.32	1378.62	1378.63	0	0	79	8.11E-07	R.VEELEMTEDIR.L	Oxidation (M)	19.21		
						909	916	475.21	948.4	948.42	-0.02	0	42	0.004966	K.NSELMDPK.C	Oxidation (M)	12.57		
						925	933	569.77	1137.53	1137.54	-0.01	0	53	0.0003406	R.QITQNTDYR.L		12.97		
						980	989	611.76	1221.51	1221.53	-0.02	0	77	1.36E-06	R.LSSDCEDQIR.I		13.49		
						990	1000	660.85	1319.68	1319.71	-0.03	0	76	1.68E-06	R.IIIQESALDYR.L		20.74		
						1077	1086	373.84	1118.5	1118.54	-0.04	0	36	0.0201925	K.HHCAAITPGR.G		11.97		
						1089	1100	743.82	1485.62	1485.61	0	0	57	0.0001408	R.QMSCLMEALEDK.R	2 Oxidation (M)	19.95		
						1089	1101	548.24	1641.69	1641.72	-0.03	1	58	0.0001093	R.QMSCLMEALEDKR.V	2 Oxidation (M)	19.16		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13473	4%	73	2	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												4	3
						145	152	494.27	986.53	986.55	-0.03	0	41	0.0062376	R.IPLNDLFR.C		22.05		
						281	289	551.29	1100.57	1100.59	-0.02	0	32	0.0496596	K.YLDFVFAVK.N		23.23		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y4L1	2%	89	2	111494	5.2	Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1												4	2
						269	278	567.78	1133.55	1133.58	-0.02	0	52	0.0004271	R.TLGGLEMELR.L	Oxidation (M)	20.57		
						283	291	524.27	1046.53	1046.55	-0.02	0	37	0.0183066	R.LAGLFNEQR.K		20.52		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11279	14%	403	6	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												5	6
						138	146	517.27	1032.53	1032.55	-0.01	0	72	5.33E-06	K.TVESITDIR.A		19.18		
						299	314	923.5	1844.99	1845.01	-0.02	0	114	2.54E-10	R.FFLQGIQLNTILPDAR.D		23.12		
						299	319	802.09	2403.23	2403.3	-0.06	1	46	0.0011556	R.FFLQGIQLNTILPDARDPAFK.A		22.77		
						327	337	576.3	1150.58	1150.6	-0.02	0	83	3.78E-07	R.ALQATVGNSYK.C		13.83		
						349	356	463.25	924.49	924.51	-0.02	0	43	0.0032748	K.AFSVNIFK.V		20.92		
						410	417	438.7	875.39	875.41	-0.02	0	46	0.002015	R.SHAGYQTI.-		13.52		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13740	9%	166	4	65745	5.9	Q13740|CD166_HUMAN CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2												5	1
						77	89	538.58	1612.71	1612.74	-0.03	1	39	0.0076692	K.SVQYDDVPEYKDR.L		17.09		
						143	152	596.33	1190.64	1190.65	-0.01	0	35	0.026833	K.ALFLETEQLK.K		20.65		
						294	305	471.56	1411.67	1411.71	-0.03	1	39	0.008849	R.SSNTYTLTDVRR.N		14.96		
						345	360	837.92	1673.82	1673.84	-0.02	0	53	0.000305	R.QIGDALPVSCTISASR.N		20.03		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P16284	8%	197	4	83396	6.5	P16284|PECA1_HUMAN Platelet endothelial cell adhesion molecule OS=Homo sapiens GN=PECAM1 PE=1 SV=1												5	1
						90	100	664.32	1326.62	1326.65	-0.02	0	55	0.0002005	K.STESYFIPEVR.I		20.56		
						210	223	516.58	1546.73	1546.77	-0.04	0	46	0.0015155	R.IISGIHMQTSESTK.S	Oxidation (M)	12.73		
						496	511	849.47	1696.92	1696.96	-0.04	0	57	0.0001219	K.VIAPVDEVQISILSSK.V		21.54		
						632	651	762.71	2285.09	2285.11	-0.02	0	38	0.0087543	K.QMPVEMSRPAVPLLNSNNEK.M	2 Oxidation (M)	19.13		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05556	7%	218	5	91714	5.3	P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=1												5	2
						125	134	554.29	1106.56	1106.56	0	0	44	0.0031939	R.SGEPQTFTLK.F		19		
						164	174	649.79	1297.57	1297.56	0	0	51	0.0006185	K.SLGTDLMNEMR.R	2 Oxidation (M)	16.91		
						182	190	492.25	982.48	982.51	-0.03	0	32	0.0458922	R.IGFGSFVEK.T		20.52		
						191	202	662.83	1323.65	1323.67	-0.02	0	47	0.0013208	K.TVMPYISTTPAK.L	Oxidation (M)	16.48		
						563	575	668.3	1334.59	1334.61	-0.02	0	45	0.0022155	R.SNGLICGGNGVCK.C		14.65		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16706	6%	346	6	131742	7.2	Q16706|MA2A1_HUMAN Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2												5	1
						61	73	749.91	1497.8	1497.82	-0.01	0	91	4.80E-08	R.LLAENNEIISNIR.D		20.21		
						418	428	608.34	1214.66	1214.67	0	0	46	0.00213	K.VLLAPLGDDFR.Y		21.41		
						547	560	779.9	1557.78	1557.8	-0.03	0	69	7.88E-06	K.FLSSSLYTALTEAR.R		21.72		
						769	776	478.22	954.43	954.45	-0.02	0	37	0.0119282	R.FDQTGLMK.Q	Oxidation (M)	13.56		
						965	974	551.27	1100.53	1100.55	-0.02	0	53	0.0003784	R.GLEQGIQDNK.I		13.61		
						1083	1094	628.8	1255.58	1255.59	-0.01	0	51	0.0006561	K.GTGLFCSTTQGK.I		17.52		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P53396	6%	265	5	121674	7	P53396|ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3												5	1
						18	28	655.83	1309.65	1309.64	0	0	61	5.34E-05	K.FICTTSAIQNR.F		17.82		
						593	607	784.47	1566.93	1566.9	0.03	0	47	0.0013371	R.TIAIIAEGIPEALTR.K		21.9		
						636	650	760.39	1518.76	1518.77	-0.01	0	77	1.23E-06	K.IGNTGGMLDNILASK.L	Oxidation (M)	20.12		
						663	676	754.35	1506.69	1506.71	-0.02	0	40	0.0066007	R.SGGMSNELNNIISR.T	Oxidation (M)	19.71		
						935	944	460.74	919.46	919.48	-0.02	0	43	0.0037716	R.FGGALDAAAK.M		15.57		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O00461	4%	97	2	81888	4.7	O00461|GOLI4_HUMAN Golgi integral membrane protein 4 OS=Homo sapiens GN=GOLIM4 PE=1 SV=1												5	1
						157	170	588.64	1762.91	1762.91	0	1	34	0.0235443	K.YLQLQQEKEQELSK.L		17.69		
						416	428	756.4	1510.78	1510.81	-0.03	0	63	3.37E-05	R.LAVQQVEEAQQLR.E		19.45		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92542	3%	113	2	79103	5.7	Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2												5	2
						392	403	686.86	1371.71	1371.72	-0.02	0	56	0.0001705	R.NQVEDLLATLEK.S		22.73		
						486	496	543.31	1084.6	1084.62	-0.02	0	57	0.0001608	K.ALADVATVLGR.A		20.74		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O94804	3%	85	2	112749	6.5	O94804|STK10_HUMAN Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1												5	1
						160	172	702.85	1403.69	1403.71	-0.02	0	35	0.024355	K.AGNVLMTLEGDIR.L	Oxidation (M)	21.63		
						447	464	611.28	1830.82	1830.91	-0.08	0	51	0.0004792	K.ASQSRPNSSALETLGGEK.L		16		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P18206	2%	128	2	124292	5.5	P18206|VINC_HUMAN Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4												5	1
						327	339	755.35	1508.69	1508.7	-0.01	0	73	3.77E-06	K.MLGQMTDQVADLR.A	2 Oxidation (M)	19.05		
						803	815	635.33	1268.65	1268.67	-0.02	0	56	0.0001845	K.AVAGNISDPGLQK.S		15.4		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	19%	766	14	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												6	3
						44	51	481.22	960.42	960.45	-0.03	0	49	0.0010703	R.TDDEVVQR.E		12.55		
						76	84	541.25	1080.49	1080.54	-0.04	0	46	0.0015082	K.FAFQAEVNR.M		19.68		
						103	114	638.31	1274.6	1274.64	-0.03	0	64	3.18E-05	R.ELISNASDALDK.I		19.46		
						143	156	510.57	1528.7	1528.77	-0.07	0	62	4.64E-05	K.NLLHVTDTGVGMTR.E	Oxidation (M)	19.02		
						169	177	491.73	981.44	981.48	-0.03	0	49	0.0007608	K.SGTSEFLNK.M		14.95		
						286	300	869.35	1736.69	1736.73	-0.04	0	43	0.0027818	K.TETVEEPMEEEEAAK.E	Oxidation (M)	13.77		
						385	395	594.33	1186.64	1186.67	-0.03	0	45	0.0024251	K.SILFVPTSAPR.G		20.65		
						396	404	508.22	1014.43	1014.47	-0.04	0	34	0.0387929	R.GLFDEYGSK.K		20.3		
						435	448	743.36	1484.7	1484.75	-0.05	0	92	3.93E-08	K.GVVDSDDLPLNVSR.E		20.34		
						538	546	524.23	1046.45	1046.49	-0.04	0	44	0.0035044	K.IYFMAGSSR.K	Oxidation (M)	16.68		
						548	557	575.75	1149.48	1149.53	-0.05	0	61	5.21E-05	K.EAESSPFVER.L		15.86		
						672	682	645.28	1288.55	1288.59	-0.04	0	50	0.0007949	K.DISTNYYASQK.K		16.64		
						725	733	497.25	992.48	992.52	-0.04	0	52	0.0004279	R.SGYLLPDTK.A		19.41		
						745	754	543.28	1084.54	1084.58	-0.04	0	49	0.0009912	R.LSLNIDPDAK.V		20.03		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P12814	13%	599	11	103563	5.3	P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2												6	1
						22	31	600.3	1198.59	1198.62	-0.03	0	38	0.012258	R.DLLLDPAWEK.Q		21.88		
						96	103	432.73	863.45	863.48	-0.03	0	39	0.0099479	K.ALDFIASK.G		19.95		
						134	147	769.36	1536.71	1536.77	-0.05	0	80	6.68E-07	R.FAIQDISVEETSAK.E		20.48		
						186	195	409.86	1226.56	1226.64	-0.08	0	55	0.0002045	R.HRPELIDYGK.L		13.95		
						215	220	374.7	747.38	747.42	-0.04	0	40	0.0100331	K.YLDIPK.M		19.2		
						347	359	493.22	1476.64	1476.71	-0.07	0	47	0.0015629	R.LSNRPAFMPSEGR.M	Oxidation (M)	13.47		
						419	431	509.24	1524.71	1524.77	-0.06	1	37	0.0135138	R.QKDYETATLSEIK.A		19.15		
						727	738	715.36	1428.71	1428.76	-0.04	0	70	6.66E-06	R.TINEVENQILTR.D		20.17		
						742	752	677.79	1353.56	1353.6	-0.03	0	70	6.32E-06	K.GISQEQMNEFR.A	Oxidation (M)	14.47		

						795	803	530.76	1059.51	1059.54	-0.03	0	44	0.0033654	R.IMSIVDPNR.L	Oxidation (M)	15.38		
						851	863	781.35	1560.68	1560.72	-0.05	0	49	0.0007827	R.ELPPDQAEYCIAR.M		19.55		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	8%	247	6	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												6	7
						156	165	545.26	1088.5	1088.55	-0.04	0	37	0.0155778	R.ALNEITESGR.I		14.42		
						166	174	485.24	968.46	968.5	-0.04	0	40	0.0062148	R.IGFGSFVDK.T		20.7		
						275	285	563.79	1125.57	1125.61	-0.04	0	38	0.0100212	K.LGAILTPNDGR.C		19.37		
						311	325	836.92	1671.83	1671.89	-0.06	0	45	0.0023148	K.LAENNIQPIFAVTSR.M		20.96		
						578	586	524.23	1046.45	1046.48	-0.03	0	52	0.000549	R.TTEGCLNPR.R		12.77		
						625	633	572.24	1142.47	1142.51	-0.04	0	35	0.0252061	K.YISCAECLK.F		15.25		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43707	8%	420	7	105245	5.3	O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2												6	1
						41	50	600.3	1198.59	1198.62	-0.03	0	38	0.012258	R.DLLLDPAWEK.Q		21.88		
						115	122	432.73	863.45	863.48	-0.03	0	39	0.0099479	K.ALDFIASK.G		19.95		
						153	166	769.36	1536.71	1536.77	-0.05	0	80	6.68E-07	R.FAIQDISVEETSAK.E		20.48		
						234	239	374.7	747.38	747.42	-0.04	0	40	0.0100331	K.YLDIPK.M		19.2		
						746	757	715.36	1428.71	1428.76	-0.04	0	70	6.66E-06	R.TINEVENQILTR.D		20.17		
						761	771	684.79	1367.57	1367.61	-0.04	0	74	2.70E-06	K.GISQEQMQEFR.A	Oxidation (M)	14.38		
						870	882	781.35	1560.68	1560.72	-0.05	0	49	0.0007827	R.ELPPDQAEYCIAR.M		19.55		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13639	7%	273	6	96246	6.4	P13639|EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4												6	1
						2	10	546.28	1090.55	1090.58	-0.03	0	51	0.000693	M.VNFTVDQIR.A		19.86		
						227	235	551.76	1101.51	1101.52	-0.01	0	48	0.0012761	K.QFAEMYVAK.F	Oxidation (M)	16.07		
						240	249	507.24	1012.46	1012.49	-0.04	0	34	0.0255303	K.GEGQLGPAER.A		12.94		
						416	426	554.3	1106.59	1106.63	-0.04	0	71	6.17E-06	R.VFSGLVSTGLK.V		20.21		
						429	438	547.26	1092.5	1092.53	-0.03	0	36	0.0170281	R.IMGPNYTPGK.K	Oxidation (M)	13.81		
						717	726	485.26	968.51	968.54	-0.03	0	33	0.0323911	R.GGGQIIPTAR.R		14.9		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05362	7%	123	3	58587	8.3	P05362|ICAM1_HUMAN Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=1 SV=2												6	1
						41	56	848.35	1694.69	1694.76	-0.07	0	45	0.0017084	R.GGSVLVTCSTSCDQPK.L		14.86		
						57	66	540.82	1079.63	1079.66	-0.03	0	42	0.0046497	K.LLGIETPLPK.K		20.83		
						135	143	487.21	972.41	972.44	-0.03	0	36	0.0224255	R.CQVEGGAPR.A		12.21		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P22314	2%	107	2	118858	5.5	P22314|UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3												6	1
						870	880	625.77	1249.53	1249.56	-0.02	0	50	0.0006506	R.AENYDIPSADR.H		16.42		
						1011	1021	652.81	1303.61	1303.64	-0.03	0	58	0.0001085	R.LDQPMTEIVSR.V	Oxidation (M)	15.73		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08238	32%	1334	22	83554	5	P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4												7	4
						42	53	638.31	1274.6	1274.64	-0.03	0	64	2.71E-05	R.ELISNASDALDK.I		19.46		
						42	55	515.59	1543.76	1543.82	-0.06	1	70	7.70E-06	R.ELISNASDALDKIR.Y		20.17		
						56	69	513.91	1538.7	1538.75	-0.05	1	40	0.0065588	R.YESLTDPSKLDSGK.E		18.54		
						73	82	597.81	1193.6	1193.64	-0.04	0	57	0.0001282	K.IDIIPNPQER.T		19.9		
						83	95	683.35	1364.69	1364.72	-0.03	0	79	9.75E-07	R.TLTLVDTGIGMTK.A	Oxidation (M)	19.99		
						96	107	621.84	1241.66	1241.7	-0.04	0	80	8.11E-07	K.ADLINNLGTIAK.S		20.52		
						187	196	656.27	1310.52	1310.56	-0.04	0	75	1.92E-06	K.EDQTEYLEER.R		17.63		
						205	219	603.63	1807.87	1807.95	-0.08	0	41	0.0055055	K.HSQFIGYPITLYLEK.E		21.57		
						292	306	924.38	1846.74	1846.79	-0.05	0	79	7.35E-07	R.NPDDITQEEYGEFYK.S		20.34		
						331	337	415.25	828.49	828.52	-0.04	0	36	0.0239868	R.ALLFIPR.R		21		
						338	348	455.56	1363.66	1363.72	-0.06	2	40	0.0069471	R.RAPFDLFENKK.K		19.77		
						339	347	540.75	1079.48	1079.53	-0.04	0	55	0.0002053	R.APFDLFENK.K		21.31		
						379	392	757.38	1512.74	1512.78	-0.04	0	101	5.85E-09	R.GVVDSEDLPLNISR.E		20.61		
						429	435	446.2	890.39	890.42	-0.03	0	38	0.0139103	K.FYEAFSK.N		19.24		
						439	448	381.17	1140.49	1140.55	-0.06	0	39	0.0080715	K.LGIHEDSTNR.R		12.6		
						457	475	731.63	2191.86	2191.93	-0.08	0	82	3.29E-07	R.YHTSQSGDEMTSLSEYVSR.M	Oxidation (M)	19.2		
						482	491	580.78	1159.54	1159.58	-0.04	0	50	0.0009063	K.SIYYITGESK.E		19.5		
						492	502	625.3	1248.59	1248.61	-0.02	0	85	2.05E-07	K.EQVANSAFVER.V		16.12		
						532	538	367.21	732.41	732.44	-0.02	0	49	0.0012801	K.SLVSVTK.E		13.86		
						558	565	505.24	1008.47	1008.51	-0.04	1	39	0.0076708	K.AKFENLCK.L		13.13		
						613	623	648.74	1295.46	1295.48	-0.02	0	46	0.0016086	R.DNSTMGYMMAK.K	3 Oxidation (M)	12.39		
						625	639	594.97	1781.88	1781.94	-0.06	0	62	4.03E-05	K.HLEINPDHPIVETLR.Q		19.64		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	28%	571	12	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												7	3
						32	39	445.22	888.42	888.46	-0.04	0	34	0.0344878	K.AVDQSIEK.K		12.56		
						78	92	584.94	1751.79	1751.85	-0.06	1	64	2.80E-05	R.GETPRVEEVGPYTYR.E		19.15		
						83	92	606.78	1211.54	1211.58	-0.04	0	60	7.11E-05	R.VEEVGPYTYR.E		19.11		
						116	121	392.69	783.36	783.39	-0.03	0	32	0.041771	K.AYVFER.D		17.85		
						154	161	481.75	961.48	961.52	-0.04	0	37	0.0154666	R.EIIEAMLK.A	Oxidation (M)	18.93		
						228	234	423.21	844.41	844.44	-0.03	0	34	0.0404341	K.IVEWNGK.T		16.16		
						263	275	823.86	1645.7	1645.74	-0.05	0	60	6.47E-05	K.DEVLYVFPSDFCR.S		22.27		
						331	348	703.65	2107.92	2107.98	-0.06	0	41	0.0047293	K.NGAPIIMSFPHFYQADER.F	Oxidation (M)	20.87		
						349	378	845.89	3379.52	3379.68	-0.15	0	33	0.0231723	R.FVSAIEGMHPNQEDHETFVDINPLTGII	Oxidation (M)	21.92		
						391	402	469.89	1406.64	1406.7	-0.07	1	46	0.0016811	K.KLDDFVETGDIR.T		19.86		

						460	472	684.77	1367.53	1367.53	0.01	0	51	0.0005005	K.GQGSMDEGTADER.A	Oxidation (M)	12.04		
						460	477	640.28	1917.81	1917.89	-0.07	1	80	5.46E-07	K.GQGSMDEGTADERAPLIR.T	Oxidation (M)	15.04		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07900	23%	1033	16	85006	4.9	P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5												7	4
						47	58	646.31	1290.61	1290.63	-0.02	0	103	3.75E-09	R.ELISNSSDALDK.I		18.63		
						47	60	520.92	1559.73	1559.82	-0.08	1	59	8.40E-05	R.ELISNSSDALDKIR.Y		19.59		
						61	74	513.91	1538.7	1538.75	-0.05	1	40	0.0065588	R.YESLTDPSKLDSGK.E		18.54		
						88	100	683.35	1364.69	1364.72	-0.03	0	79	9.75E-07	R.TLTIVDTGIGMTK.A	Oxidation (M)	19.99		
						101	112	621.84	1241.66	1241.7	-0.04	0	80	8.11E-07	K.ADLINNLGTIAK.S		20.52		
						192	201	656.27	1310.52	1310.56	-0.04	0	75	1.92E-06	K.EDQTEYLEER.R		17.63		
						300	314	917.36	1832.71	1832.77	-0.06	0	109	7.06E-10	R.NPDDITNEEYGEFYK.S		20.3		
						346	355	422.21	1263.6	1263.64	-0.03	1	53	0.0003802	R.RAPFDLFENR.K		20.79		
						347	355	554.76	1107.5	1107.53	-0.03	0	49	0.0008091	R.APFDLFENR.K		21.44		
						387	400	757.38	1512.74	1512.78	-0.04	0	101	5.85E-09	R.GVVDSEDLPLNISR.E		20.61		
						447	456	390.18	1167.52	1167.56	-0.05	0	36	0.0189818	K.LGIHEDSQNR.K		12.52		
						465	478	783.83	1565.65	1565.69	-0.05	0	49	0.0007272	R.YYTSASGDEMVSLK.D	Oxidation (M)	18.8		
						490	499	612.8	1223.59	1223.62	-0.03	0	43	0.0033891	K.HIYYITGETK.D		15.69		
						500	510	618.3	1234.6	1234.59	0	0	70	7.85E-06	K.DQVANSAFVER.L		17.55		
						540	546	374.22	746.42	746.45	-0.03	0	38	0.014303	K.TLVSVTK.E		13.65		
						621	631	610.74	1219.46	1219.48	-0.02	0	50	0.0007594	R.DNSTMGYMAAK.K	2 Oxidation (M)	12.43		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06396	11%	432	8	86043	5.9	P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1												7	1
						178	188	425.89	1274.66	1274.71	-0.05	0	36	0.0180151	K.HVVPNEVVVQR.L		13.95		
						361	368	441.72	881.43	881.45	-0.02	0	44	0.0023984	K.TASDFITK.M		15.34		
						374	390	915.45	1828.89	1828.96	-0.06	0	77	1.15E-06	K.QTQVSVLPEGGETPLFK.Q		20.96		
						578	584	378.22	754.42	754.46	-0.04	0	50	0.0005402	R.AVEVLPK.A		14.78		
						585	597	660.33	1318.64	1318.69	-0.04	0	76	2.10E-06	K.AGALNSNDAFVLK.T		20.12		
						714	728	555.91	1664.7	1664.77	-0.07	1	70	5.65E-06	K.DSQEEEKTEALTSAK.R		13.69		
						730	738	539.74	1077.47	1077.51	-0.04	0	38	0.0131702	R.YIETDPANR.D		13.3		
						742	748	379.23	756.44	756.47	-0.03	0	41	0.0060963	R.TPITVVK.Q		13.91		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08195	8%	154	3	58023	5.2	P08195|4F2_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=2												7	2
						45	59	496.24	1485.71	1485.77	-0.06	1	50	0.0007278	K.IKVAEDEAEAAAAAK.F		15.56		
						339	350	686.4	1370.79	1370.83	-0.04	0	39	0.008884	R.LLTSFLPAQLLR.L		22.97		
						410	423	753.38	1504.75	1504.75	-0.01	0	65	2.14E-05	K.GQSEDPGSLLSLFR.R		22.79		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14974	6%	247	4	98420	4.7	Q14974|IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2												7	1
						28	42	829.93	1657.84	1657.9	-0.06	0	45	0.0019731	R.AAVENLPTFLVELSR.V		23.36		
						43	54	613.32	1224.62	1224.66	-0.04	0	63	3.71E-05	R.VLANPGNSQVAR.V		13.17		
						192	206	803.43	1604.85	1604.88	-0.02	0	76	1.52E-06	K.LAATNALLNSLEFTK.A		21.97		
						235	243	478.29	954.56	954.59	-0.02	0	32	0.0444877	R.VAALQNLVK.I		19.73		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14780	3%	102	2	79433	5.6	P14780|MMP9_HUMAN Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=2												7	1
						25	36	673.35	1344.69	1344.74	-0.05	0	45	0.0022226	R.QSTLVLFPGDLR.T		21.62		
						66	76	576.86	1151.7	1151.73	-0.03	0	56	0.0001611	K.SLGPALLLLQK.Q		21.84		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	14%	352	9	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												8	2
						28	35	488.76	975.5	975.54	-0.04	0	38	0.0130607	K.QLFDQVVK.T		19.89		
						185	193	540.27	1078.52	1078.55	-0.04	0	36	0.0175475	R.EDAVLEYLK.I		20.91		
						238	246	552.77	1103.53	1103.58	-0.04	0	50	0.0008495	K.IGFPWSEIR.N		21.96		
						295	306	496.91	1487.72	1487.78	-0.06	1	37	0.0129978	R.RKPDTIEVQQMK.A	Oxidation (M)	12.15		
						372	379	494.23	986.45	986.5	-0.05	0	33	0.046668	R.ALELEQER.K		15.71		
						401	408	444.24	886.46	886.49	-0.03	0	35	0.0325341	K.EALLQASR.D		14.71		
						428	435	482.24	962.46	962.49	-0.03	0	34	0.0318729	R.ISQLEMAR.Q	Oxidation (M)	13.1		
						449	458	603.77	1205.52	1205.56	-0.04	0	51	0.0005997	K.AQMVQEDLEK.T	Oxidation (M)	13.41		
						569	577	585.74	1169.47	1169.5	-0.03	1	40	0.0072161	K.QRIDEFESM.-	Oxidation (M)	17.23		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	14%	453	8	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												8	2
						50	60	614.79	1227.57	1227.62	-0.05	0	73	4.19E-06	R.VEIIANDQGNR.I		14.54		
						61	74	783.87	1565.72	1565.77	-0.05	0	63	2.87E-05	R.ITPSYVAFTPEGER.L		20.24		
						82	96	839.38	1676.75	1676.8	-0.05	0	83	3.45E-07	K.NQLTSNPENTVFDAK.R		19.71		
						82	97	611.95	1832.83	1832.9	-0.07	1	43	0.0027831	K.NQLTSNPENTVFDAKR.L		19.18		
						124	138	535.6	1603.78	1603.86	-0.08	0	50	0.0007251	K.TKPYIQVDIGGGQTK.T		19.14		
						139	152	776.87	1551.73	1551.79	-0.05	0	57	0.0001333	K.TFAPEEISAMVLTK.M	Oxidation (M)	20.95		
						186	197	617.29	1232.57	1232.62	-0.04	0	34	0.0282969	K.DAGTIAGLNVMR.I	Oxidation (M)	19.62		
						524	532	537.76	1073.51	1073.55	-0.04	0	51	0.000665	K.ITITNDQNR.L		13.15		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15311	9%	232	6	69484	5.9	P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4												8	2
						28	35	488.76	975.5	975.54	-0.04	0	38	0.0130607	K.QLFDQVVK.T		19.89		
						238	246	552.77	1103.53	1103.58	-0.04	0	50	0.0008495	K.IGFPWSEIR.N		21.96		
						295	306	496.91	1487.72	1487.78	-0.06	1	37	0.0129978	R.RKPDTIEVQQMK.A	Oxidation (M)	12.15		

						364	371	501.74	1001.47	1001.51	-0.04	0	36	0.0212157	R.ELSEQIQR.A		13.58		
						451	458	459.22	916.43	916.45	-0.02	0	36	0.0237213	K.EAQDDLVK.T		13.28		
						578	586	560.76	1119.51	1119.56	-0.04	1	34	0.0269924	K.QRIDEFEAL.-		20.64		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15586	6%	138	3	62840	8.6	P15586|GNS_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3												8	1
						247	255	525.26	1048.51	1048.55	-0.04	0	39	0.0096675	K.AFQNVFAPR.N		20.2		
						410	421	676.31	1350.6	1350.64	-0.04	0	45	0.0022143	R.SDVLVEYQGEGR.N		19.36		
						507	519	786.8	1571.58	1571.66	-0.08	0	55	0.0002655	R.LMMLQSCSGPTCR.T	2 Oxidation (M)	13.84		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P46459	6%	253	4	83021	6.5	P46459|NSF_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=2												8	1
						188	198	573.3	1144.58	1144.61	-0.03	0	74	2.86E-06	K.AENSSLNLIGK.A		19.4		
						284	293	541.79	1081.57	1081.61	-0.05	0	46	0.0018738	K.VVNGPEILNK.Y		18.48		
						517	529	729.38	1456.74	1456.78	-0.03	0	98	1.10E-08	R.VLDDGELLVQQTK.N		20.11		
						556	566	647.82	1293.62	1293.66	-0.04	0	35	0.0235057	K.IAEESNFPFIK.I		21.13		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51659	6%	172	3	80092	9	P51659|DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3												8	1
						11	23	585.33	1168.65	1168.69	-0.04	0	55	0.0002517	R.VVLVTGAGAGLGR.A		19.67		
						316	331	734.35	1466.69	1466.74	-0.05	0	51	0.0005605	R.ATSTATSGFAGAIGQK.L		19.01		
						544	555	696.34	1390.67	1390.68	-0.02	0	67	1.59E-05	R.VLQQFADNDVSR.F		18.92		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15942	5%	78	2	62436	6.2	Q15942|ZYX_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1												8	1
						36	54	663.64	1987.89	1987.99	-0.09	0	32	0.0401007	K.VNPFRPGDSEPPPAPGAQR.A		18.53		
						254	265	538.77	1075.52	1075.57	-0.04	0	47	0.0017031	R.GPPASSPAPAPK.F		12.32		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O60488	4%	122	2	80220	8.7	O60488|ACSL4_HUMAN Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2												8	1
						340	354	791.87	1581.73	1581.79	-0.06	0	92	4.24E-08	R.IGYSSPLTLSDQSSK.I		20.02		
						577	587	582.8	1163.58	1163.62	-0.04	0	32	0.0490382	K.LQAGEYVSLGK.V		19.54		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11142	32%	1275	22	71082	5.4	P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1												9	1
						26	36	614.78	1227.55	1227.62	-0.07	0	70	9.16E-06	K.VEIIANDQGNR.T		14.21		
						37	49	744.33	1486.65	1486.69	-0.05	0	62	4.57E-05	R.TTPSYVAFTDTER.L		19.76		
						57	71	833.37	1664.72	1664.78	-0.07	0	108	9.07E-10	K.NQVAMNPTNTVFDAK.R	Oxidation (M)	19.11		
						57	72	607.94	1820.79	1820.88	-0.1	1	61	5.04E-05	K.NQVAMNPTNTVFDAKR.L	Oxidation (M)	16.51		
						78	88	635.76	1269.5	1269.55	-0.05	0	50	0.0006518	R.FDDAVVQSDMK.H	Oxidation (M)	14.95		
						103	112	394.19	1179.55	1179.61	-0.07	1	33	0.030585	K.VQVEYKGETK.S		12.52		
						113	126	816.86	1631.7	1631.78	-0.08	0	49	0.0008906	K.SFYPEEVSSMVLTK.M	Oxidation (M)	20.51		
						127	137	634.8	1267.59	1267.65	-0.06	1	69	9.64E-06	K.MKEIAEAYLGK.T	Oxidation (M)	16.64		
						129	137	497.24	992.47	992.52	-0.05	0	37	0.0147007	K.EIAEAYLGK.T		19.19		
						138	155	991.47	1980.93	1980.99	-0.06	0	73	2.82E-06	K.TVTNAVVTVPAYFNDSQR.Q		20.68		
						160	171	600.32	1198.63	1198.67	-0.03	0	76	1.98E-06	K.DAGTIAGLNVLR.I		20.94		
						172	187	830.42	1658.82	1658.89	-0.07	0	80	5.85E-07	R.IINEPTAAAIAYGLDK.K		20.9		
						172	188	596.63	1786.86	1786.98	-0.12	1	67	1.18E-05	R.IINEPTAAAIAYGLDKK.V		20.2		
						221	236	564.56	1690.65	1690.72	-0.07	0	52	0.0004054	K.STAGDTHLGGEDFDNR.M		14.78		
						300	311	494.23	1479.67	1479.75	-0.07	1	48	0.0010437	R.ARFEELNADLFR.G		20.59		
						302	311	627.28	1252.55	1252.61	-0.06	0	80	7.09E-07	R.FEELNADLFR.G		21.25		
						349	357	541.26	1080.51	1080.56	-0.05	0	51	0.0005552	K.LLQDFFNGK.E		21.07		
						349	361	522.59	1564.75	1564.82	-0.08	1	42	0.0037475	K.LLQDFFNGKELNK.S		20.73		
						452	458	387.19	772.37	772.41	-0.04	0	42	0.006073	K.DNNLLGK.F		14.56		
						510	517	495.24	988.47	988.52	-0.05	1	42	0.0050786	R.LSKEDIER.M		12.74		
						540	550	660.28	1318.54	1318.59	-0.05	0	48	0.0010681	K.NSLESYAFNMK.A	Oxidation (M)	19.67		
						602	609	472.74	943.47	943.52	-0.04	0	35	0.0277925	K.VCNPIITK.L		14.52		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13796	23%	685	12	70815	5.2	P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5												9	2
						4	15	707.76	1413.51	1413.58	-0.06	0	61	6.10E-05	R.GSVSDEEMMELR.E	2 Oxidation (M)	14.3		
						133	141	545.21	1088.41	1088.46	-0.05	0	53	0.0003746	K.ALENDPDCR.H		12.57		
						166	178	759.85	1517.69	1517.74	-0.05	0	72	4.48E-06	K.MINLSVPDTIDER.T	Oxidation (M)	20.38		
						245	253	506.79	1011.56	1011.61	-0.05	0	47	0.0015309	R.NEALIALLR.E		21.51		
						254	263	583.75	1165.49	1165.52	-0.03	0	57	0.000122	R.EGESLEDLMK.L	Oxidation (M)	18.89		
						286	297	442.21	1323.6	1323.67	-0.07	1	40	0.006868	K.IGNFSTDIKDSK.A		16.12		
						334	343	626.25	1250.48	1250.54	-0.06	0	57	0.000139	R.AECMLQQAER.L	Oxidation (M)	12.82		
						348	357	568.28	1134.55	1134.6	-0.06	0	46	0.0019186	R.QFVTATDVVR.G		19.37		
						456	468	513.24	1536.69	1536.76	-0.07	1	56	0.0001544	K.KLENCNYAVELGK.N		18.63		
						473	488	838.41	1674.8	1674.83	-0.03	0	83	3.42E-07	K.FSLVGIGGQDLNEGNR.T		21.03		
						571	584	539.9	1616.67	1616.76	-0.09	1	49	0.000895	K.TENLNDDEKLNNAK.Y		12.91		
						597	610	793.4	1584.79	1584.84	-0.05	0	64	2.61E-05	R.VYALPEDLVEVNPK.M		21.12		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38606	13%	334	7	68660	5.3	P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2												9	3
						45	56	436.89	1307.65	1307.72	-0.07	0	41	0.0061755	R.VGHSELVGEIIR.L		19.54		
						221	232	439.56	1315.67	1315.74	-0.06	0	37	0.0153624	K.LPANHPLLTGQR.V		14.04		
						257	265	481.75	961.49	961.54	-0.06	0	57	0.0001583	K.TVISQSLSK.Y		14.48		
						281	289	525.73	1049.45	1049.48	-0.03	0	36	0.0196029	R.GNEMSEVLR.D	Oxidation (M)	13.3		

						309	323	766.37	1530.72	1530.78	-0.06	0	77	1.23E-06	R.TALVANTSNMPVAAR.E	Oxidation (M)	14.17		
						339	353	579.2	1734.57	1734.66	-0.09	0	44	0.0024871	R.DMGYHVSMMADSTSR.W	3 Oxidation (M)	12.87		
						586	596	416.53	1246.57	1246.66	-0.09	2	42	0.0044252	K.FKDPLKDGEAK.I		13.43		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P34931	10%	298	5	70730	5.8	P34931|HS71L_HUMAN Heat shock 70 kDa protein 1L OS=Homo sapiens GN=HSPA1L PE=2 SV=2												9	1
						28	38	614.78	1227.55	1227.62	-0.07	0	70	9.16E-06	K.VEIIANDQGNR.T		14.21		
						39	51	744.33	1486.65	1486.69	-0.05	0	62	4.57E-05	R.TTPSYVAFTDTER.L		19.76		
						174	189	830.42	1658.82	1658.89	-0.07	0	80	5.85E-07	R.IINEPTAAAIAYGLDK.G		20.9		
						223	238	559.23	1674.66	1674.72	-0.07	0	49	0.000713	K.ATAGDTHLGGEDFDNR.L		15.08		
						542	552	652.28	1302.55	1302.59	-0.04	0	37	0.0148311	K.NALESYAFNMK.S	Oxidation (M)	19.85		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P17066	9%	308	6	71440	5.8	P17066|HSP76_HUMAN Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2												9	3
						28	38	614.78	1227.55	1227.62	-0.07	0	70	9.16E-06	R.VEILANDQGNR.T		14.21		
						39	51	744.33	1486.65	1486.69	-0.05	0	62	4.57E-05	R.TTPSYVAFTDTER.L		19.76		
						223	238	559.23	1674.66	1674.72	-0.07	0	49	0.000713	K.ATAGDTHLGGEDFDNR.L		15.08		
						351	359	541.26	1080.51	1080.56	-0.05	0	51	0.0005552	K.LLQDFFNGK.E		21.07		
						351	363	522.59	1564.75	1564.82	-0.08	1	42	0.0037475	K.LLQDFFNGKELNK.S		20.73		
						512	519	495.24	988.47	988.52	-0.05	1	34	0.0345733	R.LSKEEVER.M		12.74		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08107	9%	276	5	70294	5.5	P08107|HSP71_HUMAN Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5												9	2
						26	36	614.78	1227.55	1227.62	-0.07	0	70	9.16E-06	K.VEIIANDQGNR.T		14.21		
						37	49	744.33	1486.65	1486.69	-0.05	0	62	4.57E-05	R.TTPSYVAFTDTER.L		19.76		
						221	236	559.23	1674.66	1674.72	-0.07	0	49	0.000713	K.ATAGDTHLGGEDFDNR.L		15.08		
						349	357	555.27	1108.53	1108.57	-0.04	0	58	9.81E-05	K.LLQDFFNGR.D		21.29		
						540	550	652.28	1302.55	1302.59	-0.04	0	37	0.0148311	K.NALESYAFNMK.S	Oxidation (M)	19.85		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38646	9%	288	5	73920	5.9	P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2												9	1
						77	85	479.74	957.46	957.49	-0.03	0	54	0.0003589	K.VLENAEGAR.T		12.61		
						108	121	784.87	1567.73	1567.76	-0.03	0	33	0.0294346	R.QAVTNPNNTFYATK.R		17.29		
						207	218	621.82	1241.63	1241.67	-0.04	0	61	6.85E-05	K.DAGQISGLNVLR.V		20.55		
						395	405	645.82	1289.63	1289.67	-0.04	0	57	0.0001271	K.VQQTVQDLFGR.A		20.46		
						635	646	616.31	1230.61	1230.66	-0.05	0	83	4.00E-07	R.QAASSLQQASLK.L		13.87		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08133	5%	107	3	76168	5.4	P08133|ANXA6_HUMAN Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3												9	1
						282	290	554.25	1106.48	1106.53	-0.04	0	34	0.0272914	R.SELDMLDIR.E	Oxidation (M)	20.16		
						355	370	563.25	1686.72	1686.8	-0.08	0	38	0.0101364	K.GTVRPANDFNPDADAK.A		13.95		
						588	598	588.81	1175.6	1175.66	-0.05	0	36	0.0194167	R.DAFVAIVQSVK.N		21.34		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P29728	4%	119	3	83348	8.6	P29728|OAS2_HUMAN 2'-5'-oligoadenylate synthetase 2 OS=Homo sapiens GN=OAS2 PE=1 SV=3												9	1
						116	122	446.7	891.39	891.45	-0.05	0	34	0.0307289	K.NNFEIQK.S		14.26		
						123	134	678.36	1354.71	1354.71	0	0	44	0.0024744	K.SLDGFTIQVFTK.N		21.94		
						464	470	397.22	792.43	792.47	-0.04	0	42	0.0051036	R.VLSFSLK.S		20.33		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04843	3%	102	2	68641	6	P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1												9	2
						194	204	656.29	1310.56	1310.61	-0.05	0	51	0.0005352	R.SEDLLDYGPFR.D		21.68		
						269	278	530.25	1058.49	1058.54	-0.05	0	51	0.0005875	R.QPDSGISSIR.S		14.43		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8IYS2	3%	75	2	69684	8.4	Q8IYS2|K2013_HUMAN Uncharacterized protein KIAA2013 OS=Homo sapiens GN=KIAA2013 PE=2 SV=1												9	2
						206	214	542.76	1083.51	1083.57	-0.06	0	42	0.0047821	R.IQLNNPTER.V		14.99		
						310	316	393.71	785.41	785.44	-0.03	0	33	0.0461934	K.ALQDLAR.K		15.34		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49368	10%	208	5	61066	6.1	P49368|TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4												10	1
						238	248	640.35	1278.69	1278.71	-0.01	0	47	0.0014761	R.IVLLDSSLEYK.K		20.92		
						307	313	379.72	757.42	757.44	-0.03	0	34	0.0440209	R.ANITAIR.R		13.97		
						439	449	583.83	1165.65	1165.68	-0.03	0	54	0.0002674	R.AVAQALEVIPR.T		20.22		
						450	461	667.31	1332.61	1332.68	-0.07	0	39	0.0085112	R.TLIQNCGASTIR.L		16.52		
						508	518	593.35	1184.69	1184.71	-0.03	0	35	0.028617	K.TAVETAVLLLR.I		21.58		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31948	9%	253	5	63227	6.4	P31948|STIP1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1												10	1
						1	10	653.31	1304.6	1304.63	-0.02	1	51	0.0005305	-.MEQVNELKEK.G	Acetyl (Protein N-term); Oxidation (M)	14.79		
						110	118	532.23	1062.45	1062.48	-0.03	0	68	1.27E-05	K.EGLQNMEAR.L	Oxidation (M)	12.41		
						352	364	744.88	1487.75	1487.79	-0.03	0	66	1.59E-05	R.LAYINPDLALEEK.N		20.84		
						454	462	504.72	1007.42	1007.46	-0.04	0	34	0.0309612	K.ALDLDSSCK.E		14.88		
						534	543	558.82	1115.62	1115.64	-0.02	0	36	0.0185266	K.LMDVGLIAIR.-	Oxidation (M)	20.75		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99571	9%	147	2	44139	8.3	Q99571|P2RX4_HUMAN P2X purinoceptor 4 OS=Homo sapiens GN=P2RX4 PE=2 SV=2												10	1
						53	67	800.88	1599.74	1599.76	-0.02	0	79	8.30E-07	K.GYQETDSVVSSVTTK.V		19.25		
						128	148	660.6	1978.79	1978.84	-0.05	0	68	9.99E-06	K.SDASCTAGSAGTHSNGVSTGR.C		12.23		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q10471	9%	228	5	65433	8.6	Q10471|GALT2_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1												10	1
						94	101	447.2	892.39	892.4	-0.01	0	46	0.0016817	R.SGQDPYAR.N		12.49		
						102	113	493.24	1476.7	1476.77	-0.07	2	43	0.0034749	R.NKFNQVESDKLR.M		13.14		
						155	162	437.28	872.54	872.57	-0.03	1	39	0.0122	R.TVVSVLKK.S		13.4		
						294	302	462.25	922.49	922.52	-0.03	0	48	0.0010893	R.QGNPVAPIK.T		13.36		
						303	315	706.33	1410.65	1410.69	-0.04	0	51	0.0004909	K.TPMIAGGLFVMDK.F	2 Oxidation (M)	20.53		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16555	6%	137	3	62711	6	Q16555|DPYL2_HUMAN Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1												10	1
						259	268	516.27	1030.52	1030.54	-0.02	0	43	0.0040904	K.SSAEVIAQAR.K		13.53		
						375	390	871.37	1740.73	1740.8	-0.07	0	52	0.0003409	K.MDENQFVAVTSTNAAK.V	Oxidation (M)	19.34		
						441	451	542.81	1083.6	1083.63	-0.03	0	41	0.0054654	R.GSPLVVISQGK.I		19.69		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BYC5	4%	72	2	66930	7.4	Q9BYC5|FUT8_HUMAN Alpha-(1,6)-fucosyltransferase OS=Homo sapiens GN=FUT8 PE=1 SV=2												10	1
						139	147	536.75	1071.49	1071.53	-0.04	0	40	0.0095085	K.NLEGNELQR.H		13.88		
						404	415	667.85	1333.68	1333.71	-0.04	0	32	0.0467341	R.VYLATDDPSLLK.E		20.4		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50990	22%	622	11	60153	5.4	P50990|TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4												11	1
						63	74	667.36	1332.71	1332.74	-0.03	0	55	0.0002553	K.LFVTNDAATILR.E		20.97		
						156	165	573.79	1145.56	1145.59	-0.03	0	35	0.0267578	R.DIDEVSSLLR.T		21.36		
						172	181	584.79	1167.57	1167.59	-0.02	0	74	2.98E-06	K.QYGNEVFLAK.L		19.66		
						226	235	532.74	1063.47	1063.5	-0.03	0	48	0.0012596	K.ETEGDVTSVK.D		12.78		
						261	270	593.26	1184.51	1184.54	-0.03	0	40	0.0085682	K.TAEELMNFSK.G	Oxidation (M)	17.92		
						271	281	625.27	1248.52	1248.57	-0.04	0	71	6.23E-06	K.GEENLMDAQVK.A	Oxidation (M)	13.52		
						282	296	686.86	1371.71	1371.74	-0.03	0	99	9.72E-09	K.AIADTGANVVVTGGK.V		18.57		
						327	335	443.24	884.47	884.51	-0.03	0	34	0.0309926	K.TVGATALPR.L		14.17		
						379	390	691.28	1380.55	1380.58	-0.03	0	67	1.41E-05	R.GSTDNLMDDIER.A	Oxidation (M)	18.88		
						441	450	575.78	1149.55	1149.58	-0.03	0	64	2.73E-05	K.FAEAFEAIPR.A		20.49		
						510	520	564.83	1127.64	1127.67	-0.03	0	40	0.0078969	K.LATNAAVTVLR.V		19.36		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14618	19%	491	8	58470	8	P14618|KPYM_HUMAN Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4												11	1
						33	43	599.32	1196.62	1196.64	-0.02	0	54	0.0002778	R.LDIDSPPITAR.N		19.7		
						44	56	680.34	1358.67	1358.7	-0.03	0	65	2.26E-05	R.NTGIICTIGPASR.S		19.53		
						126	135	495.75	989.48	989.5	-0.02	0	56	0.0002101	K.GSGTAEVELK.K		13.73		
						142	151	607.27	1212.53	1212.57	-0.04	0	38	0.0129072	K.ITLDNAYMEK.C	Oxidation (M)	18.79		
						189	206	890.44	1778.86	1778.87	-0.01	0	74	2.20E-06	K.GADFLVTEVENGGSLGSK.K		21.23		
						208	224	818.92	1635.83	1635.88	-0.05	0	63	3.26E-05	K.GVNLPGAAVDLPAVSEK.D		20.62		
						295	305	571.29	1140.57	1140.6	-0.03	0	54	0.0002779	R.GDLGIEIPAEK.V		20.05		
						423	433	611.3	1220.6	1220.63	-0.03	0	88	1.06E-07	K.CCSGAIIVLTK.S		19.79		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	17%	475	9	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												11	2
						58	65	431.72	861.43	861.46	-0.03	0	43	0.004472	K.ALAPEYAK.A		13.65		
						121	130	601.79	1201.56	1201.6	-0.03	0	53	0.0003706	R.EADDIVNWLK.K		21.84		
						223	230	496.26	990.51	990.54	-0.03	0	42	0.0046646	K.ENLLDFIK.H		22.28		
						277	283	377.17	752.33	752.37	-0.04	0	31	0.0481451	K.TAAESFK.G		12.69		
						301	308	483.77	965.52	965.56	-0.03	0	42	0.0042697	R.ILEFFGLK.K		22.23		
						317	326	611.8	1221.59	1221.62	-0.03	0	49	0.0009861	R.LITLEEEMTK.Y	Oxidation (M)	19.09		
						327	338	484.56	1450.65	1450.69	-0.04	0	65	1.93E-05	K.YKPESEELTAER.I		13.6		
						425	436	655.29	1308.56	1308.59	-0.03	0	100	7.15E-09	K.MDSTANEVEAVK.V	Oxidation (M)	13.69		
						453	461	533.75	1065.48	1065.51	-0.03	0	50	0.0006524	R.TVIDYNGER.T		14.95		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q02818	11%	325	6	53846	5.2	Q02818|NUCB1_HUMAN Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4												11	1
						72	81	536.77	1071.52	1071.56	-0.04	0	64	3.47E-05	K.LQAANAEDIK.S		13.56		
						72	84	448.88	1343.63	1343.7	-0.07	1	48	0.0011443	K.LQAANAEDIKSGK.L		12.87		
						219	229	570.81	1139.6	1139.63	-0.03	0	59	8.87E-05	K.VNVPGSQAQLK.E		14.9		
						350	357	482.74	963.47	963.47	0	0	47	0.0016564	R.FEEELAAR.E		16		
						368	377	552.26	1102.51	1102.56	-0.05	0	72	5.17E-06	R.LSQETEALGR.S		13.86		
						452	461	580.8	1159.58	1159.62	-0.04	0	35	0.0272451	R.LPEVEVPQHL.-		20.45		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31146	8%	198	3	51678	6.3	P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4												11	1
						384	393	513.8	1025.58	1025.61	-0.03	0	50	0.0006739	R.DAGPLLISLK.D		21.32		
						417	432	751.84	1501.67	1501.7	-0.03	0	72	4.27E-06	R.AAPEASGTPSSDAVSR.L		12.82		
						440	449	579.31	1156.6	1156.65	-0.04	0	45	0.0023754	K.LQATVQELQK.R		15.96		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99832	5%	141	3	59842	7.5	Q99832|TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2												11	1
						1	10	608.82	1215.63	1215.66	-0.03	0	39	0.0092664	-.MMPTPVILLK.E	Acetyl (Protein N-term); 2 Oxidation (M)	21.49		
						431	440	552.81	1103.61	1103.63	-0.03	0	60	7.73E-05	K.QQLLIGAYAK.A		19.88		
						441	447	406.24	810.47	810.5	-0.03	0	41	0.0045058	K.ALEIIPR.Q		19.75		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P10809	3%	94	2	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												11	1
						397	405	451.26	900.5	900.53	-0.03	0	46	0.0025715	K.LSDGVAVLK.V		18.75		
						421	429	480.75	959.49	959.5	-0.02	0	49	0.0012825	R.VTDALNATR.A		13.3		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50991	3%	72	2	58401	8	P50991|TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4												11	1
						35	42	419.2	836.39	836.44	-0.05	0	33	0.0354469	R.FSNISAAK.A		13.13		
						532	539	466.23	930.44	930.48	-0.03	0	40	0.0096358	K.IDDVVNTR.-		13.78		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07437	30%	636	12	50095	4.8	P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2												12	2
						3	19	608.28	1821.83	1821.92	-0.09	0	58	0.0001141	R.EIVHIQAGQCGNQIGAK.F		17.35		
						47	58	651.31	1300.61	1300.63	-0.02	0	57	0.0001577	R.ISVYYNEATGGK.Y		18.96		
						63	77	816.41	1630.8	1630.82	-0.03	0	49	0.0007771	R.AILVDLEPGTMDSVR.S	Oxidation (M)	20.65		
						242	251	565.79	1129.56	1129.59	-0.02	0	55	0.000263	R.FPGQLNADLR.K		19.8		
						253	262	580.31	1158.6	1158.62	-0.02	0	65	2.50E-05	K.LAVNMVPFPR.L	Oxidation (M)	20.16		
						283	297	830.46	1658.9	1658.89	0.01	0	40	0.0058378	R.ALTVPELTQQVFDAK.N		21.97		
						298	306	549.2	1096.38	1096.41	-0.03	0	33	0.0278908	K.NMMAACDPR.H	2 Oxidation (M)	12.03		
						310	318	520.29	1038.56	1038.59	-0.02	0	60	7.53E-05	R.YLTVAAVFR.G		21.22		
						321	336	657.95	1970.82	1970.87	-0.05	1	54	0.0002453	R.MSMKEVDEQMLNVQNK.N	3 Oxidation (M)	13.25		
						325	336	731.83	1461.65	1461.68	-0.03	0	70	6.17E-06	K.EVDEQMLNVQNK.N	Oxidation (M)	14.13		
						351	359	514.75	1027.49	1027.51	-0.02	0	53	0.0003845	K.TAVCDIPPR.G		13.74		
						381	390	623.28	1244.56	1244.59	-0.03	0	42	0.0051834	R.ISEQFTAMFR.R	Oxidation (M)	20.03		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P68371	27%	585	11	50255	4.8	P68371|TBB2C_HUMAN Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1												12	2
						3	19	608.28	1821.83	1821.92	-0.09	0	58	0.0001141	R.EIVHLQAGQCGNQIGAK.F		17.35		
						63	77	809.39	1616.77	1616.81	-0.03	0	53	0.0003697	R.AVLVDLEPGTMDSVR.S	Oxidation (M)	20.38		
						242	251	565.79	1129.56	1129.59	-0.02	0	55	0.000263	R.FPGQLNADLR.K		19.8		
						253	262	580.31	1158.6	1158.62	-0.02	0	65	2.50E-05	K.LAVNMVPFPR.L	Oxidation (M)	20.16		
						283	297	854.41	1706.81	1706.85	-0.04	0	43	0.0032552	R.ALTVPELTQQMFDAK.N	Oxidation (M)	20.73		
						298	306	549.2	1096.38	1096.41	-0.03	0	33	0.0278908	K.NMMAACDPR.H	2 Oxidation (M)	12.03		
						310	318	520.29	1038.56	1038.59	-0.02	0	60	7.53E-05	R.YLTVAAVFR.G		21.22		
						321	336	657.95	1970.82	1970.87	-0.05	1	54	0.0002453	R.MSMKEVDEQMLNVQNK.N	3 Oxidation (M)	13.25		
						325	336	731.83	1461.65	1461.68	-0.03	0	70	6.17E-06	K.EVDEQMLNVQNK.N	Oxidation (M)	14.13		
						351	359	514.75	1027.49	1027.51	-0.02	0	53	0.0003845	K.TAVCDIPPR.G		13.74		
						381	390	623.28	1244.56	1244.59	-0.03	0	42	0.0051834	R.ISEQFTAMFR.R	Oxidation (M)	20.03		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BQE3	18%	422	7	50548	5	Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1												12	2
						41	60	1004.45	2006.88	2006.89	-0.01	0	124	2.54E-11	K.TIGGGDDSFNTFFSETGAGK.H		21.62		
						65	79	851.44	1700.87	1700.9	-0.03	0	63	2.89E-05	R.AVFVDLEPTVIDEVR.T		22.01		
						85	96	697.36	1392.72	1392.74	-0.03	0	53	0.0003459	R.QLFHPEQLITGK.E	Gln->pyro-Glu (N-term Q)	21.75		
						85	96	470.91	1409.72	1409.77	-0.05	0	49	0.000804	R.QLFHPEQLITGK.E		20.34		
						113	121	543.3	1084.59	1084.61	-0.02	0	87	1.77E-07	K.EIIDLVLDR.I		21.88		
						216	229	573.61	1717.82	1717.87	-0.05	0	39	0.0073663	R.NLDIERPTYTNLNR.L		19.45		
						327	336	508.28	1014.55	1014.57	-0.02	0	56	0.000198	K.DVNAAIATIK.T		19.72		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21281	16%	398	7	56807	5.6	P21281|VATB2_HUMAN Vacuolar ATP synthase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3												12	2
						30	37	437.23	872.45	872.47	-0.03	0	33	0.0495683	R.EQALAVSR.N		13.17		
						83	93	545.78	1089.55	1089.57	-0.02	0	57	0.0001818	R.SGQVLEVSGSK.A		13.69		
						94	108	760.89	1519.76	1519.79	-0.03	0	109	9.62E-10	K.AVVQVFEGTSGIDAK.K		20.2		
						121	130	560.76	1119.5	1119.52	-0.02	0	46	0.001889	R.TPVSEDMLGR.V	Oxidation (M)	13.78		
						387	400	798.94	1595.87	1595.9	-0.03	0	47	0.0011433	R.QIYPPINVLPSLSR.L		21.84		
						461	471	654.81	1307.61	1307.63	-0.01	0	38	0.0104875	R.NFIAQGPYENR.T		19.32		
						495	506	719.36	1436.71	1436.73	-0.02	0	70	7.12E-06	R.IPQSTLSEFYPR.D		20.78		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43175	11%	286	5	57356	6.3	O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4												12	2
						59	69	565.79	1129.56	1129.6	-0.03	0	60	8.20E-05	K.VTADVINAAEK.L		16.13		
						76	90	744.85	1487.69	1487.72	-0.03	0	62	4.04E-05	R.AGTGVDNVDLEAATR.K		19.4		
						147	155	450.27	898.53	898.56	-0.03	0	46	0.0015957	K.TLGILGLGR.I		21.18		
						237	247	550.3	1098.59	1098.6	-0.02	0	35	0.0227624	R.GGIVDEGALLR.A		20.29		
						385	394	536.27	1070.53	1070.57	-0.04	0	82	4.94E-07	K.QADVNLVNAK.L		14.44		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	8%	229	4	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												12	2
						46	58	720.32	1438.62	1438.66	-0.04	0	100	7.35E-09	K.TGTAEMSSILEER.I	Oxidation (M)	17.96		
						74	83	500.78	999.55	999.57	-0.02	0	36	0.0226724	R.VLSIGDGIAR.V		19.76		
						150	161	586.31	1170.6	1170.62	-0.02	0	61	6.36E-05	R.VVDALGNAIDGK.G		19.63		
						195	204	513.79	1025.57	1025.59	-0.02	0	34	0.0255611	K.AVDSLVPIGR.G		20.07		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27797	7%	116	3	48283	4.3	P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1												12	1
						49	55	369.2	736.38	736.41	-0.03	0	36	0.0181916	K.FVLSSGK.F		14.96		
						74	87	804.42	1606.83	1606.77	0.06	0	44	0.0024486	R.FYALSASFEPFSNK.G		21.93		
						279	286	496.73	991.44	991.46	-0.02	0	36	0.0210671	R.QIDNPDYK.G		12.9		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P78371	4%	141	2	57794	6	P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4												12	1
						237	248	654.33	1306.65	1306.64	0	0	51	0.0005493	K.ILIANTGMDTDK.I	Oxidation (M)	15.7		
						377	388	665.82	1329.63	1329.65	-0.03	0	57	0.0001414	R.GATQQILDEAER.S		19.54		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13667	4%	93	2	73229	5	P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2												12	1
						235	245	567.27	1132.53	1132.56	-0.03	0	51	0.0006518	K.VDATAETDLAK.R		14.39		
						350	362	729.9	1457.78	1457.75	0.03	0	42	0.0044928	K.VSQGQLVVMQPEK.F	Oxidation (M)	15.18		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06733	15%	295	6	47481	7	P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2												13	1
						16	28	703.84	1405.67	1405.71	-0.04	0	59	8.99E-05	R.GNPTVEVDLFTSK.G		20.79		
						93	103	656.77	1311.53	1311.57	-0.04	0	48	0.0010938	K.LMIEMDGTENK.S	2 Oxidation (M)	13.74		
						222	228	401.23	800.44	800.46	-0.03	0	45	0.0028973	K.EGLELLK.T		20.18		
						240	253	778.87	1555.72	1555.77	-0.05	0	57	0.0001371	K.VVIGMDVAASEFFR.S	Oxidation (M)	21.4		
						270	281	713.35	1424.69	1424.72	-0.03	0	50	0.0006301	R.YISPDQLADLYK.S		21.23		
						407	412	403.72	805.42	805.44	-0.03	0	35	0.0244664	K.YNQLLR.I		14.86		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15084	12%	192	4	48490	5	Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1												13	1
						68	77	508.29	1014.57	1014.61	-0.04	1	62	5.25E-05	K.AATALKDVVK.V		13.52		
						217	231	764.39	1526.76	1526.84	-0.08	0	43	0.0029461	K.LAAVDATVNQVLASR.Y		21.01		
						314	322	539.79	1077.57	1077.61	-0.04	0	53	0.000379	R.NSYLEVLLK.L		21.62		
						393	409	808.41	1614.81	1614.84	-0.02	0	33	0.0327681	R.GSTAPVGGGAFPTIVER.E		20.4		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61158	10%	154	4	47797	5.6	P61158|ARP3_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3												13	1
						255	264	547.77	1093.53	1093.58	-0.04	0	39	0.0086144	K.QYTGINAISK.K		16.35		
						318	329	649.32	1296.63	1296.65	-0.02	0	39	0.0072648	K.NIVLSGGSTMFR.D	Oxidation (M)	19.75		
						349	357	474.24	946.46	946.47	-0.01	0	41	0.0069078	K.LSEELSGGR.L		13.39		
						410	418	502.23	1002.44	1002.46	-0.02	0	35	0.024754	R.HNPVFGVMS.-	Oxidation (M)	18.36		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08962	8%	140	3	26474	8.1	P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2												13	16
						109	120	506.23	1515.66	1515.68	-0.02	1	33	0.0408541	R.DKVMSEFNNNFR.Q	Oxidation (M)	18.57		
						111	120	637.29	1272.56	1272.56	0.01	0	72	4.85E-06	K.VMSEFNNNFR.Q	Oxidation (M)	18.27		
						121	128	527.24	1052.46	1052.46	0	0	35	0.0211908	R.QQMENYPK.N	Oxidation (M)	12.22		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52209	8%	166	3	53619	6.8	P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3												13	1
						39	48	561.26	1120.51	1120.54	-0.03	0	42	0.0048773	K.VDDFLANEAK.G		19.62		
						77	87	596.79	1191.57	1191.58	-0.01	0	66	2.01E-05	K.AGQAVDDFIEK.L		19.57		
						120	136	796.4	1590.79	1590.8	-0.01	0	59	8.68E-05	K.GILFVGSGVSGGEEGAR.Y		20.62		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	7%	178	3	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												13	26
						135	146	438.9	1313.68	1313.73	-0.05	0	44	0.0027344	R.EHALLAYTLGVK.Q		20.27		
						256	266	513.3	1024.58	1024.6	-0.02	0	71	4.84E-06	K.IGGIGTVPVGR.V		19.27		
						431	439	457.77	913.53	913.56	-0.03	0	62	4.36E-05	R.QTVAVGVIK.A		16.09		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50395	7%	163	3	51087	6.1	P50395|GDIB_HUMAN Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2												13	1
						80	89	568.79	1135.57	1135.61	-0.04	0	37	0.0131312	K.FLMANGQLVK.M	Oxidation (M)	19.22		
						211	218	469.74	937.46	937.49	-0.03	0	48	0.0009106	K.LYSESLAR.Y		14.73		
						391	402	683.34	1364.66	1364.69	-0.03	0	77	1.34E-06	K.DLGTESQIFISR.T		20.97		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16181	4%	79	2	50933	8.8	Q16181|SEPT7_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2												13	1
						187	195	490.82	979.62	979.64	-0.02	0	39	0.0091037	K.VNIIPLIAK.A		21.18		
						417	425	537.76	1073.5	1073.55	-0.05	0	40	0.0087055	R.ILEQQNSSR.T		12.44		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P80723	29%	129	3	22680	4.6	P80723|BASP_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2												14	2
						98	121	766.69	2297.04	2297.13	-0.09	1	43	0.0025406	K.AEPPKAPEQEQAAPGPAAGGEAPK.A		12.27		
						122	149	879.39	2635.13	2635.22	-0.09	1	47	0.0010041	K.AAEAAAAPAESAAPAAGEEPSKEEGEPK.K		12.4		
						185	198	693.83	1385.65	1385.67	-0.02	0	39	0.0087489	K.ETPAATEAPSSTPK.A		12.05		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01518	28%	799	13	52222	8.3	Q01518|CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4												14	12
						2	10	567.25	1132.49	1132.52	-0.03	0	64	3.24E-05	M.ADMQNLVER.L	Acetyl (Protein N-term); Oxidation (M)	13.55		
						72	84	384.92	1535.67	1535.79	-0.12	1	41	0.0056308	K.HAEMVHTGLKLER.A	Oxidation (M)	12.09		
						85	100	879.42	1756.82	1756.88	-0.06	0	94	2.55E-08	R.ALLVTASQCQQPAENK.L		13.29		
						101	113	713.89	1425.76	1425.81	-0.05	0	60	6.45E-05	K.LSDLLAPISEQIK.E		20.84		
						156	167	747.78	1493.55	1493.59	-0.04	0	77	1.31E-06	K.EMNDAAMFYTNR.V	2 Oxidation (M)	13.46		
						295	312	460.22	1836.87	1836.97	-0.11	0	62	3.98E-05	R.SGPKPFSAPKPQTSPSPK.R		12.14		
						314	327	504.93	1511.78	1511.86	-0.08	2	54	0.0002493	R.ATKKEPAVLELEGK.K		12.84		
						317	327	404.88	1211.62	1211.68	-0.06	1	53	0.000379	K.KEPAVLELEGK.K		13.69		
						317	328	447.58	1339.71	1339.77	-0.07	2	57	0.0001537	K.KEPAVLELEGKK.W		12.8		

						318	327	542.77	1083.53	1083.58	-0.05	0	45	0.0020827	K.EPAVLELEGK.K		16.28		
						331	348	1036.99	2071.97	2072.03	-0.06	0	60	5.54E-05	R.VENQENVSNLVIEDTELK.Q		20.44		
						356	364	538.77	1075.53	1075.57	-0.04	0	58	0.0001214	K.CVNTTLQIK.G		13.33		
						423	433	618.28	1234.54	1234.59	-0.04	0	76	1.81E-06	K.NSLDCEIVSAK.S		13.73		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30101	22%	504	9	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												14	3
						63	73	596.28	1190.56	1190.59	-0.04	0	61	5.43E-05	R.LAPEYEAAATR.L		12.89		
						95	104	542.77	1083.53	1083.56	-0.03	0	38	0.0116579	K.YGVSGYPTLK.I		14.26		
						105	119	551.57	1651.69	1651.76	-0.07	1	35	0.0196814	K.IFRDGEEAGAYDGPR.T		12.98		
						297	304	439.23	876.44	876.48	-0.04	0	40	0.0074901	K.LNFAVASR.K		14.17		
						367	379	684.82	1367.62	1367.66	-0.04	0	61	5.81E-05	K.SEPIPESNDGPVK.V		12.75		
						423	433	399.89	1196.66	1196.71	-0.06	1	52	0.0004607	K.LSKDPNIVIAK.M		12.71		
						434	448	840.86	1679.71	1679.75	-0.04	0	101	5.30E-09	K.MDATANDVPSPYEVR.G	Oxidation (M)	14		
						449	460	671.33	1340.64	1340.68	-0.04	0	53	0.0003188	R.GFPTIYFSPANK.K		20.7		
						483	496	527.26	1578.75	1578.83	-0.07	0	33	0.0288992	R.EATNPPVIQEEKPK.K		12.36		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y6N5	10%	175	4	50214	9.2	Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1												14	1
						65	79	533.26	1596.76	1596.85	-0.09	1	34	0.0235443	R.KVGAENVAIVEPSER.H		13.02		
						66	79	735.36	1468.72	1468.75	-0.04	0	54	0.000294	K.VGAENVAIVEPSER.H		13.86		
						187	200	767.88	1533.74	1533.78	-0.04	0	38	0.0119137	K.EGNAIFTFPNTPVK.C		20.75		
						345	358	672.35	1342.69	1342.72	-0.03	0	49	0.0008321	K.TAAAVAAQSGILDR.T		14.04		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P39656	9%	179	4	48893	5.4	P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2												14	1
						30	40	635.37	1268.72	1268.75	-0.02	0	64	3.03E-05	R.TLVLLDNLNVR.E		21.1		
						54	60	421.21	840.4	840.44	-0.04	0	42	0.0039377	R.GFELTFK.T		20.17		
						61	71	580.29	1158.56	1158.61	-0.05	0	35	0.0239428	K.TADDPSLSLIK.Y		15.8		
						223	233	585.33	1168.65	1168.69	-0.04	0	38	0.0125874	K.NTLLIAGLQAR.N		20.04		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BS26	8%	119	3	47341	5.1	Q9BS26|TXND4_HUMAN Thioredoxin domain-containing protein 4 OS=Homo sapiens GN=TXNDC4 PE=1 SV=1												14	1
						149	158	573.78	1145.55	1145.59	-0.04	0	36	0.022103	R.DLAEITTLDR.S		20.13		
						162	170	556.27	1110.53	1110.57	-0.04	0	37	0.0123549	R.NIIGYFEQK.D		20.26		
						314	327	781.34	1560.67	1560.76	-0.09	0	46	0.0015296	K.TPADCPVIAIDSFR.H		20.79		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O60664	7%	98	2	47189	5.3	O60664|M6PBP_HUMAN Mannose-6-phosphate receptor-binding protein 1 OS=Homo sapiens GN=M6PRBP1 PE=1 SV=2												14	1
						69	84	764.42	1526.82	1526.87	-0.05	0	50	0.0007002	R.TLTAAAVSGAQPILSK.L		15.67		
						167	180	690.33	1378.65	1378.69	-0.04	0	49	0.0009642	K.SVVTGGVQSVMGSR.L	Oxidation (M)	12.93		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13489	6%	89	2	51766	4.7	P13489|RINI_HUMAN Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2												14	1
						288	302	765.87	1529.73	1529.73	0	0	54	0.0002446	K.ELSLAGNELGDEGAR.L		15.85		
						360	373	757.38	1512.74	1512.77	-0.03	0	35	0.0226163	R.ELCQGLGQPGSVLR.V		15.37		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50454	6%	112	2	46525	8.8	P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2												14	1
						47	60	737.36	1472.71	1472.73	-0.03	0	41	0.0056439	R.SAGLAFSLYQAMAK.D	Oxidation (M)	20.35		
						394	405	647.32	1292.62	1292.67	-0.05	0	71	5.89E-06	R.DTQSGSLLFIGR.L		20.88		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O14773	5%	106	2	61723	6	O14773|TPP1_HUMAN Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2												14	1
						246	259	492.23	1473.67	1473.75	-0.08	0	48	0.001207	R.LFGGNFAHQASVAR.V		13.91		
						507	520	535.59	1603.74	1603.81	-0.07	0	58	9.49E-05	R.LYQQHGAGLFDVTR.G		19.15		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60709	41%	838	13 (14)	42052	5.3	P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1												15	20
						2	18	919.38	1836.74	1836.79	-0.05	0	86	1.66E-07	M.DDDIAALVVDNGSGMCK.A	Acetyl (Protein N-term); Oxidation (M)	22.07		
						19	28	488.71	975.4	975.44	-0.04	0	62	5.01E-05	K.AGFAGDDAPR.A		13.5		
						29	39	600	1197.99	1197.7	0.29	0	63	6.96E-06	R.AVFPSIVGRPR.H		19.73		
						40	50	401.83	1202.48	1202.55	-0.07	0	56	0.0001779	R.HQGVMVGMGQK.D	2 Oxidation (M)	11.97		
						51	61	599.75	1197.48	1197.51	-0.03	0	79	8.64E-07	K.DSYVGDEAQSK.R		13.06		
						51	62	452.19	1353.55	1353.62	-0.06	1	58	9.94E-05	K.DSYVGDEAQSKR.G		12.66		
						96	113	652	1952.99	1953.06	-0.07	0	63	2.83E-05	R.VAPEEHPVLLTEAPLNPK.A		19.91		
						197	206	566.9	1131.79	1131.52	0.27	0	54	0.0002897	R.GYSFTTTAER.E		17.85		
						239	254	895.93	1789.85	1789.88	-0.03	0	102	4.11E-09	K.SYELPDGQVITIGNER.F		21.15		
						292	312	744.34	2229.99	2230.06	-0.07	0	44	0.002371	K.DLYANTVLSGGTTMYPGIADR.M	Oxidation (M)	21.2		
						313	326	527.58	1579.71	1579.79	-0.08	1	40	0.0059936	R.MQKEITALAPSTMK.I	2 Oxidation (M)	13.85		
						316	326	589.29	1176.56	1176.61	-0.04	0	51	0.0005813	K.EITALAPSTMK.I	Oxidation (M)	15.34		
						360	372	750.32	1498.63	1498.67	-0.03	0	80	6.63E-07	K.QEYDESGPSIVHR.K	Gln->pyro-Glu (N-term Q)	19.2		
						360	372	506.22	1515.64	1515.7	-0.06	0	66	2.00E-05	K.QEYDESGPSIVHR.K		14.24		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00558	13%	209	4	44985	8.3	P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3												15	1
						172	184	461.89	1382.65	1382.7	-0.05	0	44	0.0026511	R.AHSSMVGVNLPQK.A	Oxidation (M)	13.59		
						200	216	590.31	1767.91	1767.99	-0.07	0	41	0.0052473	K.ALESPERPFLAILGGAK.V		21.72		
						247	264	991.95	1981.89	1981.93	-0.04	0	87	1.13E-07	K.VLNNMEIGTSLFDEEGAK.I	Oxidation (M)	20.89		

						354	361	460.72	919.43	919.47	-0.03	0	38	0.0114164	K.ALMDEVVK.A	Oxidation (M)	13.9		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06576	7%	133	3	56525	5.3	P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3												15	1
						189	198	544.81	1087.6	1087.63	-0.03	0	35	0.0272099	K.VVDLLAPYAK.G		20.97		
						213	225	737.4	1472.79	1472.83	-0.04	0	35	0.0241314	K.TVLIMELINNVAK.A	Oxidation (M)	22.51		
						265	279	809.38	1616.75	1616.8	-0.04	0	63	2.98E-05	K.VALVYGQMNEPPGAR.A	Oxidation (M)	19.29		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O94766	6%	88	2	37270	8.4	O94766|B3GA3_HUMAN Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 OS=Homo sapiens GN=B3GAT3 PE=1 SV=2												15	3
						96	105	557.32	1112.62	1112.66	-0.04	0	35	0.0241567	R.LSQTLSLVPR.L		20.22		
						226	235	566.76	1131.5	1131.53	-0.03	0	53	0.0003511	R.FEGPQVQDGR.V		14.16		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08670	5%	89	2	53676	5.1	P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4												15	2
						101	113	529.92	1586.74	1586.79	-0.05	1	35	0.0221355	R.TNEKVELQELNDR.F		16.99		
						295	304	547.25	1092.49	1092.52	-0.03	0	54	0.0002643	K.FADLSEAANR.N		17.51		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04075	30%	746	12 (14)	39851	8.3	P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2												16	3
						2	13	717.87	1433.72	1433.72	0	0	45	0.0022361	M.PYQYPALTPEQK.K		19.37		
						2	14	521.6	1561.78	1561.81	-0.04	1	57	0.0001203	M.PYQYPALTPEQKK.E		18.2		
						15	22	470.73	939.45	939.48	-0.03	0	60	6.96E-05	K.ELSDIAHR.I		13.25		
						29	42	666.84	1331.66	1331.69	-0.03	0	71	6.07E-06	K.GILAADESTGSIAK.R		18.98		
						29	43	496.92	1487.74	1487.79	-0.05	1	48	0.0011881	K.GILAADESTGSIAKR.L		16.63		
						43	57	601.62	1801.84	1801.9	-0.06	2	33	0.0317734	K.RLQSIGTENTEENRR.F		12.43		
						44	56	745.85	1489.68	1489.7	-0.02	0	77	1.58E-06	R.LQSIGTENTEENR.R		13.51		
						44	57	549.59	1645.75	1645.8	-0.05	1	37	0.0151725	R.LQSIGTENTEENRR.F		12.78		
						61	69	522.78	1043.55	1043.56	-0.01	0	54	0.0003141	R.QLLLTADDR.V		19.33		
						88	99	448.23	1341.66	1341.7	-0.05	0	34	0.0295688	K.ADDGRPFPQVIK.S		19.11		
						100	111	396.23	1185.67	1185.71	-0.04	2	33	0.037803	K.SKGGVVGIKVDK.G		12.65		
						141	147	362.15	722.29	722.32	-0.03	0	32	0.0417081	K.DGADFAK.W		13.12		
						305	312	401.23	800.45	800.48	-0.03	0	44	0.0043551	R.ALQASALK.A		13.38		
						332	342	566.77	1131.52	1131.57	-0.05	0	92	4.61E-08	R.ALANSLACQGK.Y		13.94		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40121	22%	373	6	38779	5.9	P40121|CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=1												16	1
						116	127	451.21	1350.6	1350.62	-0.02	0	37	0.0132507	K.YQEGGVESAFHK.T		14.9		
						232	243	659.3	1316.58	1316.57	0.01	0	41	0.0062918	K.EGNPEEDLTADK.A		15.2		
						244	253	510.77	1019.52	1019.54	-0.02	0	87	1.85E-07	K.ANAQAAALYK.V		13.64		
						254	265	640.79	1279.57	1279.61	-0.03	0	87	1.34E-07	K.VSDATGQMNLTK.V	Oxidation (M)	12.52		
						307	319	695.35	1388.69	1388.74	-0.05	0	53	0.0003569	R.QAALQVAEGFISR.M		21.06		
						320	335	930.97	1859.92	1859.92	0	0	69	8.67E-06	R.MQYAPNTQVEILPQGR.E	Oxidation (M)	19.72		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08865	13%	162	3	32947	4.8	P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4												16	1
						64	80	870.93	1739.85	1739.94	-0.09	0	58	9.24E-05	R.AIVAIENPADVSVISSR.N		20.63		
						90	102	602.32	1202.62	1202.64	-0.02	0	65	2.53E-05	K.FAAATGATPIAGR.F		16.4		
						121	128	456.76	911.51	911.54	-0.03	0	39	0.008211	R.LLVVTDPR.A		19.07		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36222	6%	84	2	42998	8.7	P36222|CH3L1_HUMAN Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2												16	1
						171	182	586.34	1170.66	1170.7	-0.04	0	39	0.009827	K.QLLLSAALSAGK.V		20.89		
						183	193	606.3	1210.59	1210.61	-0.01	0	45	0.0023658	K.VTIDSSYDIAK.I		19.28		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y617	6%	113	2	40796	7.6	Q9Y617|SERC_HUMAN Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2												16	1
						6	16	557.29	1112.57	1112.6	-0.03	0	63	3.79E-05	R.QVVNFGPGPAK.L		18.55		
						52	61	593.33	1184.64	1184.65	-0.01	0	50	0.0007743	K.IINNTENLVR.E		17.07		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15365	6%	125	2	37987	6.7	Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2												16	1
						47	57	644.77	1287.52	1287.59	-0.07	0	64	2.85E-05	R.INISEGNCPER.I		14.2		
						298	306	507.76	1013.51	1013.53	-0.02	0	61	6.07E-05	R.QGANINEIR.Q		13.86		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61160	5%	77	2	45017	6.3	P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1												16	1
						98	103	366.19	730.37	730.4	-0.03	0	37	0.0234386	K.LNIDTR.N		13.77		
						107	118	685.37	1368.72	1368.73	-0.01	0	40	0.0060911	K.ILLTEPPMNPTK.N	Oxidation (M)	19.24		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61421	14%	216	5	40759	4.9	P61421|VA0D1_HUMAN Vacuolar proton pump subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1												17	1
						188	195	510.75	1019.49	1019.5	-0.01	0	33	0.0424782	K.AYLESFYK.F		20.06		
						247	257	615.83	1229.66	1229.68	-0.02	0	45	0.0022481	R.LYPEGLAQLAR.A		20.49		
						258	265	484.21	966.4	966.43	-0.03	0	32	0.0370318	R.ADDYEQVK.N		12.83		
						266	275	631.28	1260.55	1260.57	-0.02	0	33	0.0343912	K.NVADYYPEYK.L		19.41		
						276	288	652.82	1303.62	1303.64	-0.02	0	72	4.59E-06	K.LLFEGAGSNPGDK.T		19.63		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P07355	24%	479	9	38808	7.6	P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2												18	1
						2	10	564.78	1127.55	1127.56	-0.01	0	71	6.99E-06	M.STVHEILCK.L	Acetyl (Protein N-term)	19.42		
						29	37	543.74	1085.47	1085.48	-0.01	0	42	0.0053369	K.AYTNFDAER.D		15.63		
						38	47	544.28	1086.55	1086.59	-0.04	0	48	0.0015112	R.DALNIETAIK.T		20.16		
						69	77	556.27	1110.53	1110.55	-0.02	0	59	7.65E-05	R.QDIAFAYQR.R		19.38		
						105	115	611.79	1221.57	1221.59	-0.02	0	73	3.68E-06	K.TPAQYDASELK.A		15.09		
						136	145	622.8	1243.59	1243.62	-0.02	0	67	1.44E-05	R.TNQELQEINR.V		14.24		
						158	168	613.28	1224.55	1224.56	-0.02	0	41	0.0050742	K.DIISDTSGDFR.K		20.29		
						170	176	381.23	760.44	760.45	-0.01	0	48	0.0017713	K.LMVALAK.G	Oxidation (M)	15.67		
						296	302	419.19	836.37	836.39	-0.02	0	34	0.0236362	R.SEVDMLK.I	Oxidation (M)	13.21		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52907	14%	156	3	33073	5.5	P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3												18	1
						38	47	599.33	1196.65	1196.69	-0.04	0	83	3.63E-07	R.LLLNNDNLLR.E		20.55		
						104	118	771.82	1541.63	1541.68	-0.05	0	42	0.0039674	K.EASDPQPEEADGGLK.S		13.68		
						211	226	853.43	1704.85	1704.82	0.03	0	31	0.0466718	K.DVQDSLTVSNEAQTAK.E		18.77		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14847	14%	138	3	30097	6.6	Q14847|LASP1_HUMAN LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2												18	1
						76	85	601.82	1201.62	1201.61	0.01	0	48	0.001172	K.QQSELQSQVR.Y		12.99		
						97	109	709.86	1417.7	1417.72	-0.02	0	50	0.0006681	K.GFSVVADTPELQR.I		20.12		
						131	144	507.87	1520.59	1520.63	-0.05	1	39	0.0084547	R.MGPSGGEGMEPERR.D	2 Oxidation (M)	11.89		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04406	11%	180	3	36201	8.6	P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3												18	1
						201	215	706.4	1410.78	1410.78	0	0	52	0.0004335	R.GALQNIIPASTGAAK.A		19.81		
						235	248	765.89	1529.76	1529.79	-0.03	0	82	3.77E-07	R.VPTANVSVVDLTCR.L		20.03		
						264	271	415.21	828.41	828.43	-0.02	0	45	0.0026681	K.QASEGPLK.G		12.43		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04083	9%	142	3	38918	6.6	P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2												18	1
						114	124	631.79	1261.57	1261.59	-0.03	0	59	9.21E-05	K.TPAQFDADELR.A		19.47		
						167	177	607.26	1212.51	1212.53	-0.02	0	41	0.0064689	K.DITSDTSGDFR.N		18.95		
						304	312	540.74	1079.46	1079.48	-0.02	0	44	0.0026511	R.SEIDMNDIK.A	Oxidation (M)	13.51		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07195	21%	338	6	36900	5.7	P07195|LDHB_HUMAN L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2												19	1
						8	23	847.95	1693.89	1693.89	0	0	63	2.71E-05	K.LIAPVAEEEATVPNNK.I		19.43		
						78	91	504.25	1509.73	1509.77	-0.03	1	65	1.96E-05	K.IVADKDYSVTANSK.I		13.22		
						108	113	371.72	741.43	741.45	-0.02	0	43	0.0036695	R.LNLVQR.N		14.61		
						159	170	624.8	1247.58	1247.59	-0.01	0	83	3.91E-07	R.VIGSGCNLDSAR.F		13.96		
						234	244	642.3	1282.59	1282.65	-0.06	0	49	0.0008708	K.MVVESAYEVIK.L	Oxidation (M)	19.51		
						309	319	429.56	1285.66	1285.72	-0.06	2	35	0.0243674	K.LKDDEVAQLKK.S		12.83		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P02649	17%	218	5	36246	5.7	P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1												19	2
						177	185	474.77	947.52	947.52	0	0	43	0.0040789	R.LAVYQAGAR.E		14.13		
						199	207	484.77	967.52	967.55	-0.03	0	43	0.0033817	R.LGPLVEQGR.V		16.36		
						210	224	749.42	1496.83	1496.79	0.03	0	46	0.0017018	R.AATVGSLAGQPLQER.A		19.21		
						259	269	438.57	1312.69	1312.71	-0.01	1	45	0.0021514	R.AKLEEQAQQIR.L		13.09		
						270	278	517.29	1032.57	1032.54	0.04	0	42	0.0046947	R.LQAEAFQAR.L		15.14		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00338	16%	326	5	36950	8.4	P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2												19	1
						77	90	499.24	1494.69	1494.77	-0.08	1	63	3.47E-05	K.IVSGKDYNVTANSK.L		12.92		
						107	112	371.72	741.43	741.45	-0.02	0	43	0.0036695	R.LNLVQR.N		14.61		
						158	169	624.8	1247.58	1247.59	-0.01	0	83	3.91E-07	R.VIGSGCNLDSAR.F		13.96		
						233	243	632.83	1263.65	1263.67	-0.02	0	54	0.0002786	K.QVVESAYEVIK.L		19.64		
						306	315	567.77	1133.52	1133.56	-0.03	0	54	0.0003116	K.VTLTSEEEAR.L		13.61		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H444	11%	89	2	24935	4.8	Q9H444|CHM4B_HUMAN Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1												19	2
						18	28	577.29	1152.57	1152.59	-0.02	0	47	0.0014441	K.GGPTPQEAIQR.L		13.57		
						94	107	773.4	1544.78	1544.77	0.02	0	43	0.0035716	R.EALENANTNTEVLK.N		17.67		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UBR2	11%	153	3	34530	6.7	Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1												19	2
						70	81	654.83	1307.65	1307.65	0	0	62	4.56E-05	R.NVDGVNYASITR.N		19.34		
						190	199	505.74	1009.46	1009.48	-0.02	0	57	0.0001134	R.VGDYGSLSGR.E		14.52		
						275	284	371.19	1110.56	1110.59	-0.03	1	33	0.030679	R.IVTSTYKDGK.G		12.27		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62873	6%	107	2	38151	5.6	P62873|GBB1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3												19	1
						69	78	509.28	1016.54	1016.55	-0.01	0	63	3.95E-05	R.LLVSASQDGK.L		13.79		
						198	209	613.3	1224.59	1224.58	0.01	0	44	0.0026691	R.LFVSGACDASAK.L		15.99		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40926	6%	83	2	35965	8.9	P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=2												19	1
						177	185	496.76	991.5	991.53	-0.03	0	37	0.017931	R.ANTFVAELK.G		19.6		

						230	239	537.28	1072.55	1072.58	-0.02	0	46	0.0020311	R.IQEAGTEVVK.A		13.18		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50897	14%	195	3	34627	6.1	P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1												20	7
						105	122	673.31	2016.91	2016.95	-0.04	0	74	2.09E-06	K.LQQGYNAMGFSQGGQFLR.A	Oxidation (M)	20.12		
						166	174	462.73	923.44	923.47	-0.03	0	44	0.0021975	K.TLNAGAYSK.V		13.04		
						254	268	897.45	1792.89	1792.88	0	0	76	1.45E-06	K.ETIPLQETSLYTQDR.L		20.16		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61247	8%	84	2	30154	9.8	P61247|RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2												20	1
						86	94	501.77	1001.52	1001.54	-0.02	0	45	0.0026343	K.LITEDVQGK.N		14.16		
						175	187	505.92	1514.73	1514.79	-0.06	1	39	0.0094409	R.EVQTNDLKEVVNK.L		16.27		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15144	8%	116	3	34426	6.8	O15144|ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1												20	2
						1	9	559.29	1116.57	1116.6	-0.03	0	40	0.0088643	-.MILLEVNNR.I	Oxidation (M)	19.47		
						10	18	515.3	1028.59	1028.61	-0.02	0	34	0.0310742	R.IIEETLALK.F		19.77		
						180	186	472.72	943.43	943.45	-0.02	0	42	0.0061225	K.VFMQEFK.E	Oxidation (M)	16.1		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P09525	8%	94	2	36088	5.8	P09525|ANXA4_HUMAN Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4												20	1
						10	24	799.37	1596.72	1596.72	0	0	48	0.0009287	K.AASGFNAMEDAQTLR.K	Oxidation (M)	19.03		
						276	284	546.26	1090.51	1090.53	-0.02	0	45	0.0024363	R.AEIDMLDIR.A	Oxidation (M)	19.86		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63244	7%	120	2	35511	7.6	P63244|GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3												20	1
						48	57	596.77	1191.52	1191.55	-0.04	0	43	0.0034776	R.DETNYGIPQR.A		17.51		
						107	118	655.33	1308.65	1308.63	0.02	0	77	1.50E-06	K.DVLSVAFSSDNR.Q		20.9		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08758	5%	86	2	35971	4.9	P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2												20	1
						51	58	447.22	892.43	892.47	-0.03	0	52	0.0004806	R.QEISAAFK.T		16.45		
						109	117	501.3	1000.59	1000.59	-0.01	0	34	0.0313843	K.VLTEIIASR.T		19.6		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36543	17%	174	4	26186	7.7	P36543|VATE1_HUMAN Vacuolar proton pump subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1												21	2
						2	10	494.74	987.46	987.49	-0.03	0	38	0.0132971	M.ALSDADVQK.Q	Acetyl (Protein N-term)	17.72		
						34	42	554.74	1107.46	1107.51	-0.05	0	40	0.0075626	K.AEEEFNIEK.G		18.47		
						70	80	669.31	1336.61	1336.62	-0.01	0	60	6.23E-05	K.IQMSNLMNQAR.L	2 Oxidation (M)	12.6		
						213	222	495.74	989.46	989.5	-0.04	0	36	0.0226716	R.GALFGANANR.K		16.42		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62258	17%	211	4	29326	4.6	P62258|1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1												21	2
						1	12	770.86	1539.7	1539.69	0.01	1	37	0.0142724	-.MDDREDLVYQAK.L	Acetyl (Protein N-term); Oxidation (M)	18.94		
						30	42	732.36	1462.7	1462.7	0	0	79	7.83E-07	K.VAGMDVELTVEER.N	Oxidation (M)	19.29		
						43	50	454.25	906.49	906.52	-0.02	0	41	0.0064715	R.NLLSVAYK.N		19.81		
						143	153	597.79	1193.56	1193.59	-0.03	0	53	0.0003214	K.EAAENSLVAYK.A		17.59		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23396	10%	97	2	26842	9.7	P23396|RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2												21	1
						19	27	546.77	1091.53	1091.56	-0.03	0	49	0.000949	K.AELNEFLTR.E		20.34		
						228	243	795.39	1588.77	1588.79	-0.02	0	48	0.0009518	K.GGKPEPPAMPQPVPTA.-	Oxidation (M)	14.2		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27105	9%	191	3	31882	7.7	P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3												21	6
						219	232	488.23	1461.68	1461.72	-0.04	1	60	6.62E-05	R.AKVIAAEGEMNASR.A	Oxidation (M)	12.3		
						221	232	632.3	1262.58	1262.59	-0.02	0	73	3.94E-06	K.VIAAEGEMNASR.A	Oxidation (M)	12.52		
						252	263	676.37	1350.73	1350.74	-0.01	0	58	0.0001102	R.YLQTLTTIAAEK.N		20.03		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P18124	7%	78	2	29264	10.7	P18124|RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1												21	1
						89	94	359.72	717.43	717.45	-0.02	0	43	0.0054907	K.LAFVIR.I		20.21		
						167	177	585.84	1169.66	1169.68	-0.02	0	36	0.0187443	R.IALTDNALIAR.S		20.25		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61981	23%	306	6	28456	4.8	P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2												22	5
						2	10	578.81	1155.6	1155.62	-0.03	1	46	0.0019838	M.VDREQLVQK.A	Acetyl (Protein N-term)	15.44		
						20	28	524.18	1046.35	1046.4	-0.05	0	51	0.0006038	R.YDDMAAAMK.N	2 Oxidation (M)	12.26		
						29	42	822.39	1642.76	1642.78	-0.02	0	66	1.45E-05	K.NVTELNEPLSNEER.N		19.25		
						43	50	454.25	906.49	906.52	-0.02	0	48	0.0013646	R.NLLSVAYK.N		19.81		
						62	69	452.25	902.48	902.51	-0.03	0	53	0.0004209	R.VISSIEQK.T		13.14		
						133	142	540.77	1079.52	1079.55	-0.03	0	42	0.0042017	R.YLAEVATGEK.R		15.35		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31946	20%	265	5	28179	4.8	P31946|1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3												22	3
						21	29	524.18	1046.35	1046.4	-0.05	0	51	0.0006038	R.YDDMAAAMK.A	2 Oxidation (M)	12.26		
						30	43	533.57	1597.67	1597.73	-0.06	0	43	0.0037271	K.AVTEQGHELSNEER.N		12.7		
						44	51	454.25	906.49	906.52	-0.02	0	48	0.0013646	R.NLLSVAYK.N		19.81		
						63	70	452.25	902.48	902.51	-0.03	0	53	0.0004209	R.VISSIEQK.T		13.14		

						130	140	591.78	1181.54	1181.56	-0.02	0	70	6.67E-06	R.YLSEVASGDNK.Q		13.74		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27348	12%	186	3	28032	4.7	P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1												22	3
						28	41	766.86	1531.7	1531.71	-0.01	0	85	2.39E-07	K.AVTEQGAELSNEER.N		13.83		
						42	49	454.25	906.49	906.52	-0.02	0	48	0.0013646	R.NLLSVAYK.N		19.81		
						61	68	452.25	902.48	902.51	-0.03	0	53	0.0004209	R.VISSIEQK.T		13.14		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q04917	10%	136	3	28372	4.8	Q04917|1433F_HUMAN 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4												22	3
						20	28	524.18	1046.35	1046.4	-0.05	0	35	0.02322	R.YDDMASAMK.A	Oxidation (M)	12.26		
						43	50	454.25	906.49	906.52	-0.02	0	48	0.0013646	R.NLLSVAYK.N		19.81		
						62	69	452.25	902.48	902.51	-0.03	0	53	0.0004209	R.VISSIEQK.T		13.14		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07686	4%	102	2	63527	6.3	P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3												22	4
						391	400	550.34	1098.66	1098.66	0	0	52	0.0004272	K.VLDIIATINK.G		21.02		
						466	476	595.8	1189.58	1189.6	-0.02	0	50	0.0007911	K.VEPLDFGGTQK.Q		19.73		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04792	18%	254	4	22826	6	P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2												23	3
						28	37	582.29	1162.57	1162.61	-0.04	0	68	1.06E-05	R.LFDQAFGLPR.L		21.36		
						80	89	538.28	1074.54	1074.57	-0.03	0	84	3.15E-07	R.QLSSGVSEIR.H		14.98		
						189	198	471.25	940.48	940.5	-0.02	0	39	0.0096711	R.AQLGGPEAAK.S		12.82		
						189	205	548.6	1642.77	1642.82	-0.05	1	65	2.13E-05	R.AQLGGPEAAKSDETAAK.-		12.77		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51572	12%	110	2	28031	8.4	P51572|BAP31_HUMAN B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3												23	2
						168	182	572.27	1713.79	1713.85	-0.07	1	68	9.58E-06	K.LDVGNAEVKLEEENR.S		19.49		
						233	246	516.24	1545.68	1545.73	-0.05	2	42	0.0045073	K.LQAAVDGPMDKKEE.-	Oxidation (M)	12.73		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62241	11%	73	2	24475	10.3	P62241|RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2												23	2
						158	170	753.88	1505.75	1505.77	-0.02	0	36	0.0164899	K.ISSLLEEQFQQGK.L		20.45		
						185	193	476.22	950.42	950.47	-0.05	0	37	0.0150981	R.ADGYVLEGK.E		15.63		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60900	9%	109	2	27838	6.3	P60900|PSA6_HUMAN Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1												23	1
						31	43	643.35	1284.68	1284.71	-0.04	0	68	1.09E-05	K.AINQGGLTSVAVR.G		19.19		
						172	181	585.27	1168.53	1168.56	-0.03	0	40	0.0065303	K.QTESTSFLEK.K		17.02		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63104	22%	317	5	27899	4.7	P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1												24	6
						1	9	581.78	1161.54	1161.57	-0.03	1	60	7.08E-05	-.MDKNELVQK.A	Acetyl (Protein N-term); Oxidation (M)	13.03		
						28	41	774.84	1547.66	1547.71	-0.05	0	114	2.67E-10	K.SVTEQGAELSNEER.N		14.07		
						42	49	454.25	906.49	906.52	-0.03	0	40	0.0079433	R.NLLSVAYK.N		19.86		
						104	115	652.83	1303.64	1303.68	-0.04	0	50	0.0007215	K.FLIPNASQAESK.V		19.73		
						128	139	427.21	1278.6	1278.65	-0.05	1	52	0.0003927	R.YLAEVAAGDDKK.G		13.46		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43399	19%	162	3	22281	5.3	O43399|TPD54_HUMAN Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2												24	1
						1	15	831.34	1660.66	1660.74	-0.08	0	52	0.0003953	-.MDSAGQDINLNSPNK.G	Acetyl (Protein N-term); Oxidation (M)	19.12		
						129	139	595.79	1189.56	1189.59	-0.04	0	61	6.21E-05	K.TQETLSQAGQK.T		12.51		
						140	153	660.84	1319.66	1319.7	-0.04	0	50	0.0006633	K.TSAALSTVGSAISR.K		19.47		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30040	8%	132	2	29032	6.8	P30040|ERP29_HUMAN Endoplasmic reticulum protein ERp29 OS=Homo sapiens GN=ERP29 PE=1 SV=4												24	3
						37	48	662.85	1323.68	1323.71	-0.02	0	47	0.0012355	K.GALPLDTVTFYK.V		21.21		
						183	192	538.27	1074.52	1074.53	-0.01	0	85	2.69E-07	K.QGQDNLSSVK.E		12.81		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07339	21%	478	8	45037	6.1	P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1												25	13
						177	184	440.22	878.42	878.45	-0.03	0	46	0.0017974	R.QVFGEATK.Q		13.49		
						177	194	636	1904.97	1905.04	-0.06	1	67	1.15E-05	R.QVFGEATKQPGITFIAAK.F		20.04		
						185	194	514.78	1027.54	1027.57	-0.03	0	49	0.0010303	K.QPGITFIAAK.F	Gln->pyro-Glu (N-term Q)	21.22		
						195	205	628.29	1254.57	1254.61	-0.04	0	73	3.98E-06	K.FDGILGMAYPR.I	Oxidation (M)	20.52		
						223	235	801.39	1600.76	1600.82	-0.06	0	52	0.0004544	K.LVDQNIFSFYLSR.D		22.86		
						236	253	902.39	1802.76	1802.8	-0.04	0	90	6.75E-08	R.DPDAQPGGELMLGGTDSK.Y	Oxidation (M)	19.42		
						314	331	1002.99	2003.96	2004.01	-0.04	0	45	0.0020783	K.AIGAVPLIQGEYMIPCEK.V	Oxidation (M)	21.04		
						349	357	533.26	1064.51	1064.54	-0.03	0	58	0.0001217	K.LSPEDYTLK.V		19.51		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O00299	21%	98	4	27248	5.1	O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4												25	2
						2	13	729.86	1457.7	1457.74	-0.04	0	44	0.0028676	M.AEEQPQVELFVK.A	Acetyl (Protein N-term)	21.69		
						38	49	641.33	1280.64	1280.66	-0.02	0	66	1.59E-05	K.GVTFNVTTVDTK.R		19.77		
						96	113	922.98	1843.95	1843.97	-0.02	0	53	0.0003056	K.LAALNPESNTAGLDIFAK.F		21.52		
						209	216	479.23	956.44	956.47	-0.03	0	35	0.0270504	R.YLSNAYAR.E		13.93		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P07858	11%	110	3	38766	5.9	P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3												25	6
						80	87	438.71	875.41	875.45	-0.04	0	41	0.0067458	K.LPASFDAR.E		16.56		
						210	220	657.8	1313.58	1313.6	-0.02	0	35	0.023167	K.ICEPGYSPTYK.Q		16.09		
						264	281	491.21	1960.8	1960.89	-0.09	0	33	0.0262584	K.SGVYQHVTGEMMGGHAIR.I	2 Oxidation (M)	13.06		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P78417	10%	92	2	27833	6.2	P78417|GSTO1_HUMAN Glutathione transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2												25	1
						12	25	660.83	1319.65	1319.68	-0.04	0	52	0.0004071	K.GSAPPGPVPEGSIR.I		15.74		
						123	132	537.8	1073.58	1073.62	-0.05	0	40	0.009179	K.VPSLVGSFIR.S		21.26		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P45880	7%	95	2	32060	7.5	P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2												25	3
						236	247	647.32	1292.63	1292.66	-0.03	0	61	6.04E-05	K.YQLDPTASISAK.V		19.56		
						268	277	508.79	1015.57	1015.59	-0.02	0	34	0.0369445	K.LTLSALVDGK.S		20.91		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62701	6%	112	2	29807	10.2	P62701|RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2												25	1
						222	230	495.79	989.56	989.59	-0.03	0	65	2.71E-05	R.LSNIFVIGK.G		20.82		
						246	252	416.21	830.41	830.45	-0.04	0	47	0.0021611	R.LTIAEER.D		14.06		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51148	32%	432	7	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												26	3
						24	34	543.31	1084.6	1084.65	-0.05	0	54	0.000332	K.LVLLGESAVGK.S		20.26		
						122	135	698.38	1394.74	1394.79	-0.05	0	94	2.88E-08	R.QASPNIVIALAGNK.A		20.79		
						167	180	792.86	1583.7	1583.77	-0.07	0	57	0.0001406	K.TAMNVNEIFMAIAK.K	2 Oxidation (M)	21.57		
						181	196	559.94	1676.81	1676.9	-0.08	2	44	0.0028547	K.KLPKNEPQNATGAPGR.N		12.28		
						185	196	606.26	1210.51	1210.57	-0.05	0	53	0.0003532	K.NEPQNATGAPGR.N		12.15		
						197	210	523.9	1568.69	1568.77	-0.08	1	52	0.00049	R.NRGVDLQENNPASR.S		13.23		
						199	210	650.29	1298.57	1298.62	-0.05	0	80	7.01E-07	R.GVDLQENNPASR.S		14.27		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92520	19%	215	4	24950	8.5	Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1												26	4
						31	41	605.78	1209.55	1209.58	-0.03	0	57	0.0001298	K.MDASLGNLFAR.S	Oxidation (M)	21		
						73	84	559.26	1116.51	1116.56	-0.05	0	68	1.37E-05	K.MASGAANVVGPK.I	Oxidation (M)	12.8		
						85	97	747.34	1492.67	1492.73	-0.06	0	40	0.006741	K.ICLEDNVLMSGVK.N	Oxidation (M)	20.35		
						113	120	431.7	861.38	861.44	-0.06	0	50	0.0009784	K.TGEVLDTK.Y		13.06		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20339	17%	152	3 (4)	23872	8.3	P20339|RAB5A_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2												26	2
						23	33	543.31	1084.6	1084.65	-0.05	0	54	0.000332	K.LVLLGESAVGK.S		20.26		
						166	179	792.86	1583.7	1583.77	-0.07	0	57	0.0001285	K.TSMNVNEIFMAIAK.K	Oxidation (M)	21.57		
						166	179	800.85	1599.68	1599.76	-0.08	0	43	0.0029986	K.TSMNVNEIFMAIAK.K	2 Oxidation (M)	21.53		
						184	195	627.77	1253.52	1253.57	-0.06	0	41	0.0051997	K.NEPQNPGANSAR.G		12.06		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21796	16%	356	5	30868	8.6	P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2												26	4
						2	12	587.28	1172.55	1172.61	-0.06	0	73	3.79E-06	M.AVPPTYADLGK.S	Acetyl (Protein N-term)	20.66		
						33	53	730.31	2187.9	2188.01	-0.11	1	77	1.12E-06	K.TKSENGLEFTSSGSANTETTK.V		14.66		
						35	53	980.4	1958.79	1958.87	-0.08	0	88	8.63E-08	K.SENGLEFTSSGSANTETTK.V		18.82		
						97	109	700.82	1399.63	1399.66	-0.03	0	70	6.83E-06	K.LTFDSSFSPNTGK.K		20.18		
						97	110	510.24	1527.69	1527.76	-0.07	1	48	0.0011812	K.LTFDSSFSPNTGKK.N		19.43		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UL25	11%	172	2	24731	8.1	Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3												26	1
						2	16	557.24	1112.47	1112.53	-0.07	0	107	1.35E-09	M.AAAGGGGGGAAAAGR.A	Acetyl (Protein N-term)	12.67		
						180	189	604.26	1206.5	1206.56	-0.06	0	64	2.65E-05	R.MIETAQVDER.A	Oxidation (M)	13.27		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61020	11%	87	2	23920	8.3	P61020|RAB5B_HUMAN Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1												26	1
						23	33	543.31	1084.6	1084.65	-0.05	0	54	0.000332	K.LVLLGESAVGK.S		20.26		
						184	195	578.78	1155.54	1155.56	-0.02	0	33	0.0369408	K.SEPQNLGGAAGR.S		12.93		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05090	11%	83	2	21547	5.1	P05090|APOD_HUMAN Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1												26	2
						52	60	517.74	1033.46	1033.52	-0.06	0	37	0.0168513	K.IPTTFENGR.C		16.26		
						165	175	615.8	1229.59	1229.66	-0.08	0	46	0.0018872	K.NILTSNNIDVK.K		19.74		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BVK6	9%	143	2	25203	6.7	Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=1												26	3
						138	146	551.29	1100.56	1100.62	-0.05	1	39	0.009572	K.DKLSELQLR.V		19.3		
						149	159	671.34	1340.67	1340.73	-0.06	0	104	3.09E-09	R.QLVEQVEQIQK.E		19.35		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43760	9%	78	2	25079	4.8	O43760|SNG2_HUMAN Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1												26	1
						20	29	579.8	1157.59	1157.66	-0.06	0	37	0.0168953	R.FLTQPQVVAR.A		19.22		
						137	146	515.75	1029.49	1029.55	-0.05	0	41	0.0069724	K.DVLVGADSVR.A		19.09		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q7Z7H5	8%	120	2	26097	8.4	Q7Z7H5|TMED4_HUMAN Transmembrane emp24 domain-containing protein 4 OS=Homo sapiens GN=TMED4 PE=2 SV=1												26	1

						121	128	405.69	809.37	809.41	-0.04	0	35	0.0185574	R.MALFAGGK.L	Oxidation (M)	15.48		
						162	172	671.34	1340.67	1340.73	-0.06	0	85	2.24E-07	R.QLLDQVEQIQK.E		19.35		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25774	6%	101	2	38099	8.6	P25774|CATS_HUMAN Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3												26	1
						197	207	608.26	1214.51	1214.55	-0.03	0	52	0.0005193	K.GIDSDASYPYK.A		17.74		
						246	255	478.74	955.46	955.51	-0.04	0	52	0.0004422	K.GPVSVGVDAR.H		14.36		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P28070	6%	78	2	29242	5.7	P28070|PSB4_HUMAN Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4												26	1
						197	211	576.27	1725.8	1725.93	-0.13	1	34	0.0228801	R.EVLEKQPVLSQTEAR.D		16.71		
						202	211	564.76	1127.51	1127.59	-0.08	0	43	0.003967	K.QPVLSQTEAR.D		13.4		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20340	34%	425	7	23692	5.4	P20340|RAB6A_HUMAN Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3												27	4
						2	13	645.8	1289.59	1289.64	-0.05	1	95	2.15E-08	M.STGGDFGNPLRK.F	Acetyl (Protein N-term)	19.32		
						16	26	588.8	1175.59	1175.66	-0.07	0	78	1.18E-06	K.LVFLGEQSVGK.T		20.45		
						116	127	631.29	1260.57	1260.67	-0.1	0	56	0.0001826	R.GSDVIIMLVGNK.T	Oxidation (M)	20.84		
						135	143	523.73	1045.45	1045.5	-0.06	0	39	0.0112982	R.QVSIEEGER.K		13.28		
						147	158	699.32	1396.62	1396.69	-0.07	0	56	0.0001651	K.ELNVMFIETSAK.A	Oxidation (M)	20.58		
						169	183	539.92	1616.74	1616.79	-0.05	1	39	0.009054	R.RVAAALPGMESTQDR.S	Oxidation (M)	13.32		
						170	183	731.31	1460.61	1460.69	-0.08	0	62	4.47E-05	R.VAAALPGMESTQDR.S	Oxidation (M)	14.27		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61626	13%	87	2	16982	9.4	P61626|LYSC_HUMAN Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1												27	1
						33	39	406.16	810.31	810.37	-0.06	0	33	0.0267415	R.LGMDGYR.G		15.71		
						69	80	700.81	1399.61	1399.67	-0.06	0	54	0.0002783	R.STDYGIFQINSR.Y		20.92		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61106	8%	78	2	24110	5.8	P61106|RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4												27	1
						52	59	437.24	872.46	872.5	-0.04	0	42	0.0070991	R.IIEVSGQK.I		13.19		
						202	210	528.26	1054.5	1054.54	-0.04	0	36	0.0161472	R.LTSEPQPQR.E		12.32		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q06830	25%	265	5 (6)	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												28	3
						17	27	590.76	1179.5	1179.56	-0.06	0	56	0.0001789	K.ATAVMPDGQFK.D	Oxidation (M)	14.03		
						111	120	554.28	1106.54	1106.6	-0.06	0	62	4.71E-05	R.TIAQDYGVLK.A		19.68		
						141	151	597.8	1193.58	1193.64	-0.06	0	37	0.013552	R.QITVNDLPVGR.S	Gln->pyro-Glu (N-term Q)	21.47		
						141	151	606.31	1210.6	1210.67	-0.07	0	57	0.0001297	R.QITVNDLPVGR.S		19.9		
						152	158	410.19	818.37	818.41	-0.04	0	34	0.0363851	R.SVDETLR.L		13.12		
						159	168	598.79	1195.56	1195.62	-0.06	0	56	0.000157	R.LVQAFQFTDK.H		20.38		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51149	22%	177	4	23760	6.4	P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1												28	2
						11	21	529.29	1056.56	1056.62	-0.06	0	55	0.0002337	K.VIILGDSGVGK.T		19.77		
						39	48	518.76	1035.51	1035.56	-0.05	0	42	0.0051959	K.ATIGADFLTK.E		20.43		
						114	126	738.34	1474.67	1474.75	-0.07	0	44	0.0028586	R.DPENFPFVVLGNK.I		22.56		
						147	157	642.29	1282.56	1282.62	-0.05	0	36	0.0152021	K.NNIPYFETSAK.E		19.94		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62820	19%	207	4	22891	5.9	P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3												28	2
						14	24	536.3	1070.59	1070.63	-0.04	0	55	0.0002684	K.LLLIGDSGVGK.S		20.6		
						75	82	495.71	989.41	989.48	-0.07	0	54	0.0003514	R.TITSSYYR.G		14.72		
						176	187	531.73	1061.44	1061.48	-0.04	0	53	0.0004013	R.MGPGATAGGAEK.S	Oxidation (M)	11.87		
						192	198	386.71	771.4	771.45	-0.05	0	45	0.0034236	K.IQSTPVK.Q		12.21		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H0U4	17%	145	3	22328	5.5	Q9H0U4|RAB1B_HUMAN Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1												28	1
						11	21	536.3	1070.59	1070.63	-0.04	0	55	0.0002684	K.LLLIGDSGVGK.S		20.6		
						72	79	495.71	989.41	989.48	-0.07	0	54	0.0003514	R.TITSSYYR.G		14.72		
						173	187	486.54	1456.6	1456.71	-0.11	0	36	0.0169488	R.MGPGAASGGERPNLK.I	Oxidation (M)	12.47		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51153	12%	134	2	22988	9.3	P51153|RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=2 SV=1												28	4
						11	21	536.3	1070.59	1070.63	-0.04	0	55	0.0002684	K.LLLIGDSGVGK.T		20.6		
						154	167	765.31	1528.6	1528.68	-0.08	0	79	8.81E-07	K.SSMNVDEAFSSLAR.D	Oxidation (M)	20.47		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92930	12%	113	2	23740	9.2	Q92930|RAB8B_HUMAN Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2												28	1
						11	21	536.3	1070.59	1070.63	-0.04	0	55	0.0002684	K.LLLIGDSGVGK.T		20.6		
						177	190	660.75	1319.49	1319.58	-0.09	0	59	9.92E-05	K.MNDSNSAGAGGPVK.I	Oxidation (M)	12.1		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61019	12%	94	2	23702	6.1	P61019|RAB2A_HUMAN Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1												28	1
						9	19	568.29	1134.56	1134.63	-0.07	0	39	0.0104952	K.YIIIGDTGVGK.S		20.16		
						152	165	747.84	1493.66	1493.74	-0.08	0	56	0.0001828	K.TASNVEEAFINTAK.E		20.29		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P37802	12%	109	2	22548	8.4	P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3												28	1

						128	139	616.31	1230.6	1230.68	-0.08	0	50	0.0008388	R.TLMNLGGLAVAR.D	Oxidation (M)	20.12		
						161	171	640.26	1278.5	1278.58	-0.09	0	59	7.82E-05	R.NFSDNQLQEGK.N		14.77		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62913	19%	150	3	20468	9.6	P62913|RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2												31	1
						2	13	730.81	1459.6	1459.64	-0.03	1	63	4.00E-05	M.AQDQGEKENPMR.E	Acetyl (Protein N-term); Oxidation (M)	12.14		
						39	52	773.87	1545.73	1545.84	-0.11	0	52	0.0004528	K.VLEQLTGQTPVFSK.A		20.45		
						79	85	416.19	830.37	830.44	-0.07	0	35	0.0302468	K.AEEILEK.G		13.7		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23284	16%	214	3	22785	9.3	P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=1												31	2
						44	51	430.68	859.34	859.4	-0.06	0	54	0.0003597	R.IGDEDVGR.V		12.83		
						64	76	682.82	1363.62	1363.7	-0.07	0	80	7.81E-07	K.TVDNFVALATGEK.G		21.12		
						138	150	729.33	1456.64	1456.72	-0.08	0	82	4.85E-07	K.DTNGSQFFITTVK.T		20.97		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49755	9%	136	2	25131	7	P49755|TMEDA_HUMAN Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2												31	3
						117	127	650.83	1299.64	1299.71	-0.07	0	83	3.33E-07	R.IPDQLVILDMK.H	Oxidation (M)	20.84		
						144	152	366.21	1095.6	1095.67	-0.07	0	52	0.0004085	K.LKPLEVELR.R		19.41		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P84077	14%	80	2	20741	6.3	P84077|ARF1_HUMAN ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2												33	1
						20	30	552.27	1102.53	1102.61	-0.08	0	48	0.0015084	R.ILMVGLDAAGK.T	Oxidation (M)	19.76		
						128	142	823.82	1645.63	1645.76	-0.13	0	33	0.0365949	K.QDLPNAMNAAEITDK.L	Oxidation (M)	19.18		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23528	14%	127	2	18719	8.2	P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3												33	2
						2	13	572.9	1143.79	1143.61	0.17	0	85	2.73E-07	M.ASGVAVSDGVIK.V	Acetyl (Protein N-term)	19.98		
						82	92	669.26	1336.51	1336.62	-0.11	0	42	0.0040473	R.YALYDATYETK.E		19.72		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62937	47%	380	8	18229	7.7	P62937|PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2												35	2
						2	19	973.56	1945.11	1944.99	0.11	0	40	0.0053888	M.VNPTVFFDIAVDGEPLGR.V		23.49		
						20	28	528.24	1054.46	1054.53	-0.07	0	55	0.0002376	R.VSFELFADK.V		21.32		
						20	31	460.56	1378.65	1378.75	-0.1	1	46	0.0018289	R.VSFELFADKVPK.T		20.79		
						56	69	807.83	1613.64	1613.73	-0.1	0	65	1.94E-05	R.IIPGFMCQGGDFTR.H	Oxidation (M)	20.27		
						83	91	577.75	1153.49	1153.57	-0.07	0	56	0.0001948	K.FEDENFILK.H		20.62		
						132	144	513.23	1536.65	1536.73	-0.07	1	41	0.0047594	K.VKEGMNIVEAMER.F	2 Oxidation (M)	12.91		
						134	144	655.74	1309.47	1309.56	-0.09	0	40	0.0066969	K.EGMNIVEAMER.F	2 Oxidation (M)	13.61		
						155	165	624.28	1246.55	1246.62	-0.07	1	37	0.0155213	K.KITIADCGQLE.-		19.48		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62851	22%	143	3	13791	10.1	P62851|RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1												35	1
						44	52	538.28	1074.54	1074.61	-0.07	0	43	0.0037423	K.LNNLVLFDK.A		21.01		
						67	76	542.79	1083.56	1083.63	-0.07	0	46	0.0018014	K.LITPAVVSER.L		19.4		
						86	94	486.76	971.51	971.57	-0.06	0	54	0.0003819	R.AALQELLSK.G		20.36		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15819	18%	109	2	16409	7.8	Q15819|UB2V2_HUMAN Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4												35	1
						2	11	528.28	1054.55	1054.61	-0.06	1	55	0.0002099	M.AVSTGVKVPR.N	Acetyl (Protein N-term)	16.89		
						86	101	862.83	1723.64	1723.76	-0.12	0	54	0.0002737	K.INMNGINNSSGMVDAR.S	2 Oxidation (M)	13.26		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15511	17%	144	2	16367	5.5	O15511|ARPC5_HUMAN Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3												35	1
						48	60	666.81	1331.61	1331.69	-0.08	0	77	1.52E-06	R.QGNMTAALQAALK.N	Oxidation (M)	19.44		
						132	143	535.78	1069.55	1069.62	-0.07	0	67	1.61E-05	K.ALAAGGVGSIVR.V		19.35		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62263	16%	106	2	16434	10.1	P62263|RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3												35	1
						107	117	527.75	1053.49	1053.56	-0.06	0	59	7.55E-05	K.TPGPGAQSALR.A		13.13		
						129	141	715.32	1428.63	1428.71	-0.08	0	47	0.0013875	R.IEDVTPIPSDSTR.R		19.14		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q6IAA8	15%	109	2	17848	5	Q6IAA8|CK059_HUMAN UPF0404 protein C11orf59 OS=Homo sapiens GN=C11orf59 PE=1 SV=2												35	1
						21	31	584.3	1166.58	1166.65	-0.07	0	49	0.0008487	K.LLLDPSSPPTK.A		19.61		
						48	60	694.85	1387.68	1387.76	-0.07	0	60	7.02E-05	R.TDEQALLSSILAK.T		22.1		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62269	13%	87	2	17708	11	P62269|RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3												35	1
						56	66	624.25	1246.48	1246.57	-0.08	0	50	0.0006737	R.AGELTEDEVER.V		14.6		
						67	75	544.26	1086.5	1086.59	-0.08	0	37	0.0188933	R.VITIMQNPR.Q	Oxidation (M)	14.13		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61204	12%	93	2	20645	6.8	P61204|ARF3_HUMAN ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2												35	1
						20	30	552.27	1102.53	1102.61	-0.08	0	54	0.0003188	R.ILMVGLDAAGK.T	Oxidation (M)	19.75		
						118	127	545.27	1088.53	1088.62	-0.09	0	39	0.0101743	R.DAVLLVFANK.Q		21.84		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60660	25%	221	4 (5)	17090	4.6	P60660|MYL6_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2												37	1

						14	21	513.22	1024.42	1024.5	-0.08	0	35	0.0190696	K.EAFQLFDR.T		20.97		
						38	50	677.82	1353.63	1353.73	-0.1	0	81	5.09E-07	R.ALGQNPTNAEVLK.V		17.8		
						95	110	580.24	1737.7	1737.84	-0.14	1	36	0.0158808	R.VFDKEGNGTVMGAEIR.H	Oxidation (M)	15.28		
						99	110	625.26	1248.51	1248.58	-0.07	0	68	1.16E-05	K.EGNGTVMGAEIR.H	Oxidation (M)	13.24		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75348	31%	206	4	13863	8.9	O75348|VATG1_HUMAN Vacuolar proton pump subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3												38	2
						2	16	835.92	1669.82	1669.86	-0.04	0	47	0.0012732	M.ASQSQGIQQLLQAEK.R	Acetyl (Protein N-term)	21.5		
						2	17	913.93	1825.85	1825.96	-0.11	1	63	3.15E-05	M.ASQSQGIQQLLQAEKR.A	Acetyl (Protein N-term)	20.71		
						38	48	683.28	1364.55	1364.62	-0.07	0	45	0.0020743	K.EEAQAEIEQYR.L		18.76		
						81	89	594.82	1187.62	1187.6	0.02	0	51	0.0006409	K.MTILQTYFR.Q	Oxidation (M)	21.1		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07737	36%	243	4	15216	8.4	P07737|PROF1_HUMAN Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2												40	3
						57	70	735.84	1469.66	1469.75	-0.09	0	74	3.04E-06	R.SSFYVNGLTLGGQK.C		20.62		
						76	89	821.33	1640.64	1640.74	-0.1	0	71	5.53E-06	R.DSLLQDGEFSMDLR.T	Oxidation (M)	21.1		
						92	105	690.32	1378.62	1378.71	-0.09	0	56	0.0001723	K.STGGAPTFNVTVTK.T		19.32		
						109	116	445.74	889.46	889.53	-0.07	0	42	0.0050409	K.TLVLLMGK.E	Oxidation (M)	19.8		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BV40	33%	121	3	11488	6.7	Q9BV40|VAMP8_HUMAN Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1												40	2
						1	14	782.78	1563.54	1563.66	-0.12	1	41	0.0043002	-.MEEASEGGGNDRVR.N	Acetyl (Protein N-term); Oxidation (M)	12.51		
						15	24	551.75	1101.49	1101.57	-0.07	0	49	0.0010207	R.NLQSEVEGVK.N		18.97		
						25	33	560.74	1119.47	1119.53	-0.07	0	33	0.0422625	K.NIMTQNVER.I	Oxidation (M)	12.64		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P09382	30%	159	4	15048	5.3	P09382|LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2												40	2
						20	29	521.24	1040.46	1040.56	-0.1	1	40	0.0062309	R.VRGEVAPDAK.S		11.91		
						30	37	439.23	876.45	876.51	-0.06	0	43	0.0038948	K.SFVLNLGK.D		20.4		
						50	64	549.87	1646.6	1646.75	-0.15	0	33	0.0371414	R.FNAHGDANTIVCNSK.D		13.76		
						101	108	484.7	967.39	967.47	-0.08	0	43	0.0032613	K.LPDGYEFK.F		19.45		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62805	19%	83	2	11360	11.4	P62805|H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2												40	1
						25	36	442.56	1324.65	1324.75	-0.1	0	43	0.003153	R.DNIQGITKPAIR.R		16.98		
						61	68	495.25	988.49	988.57	-0.08	0	40	0.0086644	K.VFLENVIR.D		20.66		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13510	5%	107	2	45077	7.5	Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4												42	4
						82	92	612.28	1222.54	1222.6	-0.06	0	54	0.0002729	K.NMINTFVPSGK.V	Oxidation (M)	19.06		
						93	100	482.2	962.39	962.47	-0.08	0	53	0.0003769	K.VMQVVDEK.L	Oxidation (M)	12.3		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26447	17%	104	2	11949	5.8	P26447|S10A4_HUMAN Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1												43	2
						50	57	455.18	908.34	908.42	-0.09	0	46	0.0017669	R.TDEAAFQK.L		12.82		
						58	66	533.21	1064.41	1064.49	-0.08	0	60	6.67E-05	K.LMSNLDSNR.D	Oxidation (M)	12.73		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07602	7%	225	4	59899	5.1	P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2												45	6
						233	242	539.23	1076.44	1076.5	-0.06	0	64	2.93E-05	R.LGPGMADICK.N	Oxidation (M)	14		
						405	413	536.17	1070.33	1070.42	-0.09	0	35	0.0165825	K.DGGFCEVCK.K		14.74		
						430	438	507.76	1013.5	1013.58	-0.07	0	70	8.21E-06	K.QEILAALEK.G		20.11		
						439	449	656.26	1310.51	1310.6	-0.08	0	56	0.0001791	K.GCSFLPDPYQK.Q		20.24		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63218	29%	156	2	7428	9.9	P63218|GBG5_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3												45	2
						2	12	555.75	1109.49	1109.54	-0.05	1	64	2.38E-05	M.SGSSSVAAMKK.V	Acetyl (Protein N-term); Oxidation (M)	11.86		
						28	36	451.72	901.43	901.49	-0.06	0	34	0.0392599	K.VSQAAADLK.Q		12.66		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61604	40%	235	4	10925	8.9	P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2												46	3
						41	54	658.36	1314.7	1314.75	-0.05	0	86	2.04E-07	K.VLQATVVAVGSGSK.G		18.53		
						57	66	507.25	1012.48	1012.56	-0.08	0	40	0.0062814	K.GGEIQPVSVK.V		13.89		
						71	80	538.76	1075.51	1075.59	-0.08	0	54	0.0002886	K.VLLPEYGGTK.V		19.4		
						93	99	359.17	716.32	716.37	-0.05	0	54	0.0004182	R.DGDILGK.Y		14.41		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31949	37%	223	5	11847	6.6	P31949|S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2												46	3
						4	12	510.22	1018.42	1018.49	-0.08	0	49	0.0012251	K.ISSPTETER.C		12.38		
						13	23	654.29	1306.57	1306.7	-0.13	0	40	0.0073754	R.CIESLIAVFQK.Y		22.12		
						28	36	530.71	1059.41	1059.49	-0.08	0	44	0.0038762	K.DGYNYTLSK.T		17.68		
						53	62	381.17	1140.5	1140.59	-0.09	1	52	0.000413	K.NQKDPGVLDR.M		12.59		
						56	62	386.18	770.34	770.39	-0.05	0	39	0.0098296	K.DPGVLDR.M		13.85		
accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30273	22%	82	2	9775	6.5	P30273|FCERG_HUMAN High affinity immunoglobulin epsilon receptor subunit gamma OS=Homo sapiens GN=FCER1G PE=1 SV=1												46	2
						53	60	441.7	881.38	881.45	-0.06	0	33	0.0307825	K.AAITSYEK.S		13.2		
						61	71	578.25	1154.48	1154.56	-0.08	0	49	0.0008738	K.SDGVYTGLSTR.N		16.51		

accession #	coverage	score	stinct peptid	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75396	9%	92	2	24896	8.7	O75396|SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=3												46	2
						160	169	495.73	989.44	989.5	-0.07	0	48	0.0015363	R.GEALSALDSK.A		16.08		
						170	178	467.23	932.44	932.49	-0.06	0	45	0.0029124	K.ANNLSSLSK.K		13.33		

***Footnotes to Supplemental Table 7:**

Data sets were searched with the Mascot search engine (see Perkins et al. (1999)*Electrophoresis* **20**, 3551-3567).

Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).

Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.

Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest gel slice in which the protein was identified, and the total # of adjacent gel slices in which the protein was found).

Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 8. Proteins identified by HPLC-MS/MS on 5-day BCG infected human THP-1 phagosome preparation.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05023	8%	436	7	114135	5.3	P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1												1	2
						68	74	372.21	742.4	742.43	-0.03	0	49	0.0010315	R.AAEILAR.D		14.24		
						213	227	810.36	1618.7	1618.74	-0.04	0	105	2.42E-09	K.VDNSSLTGESEPQTR.S		14.11		
						228	240	760.34	1518.67	1518.7	-0.03	0	66	1.71E-05	R.SPDFTNENPLETR.N		20.69		
						446	458	616.32	1230.62	1230.65	-0.03	0	50	0.0008823	R.AVAGDASESALLK.C		19.59		
						477	487	631.34	1260.66	1260.67	-0.01	0	52	0.000488	K.IVEIPFNSTNK.Y		20.78		
						648	658	618.85	1235.68	1235.7	-0.02	0	51	0.0005475	R.LNIPVSQVNPR.D		20.16		
						728	743	753.87	1505.73	1505.74	-0.01	0	64	2.93E-05	K.ADIGVAMGIAGSDVSK.Q	Oxidation (M)	19.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15427	8%	115	3	50064	8.2	O15427|MOT4_HUMAN Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1												1	1
						2	14	593.31	1184.6	1184.6	0	0	41	0.0071432	M.GGAVVDEGPTGVK.A		14.16		
						429	441	468.92	1403.73	1403.75	-0.03	0	37	0.0136958	K.LHKPPADSGVDLR.E		13.33		
						454	465	634.79	1267.56	1267.6	-0.04	0	37	0.0123089	K.NGEVVHTPETSV.-		16.16		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15321	5%	164	3	69330	6.7	O15321|TM9S1_HUMAN Transmembrane 9 superfamily member 1 OS=Homo sapiens GN=TM9SF1 PE=2 SV=2												1	1
						38	48	594.82	1187.63	1187.66	-0.02	0	58	0.0001402	K.AGDPVILYVNK.V		20.82		
						88	96	564.28	1126.54	1126.53	0	0	42	0.0043736	R.MAESLYEIR.F	Oxidation (M)	20.21		
						436	446	624.78	1247.54	1247.54	0.01	0	64	2.95E-05	K.NNASPFDAPCR.T		17.16		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92544	5%	127	3	75211	6.1	Q92544|TM9S4_HUMAN Transmembrane 9 superfamily member 4 OS=Homo sapiens GN=TM9SF4 PE=1 SV=2												1	2
						73	81	500.76	999.51	999.53	-0.02	0	34	0.0353589	K.AENLGEVLR.G		20.25		
						85	98	818.4	1634.79	1634.83	-0.05	0	58	0.0001116	R.IVNTPFQVLMNSEK.K	Oxidation (M)	21.8		
						483	488	364.7	727.38	727.4	-0.01	0	36	0.0198653	R.TNQIPR.Q		12.77		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99805	4%	110	3	76809	7.2	Q99805|TM9S2_HUMAN Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1												1	2
						58	66	545.79	1089.57	1089.58	-0.01	0	41	0.0071204	K.AEIELFVNR.L		21.53		
						192	203	479.21	1434.6	1434.62	-0.02	0	33	0.0311329	K.DACVISSDFHER.D		19.76		
						504	509	364.7	727.38	727.4	-0.01	0	36	0.0198653	R.TNQIPR.Q		12.77		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75844	3%	69	2	55063	7.1	O75844|FACE1_HUMAN CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2												1	1
						304	314	639.27	1276.53	1276.54	-0.01	0	40	0.0079059	R.NEEEGNSEEIK.A		12.85		
						304	316	492.87	1475.59	1475.67	-0.08	1	32	0.0460731	R.NEEEGNSEEIKAK.V		12.51		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9HC07	11%	137	2	35055	6.5	Q9HC07|TM165_HUMAN Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=1 SV=1												2	2
						43	67	883.11	2646.31	2646.39	-0.08	1	85	1.48E-07	R.NKEPPAPAQQLQPQPVAVQGPEPAR.V		19.64		
						253	263	586.84	1171.66	1171.69	-0.03	0	52	0.0004632	R.SQLTTIVLAAR.E		21.29		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y490	9%	1004	18	271766	5.8	Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3												2	2
						614	624	543.31	1084.6	1084.62	-0.03	0	43	0.0041512	K.GLAGAVSELLR.S		22.4		
						625	634	507.24	1012.47	1012.49	-0.02	0	34	0.0268569	R.SAQPASAEPR.Q		12.54		
						899	910	610.3	1218.58	1218.6	-0.02	0	87	1.39E-07	R.MATNAAAQNAIK.K	Oxidation (M)	13.28		
						923	943	665.67	1993.98	1994.02	-0.04	0	76	1.62E-06	K.QAAASATQTIAAAQHAASTPK.A		19.78		
						958	971	746.94	1491.87	1491.88	-0.01	0	40	0.0066956	K.AVAEQIPLLVQGVR.G		22.09		
						1026	1035	529.3	1056.58	1056.59	-0.02	0	41	0.0060205	K.NLGTALAELR.T		21.56		
						1172	1184	450.53	1348.57	1348.61	-0.05	0	35	0.023369	K.AAGHPGDPESQQR.L		12.46		
						1321	1332	599.32	1196.62	1196.64	-0.02	0	43	0.003219	K.ALSTDPAAPNLK.S		17.63		
						1402	1415	717.86	1433.7	1433.72	-0.02	0	94	2.53E-08	K.VLGEAMTGISQNAK.N	Oxidation (M)	15.44		
						1531	1541	573.3	1144.59	1144.61	-0.02	0	59	9.78E-05	K.EVANSTANLVK.T		15		
						1594	1604	573.31	1144.6	1144.62	-0.02	0	56	0.000188	R.AAMEPIVISAK.T	Oxidation (M)	18.59		
						1605	1618	732.37	1462.74	1462.74	-0.01	0	62	4.36E-05	K.TMLESAGGLIQTAR.A	Oxidation (M)	20.49		
						1752	1766	576.28	1725.81	1725.87	-0.06	0	42	0.0044204	K.TLSHPQQMALLDQTK.T	Oxidation (M)	15.87		
						2032	2043	622.32	1242.63	1242.66	-0.03	0	74	3.03E-06	K.VLVQNAAGSQEK.L		13.5		
						2044	2057	708.88	1415.74	1415.77	-0.03	0	95	2.17E-08	K.LAQAAQSSVATITR.L		17.67		
						2090	2099	494.78	987.54	987.56	-0.02	0	45	0.0032341	K.ALGDLISATK.A		21.02		
						2120	2130	610.84	1219.66	1219.68	-0.02	0	48	0.0013418	K.VMVTNVTSLLK.T	Oxidation (M)	21.38		
						2169	2177	533.25	1064.49	1064.51	-0.02	0	33	0.0318719	K.TSTPEDFIR.M		20.44		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35579	8%	825	15	227646	5.5	P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4												2	2
						39	47	468.23	934.46	934.48	-0.02	0	33	0.0403823	K.SGFEPASLK.E		19.42		
						166	180	776.34	1550.67	1550.69	-0.02	0	59	8.60E-05	R.EDQSILCTGESGAGK.T		18.5		
						290	299	603.31	1204.6	1204.63	-0.03	0	43	0.0041165	K.TDLLLEPYNK.Y		21.25		
						359	373	804.32	1606.63	1606.69	-0.05	0	82	4.24E-07	R.NTDQASMPDNTAAQK.V	Oxidation (M)	12.5		

						408	419	653.33	1304.65	1304.66	-0.01	0	52	0.0004191	K.EQADFAIEALAK.A		21.69		
						738	745	489.75	977.49	977.5	-0.01	0	43	0.0038043	K.QACVLMIK.A	Oxidation (M)	19.29		
						746	755	597.31	1192.6	1192.61	-0.01	0	70	6.78E-06	K.ALELDSNLYR.I		20.98		
						803	810	482.23	962.44	962.49	-0.04	0	40	0.00777	R.QQQLTAMK.V	Oxidation (M)	12.76		
						1001	1014	827.39	1652.76	1652.78	-0.02	0	92	4.15E-08	R.IAEFTTNLTEEEEK.S		20.71		
						1001	1016	623.63	1867.88	1867.91	-0.03	1	58	9.73E-05	R.IAEFTTNLTEEEEKSK.S		20.18		
						1220	1234	577.28	1728.82	1728.86	-0.05	1	36	0.0142521	K.QTLENERGELANEVK.V		19.2		
						1529	1538	610.79	1219.56	1219.58	-0.01	0	40	0.0075457	R.ALEQQVEEMK.T	Oxidation (M)	14.42		
						1816	1828	765.88	1529.74	1529.76	-0.02	0	66	1.54E-05	K.IAQLEEQLDNETK.E		20.27		
						1878	1888	666.29	1330.57	1330.6	-0.03	0	53	0.0003742	R.QLEEAEEEAQR.A		14.2		
						1899	1912	791.33	1580.65	1580.66	-0.01	0	64	2.29E-05	R.ELEDATETADAMNR.E	Oxidation (M)	14.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9HD45	5%	108	3	68584	6.8	Q9HD45|TM9S3_HUMAN Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2												2	2
						60	70	652.81	1303.6	1303.63	-0.03	0	35	0.0236723	K.YFSLPFCVGSK.K		22.76		
						189	196	486.24	970.46	970.48	-0.02	0	34	0.0279731	K.IQMSYSVK.W	Oxidation (M)	13.98		
						419	429	645.3	1288.58	1288.6	-0.02	0	38	0.0113063	R.NLSGQPNFPCR.V		18.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08575	2%	123	3	148644	5.8	P08575|CD45_HUMAN Leukocyte common antigen OS=Homo sapiens GN=PTPRC PE=1 SV=2												2	2
						292	303	640.86	1279.71	1279.74	-0.03	0	36	0.0153329	K.TLILDVPPGVEK.F		21.34		
						650	660	660.85	1319.69	1319.72	-0.04	0	40	0.0072066	R.LFLAEFQSIPR.V		22.58		
						1055	1063	531.3	1060.59	1060.62	-0.03	0	48	0.0012769	K.VIVMLTELK.H	Oxidation (M)	21.07		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11717	2%	271	5	281056	5.6	P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=2												2	1
						484	491	468.75	935.48	935.51	-0.02	0	39	0.0079358	R.YDLSALVR.H		21.74		
						724	733	605.32	1208.62	1208.62	-0.01	0	61	4.91E-05	R.ATLITFLCDR.D		22.71		
						1040	1052	757.34	1512.67	1512.69	-0.02	0	79	8.86E-07	R.FVCNDDVYSGPLK.F		20.53		
						1213	1221	515.76	1029.5	1029.53	-0.03	0	38	0.0123704	R.TVEACPVVR.V		14.34		
						1536	1545	522.75	1043.49	1043.49	0	0	56	0.0002244	R.AGFTAAYSEK.G		16.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15149	0%	77	2	533404	5.7	Q15149|PLEC1_HUMAN Plectin-1 OS=Homo sapiens GN=PLEC1 PE=1 SV=2												2	1
						1234	1243	530.28	1058.54	1058.54	0.01	0	48	0.0012532	R.GTQGAEEVLR.A		15.13		
						3116	3127	642.86	1283.71	1283.71	0	0	34	0.0263316	R.SLVPAAELLESR.V		22.05		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	22%	1238	21	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												3	5
						87	98	482.25	1443.74	1443.78	-0.05	0	39	0.0097212	R.VTLRPYLTPNDR.G		19.66		
						196	204	550.73	1099.44	1099.46	-0.02	0	41	0.0066103	R.SEYMEGNVR.K	Oxidation (M)	13.07		
						205	218	502.58	1504.7	1504.77	-0.06	1	46	0.0016294	R.KVVATTQMQAADAR.K	Oxidation (M)	12.41		
						205	219	545.28	1632.81	1632.86	-0.05	2	65	2.17E-05	R.KVVATTQMQAADARK.S	Oxidation (M)	12.24		
						206	218	689.33	1376.64	1376.67	-0.03	0	109	9.20E-10	K.VVATTQMQAADAR.K	Oxidation (M)	12.8		
						220	230	672.78	1343.55	1343.55	-0.01	0	35	0.0242401	K.SFPCFDEPAMK.A	Oxidation (M)	20.64		
						242	252	609.81	1217.61	1217.63	-0.02	0	53	0.0004246	K.DLTALSNMLPK.G	Oxidation (M)	21.09		
						293	301	479.26	956.51	956.54	-0.03	0	59	9.27E-05	K.QASNGVLIR.I		14.7		
						364	379	862.9	1723.79	1723.83	-0.03	0	83	3.16E-07	R.ENSLLFDPLSSSSSNK.E		21.93		
						364	381	670.65	2008.93	2008.97	-0.04	1	60	5.67E-05	R.ENSLLFDPLSSSSSNKER.V		21.13		
						433	442	627.31	1252.6	1252.61	-0.01	0	43	0.0037458	K.DLMVLNDVYR.V	Oxidation (M)	21.36		
						486	497	709.84	1417.66	1417.68	-0.02	0	82	4.87E-07	R.MLSSFLSEDVFK.Q	Oxidation (M)	22.42		
						596	606	732.36	1462.7	1462.72	-0.02	0	57	0.0001293	R.QQQDYWLIDVR.A		22.16		
						642	648	443.75	885.48	885.5	-0.02	0	42	0.0056332	K.IQTQLQR.D		13.42		
						659	673	538.27	1611.8	1611.84	-0.04	0	92	4.75E-08	R.AQIINDAFNLASAHK.V		20.91		
						725	734	620.83	1239.65	1239.68	-0.03	0	55	0.0002415	K.QVTPLFIHFR.N	Gln->pyro-Glu (N-term Q)	22.96		
						778	793	663.97	1988.88	1988.93	-0.04	0	32	0.0330161	K.QWMENPNNNPIHPNLR.S	Oxidation (M)	19.52		
						837	843	472.26	942.51	942.53	-0.02	0	42	0.0044387	K.ELWILNR.Y		22.02		
						844	855	734.38	1466.75	1466.78	-0.02	0	78	1.11E-06	R.YLSYTLNPDLIR.K		21.71		
						924	935	635.26	1268.5	1268.53	-0.03	0	70	7.78E-06	K.DNEETGFGSGTR.A		14.3		
						956	967	740.38	1478.74	1478.74	0	0	60	6.93E-05	K.EVVLQWFTENSK.-		22.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92896	11%	585	11	138382	6.5	Q92896|GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=1												3	2
						182	197	592.94	1775.81	1775.86	-0.05	1	56	0.0001516	K.STITEIKECADEPVGK.G		19.39		
						223	232	616.79	1231.57	1231.59	-0.02	0	51	0.0005608	K.MTAIIFSDYR.L	Oxidation (M)	21		
						259	272	520.22	1557.65	1557.71	-0.06	0	34	0.0277571	K.DAHSQGEVVSCLEK.G		17.24		
						298	310	501.9	1502.68	1502.7	-0.02	0	37	0.014573	R.VAELSSDDFHLDR.H		20.24		
						323	333	634.76	1267.51	1267.53	-0.01	0	76	1.59E-06	R.FCENTQAGEGR.V		13.11		
						385	392	501.24	1000.46	1000.48	-0.01	0	38	0.0143953	R.CNVENLPR.S		14.61		
						502	516	847.38	1692.75	1692.78	-0.03	0	76	1.56E-06	R.ALNEACESVIQTACK.H		19.79		
						546	555	641.36	1280.7	1280.71	-0.01	0	40	0.0071929	R.LLELQYFISR.D		23.13		
						925	933	569.77	1137.52	1137.54	-0.02	0	51	0.0005263	R.QITQNTDYR.L		13.46		
						980	989	611.76	1221.5	1221.53	-0.03	0	77	1.56E-06	R.LSSDCEDQIR.I		13.95		
						1089	1100	743.81	1485.6	1485.61	-0.02	0	51	0.0006191	R.QMSCLMEALEDK.R	2 Oxidation (M)	20.01		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P46940	9%	637	14	189761	6.1	P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1												3	1

						81	88	455.24	908.46	908.48	-0.02	0	55	0.0002109	K.LGNFFSPK.V		20.68		
						162	174	708.37	1414.73	1414.78	-0.05	0	35	0.0195557	K.LGLAPQIQDLYGK.V		21.85		
						192	201	579.29	1156.56	1156.56	0	0	37	0.0140521	K.YGIQMPAFSK.I	Oxidation (M)	19.75		
						327	336	513.3	1024.59	1024.6	-0.02	0	45	0.0019374	R.ALQSPALGLR.G		20.06		
						857	870	785.41	1568.8	1568.82	-0.02	0	50	0.0007116	K.TLINAEDPPMVVVR.K	Oxidation (M)	20.42		
						902	916	895.93	1789.84	1789.85	-0.01	0	59	8.64E-05	R.SNQQLENDLNLMDIK.I	Oxidation (M)	20.95		
						941	953	543.9	1628.67	1628.72	-0.05	1	32	0.0464531	K.NKEQLSDMMMINK.Q	3 Oxidation (M)	13.02		
						989	997	567.79	1133.57	1133.59	-0.02	0	32	0.0441136	K.LIFQMPQNK.S	Oxidation (M)	19.57		
						1089	1096	475.74	949.46	949.48	-0.02	0	33	0.0415939	K.TDPVDIYK.S		19.21		
						1186	1194	562.82	1123.62	1123.64	-0.02	0	51	0.0005709	K.IIGNLLYYR.Y		21.49		
						1446	1455	588.78	1175.55	1175.57	-0.02	0	63	4.43E-05	K.EDSNLTLQEK.K		14.87		
						1466	1475	536.79	1071.56	1071.58	-0.02	0	51	0.0007313	K.LTELGTVDPK.N		17.93		
						1506	1516	618.82	1235.63	1235.65	-0.02	0	55	0.0002385	K.LQQTYAALNSK.A		15.71		
						1517	1528	742.33	1482.64	1482.67	-0.03	0	44	0.0028395	K.ATFYGEQVDYYK.S		20.51		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13473	4%	121	2	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												3	3
						145	152	494.27	986.53	986.55	-0.02	0	46	0.0023715	R.IPLNDLFR.C		21.89		
						153	161	526.25	1050.48	1050.5	-0.02	0	76	1.73E-06	R.CNSLSTLEK.N		15.36		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75976	3%	142	3	153919	5.7	O75976|CBPD_HUMAN Carboxypeptidase D OS=Homo sapiens GN=CPD PE=1 SV=2												3	1
						559	571	487.89	1460.64	1460.68	-0.04	0	48	0.0011031	K.YIGNMHGNEVVGR.E	Oxidation (M)	13.51		
						908	921	782.37	1562.72	1562.76	-0.04	0	59	8.56E-05	K.DLSAENGLESLMLR.S	Oxidation (M)	21.98		
						1030	1041	640.36	1278.71	1278.73	-0.02	0	35	0.0205164	R.IVIVPSLNPDGR.E		21.18		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07814	1%	68	2	172137	7	P07814|SYEP_HUMAN Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=3												3	1
						587	593	380.22	758.43	758.45	-0.02	0	34	0.0479749	K.IISLDAK.F		17.5		
						890	902	671.81	1341.61	1341.64	-0.04	0	35	0.0244812	R.NSEPAGLETPEAK.V		15.09		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14789	1%	133	2	377215	5	Q14789|GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2												3	1
						2082	2093	659.34	1316.66	1316.66	0	0	96	1.68E-08	K.VLLDDTQSEAAR.V		17.15		
						2865	2880	800.9	1599.79	1599.81	-0.02	0	37	0.0116927	R.SAAQPSTSPAEVQSLK.K		16.45		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16706	11%	642	12	131742	7.2	Q16706|MA2A1_HUMAN Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2												4	1
						61	73	749.9	1497.79	1497.82	-0.03	0	100	6.45E-09	R.LLAENNEIISNIR.D		20.8		
						183	189	481.71	961.4	961.43	-0.02	0	38	0.0141057	K.TFNDYFR.D		20.7		
						327	333	499.74	997.47	997.5	-0.03	0	34	0.0296809	K.TLEFFWR.Q		22.66		
						418	428	608.33	1214.64	1214.67	-0.02	0	56	0.0001938	K.VLLAPLGDDFR.Y		21.95		
						441	454	891.38	1780.74	1780.77	-0.03	0	47	0.0012486	K.NYQQLFDYMNSQSK.F	Oxidation (M)	20.88		
						547	560	779.91	1557.8	1557.8	0	0	33	0.0374432	K.FLSSSLYTALTEAR.R		22.44		
						649	660	754.87	1507.72	1507.77	-0.04	0	56	0.000161	R.YLVVYNPLEQDR.I		21.73		
						740	749	554.78	1107.55	1107.58	-0.03	0	49	0.0009078	K.VEDSGIFTIK.N		21.02		
						769	776	478.22	954.42	954.45	-0.03	0	32	0.0430413	R.FDQTGLMK.Q	Oxidation (M)	14.27		
						892	904	807.88	1613.75	1613.78	-0.04	0	85	2.12E-07	R.FYTDLNGYQIQPR.M		20.93		
						965	974	551.26	1100.51	1100.55	-0.04	0	51	0.0006209	R.GLEQGIQDNK.I		14.18		
						1083	1094	628.77	1255.53	1255.59	-0.06	0	64	2.77E-05	K.GTGLFCSTTQGK.I		17.87		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y4L1	9%	369	7	111494	5.2	Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1												4	1
						107	119	494.9	1481.68	1481.74	-0.05	0	34	0.0228616	K.QADNPHVALYQAR.F		15.28		
						252	262	643.82	1285.63	1285.64	-0.01	0	57	0.0001625	K.EAGMQPQLQIR.G	Oxidation (M)	16.82		
						269	278	567.77	1133.54	1133.58	-0.04	0	52	0.0004301	R.TLGGLEMELR.L	Oxidation (M)	20.53		
						283	291	524.26	1046.51	1046.55	-0.04	0	52	0.0005077	R.LAGLFNEQR.K		20.44		
						577	594	868.42	1734.83	1734.88	-0.05	0	85	1.93E-07	K.LGNTISSLFGGGTTPDAK.E		21.86		
						670	686	546.26	1635.75	1635.81	-0.06	1	49	0.0008477	K.AEAGPEGVAPAPEGEKK.Q		13.38		
						878	889	432.59	1294.74	1294.79	-0.04	0	41	0.0046657	K.LPATEKPVLLSK.D		18.04		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P16284	9%	245	5	83396	6.5	P16284|PECA1_HUMAN Platelet endothelial cell adhesion molecule OS=Homo sapiens GN=PECAM1 PE=1 SV=1												4	1
						90	100	664.31	1326.61	1326.65	-0.04	0	56	0.0001858	K.STESYFIPEVR.I		21.15		
						379	392	744.33	1486.64	1486.66	-0.02	0	76	1.67E-06	K.SDSGTYICTAGIDK.V		19.76		
						457	465	496.23	990.44	990.48	-0.04	0	45	0.002505	K.NSNDPAVFK.D		14.97		
						632	651	762.69	2285.04	2285.11	-0.08	0	35	0.0169131	K.QMPVEMSRPAVPLLNSNNEK.M	2 Oxidation (M)	19.72		
						708	717	599.77	1197.53	1197.55	-0.03	0	33	0.0342528	K.DTETVYSEVR.K		18.43		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11279	7%	168	3	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												4	6
						138	146	517.27	1032.52	1032.55	-0.02	0	67	1.55E-05	K.TVESITDIR.A		19.67		
						327	337	576.29	1150.57	1150.6	-0.03	0	68	1.07E-05	R.ALQATVGNSYK.C		14.62		
						410	417	438.7	875.39	875.41	-0.03	0	33	0.0462675	R.SHAGYQTI.-		14.22		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q08378	4%	230	5	167765	5.3	Q08378|GOGA3_HUMAN Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2												4	1

						483	494	698.79	1395.57	1395.64	-0.06	0	50	0.0007021	R.AMTDLQNMLEAK.N	2 Oxidation (M)	18.7		
						959	968	622.3	1242.58	1242.62	-0.04	0	44	0.0028969	K.QIEELQQEAR.K		15.46		
						981	990	510.25	1018.49	1018.53	-0.04	0	37	0.0193826	R.LGSDLTSAQK.E		13.91		
						1029	1043	505.56	1513.66	1513.71	-0.05	0	55	0.0002118	R.AQGGSSDSSLALHER.I		13.74		
						1233	1243	636.32	1270.62	1270.65	-0.03	0	46	0.0018769	K.LQAEADDLQIR.E		19.99		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43491	4%	153	3	113032	5.3	O43491|E41L2_HUMAN Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1												4	1
						2	13	653.33	1304.64	1304.68	-0.04	1	64	2.81E-05	M.TTEVGSVSEVKK.D	Acetyl (Protein N-term)	15.5		
						384	399	838.41	1674.81	1674.82	-0.01	0	51	0.0005493	R.GLSPAQADSQFLENAK.R		20.66		
						497	505	497.77	993.52	993.55	-0.03	0	41	0.0054818	R.LVSPEQPPK.A		13.87		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O94804	3%	114	2	112749	6.5	O94804|STK10_HUMAN Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1												4	1
						447	464	611.29	1830.86	1830.91	-0.05	0	53	0.0002802	K.ASQSRPNSSALETLGGEK.L		16.6		
						941	955	823.35	1644.69	1644.73	-0.04	0	61	5.10E-05	K.LSEEACPNPSTPSK.A		13.78		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y2J2	3%	132	2	121458	5.1	Q9Y2J2|E41L3_HUMAN Band 4.1-like protein 3 OS=Homo sapiens GN=EPB41L3 PE=1 SV=2												4	1
						912	924	687.84	1373.67	1373.68	-0.01	0	74	2.77E-06	K.AVLEQEETAAASR.E		15.72		
						953	967	733.35	1464.69	1464.75	-0.06	0	57	0.000123	K.TETISFGSVSPGGVK.L		20.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q86VP6	2%	82	2	137999	5.5	Q86VP6|CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2												4	1
						374	382	472.4	942.79	942.55	0.24	0	35	0.0076336	K.TVSPALISR.F		17.56		
						859	873	811.4	1620.79	1620.82	-0.04	0	50	0.0006733	K.SVILEAFSSPSEEVK.S		21.55		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P42704	1%	107	2	159003	5.8	P42704|LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3												4	1
						981	989	549.28	1096.55	1096.59	-0.04	0	42	0.0045906	K.IQEENVIPR.E		17.95		
						1129	1139	636.82	1271.63	1271.65	-0.02	0	65	2.24E-05	K.TVLDQQQTPSR.L		13.96		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	17%	672	13	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												5	3
						76	84	541.25	1080.49	1080.54	-0.04	0	38	0.0096928	K.FAFQAEVNR.M		20.19		
						88	95	482.28	962.55	962.58	-0.03	0	39	0.0102665	K.LIINSLYK.N		20.67		
						103	114	638.31	1274.61	1274.64	-0.03	0	82	4.41E-07	R.ELISNASDALDK.I		19.88		
						143	156	510.57	1528.7	1528.77	-0.07	0	56	0.0001684	K.NLLHVTDTGVGMTR.E	Oxidation (M)	19.39		
						169	177	491.72	981.43	981.48	-0.05	0	41	0.0054314	K.SGTSEFLNK.M		15.56		
						396	404	508.23	1014.44	1014.47	-0.03	0	39	0.0116079	R.GLFDEYGSK.K		20.72		
						435	448	743.37	1484.72	1484.75	-0.03	0	86	1.72E-07	K.GVVDSDDLPLNVSR.E		20.76		
						548	557	575.75	1149.48	1149.53	-0.05	0	62	4.66E-05	K.EAESSPFVER.L		16.39		
						588	593	353.69	705.36	705.38	-0.02	0	38	0.013229	R.FQNVAK.E		12.73		
						594	605	466.22	1395.64	1395.69	-0.05	2	42	0.0046419	K.EGVKFDESEKTK.E		13.03		
						672	682	645.29	1288.56	1288.59	-0.04	0	54	0.000305	K.DISTNYYASQK.K		17.26		
						725	733	497.25	992.48	992.52	-0.04	0	56	0.0001649	R.SGYLLPDTK.A		19.79		
						745	754	543.28	1084.54	1084.58	-0.04	0	49	0.00105	R.LSLNIDPDAK.V		20.5		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	16%	552	12	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												5	3
						156	165	545.27	1088.52	1088.55	-0.02	0	40	0.0092365	R.ALNEITESGR.I		15		
						166	174	485.24	968.46	968.5	-0.03	0	44	0.0024067	R.IGFGSFVDK.T		21.07		
						275	285	563.8	1125.58	1125.61	-0.03	0	41	0.0051871	K.LGAILTPNDGR.C		19.57		
						311	325	836.93	1671.85	1671.89	-0.05	0	56	0.0001708	K.LAENNIQPIFAVTSR.M		21.38		
						380	393	548.22	1641.65	1641.72	-0.07	0	54	0.0002326	K.VTYDSFCSNGVTHR.N		18.39		
						463	471	556.24	1110.47	1110.5	-0.02	0	38	0.0094954	K.GFLECGICR.C		20.45		
						472	479	457.19	912.37	912.4	-0.03	0	47	0.0014748	R.CDTGYIGK.N		13.64		
						489	498	576.73	1151.44	1151.49	-0.05	0	55	0.0002351	R.SSQELEGSCR.K		12.81		
						544	554	582.75	1163.48	1163.51	-0.03	0	49	0.0009199	R.YNGQVCGGPGR.G		13.07		
						578	586	524.23	1046.44	1046.48	-0.04	0	52	0.000495	R.TTEGCLNPR.R		13.21		
						625	633	572.25	1142.48	1142.51	-0.03	0	36	0.0227251	K.YISCAECLK.F		15.96		
						756	765	533.26	1064.51	1064.52	-0.01	0	41	0.0055387	K.SATTTVMNPK.F	Oxidation (M)	12.42		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P12814	6%	225	5	103563	5.3	P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2												5	1
						96	103	432.73	863.44	863.48	-0.03	0	51	0.0006726	K.ALDFIASK.G		20.36		
						347	359	493.22	1476.64	1476.71	-0.07	0	34	0.0269115	R.LSNRPAFMPSEGR.M	Oxidation (M)	14.04		
						705	714	439.85	1316.53	1316.59	-0.07	0	33	0.039607	K.HTNYTMEHIR.V	Oxidation (M)	12.6		
						742	752	677.79	1353.56	1353.6	-0.04	0	70	6.35E-06	K.GISQEQMNEFR.A	Oxidation (M)	15.22		
						795	803	530.76	1059.5	1059.54	-0.03	0	37	0.0186226	R.IMSIVDPNR.L	Oxidation (M)	16		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13639	5%	213	4	96246	6.4	P13639|EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4												5	1
						2	10	546.28	1090.54	1090.58	-0.03	0	59	0.0001066	M.VNFTVDQIR.A		20.41		
						227	235	551.74	1101.47	1101.52	-0.05	0	54	0.0003515	K.QFAEMYVAK.F	Oxidation (M)	16.74		
						240	249	507.24	1012.48	1012.49	-0.02	0	33	0.0317728	K.GEGQLGPAER.A		13.38		
						416	426	554.31	1106.61	1106.63	-0.03	0	68	1.23E-05	R.VFSGLVSTGLK.V		20.81		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43707	3%	144	3	105245	5.3	O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2												5	1
						115	122	432.73	863.44	863.48	-0.03	0	51	0.0006726	K.ALDFIASK.G		20.36		
						724	733	439.85	1316.53	1316.59	-0.07	0	33	0.039607	K.HTNYTMEHIR.V	Oxidation (M)	12.6		
						761	771	684.8	1367.58	1367.61	-0.03	0	62	4.46E-05	K.GISQEQMQEFR.A	Oxidation (M)	15.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P37840	27%	158	2	14451	4.7	P37840|SYUA_HUMAN Alpha-synuclein OS=Homo sapiens GN=SNCA PE=1 SV=1												6	5
						59	80	719.71	2156.12	2156.18	-0.06	1	74	2.38E-06	K.TKEQVTNVGGAVVTGVTAVAQK.T		20.61		
						81	96	739.88	1477.74	1477.78	-0.03	0	84	2.37E-07	K.TVEGAGSIAAATGFVK.K		20.88		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08238	15%	561	10	83554	5	P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4												6	3
						42	53	638.31	1274.61	1274.64	-0.02	0	64	2.91E-05	R.ELISNASDALDK.I		19.91		
						56	69	513.9	1538.68	1538.75	-0.07	1	39	0.0091374	R.YESLTDPSKLDSGK.E		18.91		
						73	82	597.81	1193.62	1193.64	-0.02	0	43	0.0036476	K.IDIIPNPQER.T		20.44		
						83	95	683.37	1364.72	1364.72	0	0	65	2.50E-05	R.TLTLVDTGIGMTK.A	Oxidation (M)	20.57		
						96	107	621.85	1241.68	1241.7	-0.02	0	71	6.09E-06	K.ADLINNLGTIAK.S		21.09		
						276	284	576.4	1150.79	1150.55	0.23	0	60	7.33E-05	K.YIDQEELNK.T		15.39		
						339	347	540.76	1079.5	1079.53	-0.03	0	39	0.0092774	R.APFDLFENK.K		21.97		
						482	491	580.78	1159.55	1159.58	-0.02	0	36	0.0215918	K.SIYYITGESK.E		19.95		
						492	502	625.29	1248.57	1248.61	-0.04	0	65	2.44E-05	K.EQVANSAFVER.V		16.52		
						613	623	648.74	1295.46	1295.48	-0.02	0	49	0.0008378	R.DNSTMGYMMAK.K	3 Oxidation (M)	12.9		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07900	11%	394	7	85006	4.9	P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5												6	1
						47	58	646.3	1290.58	1290.63	-0.05	0	60	7.29E-05	R.ELISNSSDALDK.I		18.82		
						61	74	513.9	1538.68	1538.75	-0.07	1	39	0.0091374	R.YESLTDPSKLDSGK.E		18.91		
						88	100	683.37	1364.72	1364.72	0	0	65	2.50E-05	R.TLTIVDTGIGMTK.A	Oxidation (M)	20.57		
						101	112	621.85	1241.68	1241.7	-0.02	0	71	6.09E-06	K.ADLINNLGTIAK.S		21.09		
						284	292	576.4	1150.79	1150.55	0.23	0	60	7.33E-05	K.YIDQEELNK.T		15.39		
						339	345	408.25	814.48	814.51	-0.03	0	33	0.043241	R.ALLFVPR.R		21.23		
						500	510	618.3	1234.58	1234.59	-0.02	0	67	1.29E-05	K.DQVANSAFVER.L		17.69		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16891	7%	213	5	84026	6.1	Q16891|IMMT_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1												6	1
						111	119	498.24	994.47	994.5	-0.03	0	38	0.00928	K.ISSVSEVMK.E	Oxidation (M)	13.47		
						258	270	460.55	1378.63	1378.64	-0.01	1	33	0.037948	K.AAMDNSEIAGEKK.S	Oxidation (M)	12.47		
						287	297	558.29	1114.56	1114.59	-0.03	0	45	0.0022564	K.AVDEAADALLK.A		20.48		
						507	516	605.77	1209.52	1209.55	-0.03	0	61	5.90E-05	K.SEFEQNLSEK.L		16.13		
						624	632	527.25	1052.48	1052.51	-0.03	0	38	0.0115893	R.GVYSEETLR.A		16.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06396	7%	304	5	86043	5.9	P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1												6	1
						361	368	441.72	881.43	881.45	-0.02	0	47	0.0012587	K.TASDFITK.M		15.82		
						585	597	660.34	1318.66	1318.69	-0.03	0	86	1.86E-07	K.AGALNSNDAFVLK.T		20.66		
						616	623	444.24	886.47	886.49	-0.01	0	40	0.0088377	K.TGAQELLR.V		16.26		
						714	728	555.92	1664.73	1664.77	-0.05	1	69	8.84E-06	K.DSQEEEKTEALTSAK.R		14.34		
						730	738	539.75	1077.49	1077.51	-0.02	0	62	4.92E-05	R.YIETDPANR.D		13.9		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	6%	115	3	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												6	2
						83	92	606.79	1211.56	1211.58	-0.03	0	41	0.0051605	R.VEEVGPYTYR.E		19.47		
						154	161	481.75	961.49	961.52	-0.02	0	35	0.0247398	R.EIIEAMLK.A	Oxidation (M)	19.21		
						460	472	684.78	1367.54	1367.53	0.01	0	38	0.0101395	K.GQGSMDEGTADER.A	Oxidation (M)	12.38		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43493	6%	115	2	51082	5.5	O43493|TGON2_HUMAN Trans-Golgi network integral membrane protein 2 OS=Homo sapiens GN=TGOLN2 PE=1 SV=2												6	1
						140	153	729.81	1457.61	1457.64	-0.03	0	56	0.0001869	K.SGAEAQTPEDSPNR.S		12.77		
						224	237	686.31	1370.6	1370.63	-0.03	0	60	7.64E-05	K.SGAEEQGPIDGPSK.S		13.69		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P42224	5%	162	4	87850	5.7	P42224|STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2												6	1
						351	359	567.8	1133.58	1133.61	-0.03	0	46	0.0020539	K.LQELNYNLK.V		20		
						362	371	412.2	1233.59	1233.64	-0.05	1	32	0.0473102	K.VLFDKDVNER.N		16.91		
						593	602	587.8	1173.59	1173.61	-0.02	0	36	0.0210594	K.DQQPGTFLLR.F		21.27		
						686	697	664.8	1327.58	1327.6	-0.02	0	50	0.0006735	K.EAPEPMELDGPK.G	Oxidation (M)	15.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P16671	5%	114	3	53589	8.2	P16671|CD36_HUMAN Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2												6	1
						57	63	413.2	824.38	824.4	-0.02	0	33	0.0297081	K.TGTEVYR.Q		13.12		
						167	173	435.7	869.38	869.41	-0.02	0	38	0.0101111	K.SSMFQVR.T	Oxidation (M)	14.39		
						224	231	461.76	921.5	921.52	-0.02	0	44	0.0029435	K.VAIIDTYK.G		19.73		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P16070	3%	137	2	82017	5.1	P16070|CD44_HUMAN CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2												6	2

						47	54	454.2	906.39	906.41	-0.03	0	34	0.0304601	R.TEAADLCK.A		13.21		
						682	694	672.33	1342.64	1342.68	-0.04	0	102	4.13E-09	K.LVINSGNGAVEDR.K		16.6		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27824	3%	82	2	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												6	1
						211	217	420.2	838.38	838.41	-0.03	0	31	0.0473221	K.TGIYEEK.H		13.6		
						574	582	544.76	1087.5	1087.51	-0.02	0	51	0.0007043	K.AEEDEILNR.S		17.17		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	20%	845	13	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												7	1
						47	60	519.26	1554.76	1554.79	-0.03	1	59	8.10E-05	K.NGRVEIIANDQGNR.I		13.99		
						50	60	614.81	1227.6	1227.62	-0.02	0	70	9.23E-06	R.VEIIANDQGNR.I		14.87		
						61	74	783.88	1565.75	1565.77	-0.02	0	76	1.57E-06	R.ITPSYVAFTPEGER.L		20.7		
						82	96	839.39	1676.77	1676.8	-0.03	0	92	4.53E-08	K.NQLTSNPENTVFDAK.R		20.16		
						82	97	611.96	1832.86	1832.9	-0.04	1	86	1.68E-07	K.NQLTSNPENTVFDAKR.L		19.59		
						123	138	578.3	1731.87	1731.95	-0.08	1	44	0.0026621	K.KTKPYIQVDIGGGQTK.T		16.83		
						124	138	535.61	1603.82	1603.86	-0.03	0	59	9.43E-05	K.TKPYIQVDIGGGQTK.T		19.63		
						186	197	617.31	1232.6	1232.62	-0.02	0	59	9.07E-05	K.DAGTIAGLNVMR.I	Oxidation (M)	20.08		
						345	352	459.73	917.45	917.47	-0.02	0	33	0.0468292	K.VLEDSDLK.K		14.65		
						448	464	918.96	1835.9	1835.93	-0.03	0	97	1.21E-08	K.SQIFSTASDNQPTVTIK.V		20.34		
						524	532	537.76	1073.51	1073.55	-0.03	0	51	0.0006573	K.ITITNDQNR.L		13.55		
						563	573	658.81	1315.61	1315.63	-0.02	0	47	0.0016499	R.NELESYAYSLK.N		21.01		
						622	633	699.39	1396.77	1396.78	-0.01	0	47	0.0013293	K.ELEEIVQPIISK.L		21.27		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	18%	560	12	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												7	1
						28	35	488.77	975.52	975.54	-0.02	0	44	0.0030829	K.QLFDQVVK.T		20.39		
						101	107	447.77	893.52	893.54	-0.02	0	37	0.0134653	R.LFFLQVK.E		22.11		
						144	156	473.25	1416.74	1416.77	-0.03	1	54	0.0003214	K.SGYLAGDKLLPQR.V		19.94		
						185	193	540.28	1078.55	1078.55	-0.01	0	45	0.0024334	R.EDAVLEYLK.I		21.36		
						295	306	496.92	1487.73	1487.78	-0.05	1	55	0.000236	R.RKPDTIEVQQMK.A	Oxidation (M)	12.59		
						296	306	444.88	1331.63	1331.68	-0.05	0	55	0.0002393	R.KPDTIEVQQMK.A	Oxidation (M)	12.94		
						360	371	505.92	1514.74	1514.78	-0.04	2	48	0.0010163	K.KAQQELEEQTRR.A		12.5		
						372	379	494.24	986.47	986.5	-0.03	0	40	0.0097279	R.ALELEQER.K		16.05		
						394	408	558.28	1671.81	1671.84	-0.03	1	38	0.011416	R.QEAEEAKEALLQASR.D		19.68		
						449	458	603.78	1205.54	1205.56	-0.02	0	57	0.0001552	K.AQMVQEDLEK.T	Oxidation (M)	13.86		
						449	460	488.56	1462.66	1462.71	-0.05	1	34	0.0284899	K.AQMVQEDLEKTR.A	Oxidation (M)	13.77		
						569	577	585.75	1169.49	1169.5	-0.01	1	57	0.0001382	K.QRIDEFESM.-	Oxidation (M)	17.83		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38646	7%	218	4	73920	5.9	P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2												7	1
						77	85	479.74	957.47	957.49	-0.02	0	50	0.0009056	K.VLENAEGAR.T		13.02		
						207	218	621.84	1241.66	1241.67	-0.02	0	43	0.0040358	K.DAGQISGLNVLR.V		21.1		
						293	307	569.6	1705.78	1705.83	-0.05	1	43	0.003427	R.ETGVDLTKDNMALQR.V	Oxidation (M)	18.49		
						635	646	616.33	1230.64	1230.66	-0.02	0	82	4.83E-07	R.QAASSLQQASLK.L		14.6		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13667	7%	198	4	73229	5	P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2												7	1
						96	103	506.23	1010.45	1010.47	-0.02	0	40	0.0073958	K.QFAPEYEK.I		15.65		
						120	131	595.82	1189.62	1189.63	-0.01	0	80	8.13E-07	K.IDATSASVLASR.F		19.72		
						235	245	567.28	1132.55	1132.56	-0.01	0	39	0.0095739	K.VDATAETDLAK.R		15		
						350	362	729.87	1457.73	1457.75	-0.03	0	41	0.0062304	K.VSQGQLVVMQPEK.F	Oxidation (M)	15.78		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P33121	5%	117	3	78919	6.8	P33121|ACSL1_HUMAN Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1												7	1
						99	112	729.86	1457.7	1457.7	0	0	50	0.00068	R.GIQVSNNGPCLGSR.K		19.15		
						208	216	507.79	1013.56	1013.58	-0.02	0	33	0.0427782	K.LLLEGVENK.L		20.25		
						341	349	526.77	1051.52	1051.55	-0.03	0	34	0.02668	K.IGFFQGDIR.L		21.45		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40939	4%	133	3	83688	9.2	P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2												7	1
						520	531	559.8	1117.59	1117.6	-0.01	0	55	0.0002276	K.DTSASAVAVGLK.Q		19.41		
						541	549	507.24	1012.46	1012.46	0	0	34	0.0279934	K.DGPGFYTTR.C		18.66		
						720	728	520.77	1039.53	1039.53	-0.01	0	43	0.0031116	R.FVDLYGAQK.I		20.03		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51659	4%	127	2	80092	9	P51659|DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3												7	1
						316	331	734.37	1466.72	1466.74	-0.02	0	55	0.0002097	R.ATSTATSGFAGAIGQK.L		19.54		
						544	555	696.34	1390.67	1390.68	-0.01	0	72	5.00E-06	R.VLQQFADNDVSR.F		19.5		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13948	3%	134	2	77636	5.3	Q13948|CASP_HUMAN Protein CASP OS=Homo sapiens GN=CUX1 PE=1 SV=2												7	1
						166	175	558.79	1115.57	1115.58	-0.01	0	37	0.0154453	K.NQAETIALEK.E		16.35		
						428	439	645.34	1288.66	1288.66	-0.01	0	98	1.19E-08	R.ITEAVATATEQR.E		14.56		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13796	25%	827	14	70815	5.2	P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5												8	2

						4	15	707.78	1413.54	1413.58	-0.04	0	58	0.0001046	R.GSVSDEEMMELR.E	2 Oxidation (M)	15.09		
						40	49	559.28	1116.55	1116.57	-0.03	0	40	0.0085437	K.AACLPLPGYR.V		20.42		
						133	141	545.22	1088.42	1088.46	-0.03	0	52	0.0005304	K.ALENDPDCR.H		13.02		
						166	178	759.85	1517.69	1517.74	-0.05	0	102	4.03E-09	K.MINLSVPDTIDER.T	Oxidation (M)	20.73		
						245	253	506.8	1011.58	1011.61	-0.03	0	44	0.0027287	R.NEALIALLR.E		21.93		
						254	263	583.75	1165.49	1165.52	-0.03	0	44	0.0024311	R.EGESLEDLMK.L	Oxidation (M)	19.12		
						264	272	535.29	1068.57	1068.62	-0.04	0	36	0.0186251	K.LSPEELLLR.W		21.8		
						286	294	497.75	993.48	993.51	-0.03	0	44	0.0026298	K.IGNFSTDIK.D		19.61		
						334	343	626.26	1250.5	1250.54	-0.04	0	57	0.0001326	R.AECMLQQAER.L	Oxidation (M)	13.28		
						348	357	568.29	1134.56	1134.6	-0.04	0	43	0.0036057	R.QFVTATDVVR.G		19.75		
						456	468	513.24	1536.7	1536.76	-0.06	1	56	0.0001693	K.KLENCNYAVELGK.N		18.9		
						473	488	838.4	1674.79	1674.83	-0.04	0	102	3.88E-09	K.FSLVGIGGQDLNEGNR.T		21.36		
						571	584	539.9	1616.69	1616.76	-0.08	1	50	0.0006514	K.TENLNDDEKLNNAK.Y		13.37		
						597	610	793.4	1584.79	1584.84	-0.05	0	97	1.24E-08	R.VYALPEDLVEVNPK.M		21.4		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31948	17%	370	8	63227	6.4	P31948|STIP1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1												8	1
						1	10	653.3	1304.59	1304.63	-0.04	1	76	1.82E-06	-.MEQVNELKEK.G	Acetyl (Protein N-term); Oxidation (M)	15.61		
						110	118	532.23	1062.45	1062.48	-0.03	0	44	0.0031811	K.EGLQNMEAR.L	Oxidation (M)	12.8		
						145	153	533.26	1064.51	1064.55	-0.04	0	42	0.004925	R.TLLSDPTYR.E		19.7		
						207	223	515.23	2056.89	2057	-0.11	2	31	0.0423022	K.KETKPEPMEEDLPENKK.Q	Oxidation (M)	12.71		
						352	364	744.88	1487.74	1487.79	-0.05	0	69	8.77E-06	R.LAYINPDLALEEK.N		21.22		
						489	505	646.58	1936.73	1936.83	-0.1	0	32	0.0358437	R.AMADPEVQQIMSDPAMR.L	3 Oxidation (M)	17.94		
						506	513	509.77	1017.52	1017.55	-0.03	0	36	0.0238234	R.LILEQMQK.D	Oxidation (M)	15.35		
						534	543	558.81	1115.61	1115.64	-0.03	0	45	0.002587	K.LMDVGLIAIR.-	Oxidation (M)	21.18		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04843	16%	414	8	68641	6	P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1												8	1
						49	65	551.95	1652.83	1652.88	-0.05	0	49	0.0008188	K.VTAEVVLAHLGGGSTSR.A		20.77		
						66	80	830.45	1658.88	1658.89	-0.01	0	49	0.0007857	R.ATSFLLALEPELEAR.L		23.3		
						117	126	490.77	979.53	979.57	-0.04	0	37	0.0151045	K.LPVALDPGAK.I		19.79		
						194	204	656.31	1310.6	1310.61	-0.02	0	52	0.0003959	R.SEDLLDYGPFR.D		22.07		
						269	278	530.26	1058.5	1058.54	-0.03	0	41	0.0062953	R.QPDSGISSIR.S		15		
						380	391	718.33	1434.65	1434.7	-0.05	0	58	0.0001014	K.NIEIDSPYEISR.A		20.64		
						525	536	651.36	1300.7	1300.74	-0.04	0	72	4.32E-06	K.ALTSEIALLQSR.L		21.31		
						537	547	431.86	1292.55	1292.6	-0.05	1	56	0.000191	R.LKTEGSDLCDR.V		13.23		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11142	13%	448	8	71082	5.4	P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1												8	2
						26	36	614.8	1227.59	1227.62	-0.03	0	67	1.57E-05	K.VEIIANDQGNR.T		14.91		
						37	49	744.33	1486.64	1486.69	-0.05	0	65	2.16E-05	R.TTPSYVAFTDTER.L		20.24		
						57	71	833.37	1664.73	1664.78	-0.05	0	105	2.24E-09	K.NQVAMNPTNTVFDAK.R	Oxidation (M)	19.57		
						57	72	607.94	1820.79	1820.88	-0.09	1	42	0.0038333	K.NQVAMNPTNTVFDAKR.L	Oxidation (M)	17.11		
						160	171	600.32	1198.63	1198.67	-0.04	0	50	0.0007335	K.DAGTIAGLNVLR.I		21.44		
						221	236	564.56	1690.66	1690.72	-0.06	0	36	0.0173738	K.STAGDTHLGGEDFDNR.M		15.7		
						349	357	541.27	1080.52	1080.56	-0.04	0	48	0.0010197	K.LLQDFFNGK.E		21.58		
						602	609	472.75	943.48	943.52	-0.04	0	34	0.0321313	K.VCNPIITK.L		15.26		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P29966	11%	173	3	31707	4.5	P29966|MARCS_HUMAN Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4												8	2
						8	30	539.76	2155.01	2155.09	-0.08	1	55	0.0001816	K.TAAKGEAAAERPGEAAVASSPSK.A		12.93		
						12	30	595.61	1783.81	1783.87	-0.06	0	57	0.0001378	K.GEAAAERPGEAAVASSPSK.A		13.19		
						138	152	750.82	1499.63	1499.67	-0.04	0	62	4.36E-05	K.AEDGATPSPSNETPK.K		13.1		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08107	10%	319	5	70294	5.5	P08107|HSP71_HUMAN Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5												8	1
						26	36	614.8	1227.59	1227.62	-0.03	0	67	1.57E-05	K.VEIIANDQGNR.T		14.91		
						37	49	744.33	1486.64	1486.69	-0.05	0	65	2.16E-05	R.TTPSYVAFTDTER.L		20.24		
						57	71	829.9	1657.79	1657.84	-0.06	0	84	2.59E-07	K.NQVALNPQNTVFDAK.R		20.37		
						221	236	559.23	1674.68	1674.72	-0.05	0	45	0.0018526	K.ATAGDTHLGGEDFDNR.L		15.79		
						349	357	555.27	1108.53	1108.57	-0.04	0	58	0.0001093	K.LLQDFFNGR.D		21.62		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H223	9%	181	4	61365	6.3	Q9H223|EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1												8	1
						15	29	686.86	1371.7	1371.71	-0.01	0	59	8.87E-05	R.AGGADAVQTVTGGLR.S		20.1		
						131	138	469.73	937.44	937.48	-0.03	0	35	0.0183375	R.FGNAFLNR.F		20.19		
						139	150	740.84	1479.67	1479.72	-0.05	0	33	0.0313747	R.FMCSQLPNQVLK.S	Oxidation (M)	20.06		
						151	165	751.38	1500.75	1500.8	-0.05	0	54	0.000293	K.SISVIDSPGILSGEK.Q		21.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q10471	9%	221	5	65433	8.6	Q10471|GALT2_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1												8	1
						94	101	447.2	892.38	892.4	-0.02	0	40	0.0083262	R.SGQDPYAR.N		12.88		
						102	113	493.24	1476.69	1476.77	-0.07	2	42	0.0043345	R.NKFNQVESDKLR.M		13.59		
						294	302	462.25	922.49	922.52	-0.03	0	46	0.0017707	R.QGNPVAPIK.T		13.81		
						303	315	706.34	1410.66	1410.69	-0.03	0	59	7.60E-05	K.TPMIAGGLFVMDK.F	2 Oxidation (M)	20.95		
						405	414	574.28	1146.54	1146.58	-0.04	0	34	0.0292777	R.NVPYGNIQSR.L		15.57		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38606	9%	214	4	68660	5.3	P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2												8	1
						221	232	439.57	1315.67	1315.74	-0.06	0	34	0.0305815	K.LPANHPLLTGQR.V		14.73		
						257	265	481.76	961.51	961.54	-0.03	0	48	0.0013564	K.TVISQSLSK.Y		15.22		
						309	323	766.37	1530.73	1530.78	-0.05	0	77	1.36E-06	R.TALVANTSNMPVAAR.E	Oxidation (M)	14.87		
						365	381	899.4	1796.79	1796.84	-0.05	0	55	0.0001816	R.LAEMPADSGYPAYLGAR.L	Oxidation (M)	20.51		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11117	7%	142	3	48713	6.3	P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3												8	1
						35	41	456.26	910.5	910.53	-0.03	0	38	0.0085231	R.FVTLLYR.H		21.13		
						242	252	672.33	1342.65	1342.69	-0.04	0	56	0.0001969	R.FLFGIYQQAEK.A		22.02		
						255	265	584.34	1166.67	1166.71	-0.04	0	48	0.0011214	R.LQGGVLLAQIR.K		21.09		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8TBA6	6%	240	4	82997	5.6	Q8TBA6|GOGA5_HUMAN Golgin subfamily A member 5 OS=Homo sapiens GN=GOLGA5 PE=1 SV=2												8	1
						308	318	637.33	1272.64	1272.67	-0.03	0	60	6.99E-05	R.LQEADQLLSTR.T		20.15		
						526	537	478.23	1431.68	1431.72	-0.04	1	37	0.0136444	K.ASKQELETELER.L		16.41		
						578	590	732.83	1463.64	1463.69	-0.05	0	85	1.92E-07	K.TLSNSSQSELENR.L		14.03		
						602	612	641.79	1281.57	1281.61	-0.05	0	60	6.40E-05	K.QTMLESLSTEK.N	Oxidation (M)	16.54		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P29401	6%	142	2	68519	7.6	P29401|TKT_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3												8	1
						187	204	695.66	2083.95	2084	-0.05	0	37	0.0110229	R.LGQSDPAPLQHQMDIYQK.R	Oxidation (M)	18.38		
						439	456	942.94	1883.86	1883.92	-0.06	0	104	2.16E-09	R.SVPTSTVFYPSDGVATEK.A		20.46		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23786	5%	75	2	74244	8.4	P23786|CPT2_HUMAN Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2												8	1
						152	161	540.25	1078.49	1078.54	-0.06	0	33	0.0390136	R.ATNMTVSAIR.F	Oxidation (M)	13.63		
						390	414	863.39	2587.15	2587.26	-0.11	0	43	0.0025772	K.DSTQTPAVTPQSQPATTDSTVTVQK.L		18.29		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q07065	5%	73	2	66097	5.6	Q07065|CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2												8	1
						273	287	549.59	1645.76	1645.82	-0.05	1	34	0.0299955	K.VASLEESEGNKQDLK.A		13.85		
						492	505	737.37	1472.72	1472.77	-0.05	0	40	0.0080646	R.SVGELPSTVESLQK.V		20.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49748	3%	104	2	70745	8.9	P49748|ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1												8	1
						265	276	578.8	1155.58	1155.61	-0.04	0	47	0.0016425	K.TPVTDPATGAVK.E		14.16		
						460	469	589.3	1176.59	1176.61	-0.02	0	58	0.0001329	R.IFEGTNDILR.L		20.68		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10809	31%	1005	18	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												9	1
						97	121	854.06	2559.15	2559.24	-0.09	0	97	9.51E-09	K.LVQDVANNTNEEAGDGTTTATVLAR.S		19.83		
						206	218	760.85	1519.69	1519.74	-0.05	0	64	2.60E-05	K.TLNDELEIIEGMK.F	Oxidation (M)	21.74		
						222	233	695.33	1388.65	1388.7	-0.04	0	44	0.0029752	R.GYISPYFINTSK.G		20.94		
						237	249	801.36	1600.7	1600.74	-0.05	0	33	0.0339172	K.CEFQDAYVLLSEK.K		21.92		
						293	301	456.78	911.54	911.58	-0.04	0	62	3.60E-05	K.VGLQVVAVK.A		19.65		
						302	309	417.18	832.35	832.38	-0.03	0	34	0.033126	K.APGFGDNR.K		13.54		
						345	359	549.62	1645.83	1645.9	-0.07	1	55	0.0002158	K.VGEVIVTKDDAMLLK.G	Oxidation (M)	19.92		
						397	405	451.25	900.49	900.53	-0.04	0	45	0.0028391	K.LSDGVAVLK.V		18.67		
						406	417	617.28	1232.54	1232.59	-0.05	0	74	3.04E-06	K.VGGTSDVEVNEK.K		13.32		
						406	418	454.55	1360.62	1360.68	-0.06	1	47	0.0014652	K.VGGTSDVEVNEKK.D		12.67		
						406	420	544.92	1631.74	1631.81	-0.07	2	87	1.31E-07	K.VGGTSDVEVNEKKDR.V		12.49		
						421	429	480.74	959.47	959.5	-0.03	0	51	0.0007015	R.VTDALNATR.A		13.63		
						447	462	886.4	1770.79	1770.85	-0.05	0	73	3.29E-06	R.CIPALDSLTPANEDQK.I		20.77		
						463	469	393.25	784.48	784.51	-0.03	0	36	0.0191335	K.IGIEIIK.R		20.45		
						463	470	471.29	940.57	940.61	-0.04	1	54	0.0002588	K.IGIEIIKR.T		19.52		
						471	481	401.56	1201.66	1201.71	-0.05	1	52	0.0004623	R.TLKIPAMTIAK.N	Oxidation (M)	16.88		
						474	481	430.73	859.45	859.48	-0.04	0	46	0.0024773	K.IPAMTIAK.N	Oxidation (M)	13.28		
						482	493	608.31	1214.6	1214.65	-0.05	0	50	0.0007896	K.NAGVEGSLIVEK.I		19.47		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14618	25%	570	10	58470	8	P14618|KPYM_HUMAN Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4												9	1
						33	43	599.31	1196.61	1196.64	-0.03	0	51	0.0004761	R.LDIDSPPITAR.N		20.05		
						44	56	680.34	1358.66	1358.7	-0.04	0	63	3.85E-05	R.NTGIICTIGPASR.S		19.87		
						93	115	822.4	2464.19	2464.28	-0.1	0	77	1.03E-06	R.TATESFASDPILYRPVAVALDTK.G		21.83		
						126	135	495.74	989.47	989.5	-0.04	0	55	0.0002757	K.GSGTAEVELK.K		14.07		
						142	151	607.28	1212.54	1212.57	-0.02	0	37	0.0152698	K.ITLDNAYMEK.C	Oxidation (M)	19.07		
						189	206	890.42	1778.82	1778.87	-0.05	0	83	3.02E-07	K.GADFLVTEVENGGSLGSK.K		21.57		
						208	224	818.93	1635.84	1635.88	-0.05	0	64	2.62E-05	K.GVNLPGAAVDLPAVSEK.D		20.99		
						295	305	571.29	1140.56	1140.6	-0.04	0	37	0.0142217	R.GDLGIEIPAEK.V		20.41		
						423	433	611.31	1220.6	1220.63	-0.03	0	62	4.52E-05	K.CCSGAIIVLTK.S		20.18		
						490	498	498.24	994.46	994.49	-0.03	0	43	0.0034558	R.VNFAMNVGK.A	Oxidation (M)	15.39		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q02818	16%	367	8	53846	5.2	Q02818|NUCB1_HUMAN Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4												9	1
						153	163	636.85	1271.69	1271.71	-0.02	0	38	0.0123717	R.DLELLIQTATR.D		22.81		

						190	200	451.22	1350.64	1350.68	-0.04	1	34	0.0242795	R.YLESLGEEQRK.E		15		
						219	229	570.8	1139.58	1139.63	-0.05	0	45	0.0020946	K.VNVPGSQAQLK.E		15.13		
						311	323	753.88	1505.74	1505.81	-0.07	0	43	0.0037344	R.LVTLEEFLASTQR.K		23.11		
						311	324	545.62	1633.83	1633.9	-0.08	1	34	0.0224865	R.LVTLEEFLASTQRK.E		22.28		
						350	357	482.73	963.44	963.47	-0.03	0	46	0.0017344	R.FEEELAAR.E		16.09		
						368	377	552.27	1102.53	1102.56	-0.03	0	78	1.37E-06	R.LSQETEALGR.S		14.25		
						452	461	580.8	1159.58	1159.62	-0.04	0	48	0.0012254	R.LPEVEVPQHL.-		20.72		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	15%	342	7	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												9	1
						196	207	475.58	1423.71	1423.77	-0.06	1	40	0.0070147	K.YQLDKDGVVLFK.K		20.63		
						301	308	483.76	965.51	965.56	-0.05	0	39	0.0081922	R.ILEFFGLK.K		22.5		
						317	326	611.79	1221.56	1221.62	-0.06	0	44	0.0030263	R.LITLEEEMTK.Y	Oxidation (M)	19.43		
						327	338	484.55	1450.62	1450.69	-0.07	0	55	0.0001778	K.YKPESEELTAER.I		14.03		
						376	386	447.86	1340.55	1340.62	-0.07	1	36	0.0160133	K.NFEDVAFDEKK.N		19.74		
						425	436	655.28	1308.55	1308.59	-0.04	0	90	7.54E-08	K.MDSTANEVEAVK.V	Oxidation (M)	14.12		
						453	461	533.74	1065.47	1065.51	-0.04	0	38	0.0113824	R.TVIDYNGER.T		15.26		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23141	8%	202	4	62766	6.2	P23141|EST1_HUMAN Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2												9	1
						93	104	674.84	1347.67	1347.71	-0.05	0	40	0.0069495	K.AGQLLSELFTNR.K		22.23		
						303	313	630.82	1259.62	1259.65	-0.03	0	43	0.0036612	K.FLSLDLQGDPR.E		21.43		
						331	339	536.75	1071.48	1071.52	-0.04	0	57	0.0002	K.TPEELQAER.N		13.72		
						524	538	796.38	1590.75	1590.8	-0.05	0	61	4.84E-05	K.EGYLQIGANTQAAQK.L		19.69		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99832	7%	179	4	59842	7.5	Q99832|TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2												9	1
						1	10	608.81	1215.62	1215.66	-0.05	0	35	0.0247693	-.MMPTPVILLK.E	Acetyl (Protein N-term); 2 Oxidation (M)	21.79		
						127	135	473.26	944.5	944.53	-0.03	0	51	0.0007311	R.TATQLAVNK.I		13.37		
						376	387	700.28	1398.54	1398.57	-0.03	0	54	0.0002577	R.GGAEQFMEETER.S	Oxidation (M)	14.95		
						441	447	406.23	810.46	810.5	-0.04	0	39	0.0077943	K.ALEIIPR.Q		20.14		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50990	7%	283	3	60153	5.4	P50990|TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4												9	1
						63	74	667.35	1332.69	1332.74	-0.05	0	97	1.41E-08	K.LFVTNDAATILR.E		21.34		
						282	296	686.86	1371.7	1371.74	-0.03	0	97	1.49E-08	K.AIADTGANVVVTGGK.V		18.45		
						441	450	575.77	1149.53	1149.58	-0.05	0	59	8.32E-05	K.FAEAFEAIPR.A		20.85		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48643	6%	145	3	60089	5.5	P48643|TCPE_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1												9	1
						133	142	547.25	1092.48	1092.52	-0.04	0	72	4.01E-06	R.IADGYEQAAR.V		13.76		
						203	214	464.56	1390.67	1390.73	-0.06	1	36	0.0199081	R.DVDFELIKVEGK.V		21.08		
						345	352	462.72	923.43	923.46	-0.03	0	39	0.0086883	R.FSELTAEK.L		14.82		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13884	5%	109	3	58367	8.8	Q13884|SNTB1_HUMAN Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3												9	1
						23	31	493.28	984.55	984.6	-0.04	0	36	0.020994	R.SGLLEVLVR.D		21.97		
						254	263	560.25	1118.49	1118.5	-0.02	0	38	0.0144941	R.SMALADPENR.Q	Oxidation (M)	13.59		
						477	485	539.76	1077.51	1077.57	-0.06	0	36	0.0203513	K.TIIQSPYEK.L		18.11		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31146	4%	100	2	51678	6.3	P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4												9	1
						384	393	513.8	1025.59	1025.61	-0.03	0	42	0.004311	R.DAGPLLISLK.D		21.66		
						440	449	579.31	1156.61	1156.65	-0.04	0	59	0.0001061	K.LQATVQELQK.R		16.01		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40227	4%	101	2	58444	6.2	P40227|TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3												9	1
						130	138	538.78	1075.54	1075.59	-0.05	0	55	0.0002439	K.ALQFLEEVK.V		21.21		
						296	307	631.82	1261.62	1261.66	-0.04	0	46	0.0018373	K.GIDPFSLDALSK.E		22.14		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8IV08	4%	86	2	55127	6	Q8IV08|PLD3_HUMAN Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1												9	3
						150	157	449.75	897.48	897.53	-0.04	0	35	0.0193259	R.QLQTLAPK.G		14.29		
						310	319	542.79	1083.57	1083.6	-0.03	0	50	0.000677	K.ALLNVVDNAR.S		20.23		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01518	31%	901	16	52222	8.3	Q01518|CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4												10	11
						2	10	567.25	1132.48	1132.52	-0.04	0	64	2.92E-05	M.ADMQNLVER.L	Acetyl (Protein N-term); Oxidation (M)	17.22		
						64	71	423.2	844.39	844.43	-0.03	0	46	0.0027526	K.EIGGDVQK.H		12.79		
						85	100	879.41	1756.81	1756.88	-0.06	0	101	5.08E-09	R.ALLVTASQCQQPAENK.L		16.83		
						101	113	713.89	1425.77	1425.81	-0.04	0	50	0.0006851	K.LSDLLAPISEQIK.E		21.67		
						114	119	382.7	763.38	763.42	-0.04	0	33	0.0363856	K.EVITFR.E		19.37		
						156	167	747.77	1493.52	1493.59	-0.07	0	80	6.70E-07	K.EMNDAAMFYTNR.V	2 Oxidation (M)	18.53		
						273	287	434.95	1735.76	1735.87	-0.11	2	37	0.0122849	K.HVSDDMKTHKNPALK.A	Oxidation (M)	11.97		
						295	312	460.23	1836.88	1836.97	-0.09	0	56	0.0001417	R.SGPKPFSAPKPQTSPSPK.R		13.23		
						314	327	504.94	1511.8	1511.86	-0.05	2	48	0.0011876	R.ATKKEPAVLELEGK.K		15.21		
						317	327	404.88	1211.61	1211.68	-0.06	1	49	0.0009631	K.KEPAVLELEGK.K		19.41		

						317	328	447.58	1339.72	1339.77	-0.06	2	49	0.0007902	K.KEPAVLELEGKK.W		14.91		
						356	364	538.77	1075.53	1075.57	-0.04	0	61	6.45E-05	K.CVNTTLQIK.G		16.57		
						365	377	492.91	1475.7	1475.78	-0.08	2	44	0.0032022	K.GKINSITVDNCKK.L		12.84		
						367	376	582.27	1162.52	1162.57	-0.04	0	71	6.04E-06	K.INSITVDNCK.K		14.2		
						367	377	431.21	1290.61	1290.66	-0.05	1	39	0.0081087	K.INSITVDNCKK.L		13.15		
						423	433	618.28	1234.54	1234.59	-0.05	0	76	1.74E-06	K.NSLDCEIVSAK.S		19.32		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30101	21%	450	10	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												10	2
						63	73	596.28	1190.55	1190.59	-0.05	0	58	0.000115	R.LAPEYEAAATR.L		15.04		
						95	104	542.77	1083.53	1083.56	-0.03	0	46	0.0017403	K.YGVSGYPTLK.I		19.85		
						105	119	551.57	1651.69	1651.76	-0.07	1	35	0.0213824	K.IFRDGEEAGAYDGPR.T		16.39		
						108	119	618.74	1235.46	1235.51	-0.04	0	45	0.0023201	R.DGEEAGAYDGPR.T		14.29		
						131	140	498.26	994.51	994.56	-0.05	0	41	0.0047266	K.QAGPASVPLR.T		14.73		
						336	344	594.75	1187.49	1187.53	-0.03	0	33	0.0434312	K.FVMQEEFSR.D	Oxidation (M)	16.7		
						367	379	684.81	1367.61	1367.66	-0.05	0	67	1.38E-05	K.SEPIPESNDGPVK.V		14.64		
						423	433	399.89	1196.66	1196.71	-0.05	1	33	0.0336046	K.LSKDPNIVIAK.M		14.56		
						449	460	671.32	1340.62	1340.68	-0.05	0	53	0.0003369	R.GFPTIYFSPANK.K		21.54		
						483	496	527.26	1578.76	1578.83	-0.07	0	38	0.0096136	R.EATNPPVIQEEKPK.K		13.67		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43175	13%	419	6	57356	6.3	O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4												10	1
						22	33	649.85	1297.68	1297.72	-0.05	0	91	5.95E-08	K.ILQDGGLQVVEK.Q		19.99		
						59	69	565.78	1129.55	1129.6	-0.05	0	83	3.66E-07	K.VTADVINAAEK.L		16.13		
						76	90	744.84	1487.67	1487.72	-0.05	0	59	8.39E-05	R.AGTGVDNVDLEAATR.K		19.72		
						147	155	450.27	898.52	898.56	-0.04	0	46	0.0018848	K.TLGILGLGR.I		21.45		
						237	247	550.29	1098.57	1098.6	-0.03	0	60	8.21E-05	R.GGIVDEGALLR.A		20.61		
						385	394	536.27	1070.53	1070.57	-0.05	0	81	7.13E-07	K.QADVNLVNAK.L		14.77		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	12%	362	6	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												10	1
						46	58	720.3	1438.59	1438.66	-0.07	0	98	1.02E-08	K.TGTAEMSSILEER.I	Oxidation (M)	17.92		
						74	83	500.77	999.53	999.57	-0.04	0	55	0.0002861	R.VLSIGDGIAR.V		20.08		
						150	161	586.3	1170.59	1170.62	-0.04	0	77	1.49E-06	R.VVDALGNAIDGK.G		19.94		
						172	182	374.22	1119.64	1119.71	-0.08	1	40	0.008227	R.VGLKAPGIIPR.I		19.68		
						195	204	513.78	1025.54	1025.59	-0.04	0	50	0.0007024	K.AVDSLVPIGR.G		20.34		
						254	261	423.23	844.45	844.5	-0.05	0	45	0.0036037	R.STVAQLVK.R		15.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08670	11%	240	5	53676	5.1	P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4												10	3
						101	113	529.92	1586.73	1586.79	-0.06	1	43	0.0036651	R.TNEKVELQELNDR.F		17.62		
						208	217	544.75	1087.48	1087.53	-0.04	0	74	3.54E-06	R.QDVDNASLAR.L		13.63		
						274	282	512.24	1022.46	1022.5	-0.04	0	33	0.0345441	R.QQYESVAAK.N		13.06		
						295	304	547.25	1092.48	1092.52	-0.04	0	56	0.0001833	K.FADLSEAANR.N		18.01		
						382	390	561.28	1120.54	1120.58	-0.04	0	34	0.0307029	R.EYQDLLNVK.M		20.52		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07437	9%	162	4	50095	4.8	P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2												10	1
						242	251	565.79	1129.56	1129.59	-0.03	0	43	0.0041496	R.FPGQLNADLR.K		20.21		
						253	262	580.3	1158.58	1158.62	-0.04	0	34	0.0290519	K.LAVNMVPFPR.L	Oxidation (M)	20.56		
						310	318	520.29	1038.56	1038.59	-0.02	0	35	0.0200779	R.YLTVAAVFR.G		21.58		
						325	336	731.82	1461.62	1461.68	-0.06	0	50	0.0007499	K.EVDEQMLNVQNK.N	Oxidation (M)	14.69		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08962	8%	92	2	26474	8.1	P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2												10	13
						111	120	637.27	1272.53	1272.56	-0.03	0	59	8.84E-05	K.VMSEFNNNFR.Q	Oxidation (M)	18.45		
						121	128	527.21	1052.4	1052.46	-0.06	0	33	0.0335411	R.QQMENYPK.N	Oxidation (M)	12.62		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08571	5%	76	2	40678	5.8	P08571|CD14_HUMAN Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2												10	3
						118	127	401.22	1200.64	1200.7	-0.05	1	33	0.0365444	R.LKELTLEDLK.I		20.43		
						263	271	456.73	911.45	911.48	-0.03	0	43	0.003322	R.ATVNPSAPR.C		12.71		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05091	4%	82	2	56859	6.6	P05091|ALDH2_HUMAN Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2												10	1
						429	436	451.73	901.45	901.49	-0.04	0	41	0.0080343	K.TIEEVVGR.A		15.91		
						437	451	764.37	1526.72	1526.77	-0.06	0	41	0.0054231	R.ANNSTYGLAAAVFTK.D		21.36		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P78371	4%	106	2	57794	6	P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4												10	1
						112	119	430.72	859.43	859.47	-0.03	0	38	0.0150306	R.EAESLIAK.K		14.34		
						157	170	747.85	1493.68	1493.74	-0.06	0	67	1.23E-05	R.QDLMNIAGTTLSSK.L	Oxidation (M)	20.16		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21281	4%	99	2	56807	5.6	P21281|VATB2_HUMAN Vacuolar ATP synthase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3												10	1
						83	93	545.77	1089.53	1089.57	-0.04	0	59	0.0001034	R.SGQVLEVSGSK.A		14.07		
						121	130	560.75	1119.49	1119.52	-0.03	0	40	0.0071161	R.TPVSEDMLGR.V	Oxidation (M)	14.16		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27797	4%	71	2	48283	4.3	P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1												10	2
						49	55	369.2	736.38	736.41	-0.03	0	33	0.037057	K.FVLSSGK.F		15.17		
						279	286	496.72	991.43	991.46	-0.03	0	38	0.0117653	R.QIDNPDYK.G		13.32		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P80723	32%	232	4	22680	4.6	P80723|BASP_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2												11	2
						98	121	766.68	2297.03	2297.13	-0.1	1	54	0.0001977	K.AEPPKAPEQEQAAPGPAAGGEAPK.A		13.68		
						150	163	471.56	1411.64	1411.73	-0.09	1	50	0.0006949	K.KTEAPAAPAAQETK.S		12.54		
						164	184	644.95	1931.83	1931.87	-0.05	0	64	2.54E-05	K.SDGAPASDSKPGSSEAAPSSK.E		12.46		
						185	198	693.82	1385.62	1385.67	-0.04	0	64	2.93E-05	K.ETPAATEAPSSTPK.A		13.11		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06576	25%	622	9	56525	5.3	P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3												11	3
						110	121	639.8	1277.59	1277.63	-0.04	0	77	1.59E-06	R.TIAMDGTEGLVR.G	Oxidation (M)	18.58		
						125	143	640.35	1918.02	1918.09	-0.07	1	46	0.0015175	K.VLDSGAPIKIPVGPETLGR.I		20.93		
						144	159	599.63	1795.88	1795.95	-0.07	1	57	0.0001075	R.IMNVIGEPIDERGPIK.T	Oxidation (M)	19.86		
						189	198	544.8	1087.59	1087.63	-0.04	0	50	0.0007686	K.VVDLLAPYAK.G		21.2		
						213	225	737.39	1472.77	1472.83	-0.06	0	61	5.63E-05	K.TVLIMELINNVAK.A	Oxidation (M)	22.75		
						265	279	809.38	1616.74	1616.8	-0.06	0	85	1.92E-07	K.VALVYGQMNEPPGAR.A	Oxidation (M)	19.28		
						311	324	718.36	1434.7	1434.75	-0.05	0	112	4.72E-10	R.FTQAGSEVSALLGR.I		21.24		
						388	406	994.48	1986.94	1987.03	-0.08	0	70	6.10E-06	R.AIAELGIYPAVDPLDSTSR.I		22.26		
						407	422	611.27	1830.78	1830.86	-0.08	0	64	2.26E-05	R.IMDPNIVGSEHYDVAR.G	Oxidation (M)	19.5		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06733	18%	430	7	47481	7	P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2												11	1
						72	80	450.26	898.51	898.55	-0.04	0	50	0.0007625	K.TIAPALVSK.K		16.61		
						90	103	556.92	1667.73	1667.77	-0.04	1	49	0.0008754	K.IDKLMIEMDGTENK.S	2 Oxidation (M)	15.61		
						222	228	401.22	800.43	800.46	-0.03	0	50	0.0010617	K.EGLELLK.T		20.48		
						240	253	778.87	1555.73	1555.77	-0.04	0	84	2.50E-07	K.VVIGMDVAASEFFR.S	Oxidation (M)	21.69		
						254	262	358.17	1071.48	1071.52	-0.05	1	39	0.0122776	R.SGKYDLDFK.S		18.88		
						270	281	713.35	1424.69	1424.72	-0.03	0	55	0.0001983	R.YISPDQLADLYK.S		21.55		
						344	358	817.39	1632.76	1632.81	-0.06	0	103	3.41E-09	K.VNQIGSVTESLQACK.L		20.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15084	16%	394	6	48490	5	Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1												11	3
						119	132	693.85	1385.7	1385.75	-0.06	0	82	4.69E-07	R.TGEAIVDAALSALR.Q		23.1		
						217	231	764.4	1526.79	1526.84	-0.06	0	86	1.69E-07	K.LAAVDATVNQVLASR.Y		21.29		
						242	256	556.59	1666.74	1666.8	-0.06	1	47	0.0011854	K.IFQKGESPVDYDGGR.T		17.97		
						246	256	576.26	1150.5	1150.49	0.02	0	47	0.0013741	K.GESPVDYDGGR.T		14.6		
						314	322	539.79	1077.57	1077.61	-0.03	0	50	0.0007024	R.NSYLEVLLK.L		21.91		
						393	409	808.4	1614.78	1614.84	-0.06	0	85	2.33E-07	R.GSTAPVGGGAFPTIVER.E		20.62		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52209	13%	312	6	53619	6.8	P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3												11	1
						52	59	401.23	800.45	800.48	-0.03	0	37	0.0215278	K.VVGAQSLK.E		13.37		
						52	64	464.57	1390.67	1390.75	-0.07	1	38	0.010472	K.VVGAQSLKEMVSK.L	Oxidation (M)	14.47		
						77	87	596.78	1191.54	1191.58	-0.04	0	73	3.70E-06	K.AGQAVDDFIEK.L		19.9		
						120	136	796.38	1590.74	1590.8	-0.06	0	82	4.15E-07	K.GILFVGSGVSGGEEGAR.Y		20.88		
						155	163	474.76	947.51	947.54	-0.04	0	33	0.0367745	K.TIFQGIAAK.V		20.08		
						332	343	714.37	1426.72	1426.76	-0.04	0	50	0.0007823	K.IISYAQGFMLLR.Q	Oxidation (M)	22.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99541	12%	222	4	48274	6.3	Q99541|ADFP_HUMAN Adipophilin OS=Homo sapiens GN=ADFP PE=1 SV=2												11	1
						94	109	853.97	1705.92	1705.97	-0.05	0	65	1.90E-05	R.LPILNQPSTQIVANAK.G		20.53		
						117	127	532.27	1062.53	1062.56	-0.03	0	38	0.0132088	K.DAVTTTVTGAK.D		14.42		
						168	182	820.38	1638.74	1638.8	-0.06	0	60	6.42E-05	R.MMQLVSSGVENALTK.S	2 Oxidation (M)	20.17		
						365	375	583.28	1164.54	1164.59	-0.04	0	59	9.89E-05	K.EVSDSLLTSSK.G		18.97		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9NVA2	12%	211	4	49652	6.4	Q9NVA2|SEP11_HUMAN Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3												11	1
						2	14	720.36	1438.71	1438.75	-0.04	0	60	6.27E-05	M.AVAVGRPSNEELR.N	Acetyl (Protein N-term)	18.71		
						84	93	612.78	1223.55	1223.58	-0.03	0	37	0.0118056	R.SYELQESNVR.L		15.78		
						176	184	490.81	979.61	979.64	-0.03	0	37	0.0123641	K.VNIIPIIAK.A		21.37		
						400	418	652.98	1955.92	1956	-0.08	0	76	1.30E-06	K.AAAQLLQSQAQQSGAQQTK.K		16.17		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	11%	246	5	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												11	14
						38	51	542.91	1625.71	1625.8	-0.08	2	38	0.0092084	R.TIEKFEKEAAEMGK.G	Oxidation (M)	14.64		
						173	179	420.21	838.4	838.44	-0.04	0	38	0.0105739	K.EVSTYIK.K		14.73		
						248	255	488.26	974.5	974.54	-0.04	0	45	0.0025902	R.LPLQDVYK.I		19.99		
						256	266	513.29	1024.57	1024.6	-0.04	0	49	0.0008535	K.IGGIGTVPVGR.V		19.46		
						431	439	457.77	913.52	913.56	-0.04	0	76	2.03E-06	R.QTVAVGVIK.A		16.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50395	9%	167	4	51087	6.1	P50395|GDIB_HUMAN Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2												11	1

						56	68	473.55	1417.62	1417.7	-0.08	1	44	0.0025931	R.FKIPGSPPESMGR.G	Oxidation (M)	19.01		
						80	89	568.79	1135.57	1135.61	-0.04	0	37	0.0158967	K.FLMANGQLVK.M	Oxidation (M)	19.55		
						211	218	469.73	937.44	937.49	-0.04	0	35	0.0178789	K.LYSESLAR.Y		15.39		
						380	390	609.35	1216.68	1216.71	-0.03	0	50	0.0006854	K.FVSISDLLVPK.D		22.79		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16181	9%	167	4	50933	8.8	Q16181|SEPT7_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2												11	1
						187	195	490.81	979.61	979.64	-0.03	0	37	0.0123641	K.VNIIPLIAK.A		21.37		
						353	364	813.29	1624.57	1624.61	-0.04	0	33	0.0324465	K.MEMEMEQVFEMK.V	4 Oxidation (M)	16.04		
						372	381	396.86	1187.57	1187.61	-0.05	1	47	0.0015842	K.LKDSEAELQR.R		13.15		
						417	425	537.76	1073.51	1073.55	-0.03	0	50	0.0009053	R.ILEQQNSSR.T		12.76		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35613	6%	70	2	42573	5.4	P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2												11	3
						174	187	470.92	1409.75	1409.79	-0.04	1	36	0.0184181	K.GGVVLKEDALPGQK.T		18.27		
						274	282	507.72	1013.43	1013.49	-0.07	0	34	0.0294052	R.FFVSSSQGR.S		16.35		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q7LGA3	6%	106	2	42140	8.8	Q7LGA3|HS2ST_HUMAN Heparan sulfate 2-O-sulfotransferase 1 OS=Homo sapiens GN=HS2ST1 PE=2 SV=1												11	1
						112	123	708.82	1415.63	1415.68	-0.05	0	66	1.82E-05	K.NNPVMSLQDQVR.F	Oxidation (M)	19.77		
						170	178	612.3	1222.59	1222.64	-0.05	0	42	0.0046672	R.LVSYYYFLR.F		22.13		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BQE3	4%	79	2	50548	5	Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1												11	1
						113	121	543.29	1084.57	1084.61	-0.04	0	46	0.0021143	K.EIIDLVLDR.I		22.22		
						327	336	508.28	1014.54	1014.57	-0.03	0	33	0.043828	K.DVNAAIATIK.T		20.13		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y6N5	13%	320	6	50214	9.2	Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1												12	1
						65	79	533.27	1596.79	1596.85	-0.06	1	38	0.0108364	R.KVGAENVAIVEPSER.H		16.21		
						66	79	735.36	1468.7	1468.75	-0.06	0	65	2.18E-05	K.VGAENVAIVEPSER.H		19.47		
						166	173	434.21	866.41	866.45	-0.04	0	43	0.0029661	K.IGSNYSVK.T		13.38		
						208	217	654.8	1307.59	1307.62	-0.03	0	43	0.0035049	K.IMYLSEAYFR.K	Oxidation (M)	21.24		
						242	253	724.84	1447.67	1447.73	-0.06	0	82	3.97E-07	K.YADALQEIIQER.N		21.73		
						397	409	754.84	1507.67	1507.72	-0.05	0	49	0.0008806	K.AEPLETFPFDQSK.E		21.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BS26	12%	225	5	47341	5.1	Q9BS26|TXND4_HUMAN Thioredoxin domain-containing protein 4 OS=Homo sapiens GN=TXNDC4 PE=1 SV=1												12	1
						141	148	479.24	956.46	956.49	-0.03	0	36	0.0188441	K.SDPIQEIR.D		17.34		
						149	158	573.78	1145.54	1145.59	-0.06	0	55	0.0002486	R.DLAEITTLDR.S		20.93		
						162	170	556.27	1110.53	1110.57	-0.04	0	41	0.0052825	R.NIIGYFEQK.D		21.15		
						314	327	781.35	1560.69	1560.76	-0.08	0	57	0.0001185	K.TPADCPVIAIDSFR.H		21.51		
						390	396	418.2	834.39	834.42	-0.03	0	35	0.0227181	K.LAPSEYR.Y		13.46		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P01891	11%	153	4	41168	6.2	P01891|1A68_HUMAN HLA class I histocompatibility antigen, A-68 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=4												12	2
						46	59	815.39	1628.77	1628.82	-0.05	0	49	0.0007604	R.FIAVGYVDDTQFVR.F		21.55		
						60	68	498.7	995.39	995.43	-0.04	0	33	0.0291622	R.FDSDAASQR.M		12.94		
						100	106	387.21	772.4	772.44	-0.04	0	38	0.0149764	R.VDLGTLR.G		19.43		
						195	205	450.88	1349.63	1349.69	-0.07	1	32	0.0455664	R.YLENGKETLQR.T		13.64		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P55084	11%	201	5	51547	9.4	P55084|ECHB_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3												12	1
						53	61	478.76	955.5	955.55	-0.05	0	38	0.0111332	R.NVVVVDGVR.T		16.65		
						62	72	607.3	1212.59	1212.64	-0.05	0	35	0.0216189	R.TPFLLSGTSYK.D		20.89		
						118	128	533.25	1064.49	1064.51	-0.03	0	41	0.0052894	R.EAALGAGFSDK.T		18.08		
						239	247	568.75	1135.49	1135.55	-0.06	0	47	0.001523	R.LEQDEYALR.S		17.95		
						339	348	623.28	1244.54	1244.54	0	0	40	0.0085431	R.DFMYVSQDPK.D	Oxidation (M)	19.08		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49411	10%	219	4	49852	7.3	P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2												12	1
						71	79	460.25	918.48	918.54	-0.05	0	36	0.0216508	K.TTLTAAITK.I		16.43		
						80	88	408.21	814.41	814.45	-0.05	0	41	0.00672	K.ILAEGGGAK.F		12.85		
						239	252	771.9	1541.79	1541.85	-0.05	0	64	2.94E-05	K.LLDAVDTYIPVPAR.D		21.64		
						316	327	593.3	1184.58	1184.61	-0.03	0	80	8.24E-07	R.AEAGDNLGALVR.G		20.13		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O60664	8%	196	3	47189	5.3	O60664|M6PBP_HUMAN Mannose-6-phosphate receptor-binding protein 1 OS=Homo sapiens GN=M6PRBP1 PE=1 SV=2												12	1
						129	140	605.27	1208.52	1208.57	-0.05	0	83	3.29E-07	K.VSGAQEMVSSAK.D	Oxidation (M)	12.55		
						167	180	690.33	1378.64	1378.69	-0.05	0	74	2.63E-06	K.SVVTGGVQSVMGSR.L	Oxidation (M)	15.17		
						231	238	528.74	1055.46	1055.5	-0.05	0	39	0.0106615	R.QEQSYFVR.L		17.43		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99536	7%	94	2	42122	5.9	Q99536|VAT1_HUMAN Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2												12	1
						256	271	795.87	1589.72	1589.76	-0.04	0	57	0.0001149	K.GVDIVMDPLGGSDTAK.G	Oxidation (M)	20.44		
						383	393	597.82	1193.63	1193.67	-0.04	1	36	0.0169435	K.VLLVPGPEKEN.-		19.87		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50552	7%	82	2	39976	9.1	P50552|VASP_HUMAN Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3												12	1
						258	273	836.33	1670.64	1670.71	-0.07	0	44	0.00238	R.SGGGGLMEEMNAMLAR.R	3 Oxidation (M)	15.38		
						299	307	486.74	971.47	971.5	-0.03	0	39	0.0100902	R.VPAQSESVR.R		12.63		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P22234	5%	84	2	47790	7	P22234|PUR6_HUMAN Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3												12	1
						2	11	529.27	1056.53	1056.58	-0.05	0	43	0.0042622	M.ATAEVLNIGK.K	Acetyl (Protein N-term)	21.29		
						236	246	623.79	1245.56	1245.63	-0.07	0	41	0.00567	K.EVTPEGLQMVK.K	Oxidation (M)	17.91		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P39656	4%	82	2	48893	5.4	P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2												12	1
						61	71	580.29	1158.56	1158.61	-0.05	0	40	0.0079832	K.TADDPSLSLIK.Y		20.31		
						343	348	373.69	745.37	745.41	-0.04	0	42	0.0062471	R.IDPFVR.T		19.73		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60709	51%	1267	16 (19)	42052	5.3	P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1												13	12
						2	18	919.37	1836.73	1836.79	-0.06	0	96	1.74E-08	M.DDDIAALVVDNGSGMCK.A	Acetyl (Protein N-term); Oxidation (M)	22.23		
						19	28	488.71	975.4	975.44	-0.04	0	72	4.92E-06	K.AGFAGDDAPR.A		13.86		
						40	50	401.84	1202.49	1202.55	-0.06	0	54	0.0002883	R.HQGVMVGMGQK.D	2 Oxidation (M)	12.19		
						51	61	599.74	1197.46	1197.51	-0.05	0	58	0.0001044	K.DSYVGDEAQSK.R		13.41		
						51	62	452.19	1353.54	1353.62	-0.07	1	54	0.0003015	K.DSYVGDEAQSKR.G		12.98		
						85	95	505.9	1514.67	1514.74	-0.07	0	72	4.73E-06	K.IWHHTFYNELR.V		19.45		
						96	113	652	1952.98	1953.06	-0.08	0	60	5.52E-05	R.VAPEEHPVLLTEAPLNPK.A		20.12		
						148	177	800.63	3198.47	3198.6	-0.13	0	75	1.31E-06	R.TTGIVMDSGDGVTHTVPIYEGYALPH	Oxidation (M)	21.24		
						184	191	499.73	997.44	997.48	-0.04	0	32	0.044512	R.DLTDYLMK.I		21.83		
						197	206	566.75	1131.48	1131.52	-0.04	0	51	0.0006101	R.GYSFTTTAER.E		17.11		
						239	254	895.93	1789.84	1789.88	-0.04	0	105	1.88E-09	K.SYELPDGQVITIGNER.F		24.32		
						291	312	787.03	2358.07	2358.15	-0.08	1	136	1.32E-12	R.KDLYANTVLSGGTTMYPGIADR.M	Oxidation (M)	20.39		
						292	312	1116.17	2230.32	2230.06	0.26	0	149	7.39E-14	K.DLYANTVLSGGTTMYPGIADR.M	Oxidation (M)	21.42		
						313	326	527.58	1579.72	1579.79	-0.08	1	46	0.0014444	R.MQKEITALAPSTMK.I	2 Oxidation (M)	14.3		
						316	326	581.3	1160.58	1160.61	-0.04	0	44	0.0034499	K.EITALAPSTMK.I		19.62		
						316	326	589.4	1176.79	1176.61	0.18	0	54	0.0003293	K.EITALAPSTMK.I	Oxidation (M)	16.76		
						360	372	750.31	1498.61	1498.67	-0.05	0	99	8.32E-09	K.QEYDESGPSIVHR.K	Gln->pyro-Glu (N-term Q)	19.36		
						360	372	506.22	1515.64	1515.7	-0.05	0	67	1.31E-05	K.QEYDESGPSIVHR.K		14.65		
						360	372	758.96	1515.9	1515.7	0.21	0	117	1.40E-10	K.QEYDESGPSIVHR.K		14.96		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63261	51%	1267	16 (22)	42108	5.3	P63261|ACTG_HUMAN Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1												13	1
						2	18	947.4	1892.79	1892.85	-0.06	0	96	1.72E-08	M.EEEIAALVIDNGSGMCK.A	Acetyl (Protein N-term); Oxidation (M)	23.3		
						19	28	488.71	975.4	975.44	-0.04	0	72	4.92E-06	K.AGFAGDDAPR.A		13.86		
						40	50	396.51	1186.5	1186.56	-0.06	0	46	0.0019352	R.HQGVMVGMGQK.D	Oxidation (M)	12.54		
						40	50	401.84	1202.49	1202.55	-0.06	0	54	0.0002883	R.HQGVMVGMGQK.D	2 Oxidation (M)	12.19		
						40	50	602.4	1202.79	1202.55	0.23	0	51	0.0006058	R.HQGVMVGMGQK.D	2 Oxidation (M)	12.28		
						51	61	599.74	1197.46	1197.51	-0.05	0	58	0.0001044	K.DSYVGDEAQSK.R		13.41		
						51	62	452.19	1353.54	1353.62	-0.07	1	54	0.0003015	K.DSYVGDEAQSKR.G		12.98		
						85	95	505.9	1514.67	1514.74	-0.07	0	72	4.73E-06	K.IWHHTFYNELR.V		19.45		
						96	113	652.01	1953	1953.06	-0.06	0	66	1.47E-05	R.VAPEEHPVLLTEAPLNPK.A		26.55		
						148	177	800.63	3198.47	3198.6	-0.13	0	75	1.31E-06	R.TTGIVMDSGDGVTHTVPIYEGYALPH	Oxidation (M)	21.24		
						184	191	499.73	997.44	997.48	-0.04	0	32	0.044512	R.DLTDYLMK.I		21.83		
						197	206	566.75	1131.48	1131.52	-0.04	0	51	0.0006101	R.GYSFTTTAER.E		17.11		
						239	254	896.05	1790.1	1789.88	0.21	0	106	1.68E-09	K.SYELPDGQVITIGNER.F		21.47		
						291	312	787.03	2358.07	2358.15	-0.08	1	136	1.32E-12	R.KDLYANTVLSGGTTMYPGIADR.M	Oxidation (M)	20.39		
						292	312	744.33	2229.98	2230.06	-0.08	0	94	2.05E-08	K.DLYANTVLSGGTTMYPGIADR.M	Oxidation (M)	21.33		
						292	312	1116.17	2230.32	2230.06	0.26	0	149	7.39E-14	K.DLYANTVLSGGTTMYPGIADR.M	Oxidation (M)	21.42		
						313	326	527.58	1579.72	1579.79	-0.08	1	46	0.0014444	R.MQKEITALAPSTMK.I	2 Oxidation (M)	14.3		
						316	326	581.3	1160.58	1160.61	-0.04	0	44	0.0034499	K.EITALAPSTMK.I		19.62		
						316	326	589.4	1176.79	1176.61	0.18	0	54	0.0003293	K.EITALAPSTMK.I	Oxidation (M)	16.76		
						360	372	750.31	1498.61	1498.67	-0.05	0	99	8.32E-09	K.QEYDESGPSIVHR.K	Gln->pyro-Glu (N-term Q)	19.36		
						360	372	506.22	1515.64	1515.7	-0.05	0	67	1.31E-05	K.QEYDESGPSIVHR.K		14.65		
						360	372	758.96	1515.9	1515.7	0.21	0	117	1.40E-10	K.QEYDESGPSIVHR.K		14.96		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30453	25%	425	7	41314	5.9	P30453|1A34_HUMAN HLA class I histocompatibility antigen, A-34 alpha chain OS=Homo sapiens GN=HLA-A PE=2 SV=1												13	1
						46	59	815.56	1629.1	1628.82	0.28	0	94	2.68E-08	R.FIAVGYVDDTQFVR.F		21.69		
						60	68	498.71	995.4	995.43	-0.03	0	43	0.0029229	R.FDSDAASQR.M		13.02		
						100	106	387.21	772.41	772.44	-0.03	0	48	0.0017156	R.VDLGTLR.G		19.31		
						122	132	621.73	1241.45	1241.48	-0.03	0	48	0.0013373	R.MYGCDVGPDGR.F	Oxidation (M)	14.03		
						195	205	450.88	1349.62	1349.69	-0.07	1	49	0.0009764	R.YLENGKETLQR.T		13.55		
						211	226	465.45	1857.78	1857.85	-0.08	0	58	9.79E-05	K.THMTHHAVSDHEATLR.C	Oxidation (M)	12.15		
						244	267	879.7	2636.07	2636.18	-0.12	0	85	1.62E-07	R.DGEDQTQDTELVETRPAGDGTFQK.W		19.58		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00558	24%	405	8	44985	8.3	P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3												13	1
						23	39	683.31	2046.92	2046.99	-0.07	1	41	0.0045166	R.VDFNVPMKNNQITNNQR.I	Oxidation (M)	18.08		
						172	184	461.89	1382.63	1382.7	-0.06	0	45	0.002497	R.AHSSMVGVNLPQK.A	Oxidation (M)	13.95		
						193	199	442.71	883.41	883.44	-0.04	0	32	0.0437924	K.ELNYFAK.A		19.67		

						200	216	590.31	1767.91	1767.99	-0.08	0	63	2.89E-05	K.ALESPERPFLAILGGAK.V		21.87		
						247	264	991.94	1981.87	1981.93	-0.06	0	78	9.67E-07	K.VLNNMEIGTSLFDEEGAK.I	Oxidation (M)	21.11		
						280	291	659.84	1317.66	1317.72	-0.06	0	42	0.004269	K.ITLPVDFVTADK.F		21.91		
						280	297	674.99	2021.95	2022.03	-0.08	1	69	6.98E-06	K.ITLPVDFVTADKFDENAK.T		21.74		
						354	361	460.73	919.44	919.47	-0.03	0	36	0.0182611	K.ALMDEVVK.A	Oxidation (M)	14.25		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15019	18%	265	4	41689	6.2	Q15019|SEPT2_HUMAN Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1												13	1
						78	91	802.39	1602.76	1602.81	-0.05	0	89	8.86E-08	R.TVQIEASTVEIEER.G		20.07		
						117	128	757.35	1512.69	1512.75	-0.05	0	54	0.0002968	K.TIISYIDEQFER.Y		22.59		
						233	249	880.45	1758.89	1758.95	-0.06	0	56	0.0001515	K.ASIPFSVVGSNQLIEAK.G		21.6		
						339	361	816.62	2446.85	2446.97	-0.12	0	67	1.50E-05	R.MQAQMQMQMQGGDGDGGALGHHV	4 Oxidation (M)	13.46		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q29960	16%	284	4	41240	6.1	Q29960|1C16_HUMAN HLA class I histocompatibility antigen, Cw-16 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=1												13	2
						46	59	815.56	1629.1	1628.82	0.28	0	94	2.68E-08	R.FIAVGYVDDTQFVR.F		21.69		
						60	68	483.2	964.38	964.43	-0.04	0	56	0.0002019	R.FDSDAASPR.G		13.15		
						195	205	450.88	1349.62	1349.69	-0.07	1	49	0.0009764	R.YLENGKETLQR.A		13.55		
						244	267	879.7	2636.07	2636.18	-0.12	0	85	1.62E-07	R.DGEDQTQDTELVETRPAGDGTFQK.W		19.58		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O94905	12%	212	3	38044	5.5	O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1												13	1
						61	72	674.83	1347.64	1347.69	-0.05	0	56	0.0001754	K.SVQTTLQTDEVK.N		16.28		
						221	232	653.82	1305.63	1305.69	-0.06	0	80	6.63E-07	K.VAQVAEITYGQK.V		18.65		
						300	314	815.84	1629.66	1629.7	-0.04	0	76	1.89E-06	K.DIPNMFMDSAGSVSK.Q	2 Oxidation (M)	19.85		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04075	36%	884	15	39851	8.3	P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2												14	2
						2	13	717.85	1433.69	1433.72	-0.03	0	70	6.78E-06	M.PYQYPALTPEQK.K		19.82		
						2	14	521.58	1561.73	1561.81	-0.08	1	33	0.0326714	M.PYQYPALTPEQKK.E		17.9		
						15	22	470.73	939.44	939.48	-0.04	0	41	0.0053562	K.ELSDIAHR.I		13.67		
						29	42	666.83	1331.65	1331.69	-0.04	0	74	3.00E-06	K.GILAADESTGSIAK.R		19.34		
						29	43	496.91	1487.72	1487.79	-0.08	1	59	8.81E-05	K.GILAADESTGSIAKR.L		16.47		
						43	57	601.63	1801.86	1801.9	-0.04	2	36	0.0135851	K.RLQSIGTENTEENRR.F		12.8		
						44	56	745.83	1489.65	1489.7	-0.05	0	96	1.86E-08	R.LQSIGTENTEENR.R		13.94		
						61	69	522.77	1043.52	1043.56	-0.04	0	49	0.000953	R.QLLLTADDR.V		19.74		
						88	99	448.22	1341.63	1341.7	-0.07	0	38	0.0108601	K.ADDGRPFPQVIK.S		19.52		
						109	134	872.08	2613.21	2613.32	-0.12	1	100	4.20E-09	K.VDKGVVPLAGTNGETTTQGLDGLSER.C		20.31		
						112	134	758.02	2271.04	2271.13	-0.09	0	92	3.79E-08	K.GVVPLAGTNGETTTQGLDGLSER.C		20.63		
						209	215	382.22	762.42	762.46	-0.04	0	36	0.021965	K.VLAAVYK.A		14.9		
						305	312	401.23	800.44	800.48	-0.04	0	45	0.0035481	R.ALQASALK.A		13.81		
						323	330	469.22	936.42	936.46	-0.04	0	37	0.0140663	K.AAQEEYVK.R		13.11		
						332	342	566.77	1131.52	1131.57	-0.05	0	78	1.28E-06	R.ALANSLACQGK.Y		14.37		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40121	25%	516	8 (9)	38779	5.9	P40121|CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=1												14	1
						97	112	967.88	1933.75	1933.85	-0.1	0	94	2.49E-08	R.EVQGNESDLFMSYFPR.G	Oxidation (M)	22		
						116	127	451.2	1350.57	1350.62	-0.05	0	47	0.0011559	K.YQEGGVESAFHK.T		15.33		
						182	187	366.19	730.37	730.4	-0.03	0	42	0.0071438	K.SNILER.N		14.42		
						192	198	386.22	770.42	770.47	-0.04	0	45	0.0020818	R.DLALAIR.D		20.49		
						232	243	659.27	1316.52	1316.57	-0.05	0	67	1.47E-05	K.EGNPEEDLTADK.A		15.55		
						244	253	510.75	1019.49	1019.54	-0.05	0	69	1.14E-05	K.ANAQAAALYK.V		14.07		
						254	265	640.79	1279.56	1279.61	-0.05	0	93	3.15E-08	K.VSDATGQMNLTK.V	Oxidation (M)	12.93		
						307	319	686.87	1371.73	1371.71	0.01	0	58	0.0001025	R.QAALQVAEGFISR.M	Gln->pyro-Glu (N-term Q)	23.66		
						307	319	695.36	1388.7	1388.74	-0.04	0	53	0.0004004	R.QAALQVAEGFISR.M		21.47		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04899	25%	322	7	40995	5.3	P04899|GNAI2_HUMAN Guanine nucleotide-binding protein G(i), alpha-2 subunit OS=Homo sapiens GN=GNAI2 PE=1 SV=3												14	1
						36	46	529.3	1056.58	1056.62	-0.04	0	33	0.0425238	K.LLLLGAGESGK.S		25.23		
						71	86	876.93	1751.85	1751.95	-0.1	0	64	2.59E-05	R.AVVYSNTIQSIMAIVK.A	Oxidation (M)	21.87		
						87	100	775.85	1549.68	1549.72	-0.04	0	42	0.0042653	K.AMGNLQIDFADPSR.A	Oxidation (M)	20.76		
						163	177	873.92	1745.83	1745.89	-0.06	0	60	6.88E-05	R.IAQSDYIPTQQDVLR.T		20.4		
						250	258	555.75	1109.48	1109.52	-0.04	0	45	0.0019688	K.LFDSICNNK.W		19.56		
						297	307	637.77	1273.53	1273.58	-0.05	0	46	0.0018764	K.YDEAASYIQSK.F		17.55		
						319	331	529.55	1585.63	1585.71	-0.08	0	33	0.0374195	K.EIYTHFTCATDTK.N		18.64		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08865	21%	331	5	32947	4.8	P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4												14	2
						43	52	568.3	1134.58	1134.63	-0.04	0	57	0.0001524	K.SDGIYIINLK.R		21.34		
						64	80	870.94	1739.87	1739.94	-0.07	0	90	6.12E-08	R.AIVAIENPADVSVISSR.N		20.98		
						90	102	602.31	1202.6	1202.64	-0.04	0	85	2.70E-07	K.FAAATGATPIAGR.F		16.25		
						103	117	849.92	1697.82	1697.85	-0.03	0	61	5.48E-05	R.FTPGTFTNQIQAAFR.E		22.14		
						121	128	456.76	911.51	911.54	-0.04	0	39	0.0080241	R.LLVVTDPR.A		19.38		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15365	13%	222	4	37987	6.7	Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2												14	1
						47	57	644.78	1287.55	1287.59	-0.04	0	72	5.08E-06	R.INISEGNCPER.I		14.55		

						102	115	721.88	1441.75	1441.8	-0.05	0	61	6.28E-05	R.LVVPATQCGSLIGK.G		20.27		
						298	306	507.75	1013.49	1013.53	-0.03	0	47	0.0016078	R.QGANINEIR.Q		14.29		
						315	325	543.76	1085.5	1085.55	-0.05	0	43	0.0043581	K.IANPVEGSSGR.Q		13.85		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08754	12%	162	4	41076	5.5	P08754|GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3												14	1
						36	46	529.3	1056.58	1056.62	-0.04	0	33	0.0425238	K.LLLLGAGESGK.S		25.23		
						91	100	373.86	1118.55	1118.61	-0.06	1	53	0.0004605	R.LKIDFGEAAR.A		19.96		
						249	257	555.75	1109.48	1109.52	-0.04	0	45	0.0019688	K.LFDSICNNK.W		19.56		
						318	330	529.55	1585.63	1585.71	-0.08	0	33	0.0374195	K.EIYTHFTCATDTK.N		18.64		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13510	6%	139	2	45077	7.5	Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4												14	3
						300	310	641.29	1280.57	1280.61	-0.04	0	65	2.11E-05	K.ESLDVYELDAK.Q		20.54		
						367	378	683.87	1365.72	1365.78	-0.06	0	74	2.51E-06	K.LTVYTTLIDVTK.G		21.78		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y617	6%	99	2	40796	7.6	Q9Y617|SERC_HUMAN Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2												14	1
						6	16	557.27	1112.53	1112.6	-0.07	0	48	0.0012678	R.QVVNFGPGPAK.L		18.51		
						52	61	593.31	1184.61	1184.65	-0.04	0	52	0.0005283	K.IINNTENLVR.E		16.77		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O94766	6%	111	2	37270	8.4	O94766|B3GA3_HUMAN Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 OS=Homo sapiens GN=B3GAT3 PE=1 SV=2												14	2
						51	59	529.28	1056.54	1056.59	-0.05	0	55	0.0002315	R.ISQLQAELR.R		19.25		
						96	105	557.32	1112.62	1112.66	-0.04	0	55	0.0002203	R.LSQTLSLVPR.L		20.58		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04406	24%	480	7	36201	8.6	P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3												15	1
						6	13	403.2	804.39	804.42	-0.04	0	33	0.0460452	K.VGVNGFGR.I		15.63		
						67	80	807.43	1612.84	1612.89	-0.05	0	94	2.51E-08	K.LVINGNPITIFQER.D		22.11		
						67	84	681.01	2040	2040.1	-0.1	1	44	0.0024043	K.LVINGNPITIFQERDPSK.I		21.53		
						146	162	917.43	1832.85	1832.91	-0.06	0	116	1.63E-10	K.IISNASCTTNCLAPLAK.V		19.84		
						201	215	706.37	1410.73	1410.78	-0.05	0	73	3.18E-06	R.GALQNIIPASTGAAK.A		20.19		
						235	248	765.87	1529.73	1529.79	-0.06	0	86	1.55E-07	R.VPTANVSVVDLTCR.L		20.37		
						264	271	415.21	828.4	828.43	-0.03	0	34	0.0364084	K.QASEGPLK.G		12.74		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04083	20%	400	7	38918	6.6	P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2												15	1
						2	9	491.73	981.45	981.48	-0.03	0	41	0.0047378	M.AMVSEFLK.Q	Acetyl (Protein N-term); Oxidation (M)	21.75		
						114	124	631.79	1261.56	1261.59	-0.04	0	76	1.90E-06	K.TPAQFDADELR.A		19.75		
						163	177	820.87	1639.72	1639.77	-0.05	1	61	4.82E-05	R.DLAKDITSDTSGDFR.N		20.51		
						167	177	607.25	1212.49	1212.53	-0.03	0	79	1.02E-06	K.DITSDTSGDFR.N		19.17		
						215	228	775.89	1549.76	1549.81	-0.05	0	70	6.68E-06	K.GTDVNVFNTILTTR.S		22.2		
						270	281	452.87	1355.59	1355.65	-0.07	0	33	0.03837	K.CATSKPAFFAEK.L		16.37		
						304	312	540.73	1079.44	1079.48	-0.04	0	42	0.0043901	R.SEIDMNDIK.A	Oxidation (M)	13.92		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05198	10%	165	3	36374	5	P05198|IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3												15	1
						235	244	615.78	1229.54	1229.6	-0.05	0	42	0.005056	R.YVMTTTTLER.T	Oxidation (M)	14.58		
						267	276	582.77	1163.52	1163.56	-0.05	0	35	0.0223218	R.GVFNVQMEPK.V	Oxidation (M)	18.77		
						277	288	674.81	1347.61	1347.65	-0.04	0	89	1.07E-07	K.VVTDTDETELAR.Q		15.59		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40926	27%	465	8	35965	8.9	P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=2												16	1
						166	176	617.34	1232.67	1232.71	-0.04	0	76	1.72E-06	K.IFGVTTLDIVR.A		21.97		
						177	185	496.76	991.5	991.53	-0.03	0	52	0.0004727	R.ANTFVAELK.G		19.84		
						204	215	685.86	1369.71	1369.76	-0.05	0	43	0.0031432	K.TIIPLISQCTPK.V		20.95		
						230	239	537.27	1072.53	1072.58	-0.04	0	60	8.64E-05	R.IQEAGTEVVK.A		13.53		
						242	257	735.83	1469.65	1469.69	-0.05	0	93	3.34E-08	K.AGAGSATLSMAYAGAR.F	Oxidation (M)	17.34		
						258	269	672.31	1342.61	1342.66	-0.05	0	68	1.09E-05	R.FVFSLVDAMNGK.E	Oxidation (M)	21.48		
						270	279	577.26	1152.51	1152.55	-0.04	0	36	0.0152261	K.EGVVECSFVK.S		19.53		
						315	324	566.78	1131.54	1131.58	-0.04	0	35	0.0219471	K.MISDAIPELK.A	Oxidation (M)	20.24		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07355	26%	477	9	38808	7.6	P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2												16	2
						29	37	543.73	1085.44	1085.48	-0.04	0	51	0.0007215	K.AYTNFDAER.D		15.9		
						38	47	544.28	1086.55	1086.59	-0.04	0	65	2.79E-05	R.DALNIETAIK.T		20.5		
						50	63	771.91	1541.81	1541.84	-0.03	0	46	0.0018218	K.GVDEVTIVNILTNR.S		22.89		
						69	77	556.26	1110.51	1110.55	-0.03	0	41	0.0055955	R.QDIAFAYQR.R		19.75		
						82	88	366.2	730.39	730.42	-0.03	0	34	0.0439472	K.ELASALK.S		14.28		
						105	115	611.78	1221.55	1221.59	-0.04	0	75	2.43E-06	K.TPAQYDASELK.A		15.46		
						136	145	622.79	1243.57	1243.62	-0.05	0	51	0.0005821	R.TNQELQEINR.V		14.72		
						158	168	613.26	1224.51	1224.56	-0.05	0	70	6.37E-06	K.DIISDTSGDFR.K		20.64		
						170	176	381.21	760.41	760.45	-0.04	0	49	0.0014365	K.LMVALAK.G	Oxidation (M)	15.86		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P02649	26%	405	7	36246	5.7	P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1												16	3

						122	132	619.73	1237.45	1237.51	-0.06	0	81	4.99E-07	R.LGADMEDVCGR.L	Oxidation (M)	13.88		
						177	185	474.75	947.48	947.52	-0.04	0	54	0.0003338	R.LAVYQAGAR.E		14.63		
						199	207	484.76	967.51	967.55	-0.04	0	43	0.0034525	R.LGPLVEQGR.V		16.64		
						210	224	749.38	1496.75	1496.79	-0.05	0	59	8.33E-05	R.AATVGSLAGQPLQER.A		19.44		
						259	269	438.56	1312.65	1312.71	-0.06	1	62	4.24E-05	R.AKLEEQAQQIR.L		13.49		
						270	278	517.26	1032.51	1032.54	-0.03	0	33	0.039229	R.LQAEAFQAR.L		15.68		
						301	317	810.87	1619.72	1619.79	-0.07	0	74	2.47E-06	K.VQAAVGTSAAPVPSDNH.-		14.81		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07195	19%	288	5	36900	5.7	P07195|LDHB_HUMAN L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2												16	1
						8	23	847.93	1693.85	1693.89	-0.04	0	59	8.20E-05	K.LIAPVAEEEATVPNNK.I		19.71		
						78	91	504.24	1509.7	1509.77	-0.07	1	76	1.43E-06	K.IVADKDYSVTANSK.I		13.71		
						92	100	457.28	912.54	912.58	-0.04	0	36	0.019877	K.IVVVTAGVR.Q		17.25		
						159	170	624.78	1247.55	1247.59	-0.04	0	76	1.65E-06	R.VIGSGCNLDSAR.F		14.46		
						309	319	429.56	1285.67	1285.72	-0.05	2	41	0.0067891	K.LKDDEVAQLKK.S		13.27		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00338	15%	265	5	36950	8.4	P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2												16	1
						91	99	457.22	912.44	912.58	-0.14	0	35	0.0220471	K.LVIITAGAR.Q		19		
						119	126	465.28	928.54	928.57	-0.04	0	37	0.0174962	K.FIIPNVVK.Y		20.91		
						158	169	624.78	1247.55	1247.59	-0.04	0	76	1.65E-06	R.VIGSGCNLDSAR.F		14.46		
						233	243	632.82	1263.63	1263.67	-0.04	0	63	3.71E-05	K.QVVESAYEVIK.L		19.93		
						306	315	567.76	1133.51	1133.56	-0.05	0	54	0.0003323	K.VTLTSEEEAR.L		14.15		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q86Y82	11%	150	3	31736	5.5	Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1												16	1
						36	44	480.26	958.51	958.54	-0.04	0	42	0.0054574	R.ISQATAQIK.N		13.14		
						76	82	423.71	845.41	845.45	-0.04	0	33	0.0490961	K.ETNELLK.E		14.59		
						83	97	813.92	1625.82	1625.86	-0.05	0	43	0.0031636	K.ELGSLPLPLSTSEQR.Q		21.35		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BWM7	10%	137	3	35823	9.3	Q9BWM7|SFXN3_HUMAN Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=2 SV=1												16	1
						136	144	473.23	944.45	944.49	-0.04	0	34	0.0399919	R.SGDTPITVR.Q		14.32		
						199	213	791.39	1580.76	1580.82	-0.05	0	66	1.62E-05	R.ELQVGIPVADEAGQR.L		20.42		
						214	222	455.23	908.45	908.5	-0.05	0	37	0.011835	R.LGYSVTAAK.Q		14.98		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05388	10%	172	3	34423	5.7	P05388|RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1												16	2
						17	26	609.32	1216.63	1216.67	-0.04	0	57	0.0001648	K.IIQLLDDYPK.C		21.17		
						84	92	484.75	967.48	967.51	-0.03	0	44	0.0025359	R.GNVGFVFTK.E		20.37		
						135	146	657.33	1312.64	1312.7	-0.07	0	71	5.42E-06	K.TSFFQALGITTK.I		22.49		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52907	9%	173	2	33073	5.5	P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3												16	2
						38	47	599.33	1196.65	1196.69	-0.04	0	85	1.93E-07	R.LLLNNDNLLR.E		20.86		
						211	226	853.39	1704.76	1704.82	-0.06	0	88	1.03E-07	K.DVQDSLTVSNEAQTAK.E		19.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14847	9%	109	2	30097	6.6	Q14847|LASP1_HUMAN LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2												16	1
						76	85	601.79	1201.56	1201.61	-0.05	0	49	0.0010542	K.QQSELQSQVR.Y		13.4		
						131	143	683.26	1364.51	1364.53	-0.02	0	61	5.93E-05	R.MGPSGGEGMEPER.R	2 Oxidation (M)	12.48		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q12907	8%	120	3	40545	6.5	Q12907|LMAN2_HUMAN Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1												16	2
						142	151	500.78	999.54	999.58	-0.03	0	46	0.0019747	R.LVPGPVFGSK.D		19.88		
						224	233	590.77	1179.53	1179.57	-0.04	0	34	0.0256749	R.LTVMTDLEDK.N	Oxidation (M)	18.78		
						238	246	524.25	1046.48	1046.52	-0.04	0	40	0.0086818	K.NCIDITGVR.L		19.35		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P29692	8%	86	2	31217	4.9	P29692|EF1D_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5												16	1
						39	48	543.78	1085.56	1085.58	-0.03	0	51	0.0007283	R.QENGASVILR.D		16.99		
						96	107	650.34	1298.67	1298.72	-0.05	0	36	0.0189547	R.GVVQELQQAISK.L		21.7		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UBR2	7%	113	2	34530	6.7	Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1												16	1
						70	81	654.8	1307.59	1307.65	-0.06	0	60	6.71E-05	R.NVDGVNYASITR.N		19.57		
						190	199	505.73	1009.45	1009.48	-0.04	0	53	0.0003389	R.VGDYGSLSGR.E		15.16		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62873	6%	138	2	38151	5.6	P62873|GBB1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3												16	1
						69	78	509.26	1016.51	1016.55	-0.04	0	65	2.45E-05	R.LLVSASQDGK.L		14.23		
						198	209	613.28	1224.54	1224.58	-0.04	0	72	3.90E-06	R.LFVSGACDASAK.L		16.42		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40925	5%	86	2	36631	6.9	P40925|MDHC_HUMAN Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4												16	2
						150	157	513.72	1025.42	1025.46	-0.04	0	35	0.0188603	K.ENFSCLTR.L		18.26		
						171	179	458.74	915.46	915.5	-0.05	0	50	0.0008592	K.LGVTANDVK.N		14.1		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21796	27%	557	7	30868	8.6	P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2												17	6
						33	53	730.32	2187.95	2188.01	-0.07	1	107	1.11E-09	K.TKSENGLEFTSSGSANTETTK.V		14.65		
						35	53	980.42	1958.83	1958.87	-0.04	0	91	4.93E-08	K.SENGLEFTSSGSANTETTK.V		18.69		
						97	109	700.82	1399.63	1399.66	-0.03	0	83	3.38E-07	K.LTFDSSFSPNTGK.K		20.39		
						97	110	510.24	1527.71	1527.76	-0.05	1	51	0.0005362	K.LTFDSSFSPNTGKK.N		19.62		
						164	174	607.31	1212.6	1212.61	-0.01	0	70	7.08E-06	R.VTQSNFAVGYK.T		18.17		
						237	256	701.72	2102.13	2102.17	-0.05	0	83	2.72E-07	K.VNNSSLIGLGYTQTLKPGIK.L		20.52		
						257	266	515.8	1029.58	1029.61	-0.03	0	72	5.15E-06	K.LTLSALLDGK.N		21.79		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P45880	22%	255	5	32060	7.5	P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2												17	2
						108	121	519.58	1555.73	1555.79	-0.06	1	44	0.0024553	K.LTFDTTFSPNTGKK.S		19.94		
						178	185	470.72	939.42	939.46	-0.03	0	32	0.040975	R.NNFAVGYR.T		16.78		
						236	247	647.33	1292.64	1292.66	-0.02	0	73	3.54E-06	K.YQLDPTASISAK.V		19.76		
						248	267	701.72	2102.13	2102.15	-0.02	0	34	0.0225638	K.VNNSSLIGVGYTQTLRPGVK.L		20.52		
						268	277	508.79	1015.57	1015.59	-0.02	0	72	5.86E-06	K.LTLSALVDGK.S		21.07		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50897	22%	349	4	34627	6.1	P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1												17	4
						105	122	1009.46	2016.9	2016.95	-0.05	0	110	6.22E-10	K.LQQGYNAMGFSQGGQFLR.A	Oxidation (M)	20.43		
						128	151	859.74	2576.21	2576.3	-0.09	0	89	5.83E-08	R.CPSPPMINLISVGGQHQGVFGLPR.C	Oxidation (M)	21.47		
						166	174	462.73	923.45	923.47	-0.02	0	57	0.0001183	K.TLNAGAYSK.V		13.34		
						254	268	897.43	1792.84	1792.88	-0.05	0	93	3.35E-08	K.ETIPLQETSLYTQDR.L		20.48		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08758	21%	364	6	35971	4.9	P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2												17	1
						30	45	852.94	1703.86	1703.89	-0.03	0	104	2.47E-09	K.GLGTDEESILTLLTSR.S		23.66		
						51	58	447.22	892.43	892.47	-0.04	0	38	0.012352	R.QEISAAFK.T		16.3		
						109	117	501.29	1000.56	1000.59	-0.03	0	54	0.0003654	K.VLTEIIASR.T		19.89		
						228	242	807.43	1612.84	1612.9	-0.06	0	66	1.67E-05	R.ETSGNLEQLLLAVVK.S		23.97		
						277	285	553.78	1105.55	1105.58	-0.03	0	52	0.0005423	R.SEIDLFNIR.K		21.74		
						291	301	645.81	1289.6	1289.63	-0.04	0	50	0.0006295	K.NFATSLYSMIK.G	Oxidation (M)	21.34		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16698	18%	240	4	36330	9.3	Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1												17	1
						98	110	667.8	1333.58	1333.65	-0.07	0	87	1.51E-07	K.ATAEQISSQTGNK.V		12.77		
						120	133	802.86	1603.71	1603.78	-0.07	0	40	0.0067519	R.DPDMVQNTVSELIK.V	Oxidation (M)	21.52		
						134	155	764.37	2290.09	2290.18	-0.09	0	77	1.10E-06	K.VAGHPNIVINNAAGNFISPTER.L		20.25		
						235	244	556.81	1111.61	1111.64	-0.03	0	36	0.0155792	R.FNVIQPGPIK.T		20.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P09525	13%	232	3	36088	5.8	P09525|ANXA4_HUMAN Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4												17	1
						10	24	799.34	1596.66	1596.72	-0.06	0	105	1.98E-09	K.AASGFNAMEDAQTLR.K	Oxidation (M)	19.18		
						226	241	833.91	1665.8	1665.85	-0.04	0	64	2.67E-05	K.SETSGSFEDALLAIVK.C		23.44		
						260	270	587.79	1173.57	1173.6	-0.03	0	63	3.98E-05	K.GLGTDDNTLIR.V		19.53		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61247	13%	123	3	30154	9.8	P61247|RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2												17	1
						129	136	469.74	937.46	937.49	-0.03	0	33	0.0315748	K.TTDGYLLR.L		19.13		
						175	187	505.92	1514.74	1514.79	-0.05	1	48	0.0010642	R.EVQTNDLKEVVNK.L		16		
						228	240	449.85	1346.53	1346.61	-0.08	0	44	0.0029774	K.LMELHGEGSSSGK.A	Oxidation (M)	12.6		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H9B4	11%	167	3	35881	9.2	Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4												17	1
						36	48	750.88	1499.75	1499.79	-0.05	0	71	5.50E-06	R.NILLTNEQLESAR.K		20.34		
						203	214	635.81	1269.6	1269.63	-0.03	0	44	0.0025867	K.VGIPVTDENGNR.L		15.74		
						224	233	550.81	1099.6	1099.63	-0.04	0	52	0.0005715	K.QAITQVVVSR.I		17.17		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P54920	7%	92	2	33667	5.2	P54920|SNAA_HUMAN Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3												17	1
						107	116	592.77	1183.53	1183.55	-0.03	0	34	0.0314689	R.AIEIYTDMGR.F	Oxidation (M)	19.22		
						286	295	588.27	1174.53	1174.55	-0.01	0	58	0.0001198	K.TIQGDEEDLR.-		14.78		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O00299	29%	372	6	27248	5.1	O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4												18	1
						2	13	729.85	1457.69	1457.74	-0.05	0	65	2.47E-05	M.AEEQPQVELFVK.A	Acetyl (Protein N-term)	21.82		
						21	29	539.74	1077.47	1077.5	-0.03	0	43	0.0035285	K.IGNCPFSQR.L		15.12		
						38	49	641.33	1280.64	1280.66	-0.02	0	72	4.51E-06	K.GVTFNVTTVDTK.R		19.93		
						96	113	922.98	1843.95	1843.97	-0.02	0	80	5.82E-07	K.LAALNPESNTAGLDIFAK.F		21.73		
						120	131	664.79	1327.56	1327.64	-0.08	0	71	5.73E-06	K.NSNPALNDNLEK.G		14.73		
						209	216	479.24	956.47	956.47	0	0	40	0.0072975	R.YLSNAYAR.E		14.3		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62258	16%	208	4	29326	4.6	P62258|1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1												18	1
						30	42	732.35	1462.68	1462.7	-0.02	0	77	1.37E-06	K.VAGMDVELTVEER.N	Oxidation (M)	19.54		

						43	50	454.25	906.48	906.52	-0.04	0	37	0.0173382	R.NLLSVAYK.N		20.11		
						87	94	497.23	992.45	992.48	-0.03	0	38	0.0113328	R.QMVETELK.L	Oxidation (M)	13.56		
						143	153	597.8	1193.58	1193.59	-0.01	0	57	0.0001585	K.EAAENSLVAYK.A		17.76		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23396	14%	162	3	26842	9.7	P23396|RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2												18	1
						19	27	546.78	1091.54	1091.56	-0.02	0	59	8.58E-05	K.AELNEFLTR.E		20.59		
						46	54	515.3	1028.6	1028.62	-0.03	0	34	0.036509	R.TEIIILATR.T		20.68		
						228	243	795.39	1588.77	1588.79	-0.02	0	37	0.0134451	K.GGKPEPPAMPQPVPTA.-	Oxidation (M)	14.77		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27105	13%	224	4	31882	7.7	P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3												18	1
						206	215	511.73	1021.44	1021.45	-0.01	0	36	0.0188134	R.AMAAEAEASR.E	Oxidation (M)	12.26		
						219	232	488.23	1461.67	1461.72	-0.05	1	57	0.0001245	R.AKVIAAEGEMNASR.A	Oxidation (M)	12.69		
						221	232	632.29	1262.56	1262.59	-0.03	0	79	1.02E-06	K.VIAAEGEMNASR.A	Oxidation (M)	12.95		
						252	263	676.36	1350.7	1350.74	-0.04	0	52	0.0003857	R.YLQTLTTIAAEK.N		20.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63104	22%	285	5	27899	4.7	P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1												19	3
						1	9	581.79	1161.56	1161.57	-0.01	1	60	7.98E-05	-.MDKNELVQK.A	Acetyl (Protein N-term); Oxidation (M)	13.21		
						28	41	774.85	1547.69	1547.71	-0.02	0	84	2.65E-07	K.SVTEQGAELSNEER.N		14.25		
						42	49	454.26	906.5	906.52	-0.02	0	45	0.0023551	R.NLLSVAYK.N		20.08		
						104	115	652.84	1303.66	1303.68	-0.02	0	52	0.000468	K.FLIPNASQAESK.V		19.95		
						128	139	427.21	1278.61	1278.65	-0.03	1	44	0.0029519	R.YLAEVAAGDDKK.G		13.69		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31946	21%	245	5	28179	4.8	P31946|1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3												19	1
						2	11	618.8	1235.59	1235.61	-0.02	1	35	0.0224089	M.TMDKSELVQK.A	Acetyl (Protein N-term); Oxidation (M)	13.43		
						30	43	533.56	1597.66	1597.73	-0.08	0	48	0.0012144	K.AVTEQGHELSNEER.N		12.9		
						44	51	454.26	906.5	906.52	-0.02	0	45	0.0023551	R.NLLSVAYK.N		20.08		
						63	70	452.25	902.49	902.51	-0.02	0	44	0.0035329	R.VISSIEQK.T		13.34		
						130	140	591.77	1181.53	1181.56	-0.02	0	74	2.54E-06	R.YLSEVASGDNK.Q		13.95		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61981	20%	269	5	28456	4.8	P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2												19	1
						2	10	578.82	1155.62	1155.62	-0.01	1	50	0.0006769	M.VDREQLVQK.A	Acetyl (Protein N-term)	15.34		
						29	42	822.38	1642.74	1642.78	-0.04	0	89	8.55E-08	K.NVTELNEPLSNEER.N		19.51		
						43	50	454.26	906.5	906.52	-0.02	0	45	0.0023551	R.NLLSVAYK.N		20.08		
						62	69	452.25	902.49	902.51	-0.02	0	44	0.0035329	R.VISSIEQK.T		13.34		
						133	142	540.76	1079.51	1079.55	-0.04	0	40	0.0061578	R.YLAEVATGEK.R		15.29		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07339	17%	389	8 (9)	45037	6.1	P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1												19	7
						177	184	440.22	878.43	878.45	-0.02	0	39	0.0093034	R.QVFGEATK.Q		13.73		
						177	194	636	1904.99	1905.04	-0.04	1	47	0.0011034	R.QVFGEATKQPGITFIAAK.F		20.29		
						185	194	514.78	1027.55	1027.57	-0.02	0	35	0.0231177	K.QPGITFIAAK.F	Gln->pyro-Glu (N-term Q)	21.43		
						185	194	523.4	1044.79	1044.6	0.19	0	31	0.0489839	K.QPGITFIAAK.F		20.25		
						195	205	628.3	1254.58	1254.61	-0.03	0	70	7.76E-06	K.FDGILGMAYPR.I	Oxidation (M)	20.77		
						236	253	902.39	1802.78	1802.8	-0.02	0	63	3.00E-05	R.DPDAQPGGELMLGGTDSK.Y	Oxidation (M)	19.64		
						349	357	533.27	1064.52	1064.54	-0.02	0	58	0.0001173	K.LSPEDYTLK.V		19.68		
						393	399	482.22	962.43	962.45	-0.02	0	33	0.0401256	R.YYTVFDR.D		20.21		
						404	411	410.71	819.4	819.42	-0.02	0	44	0.0032244	R.VGFAEAAR.L		14.34		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27348	12%	164	3	28032	4.7	P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1												19	1
						28	41	766.85	1531.69	1531.71	-0.02	0	75	2.22E-06	K.AVTEQGAELSNEER.N		14.03		
						42	49	454.26	906.5	906.52	-0.02	0	45	0.0023551	R.NLLSVAYK.N		20.08		
						61	68	452.25	902.49	902.51	-0.02	0	44	0.0035329	R.VISSIEQK.T		13.34		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30040	8%	133	2	29032	6.8	P30040|ERP29_HUMAN Endoplasmic reticulum protein ERp29 OS=Homo sapiens GN=ERP29 PE=1 SV=4												19	1
						183	192	538.26	1074.51	1074.53	-0.02	0	95	2.85E-08	K.QGQDNLSSVK.E		13.04		
						244	253	567.83	1133.64	1133.64	0	0	38	0.010575	K.SLNILTAFQK.K		21.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07686	4%	117	2	63527	6.3	P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3												19	3
						391	400	550.33	1098.64	1098.66	-0.02	0	57	0.0001603	K.VLDIIATINK.G		21.21		
						466	476	595.8	1189.59	1189.6	-0.01	0	60	7.13E-05	K.VEPLDFGGTQK.Q		19.99		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04792	26%	425	5 (6)	22826	6	P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2												20	2
						28	37	582.31	1162.6	1162.61	-0.01	0	73	3.75E-06	R.LFDQAFGLPR.L		21.41		
						80	89	529.77	1057.53	1057.54	-0.01	0	36	0.0254353	R.QLSSGVSEIR.H	Gln->pyro-Glu (N-term Q)	20.26		
						80	89	538.28	1074.55	1074.57	-0.02	0	64	2.97E-05	R.QLSSGVSEIR.H		15.15		
						172	188	953.5	1904.99	1904.98	0	0	149	6.88E-14	K.LATQSNEITIPVTFESR.A		21.15		
						189	198	471.26	940.51	940.5	0.01	0	64	2.66E-05	R.AQLGGPEAAK.S		12.88		
						189	205	548.6	1642.79	1642.82	-0.03	1	76	1.75E-06	R.AQLGGPEAAKSDETAAK.-		12.93		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61020	17%	131	3	23920	8.3	P61020|RAB5B_HUMAN Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1												20	1
						23	33	543.33	1084.65	1084.65	0	0	45	0.0026176	K.LVLLGESAVGK.S		20.44		
						166	179	768.92	1535.83	1535.8	0.03	0	37	0.0126059	K.TAMNVNDLFLAIAK.K	Oxidation (M)	22.21		
						184	195	578.79	1155.56	1155.56	0	0	49	0.0010058	K.SEPQNLGGAAGR.S		13.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60174	14%	140	3	26938	6.5	P60174|TPIS_HUMAN Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=2												20	1
						60	69	569.29	1136.57	1136.56	0	0	44	0.0028366	K.IAVAAQNCYK.V		14.06		
						176	188	489.57	1465.69	1465.72	-0.02	0	33	0.0302158	K.TATPQQAQEVHEK.L		12.49		
						195	206	617.8	1233.58	1233.59	-0.02	0	62	4.39E-05	K.SNVSDAVAQSTR.I		14.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60900	13%	174	3	27838	6.3	P60900|PSA6_HUMAN Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1												20	1
						22	30	580.8	1159.58	1159.59	-0.01	0	32	0.0494639	R.LYQVEYAFK.A		20.61		
						31	43	643.37	1284.72	1284.71	0.01	0	69	8.19E-06	K.AINQGGLTSVAVR.G		19.37		
						172	181	585.28	1168.55	1168.56	-0.02	0	73	3.78E-06	K.QTESTSFLEK.K		17.46		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50914	11%	116	2	23389	10.9	P50914|RL14_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=3												20	1
						24	35	677.89	1353.76	1353.76	-0.01	0	75	2.00E-06	K.LVAIVDVIDQNR.A		21.55		
						36	46	608.3	1214.59	1214.61	-0.02	0	41	0.0065976	R.ALVDGPCTQVR.R		16.46		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51572	9%	68	2	28031	8.4	P51572|BAP31_HUMAN B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3												20	1
						205	213	524.26	1046.5	1046.52	-0.01	0	34	0.0303814	K.AENQVLAMR.K	Oxidation (M)	13.62		
						233	246	516.24	1545.7	1545.73	-0.04	2	34	0.0250561	K.LQAAVDGPMDKKEE.-	Oxidation (M)	13.06		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30041	9%	117	2	25133	6	P30041|PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3												20	1
						133	141	504.29	1006.56	1006.55	0.01	0	49	0.0010039	R.VVFVFGPDK.K		21.06		
						145	155	596.34	1190.66	1190.67	0	0	37	0.014951	K.LSILYPATTGR.N		20.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BSR8	7%	79	2	27122	4.5	Q9BSR8|YIPF4_HUMAN Protein YIPF4 OS=Homo sapiens GN=YIPF4 PE=2 SV=1												20	1
						39	47	488.77	975.53	975.54	-0.01	0	34	0.0369799	K.LNLGGDFIK.E		20.75		
						48	56	513.26	1024.51	1024.52	-0.01	0	45	0.002076	K.ESTATTFLR.Q		19.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20340	28%	374	6	23692	5.4	P20340|RAB6A_HUMAN Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3												21	2
						2	12	581.78	1161.54	1161.54	0	0	40	0.0082242	M.STGGDFGNPLR.K	Acetyl (Protein N-term)	20.98		
						2	13	645.83	1289.64	1289.64	0	1	108	1.04E-09	M.STGGDFGNPLRK.F	Acetyl (Protein N-term)	19.89		
						16	26	588.83	1175.65	1175.66	0	0	53	0.0003827	K.LVFLGEQSVGK.T		21.02		
						135	144	579.28	1156.55	1156.57	-0.02	1	47	0.0017248	R.QVSIEEGERK.A	Gln->pyro-Glu (N-term Q)	15.71		
						147	158	699.35	1396.68	1396.69	-0.01	0	57	0.0001509	K.ELNVMFIETSAK.A	Oxidation (M)	21.19		
						170	183	731.36	1460.7	1460.69	0.01	0	70	7.46E-06	R.VAAALPGMESTQDR.S	Oxidation (M)	15.37		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92520	17%	214	4	24950	8.5	Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1												21	2
						31	41	605.78	1209.55	1209.58	-0.03	0	50	0.0006239	K.MDASLGNLFAR.S	Oxidation (M)	21.58		
						42	49	402.72	803.42	803.41	0	0	48	0.0015035	R.SALDTAAR.S		13.24		
						73	84	559.28	1116.54	1116.56	-0.02	0	70	7.96E-06	K.MASGAANVVGPK.I	Oxidation (M)	13.29		
						113	120	431.73	861.44	861.44	-0.01	0	46	0.0023961	K.TGEVLDTK.Y		13.55		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51148	16%	170	3	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												21	3
						24	34	543.32	1084.63	1084.65	-0.02	0	53	0.0003647	K.LVLLGESAVGK.S		20.8		
						185	196	606.29	1210.56	1210.57	-0.01	0	49	0.0008222	K.NEPQNATGAPGR.N		12.55		
						199	210	650.32	1298.63	1298.62	0	0	67	1.34E-05	R.GVDLQENNPASR.S		14.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75396	13%	152	3	24896	8.7	O75396|SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=3												21	1
						29	38	604.8	1207.58	1207.58	-0.01	0	44	0.0026341	R.DLQQYQSQAK.Q		14.5		
						160	169	495.75	989.49	989.5	-0.01	0	53	0.00043	R.GEALSALDSK.A		17.88		
						170	178	467.24	932.48	932.49	-0.02	0	55	0.0002737	K.ANNLSSLSK.K		14.15		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20339	11%	87	2	23872	8.3	P20339|RAB5A_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2												21	1
						23	33	543.32	1084.63	1084.65	-0.02	0	53	0.0003647	K.LVLLGESAVGK.S		20.8		
						198	209	657.34	1312.67	1312.66	0.01	0	34	0.0303897	R.GVDLTEPTQPTR.N		18.4		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43760	9%	104	2	25079	4.8	O43760|SNG2_HUMAN Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1												21	1
						20	29	579.82	1157.63	1157.66	-0.03	0	49	0.0011528	R.FLTQPQVVAR.A		19.76		
						137	146	515.78	1029.55	1029.55	0.01	0	55	0.0002655	K.DVLVGADSVR.A		19.58		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51149	36%	326	7	23760	6.4	P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1												22	1
						11	21	529.31	1056.61	1056.62	-0.01	0	57	0.0001684	K.VIILGDSGVGK.T		20.22		
						22	32	447.89	1340.64	1340.68	-0.03	1	33	0.0385017	K.TSLMNQYVNKK.F	Oxidation (M)	13.34		
						39	48	518.79	1035.56	1035.56	0	0	45	0.0022681	K.ATIGADFLTK.E		20.88		
						70	79	594.31	1186.6	1186.61	-0.01	0	38	0.0113429	R.FQSLGVAFYR.G		21.46		
						114	126	738.38	1474.74	1474.75	0	0	47	0.0013777	R.DPENFPFVVLGNK.I		23.04		
						127	132	380.19	758.37	758.39	-0.02	0	38	0.01675	K.IDLENR.Q		14.51		
						158	171	795.43	1588.84	1588.82	0.02	0	68	1.12E-05	K.EAINVEQAFQTIAR.N		22.47		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q06830	34%	359	7 (8)	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												22	1
						17	27	590.79	1179.56	1179.56	0	0	54	0.0002961	K.ATAVMPDGQFK.D	Oxidation (M)	14.6		
						28	35	470.73	939.45	939.45	0	0	42	0.0037428	K.DISLSDYK.G		20.18		
						93	110	481.51	1922.01	1922.04	-0.03	2	39	0.0079454	K.KQGGLGPMNIPLVSDPKR.T	Oxidation (M)	19.69		
						94	109	819.93	1637.84	1637.84	-0.01	0	54	0.0002812	K.QGGLGPMNIPLVSDPK.R	Oxidation (M)	20.97		
						111	120	554.3	1106.59	1106.6	0	0	56	0.0001817	R.TIAQDYGVLK.A		20.13		
						141	151	597.82	1193.62	1193.64	-0.02	0	48	0.0012618	R.QITVNDLPVGR.S	Gln->pyro-Glu (N-term Q)	21.94		
						141	151	606.34	1210.66	1210.67	-0.01	0	57	0.0001361	R.QITVNDLPVGR.S		20.4		
						159	168	598.82	1195.63	1195.62	0.01	0	58	0.0001194	R.LVQAFQFTDK.H		20.84		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48047	24%	203	5	23377	10	P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1												22	1
						41	51	573.31	1144.6	1144.58	0.03	0	32	0.0491118	R.YATALYSAASK.Q		18.12		
						65	73	513.32	1024.63	1024.63	0	1	41	0.0046545	R.VAQILKEPK.V		14.08		
						74	84	580.83	1159.65	1159.66	-0.01	0	57	0.0001517	K.VAASVLNPYVK.R		20.31		
						91	98	431.24	860.47	860.46	0	0	39	0.0104688	K.SLNDITAK.E		14.56		
						177	188	637.84	1273.67	1273.67	0	0	33	0.0387544	K.TDPSILGGMIVR.I	Oxidation (M)	20.71		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04179	22%	309	6	24878	8.3	P04179|SODM_HUMAN Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2												22	1
						69	75	411.71	821.42	821.43	-0.01	0	48	0.0011958	K.YQEALAK.G		13.25		
						76	89	712.91	1423.81	1423.8	0	0	95	2.31E-08	K.GDVTAQIALQPALK.F		20.66		
						115	122	436.76	871.5	871.5	0	0	34	0.0367715	K.GELLEAIK.R		20.48		
						115	123	514.81	1027.6	1027.6	0	1	47	0.0014882	K.GELLEAIKR.D		19.51		
						124	134	449.88	1346.63	1346.65	-0.02	2	35	0.0242734	R.DFGSFDKFKEK.L		19.87		
						195	202	502.78	1003.54	1003.55	0	0	51	0.0006977	K.NVRPDYLK.A		13.95		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P37802	22%	217	4	22548	8.4	P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3												22	1
						80	88	506.76	1011.5	1011.51	0	0	60	7.48E-05	K.IQASTMAFK.Q	Oxidation (M)	14.47		
						128	139	616.34	1230.67	1230.68	-0.01	0	59	8.97E-05	R.TLMNLGGLAVAR.D	Oxidation (M)	20.57		
						161	171	640.3	1278.58	1278.58	-0.01	0	51	0.0005836	R.NFSDNQLQEGK.N		15.39		
						172	182	609.82	1217.62	1217.62	0	0	48	0.0013964	K.NVIGLQMGTNR.G	Oxidation (M)	16.73		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H0U4	20%	183	4	22328	5.5	Q9H0U4|RAB1B_HUMAN Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1												22	1
						11	21	536.32	1070.63	1070.63	0	0	58	0.0001356	K.LLLIGDSGVGK.S		21.1		
						49	55	388.21	774.4	774.41	-0.01	0	33	0.047177	R.TIELDGK.T		14.86		
						72	79	495.74	989.47	989.48	-0.01	0	34	0.0318041	R.TITSSYYR.G		15.34		
						173	187	486.57	1456.69	1456.71	-0.02	0	58	0.0001203	R.MGPGAASGGERPNLK.I	Oxidation (M)	12.95		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62820	19%	166	4	22891	5.9	P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3												22	1
						14	24	536.32	1070.63	1070.63	0	0	58	0.0001356	K.LLLIGDSGVGK.S		21.1		
						52	58	388.21	774.4	774.41	-0.01	0	33	0.047177	R.TIELDGK.T		14.86		
						75	82	495.74	989.47	989.48	-0.01	0	34	0.0318041	R.TITSSYYR.G		15.34		
						176	187	531.74	1061.46	1061.48	-0.02	0	40	0.0080202	R.MGPGATAGGAEK.S	Oxidation (M)	12.2		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92930	15%	170	3	23740	9.2	Q92930|RAB8B_HUMAN Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2												22	1
						11	21	536.32	1070.63	1070.63	0	0	58	0.0001356	K.LLLIGDSGVGK.T		21.1		
						49	55	388.21	774.4	774.41	-0.01	0	33	0.047177	R.TIELDGK.K		14.86		
						177	190	660.84	1319.66	1319.58	0.08	0	79	9.09E-07	K.MNDSNSAGAGGPVK.I	Oxidation (M)	12.51		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51153	12%	157	2	22988	9.3	P51153|RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=2 SV=1												22	1
						11	21	536.32	1070.63	1070.63	0	0	58	0.0001356	K.LLLIGDSGVGK.T		21.1		
						154	167	765.35	1528.68	1528.68	0	0	99	8.23E-09	K.SSMNVDEAFSSLAR.D	Oxidation (M)	20.93		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61026	9%	99	2	22755	8.6	P61026|RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1												22	1
						12	22	536.32	1070.63	1070.63	0	0	58	0.0001356	K.LLLIGDSGVGK.T		21.1		
						155	161	401.23	800.44	800.44	0	0	41	0.0082035	K.ANINIEK.A		13.82		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P46781	8%	74	2	22635	10.7	P46781|RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3												22	1

						31	38	460.76	919.5	919.51	-0.01	0	39	0.010484	K.LIGEYGLR.N		20.26		
						84	91	415.72	829.43	829.45	-0.02	0	35	0.0312409	R.IGVLDEGK.M		16.99		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60660	25%	156	3	17090	4.6	P60660|MYL6_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2												26	1
						14	21	513.24	1024.46	1024.5	-0.04	0	53	0.0003171	K.EAFQLFDR.T		21.56		
						38	50	677.87	1353.72	1353.73	-0.01	0	68	1.16E-05	R.ALGQNPTNAEVLK.V		18.98		
						95	110	580.29	1737.84	1737.84	0	1	35	0.021048	R.VFDKEGNGTVMGAEIR.H	Oxidation (M)	16.24		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P39019	19%	119	3	16051	10.3	P39019|RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2												26	1
						8	16	567.8	1133.59	1133.55	0.04	0	36	0.0201638	K.DVNQQEFVR.A		17.68		
						103	111	485.79	969.57	969.59	-0.01	0	39	0.0084805	R.VLQALEGLK.M		20.68		
						134	143	471.78	941.54	941.53	0.01	0	45	0.0021064	R.IAGQVAAANK.K		12.6		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62269	12%	93	2	17708	11	P62269|RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3												26	1
						15	23	501.26	1000.51	1000.53	-0.02	0	42	0.0052026	R.VLNTNIDGR.R		14.99		
						67	75	544.3	1086.58	1086.59	0	0	51	0.0007912	R.VITIMQNPR.Q	Oxidation (M)	14.73		

***Footnotes to Supplemental Table 8:**

Data sets were searched with the Mascot search engine (see Perkins et al. (1999) *Electrophoresis* **20**, 3551-3567).

Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).

Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.

Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest gel slice in which the protein was identified, and the total # of adjacent gel slices in which the protein was found).

Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 9. Proteins identified by HPLC-MS/MS in 3-hour latex bead human THP-1 phagosome preparation.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1.

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	10%	466	9	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												2	4
						87	98	482.27	1443.78	1443.78	-0.01	0	35	0.0208314	R.VTLRPYLTPNDR.G		19.78		
						196	204	550.71	1099.41	1099.46	-0.05	0	33	0.0425146	R.SEYMEGNVR.K	Oxidation (M)	13.24		
						205	218	502.57	1504.7	1504.77	-0.07	1	40	0.0060258	R.KVVATTQMQAADAR.K	Oxidation (M)	12.58		
						206	218	689.36	1376.71	1376.67	0.04	0	70	7.46E-06	K.VVATTQMQAADAR.K	Oxidation (M)	13.11		
						242	252	609.81	1217.61	1217.63	-0.03	0	56	0.0002198	K.DLTALSNMLPK.G	Oxidation (M)	21.09		
						293	301	479.27	956.52	956.54	-0.02	0	54	0.0003245	K.QASNGVLIR.I		14.97		
						364	379	862.9	1723.79	1723.83	-0.04	0	58	9.65E-05	R.ENSLLFDPLSSSSSNK.E		21.79		
						433	442	627.3	1252.58	1252.61	-0.03	0	63	3.58E-05	K.DLMVLNDVYR.V	Oxidation (M)	21.26		
						924	935	635.27	1268.53	1268.53	0	0	60	7.76E-05	K.DNEETGFGSGTR.A		14.5		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62988	38%	81	2	8560	6.6	P62988|UBIQ_HUMAN Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1												3	9
						12	27	894.46	1786.9	1786.92	-0.02	0	41	0.0046967	K.TITLEVEPSDTIENVK.A		20.99		
						30	42	508.59	1522.73	1522.77	-0.04	1	40	0.0063358	K.IQDKEGIPPDQQR.L		13.22		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11279	9%	160	4	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												3	10
						138	146	517.4	1032.79	1032.55	0.24	0	37	0.0096108	K.TVESITDIR.A		20.55		
						327	337	576.28	1150.55	1150.6	-0.04	0	45	0.0022031	R.ALQATVGNSYK.C		16.81		
						349	356	463.26	924.5	924.51	-0.01	0	46	0.0014969	K.AFSVNIFK.V		21.43		
						410	417	438.7	875.39	875.41	-0.02	0	33	0.0406702	R.SHAGYQTI.-		14.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92542	6%	204	4	79103	5.7	Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2												3	2
						315	323	485.26	968.5	968.53	-0.03	0	45	0.0020913	K.APDVTTLPR.N		16.94		
						404	414	520.3	1038.59	1038.62	-0.03	0	39	0.0091774	K.SGAGVPAVILR.R		20.33		
						486	496	543.3	1084.59	1084.62	-0.04	0	70	7.89E-06	K.ALADVATVLGR.A		21.21		
						694	702	501.3	1000.58	1000.57	0.01	0	50	0.0008886	K.ADVLFIAPR.E		21.3		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13473	4%	122	2	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												3	4
						145	152	494.27	986.52	986.55	-0.04	0	55	0.0002571	R.IPLNDLFR.C		21.69		
						153	161	526.25	1050.48	1050.5	-0.02	0	67	1.29E-05	R.CNSLSTLEK.N		15.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P42704	3%	172	4	159003	5.8	P42704|LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3												3	1
						981	989	549.29	1096.56	1096.59	-0.03	0	33	0.0362134	K.IQEENVIPR.E		17.98		
						1099	1109	583.26	1164.5	1164.55	-0.06	0	48	0.0011293	K.GFTLNDAANSR.L		19.67		
						1129	1139	636.79	1271.57	1271.65	-0.07	0	57	0.0001533	K.TVLDQQQTPSR.L		14.04		
						1164	1176	696.86	1391.7	1391.7	0.01	0	37	0.0128159	K.MLNGLEDSIGLSK.M	Oxidation (M)	20.77		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05556	3%	78	2	91714	5.3	P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=1												3	1
						182	190	492.25	982.49	982.51	-0.02	0	34	0.0251616	R.IGFGSFVEK.T		21.12		
						191	202	662.82	1323.63	1323.67	-0.05	0	44	0.0029705	K.TVMPYISTTPAK.L	Oxidation (M)	17.03		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	10%	380	8	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												4	1
						76	84	541.26	1080.5	1080.54	-0.03	0	36	0.0170786	K.FAFQAEVNR.M		20.24		
						88	95	482.28	962.54	962.58	-0.04	0	33	0.0358444	K.LIINSLYK.N		20.77		
						385	395	594.33	1186.65	1186.67	-0.02	0	38	0.0124373	K.SILFVPTSAPR.G		21.07		
						435	448	743.37	1484.73	1484.75	-0.01	0	86	1.82E-07	K.GVVDSDDLPLNVSR.E		20.68		
						494	503	570.27	1138.52	1138.57	-0.05	0	36	0.0172674	K.LGVIEDHSNR.T		13.9		
						548	557	575.9	1149.79	1149.53	0.26	0	64	2.66E-05	K.EAESSPFVER.L		17.22		
						725	733	497.26	992.5	992.52	-0.02	0	56	0.00018	R.SGYLLPDTK.A		19.94		
						745	754	543.27	1084.53	1084.58	-0.04	0	34	0.0285218	R.LSLNIDPDAK.V		20.55		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	27%	597	11	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												5	8
						78	92	584.94	1751.79	1751.85	-0.06	1	53	0.0003072	R.GETPRVEEVGPYTYR.E		19.61		
						83	92	606.78	1211.55	1211.58	-0.03	0	62	4.54E-05	R.VEEVGPYTYR.E		19.43		
						116	121	392.69	783.37	783.39	-0.02	0	33	0.0283057	K.AYVFER.D		17.45		
						116	129	537.7	1610.08	1609.77	0.3	1	40	0.0056213	K.AYVFERDQSVGDPK.I		18.11		
						154	161	481.75	961.48	961.52	-0.03	0	46	0.0022356	R.EIIEAMLK.A	Oxidation (M)	18.73		
						263	275	823.86	1645.71	1645.74	-0.04	0	45	0.002173	K.DEVLYVFPSDFCR.S		22.49		
						331	348	703.65	2107.93	2107.98	-0.05	0	61	4.29E-05	K.NGAPIIMSFPHFYQADER.F	Oxidation (M)	21.14		
						349	378	845.92	3379.63	3379.68	-0.04	0	46	0.0008962	R.FVSAIEGMHPNQEDHETFVDIN	Oxidation (M)	22.14		
						391	402	704.5	1406.99	1406.7	0.28	1	87	1.14E-07	K.KLDDFVETGDIR.T		20.39		
						392	402	640.3	1278.58	1278.61	-0.02	0	56	0.0001734	K.LDDFVETGDIR.T		20.61		
						460	477	640.29	1917.85	1917.89	-0.03	1	69	7.98E-06	K.GQGSMDEGTADERAPLIR.T	Oxidation (M)	15.11		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08238	5%	189	3	83554	5	P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4												5	1
						96	107	621.83	1241.65	1241.7	-0.05	0	58	0.0001175	K.ADLINNLGTIAK.S		21.09		
						379	392	757.37	1512.73	1512.78	-0.04	0	81	5.34E-07	R.GVVDSEDLPLNISR.E		21.05		
						492	502	625.28	1248.54	1248.61	-0.07	0	50	0.000794	K.EQVANSAFVER.V		15.93		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	5%	139	3	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												5	3
						156	165	545.27	1088.53	1088.55	-0.01	0	41	0.0070227	R.ALNEITESGR.I		14.81		
						275	285	563.8	1125.58	1125.61	-0.03	0	54	0.0002951	K.LGAILTPNDGR.C		19.74		
						311	325	836.93	1671.84	1671.89	-0.05	0	45	0.0022726	K.LAENNIQPIFAVTSR.M		21.31		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	8%	269	5	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												6	3
						50	60	614.85	1227.69	1227.62	0.07	0	62	5.11E-05	R.VEIIANDQGNR.I		15.73		
						82	96	839.42	1676.83	1676.8	0.03	0	83	3.02E-07	K.NQLTSNPENTVFDAK.R		20.57		
						186	197	617.32	1232.63	1232.62	0.01	0	37	0.0157666	K.DAGTIAGLNVMR.I	Oxidation (M)	20.48		
						345	352	459.75	917.48	917.47	0.01	0	37	0.0162374	K.VLEDSDLK.K		15.53		
						524	532	537.79	1073.56	1073.55	0.02	0	51	0.0006773	K.ITITNDQNR.L		14.01		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15586	6%	134	3	62840	8.6	P15586|GNS_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3												6	2
						410	421	676.33	1350.64	1350.64	-0.01	0	45	0.0019781	R.SDVLVEYQGEGR.N		20.17		
						494	502	493.29	984.57	984.55	0.02	0	34	0.0284326	K.TIDPELLGK.M		20.7		
						507	519	786.82	1571.63	1571.66	-0.03	0	55	0.0002476	R.LMMLQSCSGPTCR.T	2 Oxidation (M)	14.92		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	6%	175	4	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												6	1
						372	379	494.25	986.5	986.5	-0.01	0	38	0.0143555	R.ALELEQER.K		17.57		
						428	435	482.27	962.52	962.49	0.03	0	40	0.0079327	R.ISQLEMAR.Q	Oxidation (M)	13.92		
						449	458	603.79	1205.56	1205.56	0	0	56	0.0001644	K.AQMVQEDLEK.T	Oxidation (M)	14.3		
						569	577	585.76	1169.51	1169.5	0.01	1	41	0.0057262	K.QRIDEFESM.-	Oxidation (M)	19.3		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51659	4%	99	2	80092	9	P51659|DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3												6	1
						11	23	585.31	1168.61	1168.69	-0.08	0	33	0.0337237	R.VVLVTGAGAGLGR.A		20.43		
						316	331	734.41	1466.8	1466.74	0.07	0	65	1.96E-05	R.ATSTATSGFAGAIGQK.L		20.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04843	8%	238	4	68641	6	P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1												7	1
						66	80	830.42	1658.82	1658.89	-0.07	0	67	1.36E-05	R.ATSFLLALEPELEAR.L		24.23		
						117	126	490.81	979.6	979.57	0.03	0	54	0.0002692	K.LPVALDPGAK.I		20.33		
						269	278	530.28	1058.54	1058.54	0.01	0	54	0.0003436	R.QPDSGISSIR.S		16.16		
						525	536	651.45	1300.88	1300.74	0.15	0	63	3.25E-05	K.ALTSEIALLQSR.L		22.03		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04062	7%	239	4	60134	7.3	P04062|GLCM_HUMAN Glucosylceramidase OS=Homo sapiens GN=GBA PE=1 SV=3												7	3
						160	170	649.82	1297.62	1297.58	0.04	0	82	4.41E-07	R.VPMASCDFSIR.T	Oxidation (M)	20.46		
						317	324	510.27	1018.52	1018.51	0.01	0	45	0.0027316	R.LLMLDDQR.L	Oxidation (M)	20.11		
						435	447	730.9	1459.78	1459.79	-0.01	0	66	1.89E-05	R.NFVDSPIIVDITK.D		23.11		
						473	480	401.23	800.45	800.48	-0.03	0	46	0.0026062	R.VGLVASQK.N		13.92		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38606	7%	211	4	68660	5.3	P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2												7	2
						121	129	451.76	901.51	901.5	0.01	0	34	0.0378398	R.GVNVSALSR.D		18.37		
						257	265	481.78	961.55	961.54	0.01	0	53	0.0004744	K.TVISQSLSK.Y		16.44		
						281	289	525.75	1049.49	1049.48	0.01	0	43	0.0036192	R.GNEMSEVLR.D	Oxidation (M)	14.27		
						309	323	766.4	1530.79	1530.78	0	0	81	5.30E-07	R.TALVANTSNMPVAAR.E	Oxidation (M)	15.99		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11142	5%	122	3	71082	5.4	P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1												7	1
						26	36	614.81	1227.61	1227.62	-0.01	0	37	0.017062	K.VEIIANDQGNR.T		16.08		
						160	171	600.35	1198.68	1198.67	0.02	0	50	0.0008364	K.DAGTIAGLNVLR.I		22.24		
						349	357	541.3	1080.58	1080.56	0.02	0	35	0.0191184	K.LLQDFFNGK.E		22.42		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13796	4%	74	2	70815	5.2	P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5												7	1
						348	357	568.31	1134.61	1134.6	0.01	0	32	0.0454976	R.QFVTATDVVR.G		20.38		
						571	584	539.93	1616.78	1616.76	0.01	1	42	0.0040536	K.TENLNDDEKLNNAK.Y		13.88		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38646	4%	122	2	73920	5.9	P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2												7	1
						207	218	621.85	1241.68	1241.67	0.01	0	51	0.0006123	K.DAGQISGLNVLR.V		21.64		
						635	646	616.35	1230.69	1230.66	0.03	0	71	6.08E-06	R.QAASSLQQASLK.L		15.51		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10809	24%	683	12	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												8	2
						38	58	715.7	2144.07	2144.12	-0.05	0	65	1.90E-05	R.ALMLQGVDLLADAVAVTMGPK	2 Oxidation (M)	24.99		

						97	121	854.08	2559.21	2559.24	-0.04	0	60	5.15E-05	K.LVQDVANNTNEEAGDGTTTATVLAR.S		20.41		
						222	233	695.37	1388.72	1388.7	0.02	0	61	5.94E-05	R.GYISPYFINTSK.G		21.67		
						293	301	456.8	911.58	911.58	0	0	67	1.14E-05	K.VGLQVVAVK.A		20.33		
						302	309	417.19	832.37	832.38	-0.02	0	34	0.0377719	K.APGFGDNR.K		14.04		
						345	352	422.75	843.49	843.51	-0.01	0	35	0.0288692	K.VGEVIVTK.D		15.12		
						345	359	549.64	1645.91	1645.9	0.01	1	41	0.0057419	K.VGEVIVTKDDAMLLK.G	Oxidation (M)	20.54		
						406	417	617.3	1232.6	1232.59	0.01	0	86	1.89E-07	K.VGGTSDVEVNEK.K		13.77		
						406	420	544.95	1631.83	1631.81	0.01	2	60	6.20E-05	K.VGGTSDVEVNEKKDR.V		12.94		
						421	429	480.76	959.5	959.5	0	0	60	8.41E-05	R.VTDALNATR.A		14.22		
						471	481	401.58	1201.71	1201.71	0	1	53	0.0003903	R.TLKIPAMTIAK.N	Oxidation (M)	19.2		
						482	493	608.33	1214.65	1214.65	0	0	64	3.25E-05	K.NAGVEGSLIVEK.I		20.11		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11117	6%	112	3	48713	6.3	P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3												8	2
						35	41	456.26	910.52	910.53	-0.01	0	31	0.0471625	R.FVTLLYR.H		21.76		
						255	265	584.35	1166.68	1166.71	-0.04	0	41	0.0049292	R.LQGGVLLAQIR.K		21.71		
						349	356	524.78	1047.54	1047.52	0.02	0	40	0.0085643	R.CPLQDFLR.L		22.06		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30101	5%	75	2	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												9	1
						63	73	596.29	1190.56	1190.59	-0.03	0	40	0.0068339	R.LAPEYEAAATR.L		17.09		
						367	379	684.89	1367.76	1367.66	0.1	0	34	0.0262411	K.SEPIPESNDGPVK.V		16.17		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	4%	129	2	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												9	1
						317	326	611.82	1221.62	1221.62	0	0	48	0.0011244	R.LITLEEEMTK.Y	Oxidation (M)	20.09		
						425	436	655.36	1308.7	1308.59	0.11	0	81	5.39E-07	K.MDSTANEVEAVK.V	Oxidation (M)	14.73		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	18%	474	9	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												10	1
						46	58	720.35	1438.68	1438.66	0.02	0	70	6.57E-06	K.TGTAEMSSILEER.I	Oxidation (M)	19.62		
						59	73	788.42	1574.82	1574.78	0.04	0	75	2.19E-06	R.ILGADTSVDLEETGR.V		20.89		
						74	83	500.78	999.55	999.57	-0.02	0	34	0.0332276	R.VLSIGDGIAR.V		20.58		
						134	149	812.93	1623.85	1623.88	-0.03	0	48	0.0010837	R.TGAIVDVPVGEELLGR.V		22.58		
						150	161	586.32	1170.62	1170.62	-0.01	0	61	5.92E-05	R.VVDALGNAIDGK.G		20.45		
						150	167	570.98	1709.91	1709.93	-0.02	1	45	0.0021432	R.VVDALGNAIDGKGPIGSK.T		20.54		
						172	182	374.24	1119.71	1119.71	0	1	51	0.0005418	R.VGLKAPGIIPR.I		20.28		
						195	204	513.8	1025.58	1025.59	0	0	48	0.0009629	K.AVDSLVPIGR.G		20.93		
						254	261	423.26	844.5	844.5	0	0	44	0.0039423	R.STVAQLVK.R		16.91		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21281	17%	423	8	56807	5.6	P21281|VATB2_HUMAN Vacuolar ATP synthase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3												10	1
						30	37	437.24	872.46	872.47	-0.01	0	63	5.56E-05	R.EQALAVSR.N		13.95		
						83	93	545.79	1089.56	1089.57	-0.01	0	65	2.72E-05	R.SGQVLEVSGSK.A		14.55		
						94	108	760.89	1519.78	1519.79	-0.01	0	86	1.78E-07	K.AVVQVFEGTSGIDAK.K		21.1		
						121	130	560.76	1119.51	1119.52	-0.01	0	49	0.0010262	R.TPVSEDMLGR.V	Oxidation (M)	14.64		
						131	141	397.21	1188.62	1188.63	0	0	35	0.0253664	R.VFNGSGKPIDR.G		13.6		
						387	400	799.03	1596.05	1595.9	0.15	0	53	0.000317	R.QIYPPINVLPSLSR.L		22.71		
						404	412	469.23	936.45	936.43	0.01	0	32	0.0375993	K.SAIGEGMTR.K	Oxidation (M)	12.89		
						461	471	654.82	1307.62	1307.63	-0.01	0	41	0.0055293	R.NFIAQGPYENR.T		20.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08670	17%	360	7	53676	5.1	P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4												10	5
						14	28	504.22	1509.65	1509.7	-0.05	0	41	0.0052401	R.MFGGPGTASRPSSSR.S	Oxidation (M)	13.34		
						114	120	435.73	869.44	869.43	0.01	0	33	0.0301907	R.FANYIDK.V		18.79		
						208	217	544.76	1087.5	1087.53	-0.03	0	67	1.69E-05	R.QDVDNASLAR.L		13.99		
						274	282	512.24	1022.46	1022.5	-0.04	0	47	0.0013043	R.QQYESVAAK.N		13.29		
						295	304	547.26	1092.51	1092.52	-0.01	0	57	0.0001497	K.FADLSEAANR.N		19.58		
						365	378	589.61	1765.8	1765.8	0.01	1	45	0.0017543	R.LQDEIQNMKEEMAR.H	2 Oxidation (M)	13.56		
						411	424	785.96	1569.9	1569.89	0.01	0	38	0.0116909	R.ISLPLPNFSSLNLR.E		23.94		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08962	10%	139	3	26474	8.1	P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2												10	17
						111	120	637.28	1272.56	1272.56	0	0	62	4.45E-05	K.VMSEFNNNFR.Q	Oxidation (M)	19.67		
						121	128	527.23	1052.44	1052.46	-0.02	0	44	0.0026892	R.QQMENYPK.N	Oxidation (M)	12.93		
						139	144	378.18	754.35	754.33	0.02	0	33	0.0283704	R.MQADFK.C	Oxidation (M)	13.03		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8IV08	8%	202	4	55127	6	Q8IV08|PLD3_HUMAN Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1												10	5
						150	157	449.76	897.51	897.53	-0.02	0	32	0.0449924	R.QLQTLAPK.G		14.68		
						310	319	542.81	1083.6	1083.6	-0.01	0	55	0.0002447	K.ALLNVVDNAR.S		20.76		
						397	408	658.35	1314.69	1314.69	-0.01	0	68	1.38E-05	K.LFVVPADEAQAR.I		20.8		
						458	466	538.8	1075.58	1075.6	-0.02	0	48	0.0011621	R.SQLEAIFLR.D		22.36		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UHL4	7%	116	3	54749	5.9	Q9UHL4|DPP2_HUMAN Dipeptidyl-peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=2												10	2
						26	34	508.74	1015.47	1015.47	0	0	38	0.0147418	R.APDPGFQER.F		14.51		
						113	123	596.31	1190.6	1190.6	0	0	35	0.0223702	K.SLPFGAQSTQR.G		20.02		
						204	215	647.3	1292.58	1292.59	0	0	43	0.0033493	R.DVTADFEGQSPK.C		20.1		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P34897	6%	152	3	56414	8.8	P34897|GLYM_HUMAN Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3												10	1
						201	214	774.89	1547.77	1547.83	-0.07	0	45	0.0022843	K.TGLIDYNQLALTAR.L		22.19		
						360	368	503.27	1004.52	1004.5	0.03	0	41	0.0061598	R.AMADALLER.G	Oxidation (M)	19.54		
						426	434	443.25	884.49	884.51	-0.02	0	36	0.02169	R.LGAPALTSR.Q		16.95		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O95766	5%	105	2	56286	6.1	O95766|CG028_HUMAN UPF0550 protein C7orf28 OS=Homo sapiens GN=C7orf28A PE=1 SV=1												10	1
						247	255	549.29	1096.56	1096.59	-0.03	0	42	0.0043438	K.YLTTSLFPR.H		21.84		
						282	295	757.88	1513.75	1513.78	-0.03	0	34	0.0266633	R.FLTGPLNLNDPDAK.C		21.89		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P09622	4%	117	2	54686	7.6	P09622|DLDH_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=1												10	1
						167	177	552.78	1103.55	1103.55	0.01	0	80	8.55E-07	K.ADGGTQVIDTK.N		13.82		
						496	505	504.27	1006.52	1006.51	0.01	0	38	0.0125515	R.EANLAASFGK.S		20.41		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	8%	211	4	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												11	27
						147	154	435.77	869.52	869.53	-0.02	0	42	0.0045277	K.QLIVGVNK.M		17.9		
						248	255	488.27	974.53	974.54	-0.01	0	36	0.0211882	R.LPLQDVYK.I		20.57		
						256	266	513.3	1024.58	1024.6	-0.02	0	58	0.000111	K.IGGIGTVPVGR.V		20.09		
						431	439	457.78	913.54	913.56	-0.02	0	76	1.92E-06	R.QTVAVGVIK.A		17.94		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P80723	26%	143	3	22680	4.6	P80723|BASP_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2												12	1
						98	121	766.68	2297.03	2297.13	-0.1	1	47	0.0011993	K.AEPPKAPEQEQAAPGPAAGGEAPK.A		13.93		
						164	184	644.96	1931.85	1931.87	-0.02	0	38	0.0087014	K.SDGAPASDSKPGSSEAAPSSK.E		12.67		
						185	198	693.81	1385.61	1385.67	-0.06	0	58	0.0001064	K.ETPAATEAPSSTPK.A		13.35		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
A6NI72	12%	188	3	45017	9.2	A6NI72|NCF1B_HUMAN Putative neutrophil cytosol factor 1B OS=Homo sapiens GN=NCF1B PE=5 SV=2												12	1
						57	71	852.4	1702.78	1702.8	-0.01	0	73	3.35E-06	K.EMFPIEAGAINPENR.I	Oxidation (M)	21.21		
						148	163	875.45	1748.89	1748.93	-0.04	0	56	0.000154	K.STATDITGPIILQTYR.A		22.04		
						339	355	612.28	1833.82	1833.9	-0.08	0	59	7.24E-05	R.QARPGPQSPGSPLEEER.Q		14.99		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14254	9%	156	3	41830	5.2	Q14254|FLOT2_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=1												12	1
						218	228	635.34	1268.66	1268.71	-0.05	0	32	0.0476539	K.QIAVEAQEILR.T		21.25		
						259	269	600.33	1198.65	1198.66	-0.01	0	58	0.0001237	K.QVLLAQAEAEK.I		19.73		
						308	321	742.43	1482.85	1482.85	0.01	0	34	0.0237813	K.MALVLEALPQIAAK.I	Oxidation (M)	22.56		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BTU6	9%	149	4	54388	8.5	Q9BTU6|P4K2A_HUMAN Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1												12	1
						116	123	465.24	928.46	928.5	-0.03	0	33	0.0419704	R.QAELAIER.C		16.64		
						130	146	630.33	1887.97	1887.91	0.06	1	33	0.0274591	R.IYQGSSGSYFVKDPQGR.I		19.77		
						203	210	477.29	952.56	952.57	-0.01	0	39	0.007139	K.LELNIVPR.T		21.3		
						297	305	552.33	1102.65	1102.68	-0.02	0	43	0.004145	R.LVVLDYIIR.N		23.48		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O14773	9%	209	4	61723	6	O14773|TPP1_HUMAN Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2												12	6
						246	259	492.25	1473.73	1473.75	-0.02	0	51	0.0005581	R.LFGGNFAHQASVAR.V		20.03		
						340	346	425.7	849.39	849.43	-0.04	0	42	0.0050291	R.VNTELMK.A	Oxidation (M)	13.09		
						493	506	512.97	1535.9	1535.89	0	0	43	0.0031884	R.ILSGRPPLGFLNPR.L		21.38		
						507	520	535.61	1603.8	1603.81	-0.01	0	73	3.38E-06	R.LYQQHGAGLFDVTR.G		20.6		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75955	8%	156	3	47554	7.1	O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3												12	2
						41	51	608.38	1214.74	1214.72	0.01	0	47	0.0018149	R.ISLNTLTLNVK.S		21.82		
						262	274	735.36	1468.71	1468.76	-0.05	0	50	0.0007454	R.AQQVAVQEQEIAR.R		16.22		
						393	403	608.33	1214.64	1214.69	-0.05	0	65	2.41E-05	K.VTGEVLDILTR.L		22.38		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y6N5	6%	73	2	50214	9.2	Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1												12	1
						66	79	735.38	1468.74	1468.75	-0.01	0	37	0.0152549	K.VGAENVAIVEPSER.H		19.99		
						345	358	672.37	1342.73	1342.72	0.01	0	36	0.0171465	K.TAAAVAAQSGILDR.T		20.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49411	6%	119	2	49852	7.3	P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2												12	1
						239	252	771.88	1541.75	1541.85	-0.09	0	63	3.41E-05	K.LLDAVDTYIPVPAR.D		22.25		
						316	327	593.3	1184.58	1184.61	-0.03	0	56	0.0002089	R.AEAGDNLGALVR.G		20.64		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P39656	5%	103	2	48893	5.4	P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2												12	1
						30	40	635.39	1268.77	1268.75	0.02	0	61	5.26E-05	R.TLVLLDNLNVR.E		22.64		
						223	233	585.34	1168.66	1168.69	-0.03	0	42	0.0046552	K.NTLLIAGLQAR.N		21.56		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15848	4%	72	2	60163	8.4	P15848|ARSB_HUMAN Arylsulfatase B OS=Homo sapiens GN=ARSB PE=1 SV=1												12	1

						328	338	544.32	1086.63	1086.64	-0.01	0	40	0.0097344	R.GVGFVASPLLK.Q		21.73		
						379	388	515.79	1029.56	1029.51	0.05	0	32	0.047547	K.TISEGSPSPR.I		13.17		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60709	11%	167	3	42052	5.3	P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1												13	4
						51	62	452.21	1353.6	1353.62	-0.01	1	45	0.002151	K.DSYVGDEAQSKR.G		13.35		
						96	113	652.02	1953.04	1953.06	-0.02	0	54	0.0002307	R.VAPEEHPVLLTEAPLNPK.A		20.72		
						360	372	506.23	1515.66	1515.7	-0.04	0	67	1.32E-05	K.QEYDESGPSIVHR.K		16.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04075	13%	194	4	39851	8.3	P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2												14	1
						29	42	666.85	1331.68	1331.69	-0.01	0	63	4.21E-05	K.GILAADESTGSIAK.R		19.94		
						61	69	522.78	1043.55	1043.56	-0.01	0	43	0.0039181	R.QLLLTADDR.V		20.38		
						88	99	448.24	1341.7	1341.7	-0.01	0	33	0.0334837	K.ADDGRPFPQVIK.S		20.16		
						332	342	566.78	1131.54	1131.57	-0.03	0	55	0.0002663	R.ALANSLACQGK.Y		15.34		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04899	9%	140	3	40995	5.3	P04899|GNAI2_HUMAN Guanine nucleotide-binding protein G(i), alpha-2 subunit OS=Homo sapiens GN=GNAI2 PE=1 SV=3												14	1
						36	46	529.31	1056.6	1056.62	-0.02	0	64	3.16E-05	K.LLLLGAGESGK.S		21.2		
						87	100	775.87	1549.73	1549.72	0.01	0	44	0.0024601	K.AMGNLQIDFADPSR.A	Oxidation (M)	21.24		
						199	206	463.21	924.4	924.41	-0.02	0	32	0.0422368	K.MFDVGGQR.S	Oxidation (M)	15.29		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08754	8%	130	3	41076	5.5	P08754|GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3												14	1
						36	46	529.31	1056.6	1056.62	-0.02	0	64	3.16E-05	K.LLLLGAGESGK.S		21.2		
						91	100	373.87	1118.59	1118.61	-0.01	1	34	0.0297297	R.LKIDFGEAAR.A		20.42		
						198	205	463.21	924.4	924.41	-0.02	0	32	0.0422368	K.MFDVGGQR.S	Oxidation (M)	15.29		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61421	11%	246	4	40759	4.9	P61421|VA0D1_HUMAN Vacuolar proton pump subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1												15	1
						188	195	510.74	1019.47	1019.5	-0.03	0	50	0.0007965	K.AYLESFYK.F		21.08		
						247	257	615.86	1229.7	1229.68	0.02	0	60	7.14E-05	R.LYPEGLAQLAR.A		21.56		
						258	265	484.2	966.39	966.43	-0.04	0	37	0.0126641	R.ADDYEQVK.N		13.56		
						276	288	652.81	1303.6	1303.64	-0.04	0	67	1.46E-05	K.LLFEGAGSNPGDK.T		20.52		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07355	32%	698	13	38808	7.6	P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2												16	3
						2	10	564.77	1127.53	1127.56	-0.03	0	49	0.0009783	M.STVHEILCK.L	Acetyl (Protein N-term)	20.34		
						29	37	543.75	1085.5	1085.48	0.02	0	38	0.0135923	K.AYTNFDAER.D		17.19		
						29	47	719.02	2154.05	2154.06	-0.01	1	53	0.0002754	K.AYTNFDAERDALNIETAIK.T		21.91		
						38	47	544.28	1086.55	1086.59	-0.04	0	65	2.59E-05	R.DALNIETAIK.T		21.04		
						48	63	591.36	1771.04	1770.98	0.06	1	39	0.0076837	K.TKGVDEVTIVNILTNR.S		22.52		
						50	63	771.93	1541.85	1541.84	0.01	0	89	8.23E-08	K.GVDEVTIVNILTNR.S		23.64		
						69	77	556.29	1110.57	1110.55	0.03	0	40	0.0072584	R.QDIAFAYQR.R		20.26		
						105	115	611.77	1221.52	1221.59	-0.07	0	75	2.29E-06	K.TPAQYDASELK.A		16.64		
						136	145	622.78	1243.54	1243.62	-0.07	0	57	0.000138	R.TNQELQEINR.V		15.43		
						153	169	647.31	1938.92	1938.95	-0.04	2	58	8.50E-05	K.TDLEKDIISDTSGDFRK.L		21		
						158	168	613.27	1224.52	1224.56	-0.04	0	41	0.0049133	K.DIISDTSGDFR.K		21.34		
						170	176	381.23	760.45	760.45	0	0	49	0.0012773	K.LMVALAK.G	Oxidation (M)	17.09		
						314	324	711.35	1420.68	1420.69	-0.01	0	47	0.0013126	K.SLYYYIQQDTK.G		21.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40926	17%	235	5	35965	8.9	P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=2												16	2
						177	185	496.76	991.5	991.53	-0.03	0	57	0.0001605	R.ANTFVAELK.G		20.47		
						216	229	780.86	1559.71	1559.79	-0.08	0	50	0.0006952	K.VDFPQDQLTALTGR.I		22.26		
						230	239	537.27	1072.53	1072.58	-0.05	0	36	0.0208317	R.IQEAGTEVVK.A		13.85		
						242	257	735.84	1469.67	1469.69	-0.03	0	59	9.16E-05	K.AGAGSATLSMAYAGAR.F	Oxidation (M)	19.3		
						315	324	566.78	1131.54	1131.58	-0.04	0	34	0.0322387	K.MISDAIPELK.A	Oxidation (M)	20.91		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q86Y82	12%	82	2	31736	5.5	Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1												16	2
						83	97	813.92	1625.82	1625.86	-0.04	0	45	0.0019915	K.ELGSLPLPLSTSEQR.Q		22		
						106	122	652.38	1954.12	1953.94	0.18	0	37	0.0110533	R.LMNDFSAALNNFQAVQR.R	Oxidation (M)	22.3		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04406	11%	179	3	36201	8.6	P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3												16	2
						6	13	403.21	804.4	804.42	-0.02	0	36	0.0222938	K.VGVNGFGR.I		16.95		
						67	80	807.47	1612.93	1612.89	0.04	0	90	6.90E-08	K.LVINGNPITIFQER.D		22.95		
						201	215	706.4	1410.79	1410.78	0	0	53	0.0003069	R.GALQNIIPASTGAAK.A		20.73		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50897	14%	213	4	34627	6.1	P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1												17	9
						105	122	673.32	2016.94	2016.95	-0.01	0	41	0.0042649	K.LQQGYNAMGFSQGGQFLR.A	Oxidation (M)	21.09		
						165	174	526.73	1051.45	1051.57	-0.12	1	41	0.005735	R.KTLNAGAYSK.V		12.98		
						166	174	462.73	923.44	923.47	-0.03	0	50	0.0005969	K.TLNAGAYSK.V		13.89		
						254	268	897.45	1792.88	1792.88	0	0	80	5.68E-07	K.ETIPLQETSLYTQDR.L		21.13		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UBR2	7%	113	2	34530	6.7	Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1												17	1

						70	81	654.83	1307.64	1307.65	-0.01	0	56	0.0001613	R.NVDGVNYASITR.N		20.22		
						190	199	505.74	1009.46	1009.48	-0.03	0	57	0.0001262	R.VGDYGSLSGR.E		15.9		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92820	6%	91	2	36340	6.7	Q92820|GGH_HUMAN Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2												17	2
						63	70	433.72	865.42	865.43	0	0	41	0.0054082	K.YLESAGAR.V		13.55		
						213	224	678.81	1355.61	1355.67	-0.06	0	50	0.0008072	K.FFNVLTTNTDGK.I		21.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P45880	7%	95	2	32060	7.5	P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2												18	2
						236	247	647.33	1292.64	1292.66	-0.02	0	39	0.0079975	K.YQLDPTASISAK.V		20.28		
						268	277	508.78	1015.55	1015.59	-0.04	0	56	0.0002396	K.LTLSALVDGK.S		21.71		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21796	7%	116	2	30868	8.6	P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2												18	2
						164	174	607.31	1212.61	1212.61	0	0	70	7.43E-06	R.VTQSNFAVGYK.T		19.41		
						257	266	515.81	1029.6	1029.61	-0.01	0	46	0.0019302	K.LTLSALLDGK.N		22.75		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q3B8N2	6%	90	2	39977	9.6	Q3B8N2|LEG9B_HUMAN Galectin-9B OS=Homo sapiens GN=LGALS9B PE=2 SV=3												18	3
						241	254	721.43	1440.85	1440.83	0.02	0	52	0.0004442	K.SIILSGTVLPSAQR.F		21.58		
						273	280	475.24	948.47	948.47	0	0	39	0.0112365	R.FDENAVVR.N		16.71		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27105	25%	412	6	31882	7.7	P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3												19	4
						15	25	407.53	1219.58	1219.61	-0.03	1	41	0.0066635	R.LPDSFKDSPSK.G		14.82		
						126	144	965.51	1929.01	1928.99	0.02	0	110	5.82E-10	R.VQNATLAVANITNADSATR.L		20.68		
						219	232	488.22	1461.65	1461.72	-0.07	1	53	0.0003274	R.AKVIAAEGEMNASR.A	Oxidation (M)	12.9		
						221	232	632.29	1262.57	1262.59	-0.02	0	71	6.44E-06	K.VIAAEGEMNASR.A	Oxidation (M)	13.19		
						236	251	866.46	1730.9	1730.89	0.01	0	61	5.02E-05	K.EASMVITESPAALQLR.Y	Oxidation (M)	21.12		
						252	263	676.38	1350.75	1350.74	0.01	0	77	1.38E-06	R.YLQTLTTIAAEK.N		20.9		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36543	13%	127	3	26186	7.7	P36543|VATE1_HUMAN Vacuolar proton pump subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1												19	1
						2	10	494.75	987.48	987.49	-0.01	0	35	0.0323412	M.ALSDADVQK.Q	Acetyl (Protein N-term)	18.95		
hier						70	80	669.33	1336.64	1336.62	0.01	0	54	0.0002581	K.IQMSNLMNQAR.L	2 Oxidation (M)	13.36		
						213	222	495.76	989.5	989.5	0	0	38	0.012459	R.GALFGANANR.K		18.36		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07339	22%	399	8	45037	6.1	P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1												20	14
						177	184	440.24	878.47	878.45	0.02	0	55	0.0002227	R.QVFGEATK.Q		14.34		
						185	194	514.82	1027.62	1027.57	0.05	0	37	0.0137118	K.QPGITFIAAK.F	Gln->pyro-Glu (N-term Q)	22.14		
						195	205	628.31	1254.61	1254.61	0	0	56	0.0001606	K.FDGILGMAYPR.I	Oxidation (M)	21.44		
						206	222	988.01	1974	1974.02	-0.02	0	38	0.008555	R.ISVNNVLPVFDNLMQQK.L	Oxidation (M)	23.13		
						236	253	902.43	1802.85	1802.8	0.05	0	59	7.42E-05	R.DPDAQPGGELMLGGTDSK.Y	Oxidation (M)	20.18		
						332	341	521.84	1041.66	1041.64	0.02	0	45	0.0028086	K.VSTLPAITLK.L		21.05		
						349	357	533.29	1064.56	1064.54	0.02	0	58	0.000112	K.LSPEDYTLK.V		20.32		
						404	411	410.72	819.43	819.42	0.01	0	49	0.0009919	R.VGFAEAAR.L		15.22		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07858	5%	74	2	38766	5.9	P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3												20	4
						80	87	438.75	875.48	875.45	0.03	0	42	0.0060122	K.LPASFDAR.E		18.63		
						238	245	499.75	997.49	997.48	0.01	0	34	0.0289386	K.DIMAEIYK.N	Oxidation (M)	19.97		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51572	15%	121	3	28031	8.4	P51572|BAP31_HUMAN B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3												21	1
						168	182	572.22	1713.64	1713.85	-0.22	1	52	0.0004368	K.LDVGNAEVKLEEENR.S		20.75		
						191	199	502.72	1003.42	1003.55	-0.13	1	33	0.0405223	K.LKDELASTK.Q		13.71		
						233	246	516.18	1545.53	1545.73	-0.21	2	36	0.0151856	K.LQAAVDGPMDKKEE.-	Oxidation (M)	13.76		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P02743	13%	146	3	25485	6.1	P02743|SAMP_HUMAN Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2												21	2
						65	76	703.75	1405.49	1405.66	-0.17	0	46	0.0018809	R.AYSLFSYNTQGR.D		22.14		
						77	84	497.2	992.4	992.52	-0.12	0	49	0.000824	R.DNELLVYK.E		21.36		
						87	96	578.73	1155.45	1155.59	-0.14	0	51	0.0005862	R.VGEYSLYIGR.H		21.71		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9NX63	7%	111	2	26421	8.5	Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1												21	1
						28	35	473.24	944.46	944.49	-0.04	0	60	8.67E-05	R.LSENVIDR.M		16.7		
						96	104	487.19	972.37	972.5	-0.13	0	51	0.00071	R.AAANEQLTR.A		13.54		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51148	23%	247	4	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												23	2
						24	34	543.3	1084.59	1084.65	-0.06	0	42	0.0044893	K.LVLLGESAVGK.S		21.89		
						122	135	698.37	1394.73	1394.79	-0.06	0	76	1.49E-06	R.QASPNIVIALAGNK.A		22.47		
						185	196	606.28	1210.54	1210.57	-0.03	0	59	7.60E-05	K.NEPQNATGAPGR.N		13.13		
						199	210	650.29	1298.57	1298.62	-0.05	0	69	9.77E-06	R.GVDLQENNPASR.S		15.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P51149	10%	120	3	23760	6.4	P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1												24	3
						22	31	607.25	1212.49	1212.58	-0.09	0	44	0.0031618	K.TSLMNQYVNK.K	Oxidation (M)	15.7		
						22	32	447.88	1340.63	1340.68	-0.05	1	38	0.0126032	K.TSLMNQYVNKK.F	Oxidation (M)	14.18		
						39	48	518.77	1035.52	1035.56	-0.04	0	38	0.0110576	K.ATIGADFLTK.E		22		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q06830	10%	74	2	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												24	1
						121	128	447.7	893.39	893.42	-0.03	0	33	0.0315408	K.ADEGISFR.G		20.37		
						141	151	606.31	1210.61	1210.67	-0.06	0	40	0.0062227	R.QITVNDLPVGR.S		21.48		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07686	3%	70	2	63527	6.3	P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3												24	4
						222	230	513.71	1025.41	1025.49	-0.07	0	36	0.0146354	K.TLDAMAFNK.F	Oxidation (M)	19.62		
						273	279	449.19	896.37	896.44	-0.07	0	34	0.0254489	R.MVIEYAR.L	Oxidation (M)	15.89		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63000	27%	223	5	21835	8.8	P63000|RAC1_HUMAN Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1												25	1
						6	16	530.75	1059.48	1059.54	-0.06	0	36	0.0207034	K.CVVVGDGAVGK.T		15.78		
						134	147	760.37	1518.73	1518.81	-0.08	0	44	0.0028877	K.LTPITYPQGLAMAK.E	Oxidation (M)	21.65		
						154	163	620.78	1239.55	1239.59	-0.04	0	69	8.91E-06	K.YLECSALTQR.G		20.49		
						167	174	475.73	949.44	949.49	-0.04	0	39	0.008571	K.TVFDEAIR.A		21.27		
						175	183	490.76	979.5	979.55	-0.06	0	34	0.0260679	R.AVLCPPPVK.K		19.69		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51153	12%	92	2	22988	9.3	P51153|RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=2 SV=1												25	5
						11	21	536.29	1070.56	1070.63	-0.07	0	41	0.0061996	K.LLLIGDSGVGK.T		22.31		
						154	167	765.32	1528.62	1528.68	-0.06	0	51	0.000541	K.SSMNVDEAFSSLAR.D	Oxidation (M)	22.01		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9NVJ2	10%	125	2	21753	8.7	Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1												26	7
						133	141	507.73	1013.44	1013.5	-0.06	0	62	5.50E-05	R.DLPNALDEK.Q		20.69		
						147	155	532.23	1062.44	1062.51	-0.07	0	63	3.88E-05	K.MNLSAIQDR.E	Oxidation (M)	16.05		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23284	27%	371	6	22785	9.3	P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=1												27	2
						44	51	430.68	859.35	859.4	-0.06	0	75	3.18E-06	R.IGDEDVGR.V		14.11		
						52	59	440.74	879.47	879.52	-0.05	0	33	0.0314743	R.VIFGLFGK.T		24.01		
						64	76	682.81	1363.61	1363.7	-0.09	0	78	1.16E-06	K.TVDNFVALATGEK.G		22.84		
						88	101	548.25	1641.73	1641.82	-0.09	1	54	0.0002469	R.VIKDFMIQGGDFTR.G	Oxidation (M)	21.45		
						91	101	651.75	1301.48	1301.57	-0.09	0	48	0.0010011	K.DFMIQGGDFTR.G	Oxidation (M)	22.1		
						138	150	729.33	1456.64	1456.72	-0.08	0	84	2.85E-07	K.DTNGSQFFITTVK.T		22.71		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62913	15%	118	2	20468	9.6	P62913|RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2												27	1
						2	13	730.75	1459.49	1459.64	-0.15	1	51	0.0005503	M.AQDQGEKENPMR.E	Acetyl (Protein N-term); Oxidation (M)	13.27		
						39	52	773.87	1545.72	1545.84	-0.12	0	67	1.23E-05	K.VLEQLTGQTPVFSK.A		22.01		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61225	13%	86	2	20719	4.7	P61225|RAP2B_HUMAN Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1												27	1
						6	16	486.26	970.51	970.58	-0.07	0	35	0.0224771	K.VVVLGSGGVGK.S		19.42		
						151	162	674.82	1347.63	1347.7	-0.07	0	51	0.0006222	K.ASVDELFAEIVR.Q		25.46		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61916	13%	109	2	16902	7.6	P61916|NPC2_HUMAN Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1												29	6
						26	35	525.22	1048.43	1048.49	-0.05	0	43	0.0037391	K.DCGSVDGVIK.E		18.52		
						95	103	508.72	1015.42	1015.51	-0.09	0	66	2.27E-05	K.SGINCPIQK.D		14.72		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13488	4%	204	4	93680	6.6	Q13488|VPP3_HUMAN Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 OS=Homo sapiens GN=TCIRG1 PE=1 SV=2												30	3
						29	38	566.76	1131.5	1131.63	-0.13	0	71	6.54E-06	R.LGELGLVEFR.D		23.25		
						39	49	604.26	1206.51	1206.6	-0.09	0	59	9.69E-05	R.DLNASVSAFQR.R		21.39		
						75	83	446.24	890.47	890.56	-0.09	0	42	0.0053745	R.AGLVLPPPK.G		20.38		
						104	109	365.18	728.35	728.42	-0.07	0	33	0.0499307	R.LAQELR.D		14.03		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10253	4%	168	3	106126	5.6	P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=2												30	6
						838	849	643.81	1285.61	1285.71	-0.1	0	55	0.000242	R.QQPMALAVALTK.G	Oxidation (M)	21.25		
						871	881	619.79	1237.57	1237.68	-0.12	0	39	0.0079086	R.GAYTQVIFLAR.N		22.84		
						892	903	615.78	1229.55	1229.66	-0.11	0	74	3.12E-06	R.VTSEGAGLQLQK.V		17.25		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9BV40	47%	186	4	11488	6.7	Q9BV40|VAMP8_HUMAN Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1												32	1
						1	14	782.77	1563.52	1563.66	-0.14	1	42	0.0034399	-.MEEASEGGGNDRVR.N	Acetyl (Protein N-term); Oxidation (M)	13.7		
						15	24	551.73	1101.45	1101.57	-0.12	0	56	0.0001979	R.NLQSEVEGVK.N		20.47		
						25	33	560.71	1119.41	1119.53	-0.12	0	36	0.0192278	K.NIMTQNVER.I	Oxidation (M)	13.88		
						46	59	550.24	1647.7	1647.77	-0.07	1	54	0.0002852	R.NKTEDLEATSEHFK.T		17		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75348	31%	223	3	13863	8.9	O75348|VATG1_HUMAN Vacuolar proton pump subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3												32	1

						2	17	913.93	1825.84	1825.96	-0.12	1	87	1.12E-07	M.ASQSQGIQQLLQAEKR.A	Acetyl (Protein N-term)	22.27		
						38	48	683.24	1364.46	1364.62	-0.16	0	70	6.53E-06	K.EEAQAEIEQYR.L		20.25		
						81	89	594.75	1187.49	1187.6	-0.11	0	66	1.82E-05	K.MTILQTYFR.Q	Oxidation (M)	22.92		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62888	17%	86	2	12947	9.7	P62888|RL30_HUMAN 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2												32	1
						10	17	453.18	904.35	904.46	-0.11	0	34	0.0308709	K.SLESINSR.L		14.88		
						45	56	677.3	1352.59	1352.76	-0.17	0	54	0.0002901	K.LVILANNCPALR.K		21.71		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P12830	2%	118	2	97852	4.6	P12830|CADH1_HUMAN Epithelial cadherin OS=Homo sapiens GN=CDH1 PE=1 SV=3												32	1
						66	74	537.21	1072.4	1072.52	-0.12	0	48	0.0012837	R.TAYFSLDTR.F		21.66		
						77	86	494.73	987.45	987.56	-0.11	0	69	1.06E-05	K.VGTDGVITVK.R		19.01		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q7Z7K0	17%	67	2	12823	8.9	Q7Z7K0|COXAM_HUMAN COX assembly mitochondrial protein homolog OS=Homo sapiens GN=CMC1 PE=2 SV=1												33	1
						2	11	589.23	1176.45	1176.59	-0.14	0	33	0.0368933	M.ALDPADQHLR.H	Acetyl (Protein N-term)	20.6		
						99	106	467.2	932.39	932.5	-0.11	1	35	0.0275585	R.LQKLPTSM.-	Oxidation (M)	15		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13510	5%	90	2	45077	7.5	Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4												34	5
						82	92	612.26	1222.5	1222.6	-0.1	0	39	0.0087254	K.NMINTFVPSGK.V	Oxidation (M)	20.59		
						93	100	482.21	962.4	962.47	-0.07	0	51	0.0006655	K.VMQVVDEK.L	Oxidation (M)	13.55		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P01024	2%	200	4	188569	6	P01024|CO3_HUMAN Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2												34	4
						842	848	444.19	886.37	886.45	-0.09	0	47	0.0019026	R.NEQVEIR.A		14.37		
						882	891	574.78	1147.54	1147.63	-0.09	0	36	0.0166579	R.HQQTVTIPPK.S		13.77		
						892	904	701.36	1400.71	1400.83	-0.12	0	36	0.0168335	K.SSLSVPYVIVPLK.T		23.35		
						905	913	501.9	1001.79	1001.54	0.25	0	80	4.40E-07	K.TGLQEVEVK.A		18.83		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61604	33%	153	3	10925	8.9	P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2												35	2
						41	54	658.33	1314.64	1314.75	-0.11	0	75	2.74E-06	K.VLQATVVAVGSGSK.G		20.35		
						57	66	507.23	1012.45	1012.56	-0.11	0	32	0.0474403	K.GGEIQPVSVK.V		15.88		
						71	80	538.75	1075.48	1075.59	-0.11	0	47	0.0016797	K.VLLPEYGGTK.V		20.97		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63218	26%	104	2	7428	9.9	P63218|GBG5_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3												36	1
						2	12	555.73	1109.44	1109.54	-0.1	1	65	2.14E-05	M.SGSSSVAAMKK.V	Acetyl (Protein N-term); Oxidation (M)	12.92		
						19	25	386.68	771.34	771.42	-0.09	0	39	0.0113365	R.LEAGLNR.V		14.53		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07602	6%	157	3	59899	5.1	P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2												36	2
						233	242	539.21	1076.41	1076.5	-0.09	0	37	0.0138157	R.LGPGMADICK.N	Oxidation (M)	15.95		
						430	438	507.74	1013.46	1013.58	-0.12	0	79	1.12E-06	K.QEILAALEK.G		21.73		
						439	449	656.24	1310.46	1310.6	-0.14	0	41	0.0045646	K.GCSFLPDPYQK.Q		21.86		

***Footnotes to Supplemental Table 9:**
Data sets were searched with the Mascot search engine (see Perkins et al. (1999) *Electrophoresis* **20**, 3551-3567).
Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).
Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.
Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest gel slice in which the protein was identified, and the total # of adjacent gel slices in which the protein was found).
Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 10. Proteins identified by HPLC-MS/MS in 3-day latex bead human THP-1 phagosome preparation.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1.

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27105	26%	283	6	31882	7.7	P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3												1	5
						98	111	801.53	1601.04	1600.87	0.17	0	35	0.0228255	R.TISFDIPPQEILTK.D		33.11		
						219	232	488.3	1461.88	1461.72	0.15	1	39	0.0090859	R.AKVIAAEGEMNASR.A	Oxidation (M)	18.57		
						221	232	632.37	1262.72	1262.59	0.12	0	72	4.30E-06	K.VIAAEGEMNASR.A	Oxidation (M)	19.01		
						236	251	866.55	1731.09	1730.89	0.2	0	38	0.0096185	K.EASMVITESPAALQLR.Y	Oxidation (M)	30.53		
						252	263	676.46	1350.91	1350.74	0.17	0	67	1.13E-05	R.YLQTLTTIAAEK.N		30.31		
						264	283	1072.2	2142.39	2142.18	0.21	0	31	0.0413291	K.NSTIVFPLPIDMLQGIIGAK.H	Oxidation (M)	37.1		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11279	9%	182	3	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												1	12
						138	146	517.33	1032.65	1032.55	0.1	0	53	0.0004044	K.TVESITDIR.A		28.65		
						299	314	923.61	1845.21	1845.01	0.19	0	74	2.20E-06	R.FFLQGIQLNTILPDAR.D		36.23		
						327	337	576.36	1150.71	1150.6	0.11	0	55	0.0002318	R.ALQATVGNSYK.C		22.09		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13488	5%	212	4	93680	6.6	Q13488|VPP3_HUMAN Vacuolar proton translocating ATPase 116 kDa subunit a isoform 3 OS=Homo sapiens GN=TCIRG1 PE=1 SV=2												1	5
						29	38	566.88	1131.74	1131.63	0.12	0	76	1.70E-06	R.LGELGLVEFR.D		33.28		
						277	284	460.31	918.6	918.53	0.08	0	36	0.0238435	R.FLSQVLGR.V		30.22		
						328	337	563.37	1124.73	1124.62	0.11	0	45	0.0020147	R.DLPALQEALR.D		32.28		
						338	351	497.59	1489.76	1489.65	0.11	0	54	0.0002526	R.DSSMEEGVSAVAHR.I	Oxidation (M)	20.35		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8TED4	5%	118	2	55256	6.4	Q8TED4|SPX2_HUMAN Sugar phosphate exchanger 2 OS=Homo sapiens GN=SLC37A2 PE=2 SV=2												1	1
						266	274	467.29	932.57	932.48	0.09	0	57	0.0001637	R.ESGLETVAK.C		20.79		
						278	293	861.5	1720.99	1720.82	0.16	0	60	5.52E-05	K.GPCEEPAAISFFGALR.I		35.06		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75844	5%	84	2	55063	7.1	O75844|FACE1_HUMAN CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2												1	1
						293	303	646.85	1291.68	1291.54	0.14	0	47	0.0014389	K.DIQEDSGMEPR.N	Oxidation (M)	19.79		
						304	314	639.3	1276.59	1276.54	0.05	0	38	0.0109636	R.NEEEGNSEEIK.A		18.7		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05023	3%	93	2	114135	5.3	P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1												1	1
						213	227	810.46	1618.9	1618.74	0.16	0	57	0.0001323	K.VDNSSLTGESEPQTR.S		21.18		
						228	240	760.46	1518.9	1518.7	0.21	0	36	0.0183464	R.SPDFTNENPLETR.N		30.09		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q93050	2%	94	2	97148	6	Q93050|VPP1_HUMAN Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3												1	1
						39	49	658.91	1315.81	1315.65	0.16	0	51	0.0006881	R.DLNPDVNVFQR.K		31.23		
						121	129	553.9	1105.79	1105.6	0.19	0	44	0.0029334	R.NFLELTELK.F		33.41		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15118	2%	106	2	144868	5.2	O15118|NPC1_HUMAN Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=1 SV=2												1	2
						715	726	679.44	1356.86	1356.7	0.16	0	69	8.97E-06	R.LQGETLDQQLGR.V		28.3		
						988	997	403.22	1206.63	1206.56	0.08	0	37	0.0137448	K.QRPQGGDFMR.F	Oxidation (M)	18.53		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62988	29%	70	2	8560	6.6	P62988|UBIQ_HUMAN Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV=1												2	3
						1	6	391.26	780.52	780.42	0.09	0	31	0.0468002	-.MQIFVK.T	Oxidation (M)	29.74		
						12	27	894.61	1787.2	1786.92	0.28	0	39	0.0076756	K.TITLEVEPSDTIENVK.A		37.7		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35579	4%	369	7	227646	5.5	P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4												2	1
						290	299	603.39	1204.76	1204.63	0.12	0	39	0.0090237	K.TDLLLEPYNK.Y		37.65		
						359	373	804.47	1606.93	1606.69	0.24	0	64	2.61E-05	R.NTDQASMPDNTAAQK.V	Oxidation (M)	20.69		
						746	755	597.39	1192.77	1192.61	0.16	0	43	0.0032554	K.ALELDSNLYR.I		37.09		
						1446	1454	546.86	1091.7	1091.55	0.16	0	38	0.0113352	K.FDQLLAEEK.T		35.39		
						1504	1518	572.99	1715.96	1715.72	0.23	1	32	0.0375734	R.TEMEDLMSSKDDVGK.S	2 Oxidation (M)	22.98		
						1878	1888	666.36	1330.72	1330.6	0.12	0	65	2.40E-05	R.QLEEAEEEAQR.A		24.45		
						1899	1912	791.4	1580.79	1580.66	0.13	0	89	8.86E-08	R.ELEDATETADAMNR.E	Oxidation (M)	25.83		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	12%	566	12 (13)	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												3	3
						141	152	585.42	1168.83	1168.57	0.26	0	40	0.0065373	R.GVGGSQPPDIDK.T		26.58		
						205	218	502.64	1504.91	1504.77	0.14	1	36	0.0157042	R.KVVATTQMQAADAR.K	Oxidation (M)	21.65		
						205	218	753.58	1505.14	1504.77	0.37	1	48	0.0005127	R.KVVATTQMQAADAR.K	Oxidation (M)	21.87		
						205	219	545.36	1633.07	1632.86	0.21	2	33	0.0288992	R.KVVATTQMQAADARK.S	Oxidation (M)	21.27		
						206	218	689.4	1376.79	1376.67	0.12	0	94	3.04E-08	K.VVATTQMQAADAR.K	Oxidation (M)	22.48		
						242	252	609.88	1217.75	1217.63	0.12	0	42	0.0054503	K.DLTALSNMLPK.G	Oxidation (M)	39.23		
						293	301	479.37	956.72	956.54	0.18	0	58	9.53E-05	K.QASNGVLIR.I		30.98		
						364	379	863	1723.99	1723.83	0.16	0	37	0.0114696	R.ENSLLFDPLSSSSSNK.E		40.34		

						433	442	627.39	1252.77	1252.61	0.16	0	41	0.0057882	K.DLMVLNDVYR.V	Oxidation (M)	39.59		
						642	648	443.8	885.59	885.5	0.09	0	33	0.0410914	K.IQTQLQR.D		24.26		
						712	719	463.78	925.54	925.42	0.12	0	35	0.0222967	R.SEVYGPMK.N	Oxidation (M)	23.63		
						844	855	734.43	1466.84	1466.78	0.06	0	38	0.0116033	R.YLSYTLNPDLIR.K		40.22		
						924	935	635.32	1268.62	1268.53	0.09	0	69	9.87E-06	K.DNEETGFGSGTR.A		27.09		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92542	4%	162	3	79103	5.7	Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2												3	3
						315	323	485.31	968.61	968.53	0.08	0	40	0.0060883	K.APDVTTLPR.N		34.02		
						486	496	543.39	1084.76	1084.62	0.13	0	54	0.0003193	K.ALADVATVLGR.A		39.49		
						694	702	501.37	1000.72	1000.57	0.15	0	38	0.013289	K.ADVLFIAPR.E		39.39		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13473	6%	142	3	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												4	7
						145	152	494.34	986.66	986.55	0.11	0	48	0.001426	R.IPLNDLFR.C		40.04		
						153	161	526.31	1050.6	1050.5	0.1	0	58	0.0001084	R.CNSLSTLEK.N		31.31		
						281	289	551.34	1100.67	1100.59	0.08	0	36	0.019679	K.YLDFVFAVK.N		41.36		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	12%	470	9	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												5	1
						76	84	541.33	1080.65	1080.54	0.12	0	49	0.0008384	K.FAFQAEVNR.M		35.53		
						103	114	638.39	1274.76	1274.64	0.13	0	62	4.48E-05	R.ELISNASDALDK.I		34.74		
						169	177	491.77	981.52	981.48	0.05	0	54	0.0002762	K.SGTSEFLNK.M		30.51		
						435	448	743.49	1484.97	1484.75	0.22	0	46	0.0018412	K.GVVDSDDLPLNVSR.E		36.61		
						538	546	524.28	1046.54	1046.49	0.05	0	32	0.0491595	K.IYFMAGSSR.K	Oxidation (M)	33.44		
						548	557	575.86	1149.71	1149.53	0.18	0	63	3.12E-05	K.EAESSPFVER.L		32.62		
						672	682	645.34	1288.66	1288.59	0.07	0	38	0.012871	K.DISTNYYASQK.K		32.83		
						725	733	497.3	992.59	992.52	0.07	0	55	0.0002125	R.SGYLLPDTK.A		35.01		
						745	754	543.32	1084.62	1084.58	0.05	0	43	0.0036383	R.LSLNIDPDAK.V		36.65		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	3%	74	2	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												5	1
						156	165	545.39	1088.76	1088.55	0.22	0	34	0.0290083	R.ALNEITESGR.I		28.37		
						311	325	837.08	1672.15	1671.89	0.25	0	40	0.0064007	K.LAENNIQPIFAVTSR.M		38.43		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14697	1%	76	2	107263	5.7	Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3												5	1
						158	164	437.27	872.52	872.46	0.06	0	42	0.006555	R.LDLLEDR.S		36.57		
						858	863	403.25	804.5	804.45	0.05	0	34	0.0302464	R.QEFLLR.R		36.39		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	11%	225	5	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												6	7
						83	92	606.85	1211.68	1211.58	0.1	0	51	0.0005379	R.VEEVGPYTYR.E		33.52		
						116	121	392.73	783.44	783.39	0.05	0	32	0.041388	K.AYVFER.D		33.17		
						154	161	481.8	961.58	961.52	0.07	0	39	0.0111268	R.EIIEAMLK.A	Oxidation (M)	33.39		
						392	402	640.37	1278.72	1278.61	0.11	0	57	0.00014	K.LDDFVETGDIR.T		36.15		
						460	477	640.35	1918.02	1917.89	0.14	1	47	0.0013095	K.GQGSMDEGTADERAPLIR.T	Oxidation (M)	29.34		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	15%	415	8	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												7	2
						50	60	614.86	1227.71	1227.62	0.09	0	40	0.008218	R.VEIIANDQGNR.I		26.57		
						61	74	783.98	1565.94	1565.77	0.17	0	54	0.0002441	R.ITPSYVAFTPEGER.L		35.72		
						82	96	839.56	1677.1	1676.8	0.3	0	66	1.67E-05	K.NQLTSNPENTVFDAK.R		34.42		
						186	197	617.34	1232.66	1232.62	0.04	0	39	0.0102033	K.DAGTIAGLNVMR.I	Oxidation (M)	34.37		
						345	352	459.77	917.53	917.47	0.05	0	40	0.0085806	K.VLEDSDLK.K		26.11		
						448	464	918.99	1835.97	1835.93	0.05	0	67	1.19E-05	K.SQIFSTASDNQPTVTIK.V		34.72		
						524	532	537.82	1073.62	1073.55	0.07	0	71	6.16E-06	K.ITITNDQNR.L		23.35		
						622	633	699.52	1397.02	1396.78	0.23	0	40	0.0058719	K.ELEEIVQPIISK.L		36.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	13%	356	7	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												7	2
						264	273	591.85	1181.69	1181.59	0.1	0	52	0.0004201	K.APDFVFYAPR.L		38.06		
						295	306	496.96	1487.86	1487.78	0.09	1	36	0.0179007	R.RKPDTIEVQQMK.A	Oxidation (M)	20.99		
						361	370	616.35	1230.68	1230.58	0.09	0	49	0.0010633	K.AQQELEEQTR.R		22.3		
						372	379	494.3	986.58	986.5	0.08	0	41	0.0072991	R.ALELEQER.K		30.52		
						413	427	860.52	1719.02	1718.85	0.17	0	51	0.0005444	K.TQEQLALEMAELTAR.I	Oxidation (M)	35.64		
						449	458	603.86	1205.7	1205.56	0.14	0	55	0.0002196	K.AQMVQEDLEK.T	Oxidation (M)	23.8		
						569	577	585.8	1169.58	1169.5	0.07	1	40	0.0067433	K.QRIDEFESM.-	Oxidation (M)	32.47		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15311	5%	155	3	69484	5.9	P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4												7	2
						264	273	591.85	1181.69	1181.59	0.1	0	52	0.0004201	K.APDFVFYAPR.L		38.06		
						295	306	496.96	1487.86	1487.78	0.09	1	36	0.0179007	R.RKPDTIEVQQMK.A	Oxidation (M)	20.99		
						364	371	501.84	1001.66	1001.51	0.14	0	35	0.0318952	R.ELSEQIQR.A		24.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51659	4%	94	2	80092	9	P51659|DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3												7	1
						69	81	705.87	1409.72	1409.63	0.09	0	52	0.0003947	K.AVANYDSVEEGEK.V		27.24		
						316	331	734.45	1466.88	1466.74	0.14	0	42	0.0039956	R.ATSTATSGFAGAIGQK.L		33.25		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15586	3%	52	2	62840	8.6	P15586|GNS_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3												7	1
						247	255	525.35	1048.68	1048.55	0.14	0	40	0.0073746	K.AFQNVFAPR.N		35.85		
						494	502	493.28	984.54	984.55	-0.01	0	35	0.0241043	K.TIDPELLGK.M		34.94		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38606	21%	569	10	68660	5.3	P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2												8	5
						121	129	451.77	901.54	901.5	0.04	0	48	0.0014995	R.GVNVSALSR.D		30.57		
						221	232	439.61	1315.8	1315.74	0.06	0	46	0.0022345	K.LPANHPLLTGQR.V		26.27		
						257	265	481.81	961.6	961.54	0.05	0	40	0.0081492	K.TVISQSLSK.Y		27.09		
						281	289	525.76	1049.51	1049.48	0.03	0	61	5.70E-05	R.GNEMSEVLR.D	Oxidation (M)	22.99		
						309	323	766.42	1530.82	1530.78	0.04	0	84	2.80E-07	R.TALVANTSNMPVAAR.E	Oxidation (M)	25.68		
						339	353	579.27	1734.78	1734.66	0.12	0	44	0.0024869	R.DMGYHVSMMADSTSR.W	3 Oxidation (M)	22.1		
						365	381	899.44	1796.87	1796.84	0.03	0	69	6.93E-06	R.LAEMPADSGYPAYLGAR.L	Oxidation (M)	34.2		
						537	552	934.53	1867.04	1866.83	0.21	0	63	3.25E-05	K.TVGMLSNMIAFYDMAR.R	3 Oxidation (M)	35.89		
						586	596	416.58	1246.72	1246.66	0.06	2	39	0.0096589	K.FKDPLKDGEAK.I		24.09		
						599	613	909.01	1816.01	1815.81	0.2	0	75	1.80E-06	K.SDYAQLLEDMQNAFR.S	Oxidation (M)	37.28		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P38646	11%	321	6	73920	5.9	P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2												8	1
						77	85	479.8	957.58	957.49	0.09	0	49	0.0009993	K.VLENAEGAR.T		21.33		
						86	99	725.9	1449.78	1449.71	0.07	0	65	1.96E-05	R.TTPSVVAFTADGER.L		34.59		
						188	202	847.99	1693.97	1693.84	0.12	0	47	0.0012136	K.NAVITVPAYFNDSQR.Q		36.28		
						207	218	621.91	1241.81	1241.67	0.13	0	49	0.0010018	K.DAGQISGLNVLR.V		35.84		
						293	307	569.65	1705.91	1705.83	0.08	1	40	0.0070455	R.ETGVDLTKDNMALQR.V	Oxidation (M)	31.29		
						635	646	616.38	1230.74	1230.66	0.08	0	71	6.60E-06	R.QAASSLQQASLK.L		24.93		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11142	9%	240	5	71082	5.4	P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1												8	1
						26	36	614.86	1227.7	1227.62	0.08	0	52	0.0004842	K.VEIIANDQGNR.T		26.23		
						37	49	744.41	1486.8	1486.69	0.1	0	46	0.0019164	R.TTPSYVAFTDTER.L		34.28		
						57	71	833.5	1664.99	1664.78	0.21	0	55	0.0001932	K.NQVAMNPTNTVFDAK.R	Oxidation (M)	32.59		
						160	171	600.42	1198.82	1198.67	0.15	0	45	0.0020735	K.DAGTIAGLNVLR.I		36.8		
						349	357	541.3	1080.58	1080.56	0.02	0	41	0.0047583	K.LLQDFFNGK.E		37.24		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13796	6%	144	3	70815	5.2	P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5												8	1
						166	178	759.96	1517.91	1517.74	0.17	0	65	2.15E-05	K.MINLSVPDTIDER.T	Oxidation (M)	35.45		
						348	357	568.31	1134.61	1134.6	0	0	41	0.0052843	R.QFVTATDVVR.G		33.29		
						473	488	838.48	1674.95	1674.83	0.11	0	37	0.0116084	K.FSLVGIGGQDLNEGNR.T		36.89		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08107	5%	137	3	70294	5.5	P08107|HSP71_HUMAN Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5												8	1
						26	36	614.86	1227.7	1227.62	0.08	0	52	0.0004842	K.VEIIANDQGNR.T		26.23		
						37	49	744.41	1486.8	1486.69	0.1	0	46	0.0019164	R.TTPSYVAFTDTER.L		34.28		
						349	357	555.34	1108.67	1108.57	0.1	0	39	0.0082449	K.LLQDFFNGR.D		37.55		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O00571	3%	115	2	73597	6.7	O00571|DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3												8	3
						408	418	582.34	1162.67	1162.58	0.08	0	80	7.38E-07	R.VGSTSENITQK.V		21.23		
						492	503	584.92	1167.83	1167.7	0.13	0	35	0.0163757	K.SPILVATAVAAR.G		34.81		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10809	35%	835	16	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												9	3
						38	58	715.83	2144.45	2144.12	0.33	0	66	1.51E-05	R.ALMLQGVDLLADAVAVTMGPK.G	2 Oxidation (M)	40.56		
						134	141	428.27	854.52	854.46	0.06	0	39	0.0080506	K.GANPVEIR.R		24.75		
						206	221	647.05	1938.13	1937.94	0.19	1	42	0.0036837	K.TLNDELEIIEGMKFDR.G	Oxidation (M)	37.01		
						222	233	695.39	1388.76	1388.7	0.07	0	59	9.78E-05	R.GYISPYFINTSK.G		35.66		
						251	268	640.41	1918.22	1918.06	0.16	0	45	0.0017071	K.ISSIQSIVPALEIANAHR.K		37.48		
						293	301	456.82	911.62	911.58	0.04	0	67	1.08E-05	K.VGLQVVAVK.A		32.93		
						302	309	417.21	832.4	832.38	0.02	0	50	0.0007946	K.APGFGDNR.K		22.87		
						345	359	549.68	1646.03	1645.9	0.13	1	33	0.0311734	K.VGEVIVTKDDAMLLK.G	Oxidation (M)	33.28		
						397	405	451.3	900.58	900.53	0.05	0	47	0.0016891	K.LSDGVAVLK.V		32.71		
						406	418	454.59	1360.75	1360.68	0.07	1	41	0.0059007	K.VGGTSDVEVNEKK.D		20.73		
						421	429	480.78	959.54	959.5	0.04	0	62	5.65E-05	R.VTDALNATR.A		23.09		
						430	446	842.99	1683.97	1683.9	0.07	0	76	1.62E-06	R.AAVEEGIVLGGGCALLR.C		37.09		
						447	462	886.5	1770.99	1770.85	0.14	0	32	0.0450369	R.CIPALDSLTPANEDQK.I		35.49		
						463	469	393.27	784.53	784.51	0.02	0	40	0.0065167	K.IGIEIIK.R		34.71		
						474	481	430.79	859.56	859.48	0.08	0	48	0.0015768	K.IPAMTIAK.N	Oxidation (M)	22.12		
						482	493	608.38	1214.75	1214.65	0.1	0	58	0.0001212	K.NAGVEGSLIVEK.I		32.54		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11117	11%	220	5	48713	6.3	P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3												9	4
						35	41	456.31	910.6	910.53	0.07	0	40	0.0052291	R.FVTLLYR.H		36.09		
						242	252	672.42	1342.84	1342.69	0.14	0	45	0.0023892	R.FLFGIYQQAEK.A		37.65		
						255	265	584.4	1166.79	1166.71	0.07	0	61	4.59E-05	R.LQGGVLLAQIR.K		35.75		
						349	356	524.83	1047.64	1047.52	0.12	0	40	0.0088191	R.CPLQDFLR.L		36.57		
						357	364	441.77	881.53	881.52	0.01	0	34	0.0230436	R.LTEPVVPK.D		29.02		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30101	14%	352	6	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												10	1
						63	73	596.45	1190.89	1190.59	0.29	0	69	6.31E-06	R.LAPEYEAAATR.L		27.81		
						297	304	439.27	876.53	876.48	0.05	0	43	0.0044206	K.LNFAVASR.K		32.75		
						336	344	594.83	1187.65	1187.53	0.12	0	48	0.00127	K.FVMQEEFSR.D	Oxidation (M)	30.75		
						367	379	685	1367.99	1367.66	0.33	0	68	9.10E-06	K.SEPIPESNDGPVK.V		26.09		
						434	448	840.93	1679.85	1679.75	0.1	0	84	2.86E-07	K.MDATANDVPSPYEVR.G	Oxidation (M)	32.36		
						483	496	527.31	1578.91	1578.83	0.09	0	41	0.0048405	R.EATNPPVIQEEKPK.K		22.79		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	14%	369	7	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												10	1
						70	78	501.81	1001.6	1001.55	0.05	1	42	0.0061046	K.LKAEGSEIR.L		20.67		
						277	283	377.21	752.41	752.37	0.04	0	36	0.0155079	K.TAAESFK.G		21.31		
						317	326	611.87	1221.72	1221.62	0.1	0	42	0.0040514	R.LITLEEEMTK.Y	Oxidation (M)	32.27		
						327	338	484.6	1450.77	1450.69	0.08	0	62	3.85E-05	K.YKPESEELTAER.I		23.6		
						376	385	607.3	1212.59	1212.53	0.06	0	59	9.70E-05	K.NFEDVAFDEK.K		34.35		
						425	436	655.33	1308.64	1308.59	0.05	0	93	3.28E-08	K.MDSTANEVEAVK.V	Oxidation (M)	23.47		
						453	461	533.8	1065.59	1065.51	0.08	0	35	0.02182	R.TVIDYNGER.T		27.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08962	8%	145	3	26474	8.1	P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2												10	15
						109	120	506.24	1515.71	1515.68	0.03	1	46	0.0020009	R.DKVMSEFNNNFR.Q	Oxidation (M)	31.66		
						111	120	637.31	1272.61	1272.56	0.05	0	55	0.0002221	K.VMSEFNNNFR.Q	Oxidation (M)	31.53		
						121	128	527.35	1052.69	1052.46	0.23	0	44	0.0024536	R.QQMENYPK.N	Oxidation (M)	20.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31146	8%	145	3	51678	6.3	P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4												10	1
						384	393	513.88	1025.75	1025.61	0.13	0	40	0.0056339	R.DAGPLLISLK.D		37.01		
						417	432	751.87	1501.73	1501.7	0.03	0	52	0.0004253	R.AAPEASGTPSSDAVSR.L		21.54		
						440	449	579.35	1156.68	1156.65	0.04	0	53	0.0004041	K.LQATVQELQK.R		29.47		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21281	26%	591	11	56807	5.6	P21281|VATB2_HUMAN Vacuolar ATP synthase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3												11	4
						30	37	437.26	872.51	872.47	0.04	0	40	0.0106554	R.EQALAVSR.N		22.4		
						83	93	545.8	1089.59	1089.57	0.03	0	78	1.37E-06	R.SGQVLEVSGSK.A		23.68		
						94	108	760.95	1519.88	1519.79	0.09	0	83	3.37E-07	K.AVVQVFEGTSGIDAK.K		34.03		
						110	120	649.85	1297.69	1297.6	0.09	0	47	0.0014802	K.TSCEFTGDILR.T		34.46		
						121	130	560.8	1119.59	1119.52	0.06	0	55	0.0002159	R.TPVSEDMLGR.V	Oxidation (M)	24.07		
						131	141	397.23	1188.67	1188.63	0.05	0	59	9.38E-05	R.VFNGSGKPIDR.G		21.58		
						164	185	814.44	2440.3	2440.16	0.14	0	34	0.0220292	R.IYPEEMIQTGISAIDGMNSIAR.G	2 Oxidation (M)	36.41		
						387	400	798.96	1595.91	1595.9	0.01	0	54	0.0002743	R.QIYPPINVLPSLSR.L		37.24		
						404	412	469.24	936.46	936.43	0.03	0	33	0.0351706	K.SAIGEGMTR.K	Oxidation (M)	20.31		
						461	471	654.86	1307.71	1307.63	0.09	0	46	0.0016431	R.NFIAQGPYENR.T		32.16		
						495	506	719.39	1436.76	1436.73	0.03	0	64	2.36E-05	R.IPQSTLSEFYPR.D		35.37		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	15%	404	7	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												11	2
						46	58	720.36	1438.71	1438.66	0.05	0	82	3.79E-07	K.TGTAEMSSILEER.I	Oxidation (M)	31.03		
						59	73	788.46	1574.9	1574.78	0.13	0	58	0.0001212	R.ILGADTSVDLEETGR.V		33.72		
						74	83	500.83	999.64	999.57	0.06	0	56	0.0002001	R.VLSIGDGIAR.V		33.16		
						134	149	813	1623.99	1623.88	0.11	0	44	0.0026972	R.TGAIVDVPVGEELLGR.V		36.85		
						150	161	586.34	1170.66	1170.62	0.04	0	72	4.40E-06	R.VVDALGNAIDGK.G		32.77		
						195	204	513.82	1025.63	1025.59	0.04	0	53	0.0002921	K.AVDSLVPIGR.G		33.77		
						254	261	423.34	844.66	844.5	0.16	0	40	0.0058386	R.STVAQLVK.R		28.6		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8IV08	4%	98	2	55127	6	Q8IV08|PLD3_HUMAN Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1												11	3
						310	319	542.85	1083.69	1083.6	0.09	0	48	0.0011011	K.ALLNVVDNAR.S		33.59		
						397	408	658.41	1314.81	1314.69	0.12	0	50	0.0007309	K.LFVVPADEAQAR.I		33.64		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P80723	38%	222	5	22680	4.6	P80723|BASP1_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2												13	1
						26	38	645.34	1288.67	1288.58	0.1	0	35	0.0235837	K.AEGAATEEEGTPK.E		19.66		
						39	52	714.39	1426.77	1426.66	0.11	0	40	0.0076975	K.ESEPQAAAEPAEAK.E		21.01		
						98	121	766.76	2297.27	2297.13	0.14	1	50	0.0005412	K.AEPPKAPEQEQAAPGPAAGGEAPK.A		22.2		
						164	184	644.99	1931.96	1931.87	0.09	0	52	0.0003385	K.SDGAPASDSKPGSSEAAPSSK.E		19.21		
						185	198	693.91	1385.81	1385.67	0.15	0	45	0.0023931	K.ETPAATEAPSSTPK.A		20.62		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75955	26%	521	9	47554	7.1	O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3												13	3
						19	28	493.8	985.58	985.5	0.08	0	33	0.0444982	R.SPPVMVAGGR.V	Oxidation (M)	21.14		
						41	51	608.41	1214.81	1214.72	0.09	0	68	1.18E-05	R.ISLNTLTLNVK.S		34.37		
						221	230	576.36	1150.71	1150.56	0.15	0	63	3.56E-05	K.AAYDIEVNTR.R		30.66		
						254	261	478.81	955.61	955.55	0.07	0	58	0.000105	R.VQVQVVER.A		24.47		
						262	274	735.46	1468.9	1468.76	0.14	0	66	1.61E-05	R.AQQVAVQEQEIAR.R		28.11		
						303	317	810.46	1618.91	1618.8	0.11	0	47	0.001457	K.SQLIMQAEAEAASVR.M	Oxidation (M)	33.67		
						361	377	877.52	1753.03	1752.93	0.1	0	81	4.71E-07	K.LPQVAEEISGPLTSANK.I		33.93		
						378	392	698.45	1394.89	1394.71	0.19	0	70	7.08E-06	K.ITLVSSGSGTMGAAK.V	Oxidation (M)	27.32		

						393	403	608.39	1214.77	1214.69	0.08	0	40	0.0074217	K.VTGEVLDILTR.L		36.41		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14254	19%	313	7	41830	5.2	Q14254|FLOT2_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=1												13	4
						121	128	451.78	901.54	901.5	0.04	0	42	0.006652	K.TQTAVVQR.D		19.76		
						175	184	562.33	1122.65	1122.56	0.09	0	31	0.0499829	K.SAFSEEVNIK.T		31.36		
						248	256	508.31	1014.6	1014.53	0.06	0	51	0.0006819	R.IQQIAEGEK.V		21.1		
						259	269	600.4	1198.78	1198.66	0.12	0	46	0.0017415	K.QVLLAQAEAEK.I		30.31		
						308	321	742.47	1482.93	1482.85	0.08	0	61	5.81E-05	K.MALVLEALPQIAAK.I	Oxidation (M)	35.58		
						322	328	357.26	712.51	712.45	0.06	0	36	0.0144597	K.IAAPLTK.V		22.98		
						329	341	687.92	1373.83	1373.7	0.13	0	47	0.0016229	K.VDEIVVLSGDNSK.V		32.45		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	13%	332	7	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												13	30
						38	44	447.78	893.54	893.49	0.06	1	32	0.0458369	R.TIEKFEK.E		20.79		
						85	96	468.95	1403.83	1403.72	0.11	0	32	0.042913	K.YYVTIIDAPGHR.D		31.97		
						147	154	435.81	869.61	869.53	0.07	0	46	0.0014456	K.QLIVGVNK.M		29.57		
						167	172	390.73	779.45	779.41	0.04	0	41	0.0050596	R.YEEIVK.E		23.94		
						248	255	488.33	974.64	974.54	0.1	0	51	0.0007087	R.LPLQDVYK.I		31.75		
						256	266	513.34	1024.67	1024.6	0.07	0	71	5.34E-06	K.IGGIGTVPVGR.V		30.88		
						431	439	457.81	913.61	913.56	0.05	0	62	4.30E-05	R.QTVAVGVIK.A		29.48		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y6N5	6%	139	2	50214	9.2	Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1												13	1
						66	79	735.45	1468.88	1468.75	0.13	0	72	4.36E-06	K.VGAENVAIVEPSER.H		30.62		
						345	358	672.46	1342.9	1342.72	0.18	0	67	1.33E-05	K.TAAAVAAQSGILDR.T		31.1		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O14773	9%	197	4	61723	6	O14773|TPP1_HUMAN Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2												14	4
						246	259	492.29	1473.86	1473.75	0.11	0	45	0.0021463	R.LFGGNFAHQASVAR.V		30.93		
						340	346	425.75	849.48	849.43	0.06	0	48	0.0013137	R.VNTELMK.A	Oxidation (M)	20.26		
						493	506	513.01	1536	1535.89	0.11	0	34	0.0250928	R.ILSGRPPLGFLNPR.L		33.79		
						507	520	535.63	1603.86	1603.81	0.04	0	70	6.14E-06	R.LYQQHGAGLFDVTR.G		32.14		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P48735	7%	105	3	51333	8.9	P48735|IDHP_HUMAN Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2												14	1
						46	60	570.29	1707.85	1707.78	0.07	0	37	0.0119735	K.VAKPVVEMDGDEMTR.I	2 Oxidation (M)	20.8		
						385	393	522.31	1042.6	1042.54	0.06	0	35	0.0250537	K.LDGNQDLIR.F		30.32		
						394	400	441.76	881.51	881.43	0.08	0	35	0.0165167	R.FAQMLEK.V	Oxidation (M)	22.6		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08670	17%	417	8	53676	5.1	P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4												15	15
						105	113	558.33	1114.65	1114.56	0.09	0	34	0.028193	K.VELQELNDR.F		30.62		
						160	168	530.79	1059.56	1059.52	0.04	0	60	8.17E-05	R.QVDQLTNDK.A		21.39		
						197	207	662.38	1322.75	1322.61	0.14	0	81	5.71E-07	R.EEAENTLQSFR.Q		31.4		
						208	217	544.79	1087.57	1087.53	0.05	0	91	7.24E-08	R.QDVDNASLAR.L		22.09		
						274	282	512.27	1022.53	1022.5	0.02	0	37	0.0131732	R.QQYESVAAK.N		20.61		
						295	304	547.32	1092.63	1092.52	0.11	0	40	0.0073819	K.FADLSEAANR.N		30.19		
						365	378	589.64	1765.9	1765.8	0.1	1	41	0.0046568	R.LQDEIQNMKEEMAR.H	2 Oxidation (M)	21.31		
						403	410	466.8	931.58	931.46	0.12	0	34	0.0310056	K.LLEGEESR.I		21.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y295	7%	94	2	40802	9	Q9Y295|DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1												15	1
						8	17	574.82	1147.63	1147.55	0.08	0	32	0.0472738	K.IAEIEAEMAR.T	Oxidation (M)	26.24		
						47	61	631.32	1260.63	1260.57	0.06	0	62	4.43E-05	K.GGGGGGPGEGFDVAK.T		29.41		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61421	11%	223	4	40759	4.9	P61421|VA0D1_HUMAN Vacuolar proton pump subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1												17	4
						188	195	510.82	1019.63	1019.5	0.13	0	57	0.0001702	K.AYLESFYK.F		33.66		
						247	257	615.86	1229.71	1229.68	0.03	0	49	0.0010564	R.LYPEGLAQLAR.A		34.53		
						258	265	484.26	966.51	966.43	0.08	0	50	0.0006822	R.ADDYEQVK.N		21.46		
						276	288	652.89	1303.76	1303.64	0.12	0	68	1.32E-05	K.LLFEGAGSNPGDK.T		32.6		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60709	6%	74	2	42052	5.3	P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1												17	9
						19	28	488.79	975.56	975.44	0.12	0	39	0.0099304	K.AGFAGDDAPR.A		23.85		
						316	326	589.37	1176.73	1176.61	0.12	0	34	0.0285163	K.EITALAPSTMK.I	Oxidation (M)	29.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07355	18%	290	6	38808	7.6	P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2												18	2
						38	47	544.35	1086.69	1086.59	0.1	0	34	0.039459	R.DALNIETAIK.T		34.15		
						50	63	772.1	1542.19	1541.84	0.34	0	44	0.0011889	K.GVDEVTIVNILTNR.S		38.82		
						69	77	556.35	1110.68	1110.55	0.13	0	50	0.0006635	R.QDIAFAYQR.R		32.54		
						105	115	611.82	1221.62	1221.59	0.04	0	71	5.34E-06	K.TPAQYDASELK.A		29.98		
						136	145	622.87	1243.72	1243.62	0.11	0	52	0.000548	R.TNQELQEINR.V		26.29		
						170	176	381.25	760.48	760.45	0.03	0	41	0.0089043	K.LMVALAK.G	Oxidation (M)	30.07		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04406	11%	160	3	36201	8.6	P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3												18	1

						201	215	706.45	1410.89	1410.78	0.11	0	56	0.0001869	R.GALQNIIPASTGAAK.A		33.45		
						235	248	765.93	1529.85	1529.79	0.06	0	54	0.0002591	R.VPTANVSVVDLTCR.L		33.89		
						264	271	415.25	828.49	828.43	0.06	0	50	0.0009727	K.QASEGPLK.G		20.95		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50897	26%	265	5	34627	6.1	P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1												19	8
						62	74	701.5	1400.99	1400.83	0.16	0	85	1.96E-07	K.IPGIYVLSLEIGK.T		39.17		
						105	122	1009.57	2017.13	2016.95	0.18	0	107	1.23E-09	K.LQQGYNAMGFSQGGQFLR.A	Oxidation (M)	34.23		
						128	151	859.95	2576.83	2576.3	0.53	0	34	0.036564	R.CPSPPMINLISVGGQHQGVFGLPR	Oxidation (M)	36.74		
						166	174	462.79	923.56	923.47	0.09	0	67	1.13E-05	K.TLNAGAYSK.V		22.58		
						254	268	897.57	1793.12	1792.88	0.24	0	72	4.12E-06	K.ETIPLQETSLYTQDR.L		34.36		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40926	19%	129	5	35965	8.9	P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=2												19	2
						27	45	897.14	1792.27	1792.08	0.19	0	53	0.0002674	K.VAVLGASGGIGQPLSLLLK.N		39.55		
						177	185	496.84	991.66	991.53	0.13	0	37	0.0163372	R.ANTFVAELK.G		33.32		
						230	239	537.34	1072.66	1072.58	0.08	0	59	0.0001058	R.IQEAGTEVVK.A		22.92		
						242	257	735.94	1469.87	1469.69	0.18	0	34	0.0297627	K.AGAGSATLSMAYAGAR.F	Oxidation (M)	30.76		
						315	324	566.85	1131.68	1131.58	0.1	0	50	0.0007044	K.MISDAIPELK.A	Oxidation (M)	34.06		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99623	10%	87	3	33276	9.8	Q99623|PHB2_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2												19	1
						124	131	497.86	993.71	993.48	0.23	0	36	0.0156663	R.LGLDYEER.V		32.63		
						148	157	589.38	1176.74	1176.63	0.11	0	40	0.0082704	K.FNASQLITQR.A		34.1		
						225	236	608.37	1214.72	1214.61	0.11	0	66	2.09E-05	K.IVQAEGEAEAAK.M		21.91		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UBR2	7%	73	2	34530	6.7	Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1												19	2
						70	81	654.87	1307.73	1307.65	0.08	0	43	0.0035373	R.NVDGVNYASITR.N		32.45		
						190	199	505.79	1009.57	1009.48	0.09	0	48	0.0010338	R.VGDYGSLSGR.E		28.58		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9HAV0	7%	62	2	38284	5.6	Q9HAV0|GBB4_HUMAN Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3												19	1
						2	15	885.99	1769.96	1769.89	0.07	1	41	0.0049993	M.SELEQLRQEAEQLR.N	Acetyl (Protein N-term)	37.58		
						69	78	509.33	1016.65	1016.55	0.1	0	46	0.002139	R.LLVSASQDGK.L		25.55		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36543	20%	215	5	26186	7.7	P36543|VATE1_HUMAN Vacuolar proton pump subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1												20	4
						2	10	494.81	987.61	987.49	0.12	0	33	0.0468906	M.ALSDADVQK.Q	Acetyl (Protein N-term)	31.51		
						34	42	554.82	1107.63	1107.51	0.12	0	46	0.0015812	K.AEEEFNIEK.G		31.69		
						70	80	669.36	1336.7	1336.62	0.08	0	63	3.52E-05	K.IQMSNLMNQAR.L	2 Oxidation (M)	21.58		
						138	145	487.86	973.7	973.56	0.14	1	38	0.0122252	R.KQDFPLVK.A		30.78		
						192	199	453.28	904.55	904.46	0.09	0	35	0.0261489	K.VSNTLESR.L		21.14		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q16698	8%	118	2	36330	9.3	Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1												20	1
						61	73	589.38	1176.74	1176.65	0.09	0	40	0.0081194	K.VAFITGGGTGLGK.G		33.73		
						98	110	667.89	1333.76	1333.65	0.11	0	79	9.88E-07	K.ATAEQISSQTGNK.V		21.1		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07339	30%	621	11 (12)	45037	6.1	P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1												21	18
						177	184	440.27	878.53	878.45	0.09	0	60	7.48E-05	R.QVFGEATK.Q		23.94		
						177	194	945.2	1888.39	1888.01	0.38	1	52	0.0003127	R.QVFGEATKQPGITFIAAK.F	Gln->pyro-Glu (N-term Q)	36.79		
						177	194	636.1	1905.28	1905.04	0.25	1	66	1.48E-05	R.QVFGEATKQPGITFIAAK.F		34.15		
						185	194	514.87	1027.73	1027.57	0.16	0	63	3.15E-05	K.QPGITFIAAK.F	Gln->pyro-Glu (N-term Q)	36.84		
						195	205	628.37	1254.73	1254.61	0.13	0	58	0.0001108	K.FDGILGMAYPR.I	Oxidation (M)	35.28		
						206	222	659.08	1974.23	1974.02	0.2	0	61	4.75E-05	R.ISVNNVLPVFDNLMQQK.L	Oxidation (M)	38.4		
						223	235	801.49	1600.96	1600.82	0.14	0	79	8.46E-07	K.LVDQNIFSFYLSR.D		39.67		
						236	253	902.52	1803.03	1802.8	0.23	0	55	0.0002068	R.DPDAQPGGELMLGGTDSK.Y	Oxidation (M)	32.67		
						314	331	1003.15	2004.29	2004.01	0.28	0	41	0.0048791	K.AIGAVPLIQGEYMIPCEK.V	Oxidation (M)	36.36		
						332	341	521.87	1041.73	1041.64	0.09	0	35	0.02339	K.VSTLPAITLK.L		34.49		
						349	357	533.32	1064.63	1064.54	0.09	0	52	0.0004286	K.LSPEDYTLK.V		33.06		
						404	411	410.74	819.47	819.42	0.05	0	51	0.0006244	R.VGFAEAAR.L		28.51		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08579	8%	82	2	25470	9.7	P08579|RU2B_HUMAN U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens GN=SNRPB2 PE=1 SV=1												23	1
						86	93	439.75	877.48	877.44	0.04	0	33	0.0416277	K.TDSDIISK.M		18.14		
						112	122	597.32	1192.63	1192.59	0.03	0	49	0.0008116	K.TVEQTATTTNK.K		15.84		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51572	8%	69	2	28031	8.4	P51572|BAP31_HUMAN B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3												23	1
						149	159	481.27	1440.78	1440.69	0.09	2	33	0.0351196	K.KYMEENDQLKK.G	Oxidation (M)	15.7		
						205	213	524.28	1046.54	1046.52	0.02	0	36	0.0185186	K.AENQVLAMR.K	Oxidation (M)	18.23		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21796	11%	169	3	30868	8.6	P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2												24	2
						54	61	417.75	833.48	833.45	0.03	0	35	0.0289748	K.VTGSLETK.Y		17.13		
						97	109	700.87	1399.72	1399.66	0.06	0	45	0.0024016	K.LTFDSSFSPNTGK.K		26.9		
						164	174	607.34	1212.66	1212.61	0.05	0	90	7.44E-08	R.VTQSNFAVGYK.T		25.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UL25	11%	148	2	24731	8.1	Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3												24	3
						2	16	557.3	1112.59	1112.53	0.06	0	78	1.16E-06	M.AAAGGGGGGAAAAGR.A	Acetyl (Protein N-term)	17.7		
						180	189	604.31	1206.6	1206.56	0.05	0	70	7.89E-06	R.MIETAQVDER.A	Oxidation (M)	19.27		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25774	8%	101	2	38099	8.6	P25774|CATS_HUMAN Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3												24	1
						159	174	882.45	1762.89	1762.88	0.01	0	56	0.0001629	K.LVSLSAQNLVDCSTEK.Y		27.11		
						246	255	478.79	955.56	955.51	0.05	0	46	0.0017483	K.GPVSVGVDAR.H		22.25		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51148	29%	312	5	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												25	5
						24	34	543.35	1084.68	1084.65	0.03	0	63	4.26E-05	K.LVLLGESAVGK.S		27.13		
						122	135	698.43	1394.84	1394.79	0.05	0	74	2.48E-06	R.QASPNIVIALAGNK.A		27.78		
						167	180	792.91	1583.81	1583.77	0.04	0	52	0.0003916	K.TAMNVNEIFMAIAK.K	2 Oxidation (M)	28.78		
						185	196	606.33	1210.65	1210.57	0.08	0	56	0.0001901	K.NEPQNATGAPGR.N		16.43		
						199	210	650.33	1298.64	1298.62	0.02	0	68	1.21E-05	R.GVDLQENNPASR.S		23.97		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05090	23%	211	4	21547	5.1	P05090|APOD_HUMAN Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1												25	3
						52	60	517.78	1033.54	1033.52	0.02	0	33	0.0414603	K.IPTTFENGR.C		24.66		
						152	164	712.4	1422.79	1422.74	0.05	0	51	0.0005225	R.NPNLPPETVDSLK.N		25.96		
						165	175	615.86	1229.71	1229.66	0.05	0	49	0.0010158	K.NILTSNNIDVK.K		26.13		
						177	187	654.83	1307.64	1307.58	0.06	0	79	9.24E-07	K.MTVTDQVNCPK.L	Oxidation (M)	18.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61006	19%	209	4	23824	9.2	P61006|RAB8A_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1												25	5
						11	21	536.36	1070.7	1070.63	0.07	0	43	0.0040065	K.LLLIGDSGVGK.T		27.39		
						154	167	790.44	1578.86	1578.82	0.04	0	64	2.82E-05	K.ANINVENAFFTLAR.D		30.01		
						176	190	514.95	1541.83	1541.78	0.05	1	43	0.0036183	K.KLEGNSPQGSNQGVK.I		16.27		
						177	190	707.89	1413.77	1413.68	0.09	0	60	6.92E-05	K.LEGNSPQGSNQGVK.I		16.73		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P20339	17%	167	3	23872	8.3	P20339|RAB5A_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2												25	1
						23	33	543.35	1084.68	1084.65	0.03	0	63	4.26E-05	K.LVLLGESAVGK.S		27.13		
						166	179	792.91	1583.81	1583.77	0.04	0	60	6.38E-05	K.TSMNVNEIFMAIAK.K	Oxidation (M)	28.78		
						184	195	627.82	1253.63	1253.57	0.05	0	44	0.0027668	K.NEPQNPGANSAR.G		16.33		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51153	18%	146	3	22988	9.3	P51153|RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=2 SV=1												26	7
						11	21	536.36	1070.71	1070.63	0.07	0	44	0.0027903	K.LLLIGDSGVGK.T		27.35		
						105	116	420.9	1259.69	1259.65	0.04	1	43	0.0041651	K.SIKENASAGVER.L		16.84		
						154	167	765.39	1528.77	1528.68	0.09	0	59	9.58E-05	K.SSMNVDEAFSSLAR.D	Oxidation (M)	27.22		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51149	17%	153	3	23760	6.4	P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1												26	3
						11	21	529.33	1056.65	1056.62	0.03	0	44	0.0032475	K.VIILGDSGVGK.T		26.27		
						147	157	642.34	1282.67	1282.62	0.05	0	37	0.0145849	K.NNIPYFETSAK.E		26.62		
						158	171	795.45	1588.89	1588.82	0.07	0	41	0.0048258	K.EAINVEQAFQTIAR.N		29.12		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04179	9%	97	2	24878	8.3	P04179|SODM_HUMAN Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2												26	1
						69	75	411.74	821.47	821.43	0.04	0	34	0.0301767	K.YQEALAK.G		17.91		
						76	89	712.92	1423.82	1423.8	0.02	0	64	2.83E-05	K.GDVTAQIALQPALK.F		26.92		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15153	11%	109	2	21814	7.5	P15153|RAC2_HUMAN Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1												27	2
						6	16	530.8	1059.59	1059.54	0.05	0	46	0.0022031	K.CVVVGDGAVGK.T		21.43		
						154	163	620.83	1239.64	1239.59	0.05	0	63	3.66E-05	K.YLECSALTQR.G		25.39		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63000	17%	116	3	21835	8.8	P63000|RAC1_HUMAN Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1												29	2
						6	16	530.8	1059.58	1059.54	0.04	0	41	0.006547	K.CVVVGDGAVGK.T		19.77		
						134	147	760.44	1518.86	1518.81	0.05	0	35	0.0202092	K.LTPITYPQGLAMAK.E	Oxidation (M)	25.47		
						167	174	475.78	949.54	949.49	0.05	0	39	0.0090103	K.TVFDEAIR.A		25.04		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23284	13%	109	2	22785	9.3	P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=1												29	1
						64	76	682.88	1363.74	1363.7	0.05	0	67	1.47E-05	K.TVDNFVALATGEK.G		26.78		
						138	150	729.41	1456.8	1456.72	0.08	0	44	0.0030001	K.DTNGSQFFITTVK.T		26.56		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q92930	12%	138	2	23740	9.2	Q92930|RAB8B_HUMAN Ras-related protein Rab-8B OS=Homo sapiens GN=RAB8B PE=1 SV=2												29	6
						11	21	536.35	1070.69	1070.63	0.05	0	48	0.0012521	K.LLLIGDSGVGK.T		26.17		
						177	190	660.8	1319.59	1319.58	0.01	0	90	6.76E-08	K.MNDSNSAGAGGPVK.I	Oxidation (M)	15.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60953	12%	96	2	21696	5.8	P60953|CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=1												29	2

						6	16	530.8	1059.58	1059.54	0.04	0	41	0.006547	K.CVVVGDGAVGK.T		19.77		
						134	144	414.58	1240.72	1240.67	0.05	0	54	0.0002541	K.QKPITPETAEK.L		15.96		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62820	11%	92	2	22891	5.9	P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3												29	1
						14	24	536.35	1070.69	1070.63	0.05	0	48	0.0012521	K.LLLIGDSGVGK.S		26.17		
						176	187	531.78	1061.54	1061.48	0.06	0	44	0.0032673	R.MGPGATAGGAEK.S	Oxidation (M)	15.24		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P53990	7%	115	3	39897	5.2	P53990|K0174_HUMAN Uncharacterized protein KIAA0174 OS=Homo sapiens GN=KIAA0174 PE=1 SV=1												29	3
						83	90	470.28	938.55	938.49	0.06	0	31	0.0435121	R.FGLIQSMK.E	Oxidation (M)	24.73		
						110	118	508.81	1015.61	1015.55	0.05	0	38	0.0140626	R.LQSEVAELK.I		23.34		
						138	147	559.31	1116.6	1116.55	0.05	0	45	0.0025742	R.TNQIGTVNDR.L		17		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10253	3%	160	2	106126	5.6	P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=2												31	5
						838	849	643.88	1285.75	1285.71	0.05	0	57	0.0001477	R.QQPMALAVALTK.G	Oxidation (M)	26.4		
						892	903	615.87	1229.73	1229.66	0.07	0	103	3.68E-09	R.VTSEGAGLQLQK.V		24.4		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P82979	14%	112	3	23713	6.1	P82979|HCC1_HUMAN Nuclear protein Hcc-1 OS=Homo sapiens GN=HCC1 PE=1 SV=3												32	2
						110	119	560.33	1118.65	1118.6	0.05	0	35	0.0237098	R.FNVPVSLESK.K		25.78		
						127	135	468.28	934.55	934.51	0.04	0	36	0.0215869	R.FGISSVPTK.G		24.52		
						157	166	540.31	1078.61	1078.58	0.03	0	42	0.0044691	R.FGLNVSSISR.K		25.82		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75348	21%	178	3	13863	8.9	O75348|VATG1_HUMAN Vacuolar proton pump subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3												33	2
						2	16	835.99	1669.96	1669.86	0.1	0	55	0.0001901	M.ASQSQGIQQLLQAEK.R	Acetyl (Protein N-term)	28.74		
						2	17	914.04	1826.06	1825.96	0.09	1	89	7.72E-08	M.ASQSQGIQQLLQAEKR.A	Acetyl (Protein N-term)	27.57		
						81	89	594.84	1187.67	1187.6	0.07	0	34	0.0319743	K.MTILQTYFR.Q	Oxidation (M)	28.43		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13510	5%	123	2	45077	7.5	Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4												34	5
						82	92	612.34	1222.67	1222.6	0.07	0	65	1.94E-05	K.NMINTFVPSGK.V	Oxidation (M)	25.52		
						93	100	482.28	962.55	962.47	0.08	0	58	0.0001237	K.VMQVVDEK.L	Oxidation (M)	17.05		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61604	48%	313	5	10925	8.9	P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2												35	2
						2	8	410.25	818.49	818.44	0.05	1	35	0.0262376	M.AGQAFRK.F	Acetyl (Protein N-term)	18.79		
						29	36	430.76	859.52	859.45	0.07	0	67	1.92E-05	K.GGIMLPEK.S	Oxidation (M)	24.91		
						41	54	658.43	1314.85	1314.75	0.1	0	85	2.47E-07	K.VLQATVVAVGSGSK.G		25.34		
						57	66	507.32	1012.62	1012.56	0.07	0	60	6.79E-05	K.GGEIQPVSVK.V		22.26		
						71	80	538.84	1075.66	1075.59	0.07	0	36	0.0204355	K.VLLPEYGGTK.V		26.04		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63218	26%	83	2	7428	9.9	P63218|GBG5_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3												36	1
						2	12	555.81	1109.6	1109.54	0.06	1	47	0.0013747	M.SGSSSVAAMKK.V	Acetyl (Protein N-term); Oxidation (M)	15.92		
						19	25	386.74	771.47	771.42	0.04	0	36	0.0238494	R.LEAGLNR.V		18.64		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P78556	16%	65	2	11154	9.2	P78556|CCL20_HUMAN C-C motif chemokine 20 OS=Homo sapiens GN=CCL20 PE=1 SV=1												36	1
						45	51	420.27	838.53	838.47	0.06	0	31	0.0465033	K.FIVGFTR.Q		27.27		
						71	78	444.76	887.51	887.45	0.05	0	34	0.035182	K.LSVCANPK.Q		18.34		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07602	6%	163	3	59899	5.1	P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2												36	4
						233	242	539.29	1076.57	1076.5	0.08	0	44	0.0033836	R.LGPGMADICK.N	Oxidation (M)	22.65		
						430	438	507.83	1013.64	1013.58	0.06	0	70	8.62E-06	K.QEILAALEK.G		26.92		
						439	449	656.35	1310.68	1310.6	0.09	0	50	0.0006785	K.GCSFLPDPYQK.Q		27.1		

***Footnotes to Supplemental Table10:**

Data sets were searched with the Mascot search engine (see Perkins et al. (1999)*Electrophoresis* **20**, 3551-3567).

Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).

Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.

Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest lane in which the protein was identified, and the total # of adjacent gel lanes the protein was found)

Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 11. Proteins identified by HPLC-MS/MS on 5-day latex bead human THP-1 phagosome preparation.*

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on a 1D-SDS PAGE gel.
For summary see Supplemental Table 1.

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P35579	17%	1743	34	227646	5.5	P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4												1	2
						166	180	776.35	1550.69	1550.69	0	0	40	0.0073522	R.EDQSILCTGESGAGK.T		18.62		
						290	299	603.33	1204.64	1204.63	0.01	0	47	0.0016847	K.TDLLLEPYNK.Y		20.99		
						359	373	804.33	1606.64	1606.69	-0.05	0	78	1.12E-06	R.NTDQASMPDNTAAQK.V	Oxidation (M)	12.23		
						408	419	653.34	1304.66	1304.66	0	0	71	5.52E-06	K.EQADFAIEALAK.A		21.51		
						663	670	481.24	960.47	960.48	-0.01	0	33	0.047481	R.NTNPNFVR.C		14.02		
						694	702	509.26	1016.5	1016.51	-0.01	0	33	0.0389718	R.CNGVLEGIR.I		19.66		
						712	718	462.74	923.47	923.49	-0.01	0	35	0.0215245	R.VVFQEFR.Q		20.41		
						738	745	489.76	977.51	977.5	0	0	48	0.0014102	K.QACVLMIK.A	Oxidation (M)	19.18		
						746	755	597.31	1192.6	1192.61	-0.01	0	80	6.80E-07	K.ALELDSNLYR.I		20.77		
						843	856	585.59	1753.75	1753.77	-0.02	1	34	0.0255754	R.QEEEMMAKEEELVK.V	2 Oxidation (M)	13.97		
						868	882	892.43	1782.84	1782.84	0	0	60	6.09E-05	R.LTEMETLQSQLMAEK.L	2 Oxidation (M)	20.24		
						1001	1014	827.4	1652.78	1652.78	0	0	54	0.0002554	R.IAEFTTNLTEEEEK.S		20.59		
						1001	1016	623.63	1867.88	1867.91	-0.02	1	69	6.43E-06	R.IAEFTTNLTEEEEKSK.S		19.93		
						1220	1234	577.29	1728.85	1728.86	-0.02	1	37	0.0112429	K.QTLENERGELANEVK.V		19.14		
						1248	1260	514.29	1539.85	1539.9	-0.04	2	33	0.0318784	R.KKVEAQLQELQVK.F		15.67		
						1250	1260	642.86	1283.7	1283.71	-0.01	0	79	9.58E-07	K.VEAQLQELQVK.F		20.11		
						1445	1454	407.55	1219.62	1219.64	-0.02	1	58	0.0001255	K.KFDQLLAEEK.T		19.58		
						1446	1454	546.78	1091.54	1091.55	-0.01	0	49	0.0008877	K.FDQLLAEEK.T		19.97		
						1484	1492	532.75	1063.48	1063.49	-0.01	0	41	0.0053362	R.ALEEAMEQK.A	Oxidation (M)	12.71		
						1484	1497	554.93	1661.78	1661.79	-0.02	1	62	3.98E-05	R.ALEEAMEQKAELER.L	Oxidation (M)	14.49		
						1504	1518	572.91	1715.69	1715.72	-0.03	1	46	0.0017056	R.TEMEDLMSSKDDVGK.S	2 Oxidation (M)	13.27		
						1529	1538	610.78	1219.55	1219.58	-0.03	0	45	0.0024027	R.ALEQQVEEMK.T	Oxidation (M)	14.06		
						1558	1566	531.27	1060.53	1060.56	-0.02	0	45	0.0027237	R.LEVNLQAMK.A	Oxidation (M)	18.49		
						1593	1603	465.54	1393.59	1393.6	-0.01	1	34	0.0306351	R.EMEAELEDERK.Q	Oxidation (M)	13.1		
						1662	1669	451.23	900.45	900.49	-0.04	0	34	0.0357421	R.EEILAQAK.E		14.54		
						1698	1716	697	2087.98	2087.97	0	1	54	0.0001969	R.QAQQERDELADEIANSSGK.G		19.8		
						1717	1724	415.73	829.45	829.45	-0.01	0	36	0.0245315	K.GALALEEK.R		15.24		
						1792	1802	426.55	1276.64	1276.67	-0.03	1	61	5.85E-05	K.VKLQEMEGTVK.S	Oxidation (M)	13.06		
						1794	1802	525.74	1049.46	1049.51	-0.05	0	35	0.024006	K.LQEMEGTVK.S	Oxidation (M)	12.67		
						1807	1815	452.26	902.5	902.51	-0.01	0	53	0.0004218	K.ASITALEAK.I		16.8		
						1816	1828	765.87	1529.73	1529.76	-0.03	0	62	4.52E-05	K.IAQLEEQLDNETK.E		20.06		
						1816	1830	605.97	1814.89	1814.9	-0.01	1	64	2.17E-05	K.IAQLEEQLDNETKER.Q		19.84		
						1878	1888	666.3	1330.58	1330.6	-0.02	0	77	1.62E-06	R.QLEEAEEEAQR.A		13.84		
						1899	1912	791.35	1580.68	1580.66	0.01	0	80	6.88E-07	R.ELEDATETADAMNR.E	Oxidation (M)	14.32		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y490	9%	1104	20	271766	5.8	Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3												1	2
						614	624	543.31	1084.61	1084.62	-0.02	0	42	0.0052261	K.GLAGAVSELLR.S		22.3		
						625	634	507.25	1012.5	1012.49	0	0	46	0.0016636	R.SAQPASAEPR.Q		12.36		
						899	910	610.31	1218.6	1218.6	0	0	89	9.57E-08	R.MATNAAAQNAIK.K	Oxidation (M)	13.01		
						944	957	728.4	1454.78	1454.76	0.03	0	90	7.64E-08	K.ASAGPQPLLVQSCK.A		19.45		
						958	971	746.94	1491.86	1491.88	-0.01	0	32	0.045477	K.AVAEQIPLLVQGVR.G		22.04		
						1026	1035	529.3	1056.58	1056.59	-0.01	0	45	0.0022837	K.NLGTALAELR.T		21.34		
						1191	1198	436.75	871.48	871.49	-0.01	0	40	0.0101511	K.AVTQALNR.C		13.36		
						1321	1332	599.3	1196.59	1196.64	-0.05	0	42	0.0040618	K.ALSTDPAAPNLK.S		17.53		
						1402	1415	717.86	1433.71	1433.72	-0.01	0	78	1.18E-06	K.VLGEAMTGISQNAK.N	Oxidation (M)	14.93		
						1416	1431	810.89	1619.76	1619.78	-0.02	0	41	0.0056591	K.NGNLPEFGDAISTASK.A		21.03		
						1531	1541	573.31	1144.6	1144.61	0	0	69	9.96E-06	K.EVANSTANLVK.T		14.58		
						1594	1604	573.32	1144.62	1144.62	0	0	48	0.0011673	R.AAMEPIVISAK.T	Oxidation (M)	18.7		
						1605	1618	732.38	1462.74	1462.74	-0.01	0	59	9.01E-05	K.TMLESAGGLIQTAR.A	Oxidation (M)	20.19		
						1619	1625	370.72	739.42	739.43	-0.02	0	31	0.0433239	R.ALAVNPR.D		13.49		
						1752	1766	576.29	1725.86	1725.87	-0.01	0	48	0.001015	K.TLSHPQQMALLDQTK.T	Oxidation (M)	15.5		
						2032	2043	622.33	1242.65	1242.66	-0.01	0	80	7.55E-07	K.VLVQNAAGSQEK.L		13.23		
						2044	2057	708.89	1415.76	1415.77	-0.01	0	80	6.44E-07	K.LAQAAQSSVATITR.L		17.84		
						2090	2099	494.78	987.55	987.56	-0.01	0	73	4.17E-06	K.ALGDLISATK.A		20.81		
						2169	2177	533.25	1064.49	1064.51	-0.02	0	41	0.0055006	K.TSTPEDFIR.M		20.15		
						2351	2361	516.3	1030.59	1030.6	-0.01	0	38	0.0133896	K.SIAAATSALVK.A		19.89		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P15144	9%	492	9	109870	5.3	P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4												2	2
						205	219	545.28	1632.81	1632.86	-0.05	2	55	0.0001896	R.KVVATTQMQAADARK.S	Oxidation (M)	12.2		
						206	218	689.34	1376.66	1376.67	-0.01	0	82	4.80E-07	K.VVATTQMQAADAR.K	Oxidation (M)	12.82		
						242	252	609.82	1217.63	1217.63	-0.01	0	37	0.0155245	K.DLTALSNMLPK.G	Oxidation (M)	21.22		
						293	301	479.27	956.53	956.54	-0.01	0	66	1.90E-05	K.QASNGVLIR.I		14.91		
						364	379	862.9	1723.79	1723.83	-0.04	0	41	0.0054771	R.ENSLLFDPLSSSSSNK.E		22.01		
						364	381	670.64	2008.91	2008.97	-0.06	1	40	0.0058471	R.ENSLLFDPLSSSSSNKER.V		21.27		
						642	648	443.75	885.49	885.5	-0.01	0	39	0.0100636	K.IQTQLQR.D		13.47		
						844	855	734.39	1466.76	1466.78	-0.02	0	67	1.42E-05	R.YLSYTLNPDLIR.K		21.84		
						924	935	635.28	1268.54	1268.53	0.01	0	65	2.47E-05	K.DNEETGFGSGTR.A		14.43		
																		Strongest gel	# gel slices

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	slice	found
P11279	5%	98	2	45367	9	P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3												2	1
						138	146	517.28	1032.54	1032.55	-0.01	0	54	0.0003488	K.TVESITDIR.A		19.73		
						327	337	576.28	1150.55	1150.6	-0.05	0	45	0.0023935	R.ALQATVGNSYK.C		14.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07814	4%	299	6	172137	7	P07814|SYEP_HUMAN Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=3												2	2
						426	435	558.32	1114.63	1114.63	0	0	58	0.0001289	R.LNLNNTVLSK.R		20.13		
						587	593	380.22	758.43	758.45	-0.03	0	44	0.0039996	K.IISLDAK.F		17.68		
						757	765	471.77	941.53	941.53	0	0	37	0.0131988	R.VAVQGDVVR.E		14.21		
						890	902	671.81	1341.61	1341.64	-0.03	0	48	0.0011557	R.NSEPAGLETPEAK.V		15.17		
						992	1009	794.36	1586.71	1586.73	-0.02	0	54	0.0003091	K.NQGGGLSSSGAGEGQGPK.K		12.99		
						1390	1400	602.8	1203.58	1203.6	-0.02	0	61	5.94E-05	K.LTVAENEAETK.L		13.95		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y4L1	4%	146	3	111494	5.2	Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1												2	1
						283	291	524.28	1046.54	1046.55	-0.01	0	51	0.0007122	R.LAGLFNEQR.K		20.43		
						670	686	546.27	1635.78	1635.81	-0.03	1	52	0.0004142	K.AEAGPEGVAPAPEGEKK.Q		13.38		
						878	889	432.6	1294.76	1294.79	-0.02	0	44	0.0026561	K.LPATEKPVLLSK.D		18.85		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q32MZ4	3%	141	2	89826	4.6	Q32MZ4|LRRF1_HUMAN Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2												2	1
						618	631	758.37	1514.72	1514.72	0	0	59	8.93E-05	K.SAVEAQNEVTENPK.Q		13.73		
						707	719	650.81	1299.61	1299.63	-0.03	0	82	4.74E-07	K.IDGATQSSPAEPK.S		13.21		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P41252	3%	140	3	146178	5.9	P41252|SYIC_HUMAN Isoleucyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=1												2	1
						423	432	616.8	1231.59	1231.62	-0.03	0	57	0.0001432	R.VENMVDQLLR.N	Oxidation (M)	20.61		
						629	638	587.34	1172.66	1172.69	-0.04	0	35	0.0289747	R.LYLINSPVVR.A		21.31		
						922	933	733.36	1464.71	1464.71	0	0	48	0.0010514	K.QLSSEELEQFQK.T		20.34		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43491	2%	77	2	113032	5.3	O43491|E41L2_HUMAN Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1												2	1
						2	13	653.34	1304.66	1304.68	-0.03	1	46	0.0016761	M.TTEVGSVSEVKK.D	Acetyl (Protein N-term)	15.95		
						497	505	497.77	993.52	993.55	-0.03	0	34	0.0277282	R.LVSPEQPPK.A		13.9		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q00610	2%	135	3	193260	5.5	Q00610|CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5												2	1
						572	583	456.88	1367.63	1367.69	-0.06	0	54	0.0002884	K.NNRPSEGPLQTR.L		13.12		
						882	892	667.82	1333.62	1333.63	-0.01	0	32	0.0414604	K.IYIDSNNNPER.F		15.86		
						1398	1406	563.79	1125.57	1125.58	-0.02	0	49	0.0009077	K.VANVELYYR.A		20.17		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14625	16%	665	13	92696	4.8	P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1												3	3
						76	84	541.27	1080.52	1080.54	-0.01	0	42	0.0045233	K.FAFQAEVNR.M		20.16		
						88	95	482.29	962.57	962.58	-0.01	0	40	0.0082875	K.LIINSLYK.N		20.79		
						103	114	638.32	1274.62	1274.64	-0.01	0	71	5.40E-06	R.ELISNASDALDK.I		19.9		
						103	116	515.61	1543.8	1543.82	-0.02	1	50	0.0007579	R.ELISNASDALDKIR.L		20.66		
						143	156	510.59	1528.74	1528.77	-0.02	0	56	0.0001649	K.NLLHVTDTGVGMTR.E	Oxidation (M)	19.45		
						169	177	491.74	981.46	981.48	-0.01	0	44	0.002807	K.SGTSEFLNK.M		15.87		
						435	448	743.38	1484.74	1484.75	0	0	82	4.30E-07	K.GVVDSDDLPLNVSR.E		20.74		
						538	546	524.24	1046.46	1046.49	-0.03	0	36	0.0197064	K.IYFMAGSSR.K	Oxidation (M)	18.09		
						548	557	575.76	1149.52	1149.53	-0.01	0	66	1.91E-05	K.EAESSPFVER.L		17.09		
						594	605	466.22	1395.64	1395.69	-0.04	2	42	0.00461	K.EGVKFDESEKTK.E		13.06		
						672	682	645.29	1288.56	1288.59	-0.03	0	56	0.00021	K.DISTNYYASQK.K		18.31		
						725	733	497.26	992.5	992.52	-0.01	0	52	0.0004659	R.SGYLLPDTK.A		19.94		
						745	754	543.29	1084.56	1084.58	-0.01	0	37	0.0164126	R.LSLNIDPDAK.V		20.52		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P12814	8%	337	6	103563	5.3	P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2												3	1
						96	103	432.74	863.47	863.48	-0.01	0	50	0.0007957	K.ALDFIASK.G		20.48		
						134	147	769.39	1536.76	1536.77	-0.01	0	73	3.23E-06	R.FAIQDISVEETSAK.E		21.01		
						347	359	493.23	1476.68	1476.71	-0.04	0	38	0.01309	R.LSNRPAFMPSEGR.M	Oxidation (M)	14.11		
						727	738	715.38	1428.75	1428.76	-0.01	0	67	1.31E-05	R.TINEVENQILTR.D		20.7		
						742	752	677.8	1353.58	1353.6	-0.01	0	67	1.35E-05	K.GISQEQMNEFR.A	Oxidation (M)	15.34		
						795	803	530.77	1059.53	1059.54	-0.01	0	43	0.0044982	R.IMSIVDPNR.L	Oxidation (M)	16.43		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P34932	6%	249	4	95127	5.1	P34932|HSP74_HUMAN Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4												3	1
						222	234	661.35	1320.69	1320.7	-0.01	0	94	2.83E-08	K.VLATAFDTTLGGR.K		21.06		
						361	374	760.37	1518.73	1518.75	-0.02	0	49	0.0008214	K.ELSTTLNADEAVTR.G		19.98		
						544	557	750.33	1498.64	1498.61	0.03	0	46	0.0018395	K.AESEEMETSQAGSK.D	Oxidation (M)	12.32		
						755	764	567.3	1132.58	1132.58	0	0	60	7.26E-05	K.QSLTMDPVVK.S	Oxidation (M)	15.47		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43707	5%	280	4	105245	5.3	O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2												3	1
						115	122	432.74	863.47	863.48	-0.01	0	50	0.0007957	K.ALDFIASK.G		20.48		
						153	166	769.39	1536.76	1536.77	-0.01	0	73	3.23E-06	R.FAIQDISVEETSAK.E		21.01		
						746	757	715.38	1428.75	1428.76	-0.01	0	67	1.31E-05	R.TINEVENQILTR.D		20.7		

						761	771	684.81	1367.6	1367.61	-0.02	0	59	7.78E-05	K.GISQEQMQEFR.A	Oxidation (M)	15.3		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13639	3%	160	3	96246	6.4	P13639|EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4												3	2
						2	10	546.3	1090.58	1090.58	0	0	59	0.0001046	M.VNFTVDQIR.A		20.34		
						227	235	551.77	1101.52	1101.52	0	0	44	0.0030123	K.QFAEMYVAK.F	Oxidation (M)	17.61		
						416	426	554.32	1106.62	1106.63	-0.01	0	57	0.0001593	R.VFSGLVSTGLK.V		20.83		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05107	3%	146	2	87976	6.7	P05107|ITB2_HUMAN Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2												3	2
						166	174	485.25	968.49	968.5	-0.01	0	55	0.0002347	R.IGFGSFVDK.T		21.23		
						311	325	836.95	1671.89	1671.89	-0.01	0	60	6.58E-05	K.LAENNIQPIFAVTSR.M		21.55		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q8WUM4	3%	110	3	96590	6.1	Q8WUM4|PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1												3	1
						270	276	411.2	820.39	820.41	-0.02	0	36	0.018968	K.FGEEIAR.L		15.91		
						340	350	585.32	1168.62	1168.65	-0.03	0	38	0.0122726	K.STPVNVPISQK.F		16.61		
						567	574	459.23	916.45	916.45	0	0	36	0.0217841	R.EGLENDLK.S		16.39		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11586	3%	102	2	102180	6.9	P11586|C1TC_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3												3	1
						505	517	752.86	1503.7	1503.71	-0.01	0	55	0.0002305	K.TDPTTLTDEEINR.F		19.81		
						879	889	585.35	1168.69	1168.7	-0.01	0	49	0.0009161	K.GVPTGFILPIR.D		22.35		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P22314	2%	129	2	118858	5.5	P22314|UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3												3	1
						679	693	812.44	1622.86	1622.9	-0.04	0	60	6.70E-05	R.LAGTQPLEVLEAVQR.S		22.17		
						1011	1021	652.82	1303.63	1303.64	-0.01	0	70	7.18E-06	R.LDQPMTEIVSR.V	Oxidation (M)	17.13		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14697	2%	73	2	107263	5.7	Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3												3	1
						158	164	437.23	872.46	872.46	-0.01	0	34	0.0370002	R.LDLLEDR.S		20.61		
						165	173	486.79	971.56	971.58	-0.02	0	40	0.0097477	R.SLLLSVNAR.G		20.57		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08238	22%	977	17	83554	5	P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4												5	4
						42	53	638.32	1274.62	1274.64	-0.02	0	82	4.56E-07	R.ELISNASDALDK.I		19.81		
						56	69	513.92	1538.73	1538.75	-0.02	1	50	0.0007208	R.YESLTDPSKLDSGK.E		18.94		
						73	82	597.82	1193.62	1193.64	-0.02	0	60	7.59E-05	K.IDIIPNPQER.T		20.25		
						83	95	683.36	1364.7	1364.72	-0.03	0	70	6.34E-06	R.TLTLVDTGIGMTK.A	Oxidation (M)	20.47		
						96	107	621.85	1241.68	1241.7	-0.02	0	72	4.75E-06	K.ADLINNLGTIAK.S		21.04		
						187	196	656.29	1310.57	1310.56	0.01	0	63	3.41E-05	K.EDQTEYLEER.R		18.2		
						276	284	576.27	1150.53	1150.55	-0.02	0	49	0.0008852	K.YIDQEELNK.T		15.25		
						338	347	412.87	1235.58	1235.63	-0.05	1	34	0.0262071	R.RAPFDLFENK.K		21.08		
						338	348	455.56	1363.66	1363.72	-0.06	2	42	0.0044036	R.RAPFDLFENKK.K		20.2		
						339	347	540.76	1079.5	1079.53	-0.02	0	49	0.0008559	R.APFDLFENK.K		21.86		
						379	392	757.39	1512.77	1512.78	0	0	106	1.70E-09	R.GVVDSEDLPLNISR.E		21.17		
						429	435	446.21	890.4	890.42	-0.02	0	43	0.00479	K.FYEAFSK.N		19.59		
						439	448	381.18	1140.51	1140.55	-0.04	0	38	0.0109132	K.LGIHEDSTNR.R		13.04		
						482	491	580.78	1159.55	1159.58	-0.02	0	48	0.0014298	K.SIYYITGESK.E		19.86		
						492	502	625.3	1248.58	1248.61	-0.03	0	65	2.05E-05	K.EQVANSAFVER.V		16.73		
						532	538	367.22	732.43	732.44	-0.01	0	39	0.0109706	K.SLVSVTK.E		14.34		
						613	623	648.78	1295.55	1295.48	0.06	0	36	0.0180379	R.DNSTMGYMMAK.K	3 Oxidation (M)	12.78		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07900	18%	776	13	85006	4.9	P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5												5	3
						47	58	646.32	1290.62	1290.63	-0.01	0	82	4.29E-07	R.ELISNSSDALDK.I		18.98		
						61	74	513.92	1538.73	1538.75	-0.02	1	50	0.0007208	R.YESLTDPSKLDSGK.E		18.94		
						88	100	683.36	1364.7	1364.72	-0.03	0	70	6.34E-06	R.TLTIVDTGIGMTK.A	Oxidation (M)	20.47		
						101	112	621.85	1241.68	1241.7	-0.02	0	72	4.75E-06	K.ADLINNLGTIAK.S		21.04		
						192	201	656.29	1310.57	1310.56	0.01	0	63	3.41E-05	K.EDQTEYLEER.R		18.2		
						284	292	576.27	1150.53	1150.55	-0.02	0	49	0.0008852	K.YIDQEELNK.T		15.25		
						346	355	632.82	1263.62	1263.64	-0.01	1	39	0.0090779	R.RAPFDLFENR.K		21.39		
						347	355	554.76	1107.51	1107.53	-0.03	0	49	0.0009397	R.APFDLFENR.K		22		
						387	400	757.39	1512.77	1512.78	0	0	106	1.70E-09	R.GVVDSEDLPLNISR.E		21.17		
						447	456	390.18	1167.53	1167.56	-0.04	0	37	0.013625	K.LGIHEDSQNR.K		12.95		
						490	499	612.81	1223.61	1223.62	-0.01	0	42	0.0044268	K.HIYYITGETK.D		16.38		
						500	510	618.3	1234.58	1234.59	-0.02	0	73	3.31E-06	K.DQVANSAFVER.L		18.03		
						540	546	374.22	746.42	746.45	-0.03	0	44	0.0040311	K.TLVSVTK.E		14.12		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06396	9%	428	7	86043	5.9	P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1												5	1
						62	72	418.89	1253.64	1253.69	-0.05	1	33	0.0308306	K.AGKEPGLQIWR.V		20.07		
						178	188	425.9	1274.67	1274.71	-0.04	0	32	0.0409862	K.HVVPNEVVVQR.L		14.52		
						585	597	660.34	1318.67	1318.69	-0.01	0	92	5.16E-08	K.AGALNSNDAFVLK.T		20.56		
						616	623	444.24	886.46	886.49	-0.02	0	63	4.64E-05	K.TGAQELLR.V		16.42		
						714	728	555.92	1664.73	1664.77	-0.05	1	48	0.0009781	K.DSQEEEKTEALTSAK.R		14.3		
						730	738	539.75	1077.49	1077.51	-0.02	0	62	5.01E-05	R.YIETDPANR.D		13.82		
						742	748	379.23	756.45	756.47	-0.02	0	35	0.0256759	R.TPITVVK.Q		14.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27824	6%	156	3	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												5	1
						211	217	420.2	838.38	838.41	-0.03	0	36	0.0157784	K.TGIYEEK.H		13.52		
						552	573	616.3	2461.17	2461.12	0.05	2	53	0.0002724	K.QKSDAEEDGGTVSQEEEDRKPK.A		12.73		
						574	582	544.76	1087.5	1087.51	-0.02	0	67	1.55E-05	K.AEEDEILNR.S		17.47		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14108	5%	87	2	54712	5	Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2												5	1
						83	92	606.78	1211.55	1211.58	-0.03	0	45	0.0021862	R.VEEVGPYTYR.E		19.46		
						391	402	469.9	1406.67	1406.7	-0.04	1	42	0.0040419	K.KLDDFVETGDIR.T		20.38		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14974	3%	129	3	98420	4.7	Q14974|IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2												5	1
						43	54	613.32	1224.62	1224.66	-0.03	0	42	0.0042108	R.VLANPGNSQVAR.V		13.86		
						235	243	478.29	954.57	954.59	-0.01	0	43	0.0035419	R.VAALQNLVK.I		20.12		
						550	557	489.75	977.49	977.52	-0.03	0	44	0.0030922	K.TTLVIMER.L	Oxidation (M)	17.16		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11021	27%	997	16	72402	5.1	P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2												6	2
						47	60	519.26	1554.76	1554.79	-0.02	1	62	4.57E-05	K.NGRVEIIANDQGNR.I		13.88		
						50	60	614.81	1227.61	1227.62	-0.01	0	70	9.04E-06	R.VEIIANDQGNR.I		14.76		
						61	74	783.89	1565.76	1565.77	-0.02	0	68	8.91E-06	R.ITPSYVAFTPEGER.L		20.64		
						82	96	839.4	1676.79	1676.8	-0.01	0	107	1.34E-09	K.NQLTSNPENTVFDAK.R		20.1		
						82	97	611.96	1832.85	1832.9	-0.05	1	89	8.06E-08	K.NQLTSNPENTVFDAKR.L		19.57		
						124	138	535.61	1603.82	1603.86	-0.04	0	67	1.43E-05	K.TKPYIQVDIGGGQTK.T		19.61		
						186	197	617.31	1232.61	1232.62	-0.01	0	44	0.0029427	K.DAGTIAGLNVMR.I	Oxidation (M)	20.01		
						198	214	605.99	1814.96	1814.99	-0.03	1	89	6.45E-08	R.IINEPTAAAIAYGLDKR.E		20.95		
						325	336	510.24	1527.69	1527.74	-0.05	1	50	0.0006892	R.AKFEELNMDLFR.S	Oxidation (M)	20.81		
						353	367	530.28	1587.81	1587.85	-0.04	1	37	0.01494	K.KSDIDEIVLVGGSTR.I		20.5		
						371	376	364.73	727.44	727.46	-0.02	0	39	0.0100392	K.IQQLVK.E		13.66		
						448	464	918.96	1835.91	1835.93	-0.02	0	98	1.09E-08	K.SQIFSTASDNQPTVTIK.V		20.24		
						524	532	537.77	1073.52	1073.55	-0.02	0	56	0.0001944	K.ITITNDQNR.L		13.49		
						541	554	418.19	1668.72	1668.77	-0.05	2	35	0.0199412	R.MVNDAEKFAEEDKK.L	Oxidation (M)	13.53		
						620	633	551.99	1652.94	1652.97	-0.03	2	53	0.0002885	K.KKELEEIVQPIISK.L		20.06		
						622	633	699.4	1396.78	1396.78	0	0	38	0.012695	K.ELEEIVQPIISK.L		21.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26038	17%	610	14	67892	6.1	P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3												6	1
						28	35	488.77	975.52	975.54	-0.02	0	44	0.003133	K.QLFDQVVK.T		20.28		
						101	107	447.77	893.52	893.54	-0.02	0	33	0.0322266	R.LFFLQVK.E		22.06		
						185	193	540.28	1078.54	1078.55	-0.01	0	62	4.83E-05	R.EDAVLEYLK.I		21.35		
						295	306	496.92	1487.73	1487.78	-0.05	1	53	0.000345	R.RKPDTIEVQQMK.A	Oxidation (M)	12.48		
						296	306	444.88	1331.63	1331.68	-0.05	0	42	0.0053082	R.KPDTIEVQQMK.A	Oxidation (M)	12.83		
						360	371	505.92	1514.74	1514.78	-0.04	2	38	0.0104235	K.KAQQELEEQTRR.A		12.44		
						361	370	616.3	1230.58	1230.58	-0.01	0	35	0.0244704	K.AQQELEEQTR.R		13.09		
						401	408	444.24	886.47	886.49	-0.02	0	35	0.0288628	K.EALLQASR.D		14.98		
						428	435	482.24	962.46	962.49	-0.02	0	45	0.002497	R.ISQLEMAR.Q	Oxidation (M)	13.44		
						449	458	603.78	1205.55	1205.56	-0.01	0	71	5.60E-06	K.AQMVQEDLEK.T	Oxidation (M)	13.8		
						449	460	488.56	1462.67	1462.71	-0.04	1	35	0.0236423	K.AQMVQEDLEKTR.A	Oxidation (M)	13.75		
						524	533	523.4	1044.79	1044.56	0.23	0	40	0.0061384	K.ALTSELANAR.D		18.43		
						524	537	502.25	1503.72	1503.75	-0.03	1	37	0.0149882	K.ALTSELANARDESK.K		15.94		
						569	577	585.74	1169.47	1169.5	-0.03	1	42	0.0043783	K.QRIDEFESM.-	Oxidation (M)	17.82		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P01876	10%	157	3	38486	6.1	P01876|IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2												6	1
						154	168	770.86	1539.71	1539.72	-0.01	0	39	0.0093864	R.DASGVTFTWTPSSGK.S		21.26		
						201	212	688.31	1374.61	1374.61	0	0	57	0.0001512	K.TFTCTAAYPESK.T		17.03		
						264	273	607.31	1212.61	1212.63	-0.01	0	61	5.17E-05	R.WLQGSQELPR.E		19.97		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15942	7%	138	3	62436	6.2	Q15942|ZYX_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1												6	1
						36	54	663.66	1987.95	1987.99	-0.04	0	39	0.0083397	K.VNPFRPGDSEPPPAPGAQR.A		19.13		
						254	265	538.77	1075.53	1075.57	-0.03	0	57	0.0001514	R.GPPASSPAPAPK.F		12.61		
						376	386	630.31	1258.61	1258.61	0	0	43	0.0036326	R.QNVAVNELCGR.C		18.34		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q13310	4%	69	2	71080	9.3	Q13310|PABP4_HUMAN Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1												6	1
						68	78	641.82	1281.63	1281.63	0	0	59	7.56E-05	R.ALDTMNFDVIK.G	Oxidation (M)	20.73		
						313	324	635.81	1269.61	1269.62	-0.02	0	38	0.0120431	K.EFSPFGSITSAK.V		21.39		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P13796	20%	590	11	70815	5.2	P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=5												7	2
						4	15	707.79	1413.56	1413.58	-0.02	0	45	0.0025465	R.GSVSDEEMMELR.E	2 Oxidation (M)	14.78		
						133	141	545.23	1088.44	1088.46	-0.02	0	47	0.001766	K.ALENDPDCR.H		12.86		
						166	178	759.86	1517.71	1517.74	-0.03	0	52	0.0004418	K.MINLSVPDTIDER.T	Oxidation (M)	20.78		
						245	253	506.8	1011.59	1011.61	-0.01	0	48	0.0012217	R.NEALIALLR.E		22		
						254	263	583.76	1165.51	1165.52	-0.01	0	61	5.92E-05	R.EGESLEDLMK.L	Oxidation (M)	19.24		
						286	294	497.76	993.5	993.51	-0.01	0	65	2.23E-05	K.IGNFSTDIK.D		19.59		

						334	343	626.27	1250.52	1250.54	-0.02	0	54	0.0002709	R.AECMLQQAER.L	Oxidation (M)	13.08		
						348	357	568.3	1134.58	1134.6	-0.02	0	54	0.0002792	R.QFVTATDVVR.G		19.73		
						473	488	838.41	1674.8	1674.83	-0.03	0	67	1.17E-05	K.FSLVGIGGQDLNEGNR.T		21.43		
						571	584	539.91	1616.71	1616.76	-0.06	1	48	0.0010467	K.TENLNDDEKLNNAK.Y		13.25		
						611	622	718.32	1434.62	1434.64	-0.02	0	50	0.0006474	K.MVMTVFACLMGK.G	3 Oxidation (M)	20.86		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P11142	19%	680	11	71082	5.4	P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1												7	2
						26	36	614.81	1227.6	1227.62	-0.02	0	67	1.48E-05	K.VEIIANDQGNR.T		14.6		
						37	49	744.35	1486.68	1486.69	-0.02	0	65	2.41E-05	R.TTPSYVAFTDTER.L		20.3		
						57	71	833.38	1664.74	1664.78	-0.04	0	87	1.36E-07	K.NQVAMNPTNTVFDAK.R	Oxidation (M)	19.51		
						57	72	607.94	1820.8	1820.88	-0.09	1	56	0.0001643	K.NQVAMNPTNTVFDAKR.L	Oxidation (M)	17.46		
						78	88	635.77	1269.53	1269.55	-0.03	0	60	7.88E-05	R.FDDAVVQSDMK.H	Oxidation (M)	15.43		
						160	171	600.32	1198.63	1198.67	-0.04	0	65	2.59E-05	K.DAGTIAGLNVLR.I		21.39		
						172	188	596.65	1786.94	1786.98	-0.04	1	79	7.21E-07	R.IINEPTAAAIAYGLDKK.V		20.82		
						221	236	564.57	1690.7	1690.72	-0.02	0	35	0.0227628	K.STAGDTHLGGEDFDNR.M		15.38		
						302	311	627.31	1252.6	1252.61	-0.01	0	49	0.0007898	R.FEELNADLFR.G		21.78		
						349	357	541.28	1080.54	1080.56	-0.02	0	52	0.000435	K.LLQDFFNGK.E		21.56		
						452	458	387.2	772.39	772.41	-0.02	0	34	0.0375324	K.DNNLLGK.F		14.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08107	12%	320	6	70294	5.5	P08107|HSP71_HUMAN Heat shock 70 kDa protein 1 OS=Homo sapiens GN=HSPA1A PE=1 SV=5												7	1
						26	36	614.81	1227.6	1227.62	-0.02	0	67	1.48E-05	K.VEIIANDQGNR.T		14.6		
						37	49	744.35	1486.68	1486.69	-0.02	0	65	2.41E-05	R.TTPSYVAFTDTER.L		20.3		
						57	71	829.92	1657.82	1657.84	-0.02	0	60	5.96E-05	K.NQVALNPQNTVFDAK.R		20.38		
						78	88	619.78	1237.54	1237.56	-0.02	0	36	0.0159993	K.FGDPVVQSDMK.H	Oxidation (M)	15.86		
						221	236	559.25	1674.73	1674.72	0.01	0	43	0.0034816	K.ATAGDTHLGGEDFDNR.L		15.69		
						349	357	555.28	1108.55	1108.57	-0.01	0	49	0.0007665	K.LLQDFFNGR.D		21.7		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P29966	10%	114	2	31707	4.5	P29966|MARCS_HUMAN Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4												7	1
						12	30	595.62	1783.83	1783.87	-0.04	0	54	0.0002324	K.GEAAAERPGEAAVASSPSK.A		13.03		
						138	152	750.83	1499.65	1499.67	-0.02	0	60	7.16E-05	K.AEDGATPSPSNETPK.K		12.95		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08133	10%	227	6	76168	5.4	P08133|ANXA6_HUMAN Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3												7	1
						103	113	553.28	1104.55	1104.53	0.02	0	49	0.0011452	K.DAISGIGTDEK.C		16.64		
						157	166	573.33	1144.64	1144.66	-0.03	0	36	0.0200072	K.MLVVLLQGTR.E	Oxidation (M)	20.91		
						221	231	391.54	1171.6	1171.66	-0.05	0	43	0.0039697	K.TTGKPIEASIR.G		13.34		
						251	259	550.24	1098.46	1098.5	-0.03	0	35	0.023531	R.STPEYFAER.L		18.98		
						355	370	563.26	1686.74	1686.8	-0.05	0	31	0.0467612	K.GTVRPANDFNPDADAK.A		14.34		
						547	554	529.26	1056.51	1056.51	0	0	33	0.0388716	R.FMTILCTR.S	Oxidation (M)	20.12		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P17066	8%	227	4	71440	5.8	P17066|HSP76_HUMAN Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2												7	2
						28	38	614.81	1227.6	1227.62	-0.02	0	67	1.48E-05	R.VEILANDQGNR.T		14.6		
						39	51	744.35	1486.68	1486.69	-0.02	0	65	2.41E-05	R.TTPSYVAFTDTER.L		20.3		
						223	238	559.25	1674.73	1674.72	0.01	0	43	0.0034816	K.ATAGDTHLGGEDFDNR.L		15.69		
						351	359	541.28	1080.54	1080.56	-0.02	0	52	0.000435	K.LLQDFFNGK.E		21.56		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04062	3%	75	2	60134	7.3	P04062|GLCM_HUMAN Glucosylceramidase OS=Homo sapiens GN=GBA PE=1 SV=3												7	1
						317	324	510.25	1018.49	1018.51	-0.02	0	39	0.0099865	R.LLMLDDQR.L	Oxidation (M)	19.64		
						333	342	521.78	1041.55	1041.57	-0.02	0	36	0.0206613	K.VVLTDPEAAK.Y		15.9		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04843	3%	89	2	68641	6	P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1												7	1
						117	126	490.78	979.54	979.57	-0.03	0	38	0.0106195	K.LPVALDPGAK.I		19.81		
						269	278	530.26	1058.51	1058.54	-0.03	0	50	0.0007329	R.QPDSGISSIR.S		14.86		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40227	14%	367	7	58444	6.2	P40227|TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3												8	1
						46	55	503.75	1005.48	1005.52	-0.03	0	36	0.0218625	K.MLVSGAGDIK.L	Oxidation (M)	14.9		
						118	127	539.78	1077.54	1077.57	-0.03	0	50	0.000831	R.IITEGFEAAK.E		19.46		
						130	138	538.79	1075.57	1075.59	-0.03	0	53	0.0004278	K.ALQFLEEVK.V		21.22		
						146	153	458.75	915.49	915.5	-0.01	0	40	0.0099333	R.ETLIDVAR.T		20.03		
						200	208	511.26	1020.51	1020.51	0	0	61	5.84E-05	K.SETDTSLIR.G		15.63		
						296	307	631.83	1261.64	1261.66	-0.02	0	66	1.87E-05	K.GIDPFSLDALSK.E		22.27		
						450	465	881.47	1760.92	1760.93	-0.01	0	62	3.62E-05	K.VLAQNSGFDLQETLVK.I		21.31		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P49368	11%	304	6	61066	6.1	P49368|TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4												8	1
						129	138	561.78	1121.54	1121.56	-0.02	0	49	0.0008507	K.ALDDMISTLK.K	Oxidation (M)	19.9		
						238	248	640.35	1278.69	1278.71	-0.02	0	64	2.95E-05	R.IVLLDSSLEYK.K		21.36		
						307	313	379.71	757.41	757.44	-0.03	0	37	0.0226395	R.ANITAIR.R		14.33		
						390	399	625.77	1249.52	1249.55	-0.03	0	49	0.0009825	R.NLQDAMQVCR.N	Oxidation (M)	13.81		
						439	449	583.84	1165.66	1165.68	-0.02	0	63	3.63E-05	R.AVAQALEVIPR.T		20.61		
						450	461	667.32	1332.63	1332.68	-0.05	0	45	0.0021827	R.TLIQNCGASTIR.L		17.67		
																		Strongest gel	# gel slices

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	slice	found
P48643	10%	255	6	60089	5.5	P48643|TCPE_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1												8	1
						28	35	445.74	889.47	889.49	-0.02	0	36	0.0243507	R.LMGLEALK.S	Oxidation (M)	19.86		
						133	142	547.25	1092.49	1092.52	-0.03	0	63	3.48E-05	R.IADGYEQAAR.V		13.85		
						203	214	464.57	1390.7	1390.73	-0.04	1	43	0.0034756	R.DVDFELIKVEGK.V		21.13		
						345	352	462.73	923.45	923.46	-0.01	0	45	0.0020603	R.FSELTAEK.L		14.94		
						382	388	410.25	818.48	818.5	-0.02	0	35	0.0291021	R.AVTIFIR.G		20.56		
						515	525	645.83	1289.65	1289.68	-0.03	0	37	0.0152766	K.QQISLATQMVR.M	Oxidation (M)	18.02		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P10809	9%	276	5	61187	5.7	P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2												8	1
						397	405	451.26	900.51	900.53	-0.02	0	34	0.0360729	K.LSDGVAVLK.V		19.02		
						406	417	617.29	1232.56	1232.59	-0.03	0	73	3.61E-06	K.VGGTSDVEVNEK.K		13.37		
						421	429	480.74	959.47	959.5	-0.03	0	37	0.0200928	R.VTDALNATR.A		13.68		
						471	481	401.56	1201.65	1201.71	-0.06	1	41	0.0060385	R.TLKIPAMTIAK.N	Oxidation (M)	17.76		
						482	493	608.33	1214.64	1214.65	-0.01	0	58	0.0001201	K.NAGVEGSLIVEK.I		19.59		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P54577	8%	206	4	59448	6.6	P54577|SYYC_HUMAN Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4												8	1
						103	114	651.84	1301.67	1301.69	-0.02	0	50	0.0007473	K.AMLESIGVPLEK.L	Oxidation (M)	20.52		
						311	319	487.26	972.5	972.52	-0.02	0	35	0.0307427	K.NSVEVALNK.L		15.11		
						357	367	628.8	1255.58	1255.6	-0.03	0	45	0.0024319	K.NSEPEEVIPSR.L		16.54		
						392	400	493.24	984.47	984.49	-0.02	0	46	0.0021007	K.IDVGEAEPR.T		15.07		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O75083	6%	134	4	66836	6.2	O75083|WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4												8	1
						8	17	573.31	1144.6	1144.62	-0.02	0	32	0.0482154	K.VFASLPQVER.G		20.3		
						29	38	564.28	1126.54	1126.54	0	0	35	0.0236504	K.GNNFLYTNGK.C		19.15		
						117	124	400.72	799.43	799.46	-0.02	0	33	0.048019	R.IAVVGEGR.E		14.02		
						148	155	444.25	886.49	886.51	-0.03	0	34	0.035509	K.VINSVDIK.Q		15.42		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P17987	6%	139	3	60819	5.8	P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=CCT1 PE=1 SV=1												8	1
						1	11	633.33	1264.64	1264.58	0.07	0	52	0.0004418	-.MEGPLSVFGDR.S	Acetyl (Protein N-term); Oxidation (M)	22.75		
						434	443	574.3	1146.59	1146.6	-0.02	0	38	0.013321	R.EQLAIAEFAR.S		21		
						500	510	594.82	1187.63	1187.66	-0.02	0	50	0.0008786	K.QAGVFEPTIVK.V		20.21		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23141	3%	97	2	62766	6.2	P23141|EST1_HUMAN Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2												8	1
						331	339	536.75	1071.49	1071.52	-0.03	0	50	0.0010693	K.TPEELQAER.N		13.76		
						483	491	510.23	1018.44	1018.46	-0.02	0	47	0.0017395	K.EGASEEEIR.L		13.15		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07237	23%	594	11	57480	4.8	P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3												9	1
						70	78	501.77	1001.52	1001.55	-0.03	1	36	0.0222668	K.LKAEGSEIR.L		12.74		
						82	97	890.91	1779.81	1779.83	-0.02	0	95	2.10E-08	K.VDATEESDLAQQYGVR.G		20.41		
						201	207	389.22	776.42	776.44	-0.02	0	45	0.0029025	K.DGVVLFK.K		20.77		
						214	222	519.24	1036.46	1036.48	-0.02	0	36	0.0153077	R.NNFEGEVTK.E		14.27		
						277	283	377.18	752.35	752.37	-0.02	0	34	0.0206801	K.TAAESFK.G		13.05		
						286	300	611.95	1832.84	1832.91	-0.07	0	48	0.0008985	K.ILFIFIDSDHTDNQR.I		22.28		
						301	308	483.78	965.54	965.56	-0.02	0	40	0.0072177	R.ILEFFGLK.K		22.64		
						317	326	611.81	1221.6	1221.62	-0.02	0	49	0.0010114	R.LITLEEEMTK.Y	Oxidation (M)	19.43		
						327	338	484.56	1450.65	1450.69	-0.04	0	69	7.26E-06	K.YKPESEELTAER.I		14.1		
						376	386	447.87	1340.59	1340.62	-0.03	1	57	0.000146	K.NFEDVAFDEKK.N		19.74		
						425	436	655.29	1308.57	1308.59	-0.02	0	85	2.38E-07	K.MDSTANEVEAVK.V	Oxidation (M)	14.14		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50990	23%	660	11	60153	5.4	P50990|TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4												9	1
						63	74	667.37	1332.72	1332.74	-0.02	0	101	5.43E-09	K.LFVTNDAATILR.E		21.31		
						156	165	573.79	1145.57	1145.59	-0.03	0	39	0.0108256	R.DIDEVSSLLR.T		21.84		
						226	235	532.76	1063.5	1063.5	0	0	49	0.0008654	K.ETEGDVTSVK.D		13.18		
						271	281	625.28	1248.54	1248.57	-0.03	0	64	3.00E-05	K.GEENLMDAQVK.A	Oxidation (M)	13.97		
						282	296	686.86	1371.71	1371.74	-0.03	0	92	4.75E-08	K.AIADTGANVVVTGGK.V		18.46		
						327	335	443.25	884.49	884.51	-0.01	0	46	0.0020571	K.TVGATALPR.L		14.58		
						379	390	691.3	1380.58	1380.58	0	0	83	3.60E-07	R.GSTDNLMDDIER.A	Oxidation (M)	19.03		
						391	400	533.25	1064.49	1064.51	-0.02	0	44	0.0026879	R.AVDDGVNTFK.V		16.5		
						408	421	677.88	1353.75	1353.75	0	0	35	0.0206846	R.LVPGGGATEIELAK.Q		20.01		
						441	450	575.79	1149.56	1149.58	-0.02	0	62	4.56E-05	K.FAEAFEAIPR.A		20.9		
						510	520	564.83	1127.65	1127.67	-0.02	0	48	0.0013257	K.LATNAAVTVLR.V		19.79		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P14618	17%	363	7	58470	8	P14618|KPYM_HUMAN Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4												9	2
						33	43	599.33	1196.64	1196.64	0	0	49	0.0008067	R.LDIDSPPITAR.N		20.1		
						44	56	680.35	1358.69	1358.7	-0.01	0	44	0.0030569	R.NTGIICTIGPASR.S		19.92		
						126	135	495.75	989.48	989.5	-0.02	0	43	0.0040316	K.GSGTAEVELK.K		14.19		
						142	151	607.29	1212.56	1212.57	-0.01	0	46	0.0016666	K.ITLDNAYMEK.C	Oxidation (M)	19.12		
						189	206	890.43	1778.84	1778.87	-0.03	0	92	3.30E-08	K.GADFLVTEVENGGSLGSK.K		21.62		
						208	224	818.94	1635.86	1635.88	-0.03	0	50	0.0007182	K.GVNLPGAAVDLPAVSEK.D		21.04		
						295	305	571.3	1140.59	1140.6	-0.01	0	40	0.0079424	R.GDLGIEIPAEK.V		20.46		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50991	16%	446	9	58401	8	P50991|TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4												9	1
						35	42	419.22	836.42	836.44	-0.02	0	36	0.0148108	R.FSNISAAK.A		13.53		
						66	79	709.37	1416.73	1416.75	-0.02	0	56	0.0001828	K.GDVTITNDGATILK.Q		20.32		
						161	174	739.88	1477.75	1477.76	-0.01	0	81	5.60E-07	R.ETLLNSATTSLNSK.V		20.23		
						281	288	467.29	932.56	932.57	-0.01	0	38	0.0144878	R.AYILNLVK.Q		21.22		
						385	391	394.24	786.47	786.5	-0.02	0	34	0.037482	K.TVTIVVR.G		16.37		
						392	403	448.89	1343.65	1343.7	-0.05	1	51	0.0006435	R.GSNKLVIEEAER.S		15.41		
						396	403	479.76	957.5	957.51	-0.01	0	34	0.0327298	K.LVIEEAER.S		16.63		
						420	435	775.94	1549.87	1549.88	-0.01	0	68	9.98E-06	R.ALIAGGGAPEIELALR.L		21.88		
						532	539	466.24	930.46	930.48	-0.02	0	48	0.0015663	K.IDDVVNTR.-		14.23		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30101	16%	351	7	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												9	2
						63	73	596.28	1190.55	1190.59	-0.04	0	42	0.0053539	R.LAPEYEAAATR.L		15.54		
						131	140	498.27	994.53	994.56	-0.03	0	43	0.0029823	K.QAGPASVPLR.T		15.11		
						336	344	594.75	1187.48	1187.53	-0.04	0	48	0.0011682	K.FVMQEEFSR.D	Oxidation (M)	17.2		
						367	379	684.83	1367.65	1367.66	-0.01	0	71	5.87E-06	K.SEPIPESNDGPVK.V		15.06		
						423	433	399.91	1196.69	1196.71	-0.02	1	37	0.0120614	K.LSKDPNIVIAK.M		14.93		
						472	482	685.85	1369.68	1369.69	-0.01	0	35	0.0201546	R.ELSDFISYLQR.E		23.08		
						483	496	527.27	1578.8	1578.83	-0.03	0	44	0.0026296	R.EATNPPVIQEEKPK.K		13.79		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99832	13%	329	6	59842	7.5	Q99832|TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2												9	1
						1	10	608.83	1215.65	1215.66	-0.01	0	48	0.0011374	-.MMPTPVILLK.E	Acetyl (Protein N-term); 2 Oxidation (M)	21.93		
						78	84	380.23	758.44	758.45	-0.01	0	36	0.0248894	K.TLVDIAK.S		18.16		
						376	387	700.29	1398.57	1398.57	0	0	76	1.84E-06	R.GGAEQFMEETER.S	Oxidation (M)	15.15		
						402	418	846.9	1691.8	1691.8	-0.01	0	67	1.20E-05	K.NDSVVAGGGAIEMELSK.Y	Oxidation (M)	20.59		
						441	447	406.25	810.48	810.5	-0.02	0	41	0.0048281	K.ALEIIPR.Q		20.15		
						448	463	897.42	1792.82	1792.84	-0.02	0	62	4.04E-05	R.QLCDNAGFDATNILNK.L		21.13		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31146	8%	221	4	51678	6.3	P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4												9	1
						384	393	513.8	1025.59	1025.61	-0.02	0	45	0.0020398	R.DAGPLLISLK.D		21.8		
						417	432	751.85	1501.69	1501.7	-0.01	0	74	2.70E-06	R.AAPEASGTPSSDAVSR.L		13.22		
						439	449	429.24	1284.7	1284.74	-0.04	1	34	0.0311191	R.KLQATVQELQK.R		14.49		
						440	449	579.32	1156.62	1156.65	-0.03	0	68	1.20E-05	K.LQATVQELQK.R		16.2		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06744	8%	183	3	63335	8.4	P06744|G6PI_HUMAN Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4												9	1
						107	116	522.28	1042.54	1042.57	-0.03	0	45	0.0023544	R.SNTPILVDGK.D		16.46		
						195	211	916.51	1831.01	1831.01	0	0	61	5.11E-05	K.TLAQLNPESSLFIIASK.T		22.86		
						212	226	828.4	1654.79	1654.8	-0.01	0	77	1.22E-06	K.TFTTQETITNAETAK.E		19.48		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01518	42%	1311	22	52222	8.3	Q01518|CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=4												10	3
						2	10	567.26	1132.5	1132.52	-0.02	0	66	1.81E-05	M.ADMQNLVER.L	Acetyl (Protein N-term); Oxidation (M)	17.48		
						2	13	766.37	1530.72	1530.75	-0.02	1	31	0.0497159	M.ADMQNLVERLER.A	Acetyl (Protein N-term); Oxidation (M)	20.9		
						64	71	423.21	844.41	844.43	-0.02	0	46	0.0023429	K.EIGGDVQK.H		12.77		
						85	100	879.44	1756.86	1756.88	-0.01	0	107	1.12E-09	R.ALLVTASQCQQPAENK.L		17.18		
						101	113	713.89	1425.76	1425.81	-0.05	0	51	0.0006092	K.LSDLLAPISEQIK.E		23.65		
						101	113	713.9	1425.79	1425.81	-0.02	0	70	7.46E-06	K.LSDLLAPISEQIK.E		21.61		
						114	119	382.71	763.4	763.42	-0.02	0	33	0.0381004	K.EVITFR.E		19.24		
						156	167	747.79	1493.57	1493.59	-0.02	0	80	6.92E-07	K.EMNDAAMFYTNR.V	2 Oxidation (M)	18.58		
						273	287	434.96	1735.8	1735.87	-0.07	2	37	0.0122004	K.HVSDDMKTHKNPALK.A	Oxidation (M)	11.95		
						295	312	460.24	1836.94	1836.97	-0.04	0	64	2.37E-05	R.SGPKPFSAPKPQTSPSPK.R		13.3		
						314	327	504.94	1511.81	1511.86	-0.05	2	62	4.53E-05	R.ATKKEPAVLELEGK.K		15.55		
						317	327	404.89	1211.65	1211.68	-0.03	1	58	0.0001215	K.KEPAVLELEGK.K		19.2		
						317	328	447.58	1339.72	1339.77	-0.05	2	68	1.01E-05	K.KEPAVLELEGKK.W		15.24		
						318	327	542.8	1083.58	1083.58	0	0	61	5.87E-05	K.EPAVLELEGK.K		20.27		
						331	348	1037.01	2072.01	2072.03	-0.02	0	133	2.94E-12	R.VENQENVSNLVIEDTELK.Q		21.21		
						356	364	538.78	1075.54	1075.57	-0.03	0	48	0.0011409	K.CVNTTLQIK.G		16.91		
						365	377	492.92	1475.73	1475.78	-0.04	2	66	1.74E-05	K.GKINSITVDNCKK.L		12.82		
						367	376	582.28	1162.55	1162.57	-0.02	0	65	2.15E-05	K.INSITVDNCK.K		14.36		
						367	377	431.21	1290.62	1290.66	-0.04	1	41	0.0055202	K.INSITVDNCKK.L		13.17		
						405	412	436.26	870.51	870.52	-0.01	0	39	0.0094252	K.VPTISINK.T		17.88		
						423	433	618.29	1234.57	1234.59	-0.02	0	71	6.35E-06	K.NSLDCEIVSAK.S		19.15		
						434	458	943.1	2826.28	2826.31	-0.03	0	66	1.17E-05	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	Oxidation (M)	22.45		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O43175	17%	513	8	57356	6.3	O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4												10	1
						22	33	649.86	1297.7	1297.72	-0.02	0	85	2.42E-07	K.ILQDGGLQVVEK.Q		19.86		
						59	69	565.79	1129.56	1129.6	-0.03	0	65	2.81E-05	K.VTADVINAAEK.L		16.56		
						76	90	744.86	1487.7	1487.72	-0.02	0	79	8.37E-07	R.AGTGVDNVDLEAATR.K		19.6		
						138	146	506.74	1011.46	1011.47	-0.01	0	34	0.0277944	K.FMGTELNGK.T	Oxidation (M)	14.14		
						147	155	450.27	898.52	898.56	-0.04	0	42	0.004152	K.TLGILGLGR.I		21.43		
						237	247	550.31	1098.6	1098.6	-0.01	0	53	0.0003542	R.GGIVDEGALLR.A		20.67		
						352	364	673.38	1344.75	1344.76	-0.01	0	70	8.32E-06	K.GTIQVITQGTSLK.N		20.04		

						385	394	536.29	1070.56	1070.57	-0.01	0	85	2.31E-07	K.QADVNLVNAK.L		15.03		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P21796	16%	352	5	30868	8.6	P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2												10	5
						33	53	730.33	2187.96	2188.01	-0.05	1	84	2.05E-07	K.TKSENGLEFTSSGSANTETTK.V		15.11		
						35	53	980.44	1958.86	1958.87	-0.01	0	80	5.48E-07	K.SENGLEFTSSGSANTETTK.V		19.02		
						97	109	700.83	1399.65	1399.66	-0.01	0	102	4.06E-09	K.LTFDSSFSPNTGK.K		20.49		
						97	110	510.26	1527.74	1527.76	-0.01	1	44	0.0025081	K.LTFDSSFSPNTGKK.N		19.78		
						164	174	607.3	1212.59	1212.61	-0.02	0	40	0.0065288	R.VTQSNFAVGYK.T		18.49		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P78371	11%	313	6	57794	6	P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4												10	1
						2	13	651.37	1300.72	1300.74	-0.02	0	44	0.0031969	M.ASLSLAPVNIFK.A	Acetyl (Protein N-term)	23.91		
						58	72	782.89	1563.77	1563.78	-0.01	0	52	0.0003946	R.DASLMVTNDGATILK.N	Oxidation (M)	20.45		
						112	119	430.73	859.45	859.47	-0.02	0	60	0.0001047	R.EAESLIAK.K		14.45		
						237	248	654.32	1306.62	1306.64	-0.02	0	44	0.002916	K.ILIANTGMDTDK.I	Oxidation (M)	16.08		
						237	250	516.94	1547.81	1547.82	-0.01	1	36	0.0180614	K.ILIANTGMDTDKIK.I	Oxidation (M)	17.61		
						377	388	665.83	1329.64	1329.65	-0.01	0	47	0.0016571	R.GATQQILDEAER.S		19.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q5VTE0	9%	254	5 (6)	50495	9.2	Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1AL3 PE=5 SV=1												10	10
						38	44	447.74	893.47	893.49	-0.01	1	33	0.0356347	R.TIEKFEK.E		13.12		
						147	154	427.25	852.49	852.51	-0.02	0	37	0.0122834	K.QLIVGVNK.M	Gln->pyro-Glu (N-term Q)	21.25		
						173	179	420.22	838.44	838.44	-0.01	0	47	0.0011123	K.EVSTYIK.K		15.15		
						256	266	513.31	1024.6	1024.6	-0.01	0	71	4.66E-06	K.IGGIGTVPVGR.V		19.73		
						431	439	449.27	896.52	896.53	-0.01	0	55	0.0001916	R.QTVAVGVIK.A	Gln->pyro-Glu (N-term Q)	20.77		
						431	439	457.9	913.79	913.56	0.23	0	68	2.37E-06	R.QTVAVGVIK.A		18.82		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52209	9%	210	4	53619	6.8	P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3												10	3
						39	48	561.28	1120.55	1120.54	0.01	0	53	0.0004219	K.VDDFLANEAK.G		20.12		
						52	64	464.58	1390.72	1390.75	-0.02	1	34	0.0283812	K.VVGAQSLKEMVSK.L	Oxidation (M)	15.19		
						77	87	596.79	1191.57	1191.58	-0.01	0	86	1.97E-07	K.AGQAVDDFIEK.L		20.08		
						155	163	474.78	947.54	947.54	0	0	39	0.0096504	K.TIFQGIAAK.V		20.29		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50502	8%	133	3	41477	5.2	P50502|F10A1_HUMAN Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2												10	2
						119	132	735.91	1469.81	1469.77	0.04	0	57	0.0001499	K.VAAIEALNDGELQK.A		20.51		
						133	142	553.8	1105.59	1105.6	-0.01	0	40	0.0075545	K.AIDLFTDAIK.L		22.08		
						147	153	396.25	790.48	790.5	-0.02	0	36	0.0234431	R.LAILYAK.R		20.25		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O60664	6%	113	2	47189	5.3	O60664|M6PBP_HUMAN Mannose-6-phosphate receptor-binding protein 1 OS=Homo sapiens GN=M6PRBP1 PE=1 SV=2												10	2
						129	140	605.28	1208.54	1208.57	-0.03	0	68	1.05E-05	K.VSGAQEMVSSAK.D	Oxidation (M)	12.63		
						167	180	690.36	1378.71	1378.69	0.02	0	45	0.0021047	K.SVVTGGVQSVMGSR.L	Oxidation (M)	16.4		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06733	5%	132	3	47481	7	P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2												10	3
						222	228	401.23	800.45	800.46	-0.02	0	51	0.000877	K.EGLELLK.T		20.69		
						407	412	403.73	805.44	805.44	0	0	38	0.012234	K.YNQLLR.I		16.02		
						413	420	452.73	903.44	903.45	-0.02	0	43	0.0040857	R.IEEELGSK.A		13.68		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P50454	5%	65	2	46525	8.8	P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2												10	2
						301	308	399.74	797.47	797.5	-0.03	0	33	0.0337376	K.AVAISLPK.G		20.03		
						394	405	647.34	1292.66	1292.67	-0.01	0	32	0.0449731	R.DTQSGSLLFIGR.L		22.03		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P25705	5%	84	2	59828	9.2	P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1												10	1
						74	83	500.78	999.56	999.57	-0.02	0	34	0.0344745	R.VLSIGDGIAR.V		20.09		
						134	149	812.93	1623.85	1623.88	-0.03	0	50	0.0005942	R.TGAIVDVPVGEELLGR.V		22.01		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9UNH7	5%	65	2	46905	5.8	Q9UNH7|SNX6_HUMAN Sorting nexin-6 OS=Homo sapiens GN=SNX6 PE=1 SV=1												11	1
						61	68	489.76	977.5	977.49	0.01	0	32	0.0486713	K.QNEFSVVR.Q		18.29		
						194	204	516.3	1030.58	1030.57	0.01	0	33	0.041093	K.SADGVIVSGVK.D		16.47		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06576	4%	79	2	56525	5.3	P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3												11	1
						110	121	639.8	1277.58	1277.63	-0.05	0	44	0.0026329	R.TIAMDGTEGLVR.G	Oxidation (M)	18.85		
						202	212	488.27	974.52	974.55	-0.03	0	34	0.0326659	K.IGLFGGAGVGK.T		20.77		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60709	36%	746	13 (14)	42052	5.3	P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1												14	12
						2	18	919.39	1836.76	1836.79	-0.03	0	50	0.0006172	M.DDDIAALVVDNGSGMCK.A	Acetyl (Protein N-term); Oxidation (M)	22.75		
						19	28	488.72	975.43	975.44	-0.02	0	73	4.23E-06	K.AGFAGDDAPR.A		14.23		
						40	50	401.85	1202.54	1202.55	-0.02	0	49	0.0010147	R.HQGVMVGMGQK.D	2 Oxidation (M)	12.22		
						51	61	599.76	1197.5	1197.51	-0.01	0	61	5.32E-05	K.DSYVGDEAQSK.R		13.67		

						51	62	452.2	1353.58	1353.62	-0.04	1	65	2.08E-05	K.DSYVGDEAQSKR.G		13.15		
						96	113	652.01	1953.02	1953.06	-0.04	0	56	0.0001578	R.VAPEEHPVLLTEAPLNPK.A		20.4		
						184	191	507.74	1013.47	1013.47	0	0	38	0.012683	R.DLTDYLMK.I	Oxidation (M)	21.1		
						197	206	566.77	1131.53	1131.52	0.01	0	53	0.0003568	R.GYSFTTTAER.E		18.92		
						239	254	895.95	1789.88	1789.88	-0.01	0	93	3.59E-08	K.SYELPDGQVITIGNER.F		21.8		
						313	326	527.6	1579.77	1579.79	-0.03	1	43	0.0030881	R.MQKEITALAPSTMK.I	2 Oxidation (M)	15.1		
						316	326	589.31	1176.6	1176.61	-0.01	0	53	0.0003634	K.EITALAPSTMK.I	Oxidation (M)	17.13		
						329	335	398.24	794.47	794.47	0	0	41	0.0047096	K.IIAPPER.K		14.36		
						360	372	750.35	1498.69	1498.67	0.02	0	61	5.90E-05	K.QEYDESGPSIVHR.K	Gln->pyro-Glu (N-term Q)	19.7		
						360	372	506.23	1515.68	1515.7	-0.01	0	72	4.82E-06	K.QEYDESGPSIVHR.K		15.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00558	7%	113	3	44985	8.3	P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3												14	1
						23	30	483.24	964.46	964.47	-0.01	0	38	0.010931	R.VDFNVPMK.N	Oxidation (M)	19.44		
						172	184	461.9	1382.67	1382.7	-0.02	0	35	0.0202968	R.AHSSMVGVNLPQK.A	Oxidation (M)	14.49		
						354	361	460.74	919.46	919.47	-0.01	0	39	0.0087605	K.ALMDEVVK.A	Oxidation (M)	14.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04075	35%	758	13 (14)	39851	8.3	P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2												15	2
						15	22	470.74	939.48	939.48	0	0	55	0.0002139	K.ELSDIAHR.I		13.95		
						29	42	666.86	1331.7	1331.69	0.01	0	79	9.79E-07	K.GILAADESTGSIAK.R		19.62		
						29	43	496.94	1487.79	1487.79	0	1	52	0.0004676	K.GILAADESTGSIAKR.L		18.75		
						43	57	601.63	1801.87	1801.9	-0.03	2	40	0.0060543	K.RLQSIGTENTEENRR.F		12.96		
						44	56	745.86	1489.71	1489.7	0.01	0	84	2.61E-07	R.LQSIGTENTEENR.R		14.34		
						44	57	549.61	1645.81	1645.8	0.01	1	34	0.0282524	R.LQSIGTENTEENRR.F		13.35		
						61	69	522.79	1043.57	1043.56	0.01	0	69	1.04E-05	R.QLLLTADDR.V		19.97		
						88	99	448.24	1341.69	1341.7	-0.01	0	46	0.0017572	K.ADDGRPFPQVIK.S		19.75		
						100	111	396.24	1185.69	1185.71	-0.02	2	33	0.0400843	K.SKGGVVGIKVDK.G		13.22		
						112	134	758.05	2271.13	2271.13	0	0	96	1.47E-08	K.GVVPLAGTNGETTTQGLDGLSER.C		20.94		
						141	147	362.16	722.31	722.32	-0.02	0	32	0.0391145	K.DGADFAK.W		13.73		
						209	215	382.23	762.44	762.46	-0.02	0	35	0.0326386	K.VLAAVYK.A		15.68		
						305	312	401.24	800.47	800.48	-0.01	0	48	0.0017458	R.ALQASALK.A		14.08		
						332	342	566.79	1131.57	1131.57	0	0	59	0.0001063	R.ALANSLACQGK.Y		14.95		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40121	14%	295	5 (6)	38779	5.9	P40121|CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=1												15	1
						192	198	386.24	770.46	770.47	-0.01	0	32	0.0421824	R.DLALAIR.D		20.72		
						244	253	510.77	1019.52	1019.54	-0.02	0	43	0.003937	K.ANAQAAALYK.V		14.51		
						254	265	640.81	1279.61	1279.61	0	0	90	6.36E-08	K.VSDATGQMNLTK.V	Oxidation (M)	13.04		
						307	319	686.88	1371.74	1371.71	0.02	0	38	0.0120987	R.QAALQVAEGFISR.M	Gln->pyro-Glu (N-term Q)	24.26		
						307	319	695.35	1388.69	1388.74	-0.05	0	58	0.0001195	R.QAALQVAEGFISR.M		21.73		
						336	341	360.69	719.37	719.39	-0.02	0	39	0.0099463	R.ESPIFK.Q		16.63		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08865	13%	207	3	32947	4.8	P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4												15	1
						64	80	870.99	1739.97	1739.94	0.03	0	96	1.58E-08	R.AIVAIENPADVSVISSR.N		21.29		
						90	102	602.34	1202.66	1202.64	0.02	0	76	1.92E-06	K.FAAATGATPIAGR.F		18.36		
						121	128	456.78	911.54	911.54	0	0	35	0.0184636	R.LLVVTDPR.A		19.71		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15365	9%	163	3	37987	6.7	Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2												15	1
						47	57	644.8	1287.58	1287.59	-0.01	0	61	6.11E-05	R.INISEGNCPER.I		15.25		
						298	306	507.76	1013.51	1013.53	-0.01	0	60	8.28E-05	R.QGANINEIR.Q		14.77		
						315	325	543.77	1085.53	1085.55	-0.01	0	42	0.0053369	K.IANPVEGSSGR.Q		14.12		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04899	7%	97	2	40995	5.3	P04899|GNAI2_HUMAN Guanine nucleotide-binding protein G(i), alpha-2 subunit OS=Homo sapiens GN=GNAI2 PE=1 SV=3												15	1
						36	46	529.32	1056.62	1056.62	0	0	58	0.0001266	K.LLLLGAGESGK.S		20.81		
						87	100	775.89	1549.76	1549.72	0.04	0	39	0.0084712	K.AMGNLQIDFADPSR.A	Oxidation (M)	20.9		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P08754	6%	96	2	41076	5.5	P08754|GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3												15	1
						36	46	529.32	1056.62	1056.62	0	0	58	0.0001266	K.LLLLGAGESGK.S		20.81		
						91	100	373.87	1118.6	1118.61	-0.01	1	38	0.0137381	R.LKIDFGEAAR.A		20.24		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9Y617	6%	88	2	40796	7.6	Q9Y617|SERC_HUMAN Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2												15	1
						6	16	557.31	1112.6	1112.6	0	0	33	0.0401826	R.QVVNFGPGPAK.L		19.49		
						52	61	593.34	1184.66	1184.65	0.01	0	56	0.0002187	K.IINNTENLVR.E		18.97		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04406	16%	264	5	36201	8.6	P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3												16	1
						67	80	807.4	1612.78	1612.89	-0.11	0	64	2.50E-05	K.LVINGNPITIFQER.D		23.38		
						67	84	680.99	2039.96	2040.1	-0.14	1	35	0.0185348	K.LVINGNPITIFQERDPSK.I		22.64		
						201	215	706.36	1410.7	1410.78	-0.08	0	55	0.0002005	R.GALQNIIPASTGAAK.A		21.07		
						235	248	765.86	1529.71	1529.79	-0.08	0	49	0.0009322	R.VPTANVSVVDLTCR.L		21.46		
						264	271	415.2	828.38	828.43	-0.05	0	61	7.73E-05	K.QASEGPLK.G		13.18		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P07355	14%	237	5	38808	7.6	P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2												16	1
						2	10	564.76	1127.51	1127.56	-0.06	0	35	0.0270681	M.STVHEILCK.L	Acetyl (Protein N-term)	20.68		
						38	47	544.28	1086.54	1086.59	-0.06	0	46	0.0024906	R.DALNIETAIK.T		21.42		
						69	77	556.25	1110.49	1110.55	-0.05	0	47	0.0012298	R.QDIAFAYQR.R		20.59		
						136	145	622.78	1243.55	1243.62	-0.07	0	55	0.0002483	R.TNQELQEINR.V		16.13		
						158	168	613.25	1224.48	1224.56	-0.08	0	54	0.0002536	K.DIISDTSGDFR.K		21.59		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04083	13%	204	4	38918	6.6	P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2												16	1
						114	124	631.75	1261.49	1261.59	-0.1	0	61	6.56E-05	K.TPAQFDADELR.A		20.55		
						167	177	607.24	1212.47	1212.53	-0.06	0	60	8.13E-05	K.DITSDTSGDFR.N		20.16		
						215	228	775.87	1549.72	1549.81	-0.09	0	43	0.0031185	K.GTDVNVFNTILTTR.S		23.55		
						304	312	540.71	1079.41	1079.48	-0.08	0	42	0.0043911	R.SEIDMNDIK.A	Oxidation (M)	14.7		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q14847	10%	171	3	30097	6.6	Q14847|LASP1_HUMAN LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2												16	1
						74	85	481.9	1442.69	1442.78	-0.09	1	63	3.56E-05	R.LKQQSELQSQVR.Y		13.79		
						76	85	601.78	1201.55	1201.61	-0.06	0	43	0.003953	K.QQSELQSQVR.Y		13.92		
						97	109	709.84	1417.66	1417.72	-0.06	0	65	2.49E-05	K.GFSVVADTPELQR.I		21.38		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52907	9%	108	2	33073	5.5	P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3												16	1
						38	47	599.33	1196.64	1196.69	-0.05	0	66	1.60E-05	R.LLLNNDNLLR.E		21.9		
						104	118	771.8	1541.59	1541.68	-0.09	0	41	0.0050256	K.EASDPQPEEADGGLK.S		15.22		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P05388	7%	97	2	34423	5.7	P05388|RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1												16	1
						84	92	484.74	967.46	967.51	-0.05	0	33	0.028651	R.GNVGFVFTK.E		21.33		
						135	146	657.32	1312.63	1312.7	-0.07	0	63	3.36E-05	K.TSFFQALGITTK.I		23.95		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15084	6%	89	2	48490	5	Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1												16	2
						217	231	764.38	1526.74	1526.84	-0.1	0	40	0.0058109	K.LAAVDATVNQVLASR.Y		22.25		
						374	386	742.32	1482.63	1482.71	-0.08	0	49	0.0008714	K.GSFSEQGINEFLR.E		22.55		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P40925	6%	89	2	36631	6.9	P40925|MDHC_HUMAN Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4												16	1
						171	179	458.72	915.43	915.5	-0.07	0	49	0.0011511	K.LGVTANDVK.N		14.91		
						299	310	697.33	1392.64	1392.7	-0.07	0	40	0.0067445	K.FVEGLPINDFSR.E		22.59		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07195	21%	304	6	36900	5.7	P07195|LDHB_HUMAN L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2												17	1
						8	23	847.96	1693.9	1693.89	0.01	0	54	0.0002472	K.LIAPVAEEEATVPNNK.I		20.03		
						78	91	504.26	1509.76	1509.77	-0.01	1	31	0.0448065	K.IVADKDYSVTANSK.I		14.06		
						108	113	371.73	741.44	741.45	-0.01	0	38	0.0104138	R.LNLVQR.N		16.09		
						159	170	624.82	1247.63	1247.59	0.03	0	77	1.64E-06	R.VIGSGCNLDSAR.F		15.2		
						234	244	642.32	1282.63	1282.65	-0.02	0	46	0.001489	K.MVVESAYEVIK.L	Oxidation (M)	20.2		
						309	319	429.57	1285.7	1285.72	-0.02	2	58	0.0001221	K.LKDDEVAQLKK.S		13.53		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00338	15%	251	5	36950	8.4	P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2												17	1
						77	90	499.26	1494.75	1494.77	-0.02	1	40	0.0070942	K.IVSGKDYNVTANSK.L		13.66		
						91	99	457.28	912.56	912.58	-0.02	0	43	0.0035626	K.LVIITAGAR.Q		20.16		
						107	112	371.73	741.44	741.45	-0.01	0	38	0.0104138	R.LNLVQR.N		16.09		
						158	169	624.82	1247.63	1247.59	0.03	0	77	1.64E-06	R.VIGSGCNLDSAR.F		15.2		
						306	315	567.78	1133.55	1133.56	0	0	53	0.0003393	K.VTLTSEEEAR.L		14.63		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P29692	8%	120	2	31217	4.9	P29692|EF1D_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5												17	1
						39	48	543.8	1085.59	1085.58	0	0	60	7.45E-05	R.QENGASVILR.D		18.59		
						84	95	679.87	1357.72	1357.72	0	0	59	8.94E-05	R.IASLEVENQSLR.G		19.98		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P09525	17%	285	5	36088	5.8	P09525|ANXA4_HUMAN Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4												18	1
						10	24	799.35	1596.69	1596.72	-0.03	0	76	1.72E-06	K.AASGFNAMEDAQTLR.K	Oxidation (M)	19.48		
						142	150	567.74	1133.47	1133.48	-0.01	0	38	0.0112123	R.SDTSFMFQR.V	Oxidation (M)	19.75		
						151	160	479.79	957.57	957.56	0	0	38	0.0152035	R.VLVSLSAGGR.D		19.83		
						260	270	587.81	1173.61	1173.6	0.01	0	65	2.56E-05	K.GLGTDDNTLIR.V		19.88		
						276	284	546.28	1090.54	1090.53	0	0	69	1.08E-05	R.AEIDMLDIR.A	Oxidation (M)	20.44		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P06753	15%	261	5	32856	4.7	P06753|TPM3_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1												18	1
						78	90	658.82	1315.62	1315.64	-0.01	0	48	0.0012661	K.AADAEAEVASLNR.R		18.49		
						78	91	491.58	1471.73	1471.74	-0.01	1	42	0.0040082	K.AADAEAEVASLNRR.I		15.66		
						92	101	622.33	1242.65	1242.65	0	0	80	6.56E-07	R.IQLVEEELDR.A		20.7		
						141	149	574.3	1146.58	1146.6	-0.02	0	50	0.0007405	K.MELQEIQLK.E	Oxidation (M)	20.14		
						169	178	578.84	1155.67	1155.65	0.02	0	41	0.0057083	K.LVIIEGDLER.T		20.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

P67936	15%	192	4	28619	4.7	P67936|TPM4_HUMAN Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3												18	1
						45	54	508.27	1014.53	1014.51	0.02	0	37	0.0186102	K.AEGDVAALNR.R		14.58		
						56	65	622.33	1242.65	1242.65	0	0	80	6.56E-07	R.IQLVEEELDR.A		20.7		
						105	113	591.28	1180.55	1180.55	0	0	36	0.0168963	K.MEIQEMQLK.E	2 Oxidation (M)	14.02		
						216	223	481.74	961.46	961.46	0	0	40	0.0079505	K.TIDDLEEK.L		15.14		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P36543	9%	106	2	26186	7.7	P36543|VATE1_HUMAN Vacuolar proton pump subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1												18	1
						2	10	494.75	987.48	987.49	-0.01	0	40	0.008313	M.ALSDADVQK.Q	Acetyl (Protein N-term)	19.01		
						70	80	669.31	1336.61	1336.62	-0.02	0	66	1.76E-05	K.IQMSNLMNQAR.L	2 Oxidation (M)	13.19		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P47756	9%	132	2	31616	5.4	P47756|CAPZB_HUMAN F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4												18	1
						182	195	677.32	1352.63	1352.64	0	0	96	1.77E-08	K.SGSGTMNLGGSLTR.Q	Oxidation (M)	15.4		
						216	225	421.54	1261.61	1261.63	-0.02	1	36	0.0198697	R.LVEDMENKIR.S	Oxidation (M)	13.28		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
A6NL28	7%	90	2	26595	4.5	A6NL28|TPM3L_HUMAN Putative tropomyosin alpha-3 chain-like protein OS=Homo sapiens PE=5 SV=2												18	1
						80	88	574.3	1146.58	1146.6	-0.02	0	50	0.0007405	K.MELQEIQLK.E	Oxidation (M)	20.14		
						138	144	439.22	876.43	876.44	0	0	40	0.0084428	R.LMDQNLK.C	Oxidation (M)	12.89		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O15144	6%	84	2	34426	6.8	O15144|ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1												18	1
						1	9	559.3	1116.59	1116.6	-0.01	0	40	0.0077027	-.MILLEVNNR.I	Oxidation (M)	20.09		
						10	18	515.3	1028.59	1028.61	-0.02	0	44	0.0032614	R.IIEETLALK.F		20.36		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O00299	15%	159	3	27248	5.1	O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4												19	1
						2	13	729.84	1457.66	1457.74	-0.08	0	39	0.0085806	M.AEEQPQVELFVK.A	Acetyl (Protein N-term)	23.1		
						38	49	641.31	1280.6	1280.66	-0.06	0	63	3.03E-05	K.GVTFNVTTVDTK.R		20.84		
						120	131	664.79	1327.57	1327.64	-0.07	0	57	0.0001593	K.NSNPALNDNLEK.G		16.13		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62701	10%	150	3	29807	10.2	P62701|RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2												19	1
						192	198	386.72	771.42	771.46	-0.04	0	41	0.0085601	R.IGVITNR.E		15.07		
						212	221	526.73	1051.44	1051.47	-0.03	0	54	0.0002426	K.DANGNSFATR.L		14.12		
						222	230	495.77	989.52	989.59	-0.07	0	55	0.0002627	R.LSNIFVIGK.G		22.1		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23396	9%	82	2	26842	9.7	P23396|RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2												19	1
						19	27	546.76	1091.5	1091.56	-0.06	0	33	0.0333647	K.AELNEFLTR.E		21.58		
						215	227	735.85	1469.69	1469.76	-0.07	0	49	0.000905	K.DEILPTTPISEQK.G		21.14		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P63104	27%	376	6	27899	4.7	P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1												20	2
						1	9	581.8	1161.59	1161.57	0.02	1	65	2.57E-05	-.MDKNELVQK.A	Acetyl (Protein N-term); Oxidation (M)	13.55		
						28	41	774.86	1547.72	1547.71	0.01	0	114	2.61E-10	K.SVTEQGAELSNEER.N		15.29		
						42	49	454.27	906.52	906.52	0	0	45	0.0023659	R.NLLSVAYK.N		20.36		
						104	115	652.85	1303.68	1303.68	0.01	0	56	0.0001942	K.FLIPNASQAESK.V		20.19		
						128	139	427.22	1278.64	1278.65	-0.01	1	44	0.0026798	R.YLAEVAAGDDKK.G		14.25		
						213	222	603.33	1204.65	1204.65	0	0	52	0.0005279	K.DSTLIMQLLR.D	Oxidation (M)	23.08		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P31946	25%	313	6	28179	4.8	P31946|1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3												20	1
						2	11	618.81	1235.61	1235.61	0	1	43	0.0037968	M.TMDKSELVQK.A	Acetyl (Protein N-term); Oxidation (M)	13.77		
						30	43	533.59	1597.74	1597.73	0	0	64	2.43E-05	K.AVTEQGHELSNEER.N		13.16		
						44	51	454.27	906.52	906.52	0	0	45	0.0023659	R.NLLSVAYK.N		20.36		
						63	70	452.26	902.5	902.51	0	0	48	0.0015351	R.VISSIEQK.T		13.68		
						130	140	591.79	1181.56	1181.56	0	0	62	3.88E-05	R.YLSEVASGDNK.Q		14.51		
						215	224	603.33	1204.65	1204.65	0	0	52	0.0005279	K.DSTLIMQLLR.D	Oxidation (M)	23.08		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P61981	24%	294	6	28456	4.8	P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2												20	1
						2	10	578.82	1155.63	1155.62	0.01	1	38	0.0121761	M.VDREQLVQK.A	Acetyl (Protein N-term)	17.06		
						29	42	822.4	1642.79	1642.78	0.01	0	77	1.16E-06	K.NVTELNEPLSNEER.N		19.66		
						43	50	454.27	906.52	906.52	0	0	45	0.0023659	R.NLLSVAYK.N		20.36		
						62	69	452.26	902.5	902.51	0	0	48	0.0015351	R.VISSIEQK.T		13.68		
						133	142	540.78	1079.55	1079.55	0	0	34	0.0241783	R.YLAEVATGEK.R		16.84		
						218	227	603.33	1204.65	1204.65	0	0	52	0.0005279	K.DSTLIMQLLR.D	Oxidation (M)	23.08		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30040	18%	279	4	29032	6.8	P30040|ERP29_HUMAN Endoplasmic reticulum protein ERp29 OS=Homo sapiens GN=ERP29 PE=1 SV=4												20	1
						37	48	662.84	1323.67	1323.71	-0.03	0	51	0.0005519	K.GALPLDTVTFYK.V		21.86		
						183	192	538.27	1074.52	1074.53	-0.01	0	92	5.07E-08	K.QGQDNLSSVK.E		13.29		
						209	223	862.91	1723.8	1723.77	0.03	0	68	9.90E-06	K.ILDQGEDFPASEMTR.I	Oxidation (M)	19.93		
						244	253	567.84	1133.67	1133.64	0.03	0	68	1.25E-05	K.SLNILTAFQK.K		22.21		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P27348	16%	226	4	28032	4.7	P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1												20	1

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
						28	41	766.87	1531.72	1531.71	0.01	0	82	4.71E-07	K.AVTEQGAELSNEER.N		14.77		
						42	49	454.27	906.52	906.52	0	0	45	0.0023659	R.NLLSVAYK.N		20.36		
						61	68	452.26	902.5	902.51	0	0	48	0.0015351	R.VISSIEQK.T		13.68		
						213	222	603.33	1204.65	1204.65	0	0	52	0.0005279	K.DSTLIMQLLR.D	Oxidation (M)	23.08		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07339	11%	210	5	45037	6.1	P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1												20	2
						177	184	440.24	878.47	878.45	0.02	0	45	0.0024983	R.QVFGEATK.Q		14.16		
						177	194	636.03	1905.06	1905.04	0.03	1	45	0.0018696	R.QVFGEATKQPGITFIAAK.F		20.63		
						332	341	521.83	1041.65	1041.64	0.01	0	42	0.0048035	K.VSTLPAITLK.L		20.67		
						349	357	533.28	1064.54	1064.54	0	0	40	0.0067828	K.LSPEDYTLK.V		20.1		
						404	411	410.72	819.42	819.42	-0.01	0	38	0.0133185	R.VGFAEAAR.L		15.24		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P26373	9%	76	2	24304	11.7	P26373|RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4												20	1
						75	82	475.76	949.5	949.49	0.01	0	37	0.0140291	R.GFSLEELR.V		21.33		
						106	116	616.81	1231.61	1231.62	0	0	39	0.0104183	K.STESLQANVQR.L		14.38		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P45880	7%	107	2	32060	7.5	P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2												20	3
						236	247	647.34	1292.67	1292.66	0.01	0	50	0.0006823	K.YQLDPTASISAK.V		20.06		
						268	277	508.81	1015.62	1015.59	0.02	0	56	0.0002055	K.LTLSALVDGK.S		21.42		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P00918	7%	99	2	29285	6.9	P00918|CAH2_HUMAN Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2												20	1
						159	167	494.28	986.55	986.56	-0.01	0	46	0.0024045	K.VVDVLDSIK.T		21.02		
						172	181	585.27	1168.53	1168.51	0.02	0	53	0.000328	K.SADFTNFDPR.G		20.45		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P04792	13%	166	3 (4)	22826	6	P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2												21	3
						80	89	529.78	1057.55	1057.54	0.01	0	62	5.96E-05	R.QLSSGVSEIR.H	Gln->pyro-Glu (N-term Q)	20.49		
						80	89	538.4	1074.79	1074.57	0.22	0	70	6.40E-06	R.QLSSGVSEIR.H		16.33		
						189	198	471.27	940.53	940.5	0.03	0	53	0.0003101	R.AQLGGPEAAK.S		12.95		
						189	205	548.61	1642.82	1642.82	0	1	44	0.0027423	R.AQLGGPEAAKSDETAAK.-		13.02		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P52566	10%	97	2	23031	5.1	P52566|GDIR2_HUMAN Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3												22	2
						51	63	656.31	1310.6	1310.71	-0.11	0	56	0.0001533	K.TLLGDGPVVTDPK.A		20.97		
						64	71	428.23	854.44	854.5	-0.06	0	41	0.0051123	K.APNVVVTR.L		14.2		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q06830	44%	479	10 (11)	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												23	2
						17	27	590.79	1179.57	1179.56	0.01	0	48	0.0011233	K.ATAVMPDGQFK.D	Oxidation (M)	16.73		
						28	35	470.74	939.47	939.45	0.01	0	33	0.0304928	K.DISLSDYK.G		20.21		
						93	110	481.52	1922.03	1922.04	-0.01	2	37	0.0121651	K.KQGGLGPMNIPLVSDPKR.T	Oxidation (M)	19.73		
						94	109	819.93	1637.85	1637.84	0	0	47	0.0013004	K.QGGLGPMNIPLVSDPK.R	Oxidation (M)	20.86		
						94	110	599	1793.97	1793.95	0.02	1	43	0.003348	K.QGGLGPMNIPLVSDPKR.T	Oxidation (M)	20.34		
						111	120	554.32	1106.62	1106.6	0.02	0	69	8.30E-06	R.TIAQDYGVLK.A		20.12		
						129	140	680.4	1358.79	1358.79	0	1	41	0.0063929	R.GLFIIDDKGILR.Q		21.95		
						141	151	597.85	1193.68	1193.64	0.04	0	54	0.0002642	R.QITVNDLPVGR.S	Gln->pyro-Glu (N-term Q)	21.91		
						141	151	606.35	1210.69	1210.67	0.03	0	58	0.0001169	R.QITVNDLPVGR.S		20.29		
						152	158	410.22	818.42	818.41	0.01	0	45	0.0030334	R.SVDETLR.L		13.68		
						159	168	598.82	1195.63	1195.62	0.01	0	59	8.43E-05	R.LVQAFQFTDK.H		20.77		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q9H0U4	13%	102	2	22328	5.5	Q9H0U4|RAB1B_HUMAN Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1												23	1
						11	21	536.33	1070.65	1070.63	0.01	0	59	9.04E-05	K.LLLIGDSGVGK.S		21.08		
						173	187	486.58	1456.73	1456.71	0.02	0	42	0.0044786	R.MGPGAASGGERPNLK.I	Oxidation (M)	13.02		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P37802	12%	87	2	22548	8.4	P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3												23	1
						128	139	616.34	1230.67	1230.68	-0.01	0	50	0.000765	R.TLMNLGGLAVAR.D	Oxidation (M)	20.64		
						161	171	640.31	1278.6	1278.58	0.01	0	37	0.0125343	R.NFSDNQLQEGK.N		15.88		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P32119	11%	97	2 (3)	22049	5.7	P32119|PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5												23	1
						17	26	489.76	977.5	977.52	-0.02	0	40	0.0086951	K.ATAVVDGAFK.E		18.34		
						140	150	597.85	1193.68	1193.64	0.04	0	54	0.0002642	R.QITVNDLPVGR.S	Gln->pyro-Glu (N-term Q)	21.91		
						140	150	606.35	1210.69	1210.67	0.03	0	58	0.0001169	R.QITVNDLPVGR.S		20.29		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P51149	10%	86	2	23760	6.4	P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1												23	1
						11	21	529.32	1056.63	1056.62	0.01	0	49	0.0009894	K.VIILGDSGVGK.T		20.25		
						39	48	518.79	1035.57	1035.56	0.01	0	37	0.0156193	K.ATIGADFLTK.E		20.91		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q99497	7%	70	2	20050	6.3	Q99497|PARK7_HUMAN Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2												23	1
						6	12	364.26	726.51	726.5	0.01	0	33	0.0249107	R.ALVILAK.G		19.94		
						183	189	378.23	754.45	754.46	-0.01	1	37	0.0120055	K.APLVLKD.-		17.08		

accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23284	22%	203	4	22785	9.3	P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=1												25	2
						44	51	430.69	859.37	859.4	-0.04	0	45	0.0034048	R.IGDEDVGR.V		13.63		
						64	76	682.83	1363.64	1363.7	-0.05	0	69	8.95E-06	K.TVDNFVALATGEK.G		22.37		
						91	101	651.77	1301.53	1301.57	-0.05	0	33	0.0371105	K.DFMIQGGDFTR.G	Oxidation (M)	21.59		
						138	150	729.34	1456.67	1456.72	-0.05	0	58	0.0001047	K.DTNGSQFFITTVK.T		22.15		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
O14950	12%	124	2	19824	4.7	O14950|MRLC2_HUMAN Myosin regulatory light chain MRLC2 OS=Homo sapiens GN=MYLC2B PE=1 SV=2												25	2
						36	45	627.23	1252.44	1252.55	-0.11	0	48	0.0010075	K.EAFNMIDQNR.D	Oxidation (M)	17.1		
						94	104	614.78	1227.55	1227.61	-0.06	0	76	2.21E-06	K.LNGTDPEDVIR.N		20.37		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P16949	13%	127	2	17292	5.8	P16949|STMN1_HUMAN Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3												26	1
						44	52	537.76	1073.51	1073.56	-0.05	0	53	0.0003898	K.DLSLEEIQK.K		21.11		
						86	95	583.26	1164.51	1164.54	-0.04	0	46	0.0019192	K.AIEENNNFSK.M		14.2		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P23528	12%	122	2	18719	8.2	P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3												26	1
						2	13	572.79	1143.56	1143.61	-0.06	0	85	2.72E-07	M.ASGVAVSDGVIK.V	Acetyl (Protein N-term)	20.98		
						14	21	512.76	1023.5	1023.52	-0.02	1	37	0.0141741	K.VFNDMKVR.K	Oxidation (M)	13.23		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62937	24%	163	4	18229	7.7	P62937|PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2												27	1
						20	28	528.26	1054.51	1054.53	-0.02	0	48	0.0010002	R.VSFELFADK.V		22.7		
						83	91	577.76	1153.51	1153.57	-0.06	0	39	0.0096526	K.FEDENFILK.H		21.88		
						134	144	655.78	1309.54	1309.56	-0.03	0	36	0.0158677	K.EGMNIVEAMER.F	2 Oxidation (M)	14.87		
						155	165	624.28	1246.55	1246.62	-0.08	1	39	0.0084514	K.KITIADCGQLE.-		20.41		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P62851	22%	137	3	13791	10.1	P62851|RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1												27	1
						44	52	538.29	1074.57	1074.61	-0.03	0	36	0.0207079	K.LNNLVLFDK.A		22.27		
						67	76	542.79	1083.56	1083.63	-0.07	0	50	0.0007122	K.LITPAVVSER.L		20.45		
						86	94	486.78	971.54	971.57	-0.03	0	51	0.0006744	R.AALQELLSK.G		21.54		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q15819	18%	107	2	16409	7.8	Q15819|UB2V2_HUMAN Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4												27	1
						2	11	528.29	1054.56	1054.61	-0.05	1	45	0.0024104	M.AVSTGVKVPR.N	Acetyl (Protein N-term)	18.9		
						86	101	862.92	1723.83	1723.76	0.07	0	62	3.88E-05	K.INMNGINNSSGMVDAR.S	2 Oxidation (M)	14.35		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P30044	10%	78	2	22298	8.8	P30044|PRDX5_HUMAN Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=3												27	1
						149	159	545.25	1088.49	1088.59	-0.09	0	39	0.011548	R.LLADPTGAFGK.E		21.19		
						181	191	619.8	1237.59	1237.64	-0.05	0	41	0.0055348	R.FSMVVQDGIVK.A	Oxidation (M)	20.28		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P60660	17%	135	2	17090	4.6	P60660|MYL6_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2												28	2
						38	50	677.85	1353.68	1353.73	-0.05	0	82	4.37E-07	R.ALGQNPTNAEVLK.V		19.57		
						99	110	625.26	1248.5	1248.58	-0.07	0	53	0.0003388	K.EGNGTVMGAEIR.H	Oxidation (M)	14.19		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
P07737	18%	107	2	15216	8.4	P07737|PROF1_HUMAN Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2												29	1
						92	105	690.33	1378.64	1378.71	-0.07	0	57	0.0001313	K.STGGAPTFNVTVTK.T		20.37		
						106	116	617.85	1233.68	1233.7	-0.02	1	50	0.0008072	K.TDKTLVLLMGK.E	Oxidation (M)	20.41		
accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
Q01469	13%	75	2	15497	6.6	Q01469|FABP5_HUMAN Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3												29	1
						25	33	464.26	926.51	926.55	-0.05	0	32	0.0423292	K.ELGVGIALR.K		21.41		
						73	81	513.22	1024.42	1024.45	-0.03	0	43	0.0033755	K.FEETTADGR.K		13.45		

***Footnotes to Supplemental Table 11:**

Data sets were searched with the Mascot search engine (see Perkins et al. (1999) *Electrophoresis* **20**, 3551-3567).

Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in some cases the number of observed redundant peptide sequences is indicated in parentheses), and the sequence coverage of the protein (%).

Listed is the Mascot protein score as well as the score and expectation value for the individual peptides.

Additional columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest gel slice in which the protein was identified, and the total # of adjacent gel slices in which the protein was found).

Proteins identified by single-peptide assigments for this experiment are not listed in this Table but in Supplemental Table 12.

Supplemental Table 12. Proteins identified by single-peptide based assignments by HPLC-MS/MS in various BCG infected human THP-1 phagosome preparations and in latex bead human THP-1 phagosome preparations.

See Methods (main manuscript) for critereia used for single peptide based protein assignments. As additional criteria, we required that each specific protein identification based on a single peptide assignment be observed in more than one independent biological experiment, either as part of a regular protein assignment observed together with multiple other peptides of that specific protein, or as another independent single-peptide based protein assignment.

ESI-MS/MS raw data obtained on a QSTAR Pulsar i instrument and Mascot search results for
trypsin digestion of proteins separated on 1D-SDS PAGE gels and identified by single-peptide assignments.
Also see Supplemental Document showing MS/MS spectra and fragment ion mass lists.

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	O75390	2%	143	1	51908	8.4	O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2												10	1
							383	393	605.36	1208.7	1208.71	-0.01	0	50	6.80E-04	K.IVPNVLLEQGK.A		20.78		
BCG (3 days, a), [ST6]	O75390	2%	62	1	51908	8.4	O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2												14	1
							383	393	605.37	1208.72	1208.71	0	0	41	5.60E-03	K.IVPNVLLEQGK.A		31.16		
BCG (3 days, b), [ST7]	O75390	2%	40	1	51908	8.4	O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2												14	1
							383	393	605.34	1208.67	1208.71	-0.05	0	40	7.30E-03	K.IVPNVLLEQGK.A		18.76		
BCG (5 days), [ST8]	O75390	2%	60	1	51908	8.4	O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2												12	1
							383	393	605.34	1208.66	1208.71	-0.05	0	39	9.00E-03	K.IVPNVLLEQGK.A		20.53		
beads (3 hours), [ST9]	O75390	2%	41	1	51908	8.4	O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2												12	1
							383	393	605.35	1208.69	1208.71	-0.02	0	41	4.70E-03	K.IVPNVLLEQGK.A		21.08		
beads (3 days), [ST10]	O75390	2%	40	1	51908	8.4	O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2												14	1
							383	393	605.4	1208.79	1208.71	0.08	0	34	2.60E-02	K.IVPNVLLEQGK.A		33.06		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q01628	12%	111	1	14794	6.5	Q01628|IFM3_HUMAN Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2												32	2
							89	104	793.27	1584.54	1584.75	-0.21	0	111	5.00E-10	K.MVGDVTGAQAYASTAK.C	Oxidation (M)	19.52		
BCG (1 day), [ST5]	Q01628	12%	39	1	14794	6.5	Q01628|IFM3_HUMAN Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2												43	1
							89	104	793.23	1584.44	1584.75	-0.3	0	39	5.10E-03	K.MVGDVTGAQAYASTAK.C	Oxidation (M)	15.2		
BCG (3 days, a), [ST6]	Q01628	12%	65	1	14794	6.5	Q01628|IFM3_HUMAN Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2												33	2
							89	104	793.39	1584.77	1584.75	0.03	0	65	2.30E-05	K.MVGDVTGAQAYASTAK.C	Oxidation (M)	24.83		
BCG (3 days, b), [ST7]	Q01628	12%	89	1	14794	6.5	Q01628|IFM3_HUMAN Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2												45	3
							89	104	793.32	1584.62	1584.75	-0.13	0	89	8.80E-08	K.MVGDVTGAQAYASTAK.C	Oxidation (M)	16.4		
beads (3 hours), [ST9]	Q01628	12%	116	1	14794	6.5	Q01628|IFM3_HUMAN Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2												36	3
							89	104	793.3	1584.58	1584.75	-0.17	0	116	1.50E-10	K.MVGDVTGAQAYASTAK.C	Oxidation (M)	19.73		
beads (3 days), [ST10]	Q01628	12%	93	1	14794	6.5	Q01628|IFM3_HUMAN Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2												36	2
							89	104	793.42	1584.83	1584.75	0.09	0	93	3.50E-08	K.MVGDVTGAQAYASTAK.C	Oxidation (M)	24.57		
other possible isoforms *		P13164	IFM1_HUMAN Interferon-induced transmembrane protein 1																	
		Q01629	IFM2_HUMAN Interferon-induced transmembrane protein 2																	

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P30048	3%	47	1	28017	7.7	P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3												37	1
							208	214	417.15	832.29	832.43	-0.14	0	47	1.70E-03	R.SVEETLR.L		13.01		
BCG (3 days, a), [ST6]	P30048	4%	57	1	28017	7.7	P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3												27	2
							74	83	511.29	1020.57	1020.52	0.05	0	32	4.90E-02	K.GTAVVNGEFK.D		23.92		
BCG (3 days, b), [ST7]	P30048	4%	82	1	28017	7.7	P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3												27	1
							74	83	511.23	1020.45	1020.52	-0.07	0	40	7.30E-03	K.GTAVVNGEFK.D		14.7		
BCG (5 days), [ST8]	P30048	3%	64	1	28017	7.7	P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3												21	2
							208	214	417.21	832.41	832.43	-0.01	0	42	5.50E-03	R.SVEETLR.L		13.94		
beads (3 hours), [ST9]	P30048	3%	66	1	28017	7.7	P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3												27	1
							208	214	417.2	832.38	832.43	-0.05	0	37	1.80E-02	R.SVEETLR.L		14.87		
beads (3 days), [ST10]	P30048	4%	49	1	28017	7.7	P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3												26	2
							74	83	511.29	1020.58	1020.52	0.05	0	39	9.00E-03	K.GTAVVNGEFK.D		24.06		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P14314	2%	53	1	60357	4.3	P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2												19	1
							125	135	654.23	1306.44	1306.62	-0.18	0	53	3.40E-04	R.ESLQQMAEVTR.E	Oxidation (M)	14.16		
BCG (3 days, a), [ST6]	P14314	2%	42	1	60357	4.3	P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2												6	1
							125	135	654.39	1306.77	1306.62	0.15	0	42	4.80E-03	R.ESLQQMAEVTR.E	Oxidation (M)	22.96		
BCG (3 days, b), [ST7]	P14314	2%	86	1	60357	4.3	P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2												7	1
							125	135	654.29	1306.57	1306.62	-0.05	0	60	7.30E-05	R.ESLQQMAEVTR.E	Oxidation (M)	14.65		
BCG (5 days), [ST8]	P14314	2%	129	1	60357	4.3	P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2												6	1
							125	135	654.3	1306.58	1306.62	-0.04	0	58	1.00E-04	R.ESLQQMAEVTR.E	Oxidation (M)	15.3		
beads (5 days), [ST11]	P14314	2%	92	1	60357	4.3	P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2												5	1
							125	135	654.29	1306.56	1306.62	-0.06	0	72	4.50E-06	R.ESLQQMAEVTR.E	Oxidation (M)	15.43		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q00325	3%	86	1	40525	9.4	Q00325|MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2												1	2
							190	201	681.26	1360.5	1360.71	-0.21	0	48	1.10E-03	R.IQTQPGYANTLR.D		15.11		
BCG (3 days, a), [ST6]	Q00325	3%	52	1	40525	9.4	Q00325|MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2												1	1
							190	201	681.41	1360.81	1360.71	0.1	0	43	3.40E-03	R.IQTQPGYANTLR.D		25.78		
BCG (3 days, b), [ST7]	Q00325	3%	51	1	40525	9.4	Q00325|MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2												1	2
							190	201	681.33	1360.65	1360.71	-0.06	0	42	4.30E-03	R.IQTQPGYANTLR.D		16.78		
BCG (5 days), [ST8]	Q00325	3%	45	1	40525	9.4	Q00325|MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2												2	1
							190	201	681.35	1360.68	1360.71	-0.03	0	45	2.60E-03	R.IQTQPGYANTLR.D		17.23		
beads (3 days), [ST10]	Q00325	3%	64	1	40525	9.4	Q00325|MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2												1	1
							190	201	681.45	1360.88	1360.71	0.17	0	52	5.20E-04	R.IQTQPGYANTLR.D		26.73		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P26373	5%	46	1	24304	11.7	P26373|RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4												23	2
							106	116	616.83	1231.65	1231.62	0.03	0	46	1.90E-03	K.STESLQANVQR.L		19.93		
BCG (3 days, b), [ST7]	P26373	5%	42	1	24304	11.7	P26373|RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4												23	2
							106	116	616.8	1231.59	1231.62	-0.03	0	43	4.30E-03	K.STESLQANVQR.L		13.55		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P11234	5%	63	1	23508	6.2	P11234|RALB_HUMAN Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1												20	1
							17	27	510.27	1018.53	1018.55	-0.02	0	35	3.10E-02	K.VIMVGSGGVGK.S	Oxidation (M)	15.02		
BCG (3 days, b), [ST7]	P11234	5%	75	1	23508	6.2	P11234|RALB_HUMAN Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1												26	1
							17	27	510.25	1018.49	1018.55	-0.06	0	42	5.60E-03	K.VIMVGSGGVGK.S	Oxidation (M)	14.48		
BCG (5 days), [ST8]	P11234	5%	38	1	23508	6.2	P11234|RALB_HUMAN Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1												20	1

							17	27	510.28	1018.54	1018.55	-0.01	0	38	1.40E-02	K.VIMVGSGGVGK.S	Oxidation (M)	14.54		

other possible isoform P11233 RALA_HUMAN Ras-related protein Ral-A precursor

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P61224	6%	57	1	21040	5.7	P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1												23	2
							6	16	493.26	984.51	984.6	-0.08	0	57	1.40E-04	K.LVVLGSGGVGK.S		20.93		
BCG (3 days, a), [ST6]	P61224	6%	79	1	21040	5.7	P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1												29	2
							6	16	493.33	984.64	984.6	0.05	0	39	9.10E-03	K.LVVLGSGGVGK.S		25.91		
BCG (3 days, b), [ST7]	P61224	6%	63	1	21040	5.7	P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1												30	2
							6	16	493.27	984.53	984.6	-0.06	0	61	5.70E-05	K.LVVLGSGGVGK.S		19.29		
beads (3 hours), [ST9]	P61224	6%	60	1	21040	5.7	P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1												26	2
							6	16	493.26	984.51	984.6	-0.09	0	60	7.80E-05	K.LVVLGSGGVGK.S		20.65		
beads (3 days), [ST10]	P61224	6%	101	1	21040	5.7	P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1												29	3
							6	16	493.32	984.63	984.6	0.04	0	66	2.00E-05	K.LVVLGSGGVGK.S		24.43		
beads (5 days), [ST11]	P61224	6%	55	1	21040	5.7	P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1												24	1
							6	16	493.28	984.54	984.6	-0.06	0	55	2.40E-04	K.LVVLGSGGVGK.S		20.19		

other possible isoform P62834 RAP1A_HUMAN Ras-related protein Rap-1A precursor

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q3B8N2	2%	49	1	39977	9.6	Q3B8N2|LEG9B_HUMAN Galectin-9B OS=Homo sapiens GN=LGALS9B PE=2 SV=3												20	3
							273	280	475.28	948.55	948.47	0.08	0	49	1.10E-03	R.FDENAVVR.N		24.12		
BCG (3 days, b), [ST7]	Q3B8N2	2%	45	1	39977	9.6	Q3B8N2|LEG9B_HUMAN Galectin-9B OS=Homo sapiens GN=LGALS9B PE=2 SV=3												17	3
							273	280	475.22	948.43	948.47	-0.04	0	45	2.70E-03	R.FDENAVVR.N		15.37		
BCG (5 days), [ST8]	Q3B8N2	2%	42	1	39977	9.6	Q3B8N2|LEG9B_HUMAN Galectin-9B OS=Homo sapiens GN=LGALS9B PE=2 SV=3												15	1
							273	280	475.22	948.43	948.47	-0.03	0	42	5.20E-03	R.FDENAVVR.N		15.76		
beads (3 days), [ST10]	Q3B8N2	2%	45	1	39977	9.6	Q3B8N2|LEG9B_HUMAN Galectin-9B OS=Homo sapiens GN=LGALS9B PE=2 SV=3												32	1
							273	280	475.26	948.5	948.47	0.03	0	45	2.60E-03	R.FDENAVVR.N		23.26		

other possible isoform Q6DKI2 LEG9C_HUMAN Galectin-9C (Galectin-9-like protein B)

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q15907	5%	76	1	24588	5.6	Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4												20	1
							14	24	522.29	1042.56	1042.6	-0.04	0	57	1.50E-04	K.VVLIGDSGVGK.S		19.9		
BCG (3 days, b), [ST7]	Q15907	5%	40	1	24588	5.6	Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4												27	1
							14	24	522.28	1042.54	1042.6	-0.06	0	40	7.50E-03	K.VVLIGDSGVGK.S		19.45		
BCG (5 days), [ST8]	Q15907	5%	121	1	24588	5.6	Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4												21	1
							14	24	522.31	1042.6	1042.6	-0.01	0	54	3.20E-04	K.VVLIGDSGVGK.S		19.93		
beads (3 hours), [ST9]	Q15907	5%	44	1	24588	5.6	Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4												23	1
							14	24	522.28	1042.55	1042.6	-0.05	0	44	3.60E-03	K.VVLIGDSGVGK.S		20.94		
beads (3 days), [ST10]	Q15907	5%	50	1	24588	5.6	Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4												25	1
							14	24	522.33	1042.64	1042.6	0.04	0	37	1.60E-02	K.VVLIGDSGVGK.S		26		

other possible isoform P62491 RB11A_HUMAN Ras-related protein Rab-11A (Rab-11)

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q9NVJ2	5%	120	1	21753	8.7	Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1												39	1
							147	155	532.17	1062.33	1062.51	-0.18	0	84	2.70E-07	K.MNLSAIQDR.E	Oxidation (M)	13.4		
BCG (3 days, a), [ST6]	Q9NVJ2	5%	77	1	21753	8.7	Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1												30	3
							147	155	532.28	1062.54	1062.51	0.03	0	77	1.40E-06	K.MNLSAIQDR.E	Oxidation (M)	22.5		
BCG (3 days, b), [ST7]	Q9NVJ2	5%	98	1	21753	8.7	Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1												31	2
							147	155	532.24	1062.47	1062.51	-0.04	0	78	1.30E-06	K.MNLSAIQDR.E	Oxidation (M)	14.37		
beads (3 days), [ST10]	Q9NVJ2	5%	55	1	21753	8.7	Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1												29	2
							133	141	507.78	1013.55	1013.5	0.04	0	36	2.00E-02	R.DLPNALDEK.Q		24.47		

other possible isoform Q96BM9 ARL8A_HUMAN ADP-ribosylation factor-like protein 8A

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	O75964	11%	88	1	11421	9.7	O75964|ATP5L_HUMAN ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3												33	1
							56	66	576.23	1150.45	1150.6	-0.15	0	88	1.10E-07	K.IVNSAQTGSFK.Q		14.8		
BCG (3 days, a), [ST6]	O75964	11%	49	1	11421	9.7	O75964|ATP5L_HUMAN ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3												36	1
							56	66	576.31	1150.61	1150.6	0.01	0	49	9.90E-04	K.IVNSAQTGSFK.Q		19.9		
BCG (3 days, b), [ST7]	O75964	11%	64	1	11421	9.7	O75964|ATP5L_HUMAN ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3												46	2
							56	66	576.27	1150.52	1150.6	-0.08	0	64	2.60E-05	K.IVNSAQTGSFK.Q		13.24		
beads (3 hours), [ST9]	O75964	11%	70	1	11421	9.7	O75964|ATP5L_HUMAN ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3												35	1
							56	66	576.25	1150.49	1150.6	-0.1	0	58	1.00E-04	K.IVNSAQTGSFK.Q		14.93		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P04040	2%	67	1	59947	6.9	P04040|CATA_HUMAN Catalase OS=Homo sapiens GN=CAT PE=1 SV=3												10	1
							432	444	747.43	1492.85	1492.69	0.16	0	46	1.90E-03	R.FNTANDDNVTQVR.A		24.21		
BCG (3 days, b), [ST7]	P04040	2%	61	1	59947	6.9	P04040|CATA_HUMAN Catalase OS=Homo sapiens GN=CAT PE=1 SV=3												11	1
							432	444	747.34	1492.66	1492.69	-0.03	0	61	6.40E-05	R.FNTANDDNVTQVR.A		15.38		
BCG (5 days), [ST8]	P04040	2%	120	1	59947	6.9	P04040|CATA_HUMAN Catalase OS=Homo sapiens GN=CAT PE=1 SV=3												9	1
							432	444	747.33	1492.65	1492.69	-0.04	0	93	3.70E-08	R.FNTANDDNVTQVR.A		15.48		
beads (5 days), [ST11]	P04040	2%	57	1	59947	6.9	P04040|CATA_HUMAN Catalase OS=Homo sapiens GN=CAT PE=1 SV=3												8	1
							432	444	747.34	1492.67	1492.69	-0.02	0	57	1.30E-04	R.FNTANDDNVTQVR.A		15.94		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P47756	5%	124	1	31616	5.4	P47756|CAPZB_HUMAN F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4												21	1
							182	195	677.34	1352.66	1352.64	0.03	0	90	6.60E-08	K.SGSGTMNLGGSLTR.Q	Oxidation (M)	22.87		
BCG (3 days, b), [ST7]	P47756	5%	84	1	31616	5.4	P47756|CAPZB_HUMAN F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4												21	2
							182	195	677.32	1352.63	1352.64	0	0	78	9.90E-07	K.SGSGTMNLGGSLTR.Q	Oxidation (M)	14.42		
BCG (5 days), [ST8]	P47756	5%	77	1	31616	5.4	P47756|CAPZB_HUMAN F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4												17	1
							182	195	677.3	1352.59	1352.64	-0.04	0	77	1.20E-06	K.SGSGTMNLGGSLTR.Q	Oxidation (M)	14.82		
beads (3 days), [ST10]	P47756	5%	41	1	31616	5.4	P47756|CAPZB_HUMAN F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4												21	1
							182	195	677.36	1352.7	1352.64	0.06	0	41	5.60E-03	K.SGSGTMNLGGSLTR.Q	Oxidation (M)	28.23		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9HB40	2%	67	1	51083	5.6	Q9HB40|RISC_HUMAN Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1												19	4
							233	243	592.83	1183.64	1183.66	-0.02	0	67	1.50E-05	K.VAEQVLNAVNK.G		19.39		
BCG (3 days, b), [ST7]	Q9HB40	2%	83	1	51083	5.6	Q9HB40|RISC_HUMAN Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1												25	5
							233	243	592.81	1183.6	1183.66	-0.06	0	83	3.40E-07	K.VAEQVLNAVNK.G		18.64		
BCG (5 days), [ST8]	Q9HB40	2%	68	1	51083	5.6	Q9HB40|RISC_HUMAN Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1												20	2
							233	243	592.83	1183.65	1183.66	-0.01	0	68	1.20E-05	K.VAEQVLNAVNK.G		19.07		

beads (3 hours), [ST9]	Q9HB40	2%	84	1	51083	5.6	Q9HB40|RISC_HUMAN Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1												21	1
							233	243	592.77	1183.53	1183.66	-0.12	0	84	2.70E-07	K.VAEQVLNAVNK.G		20.23		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P27449	12%	37	1	15725	8	P27449|VATL_HUMAN Vacuolar ATP synthase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1												2	1
							37	54	652.31	1953.9	1953.93	-0.04	0	37	1.10E-02	K.SGTGIAAMSVMRPEQIMK.S	3 Oxidation (M)	16		
BCG (1 day), [ST5]	P27449	12%	38	1	15725	8	P27449|VATL_HUMAN Vacuolar ATP synthase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1												1	1
							37	54	652.21	1953.6	1953.93	-0.34	0	38	8.00E-03	K.SGTGIAAMSVMRPEQIMK.S	3 Oxidation (M)	13.74		
BCG (5 days), [ST8]	P27449	12%	46	1	15725	8	P27449|VATL_HUMAN Vacuolar ATP synthase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1												2	1
							37	54	652.31	1953.9	1953.93	-0.03	0	46	1.40E-03	K.SGTGIAAMSVMRPEQIMK.S	3 Oxidation (M)	15.39		
beads (3 hours), [ST9]	P27449	12%	43	1	15725	8	P27449|VATL_HUMAN Vacuolar ATP synthase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1												2	1
							37	54	652.3	1953.87	1953.93	-0.06	0	43	3.00E-03	K.SGTGIAAMSVMRPEQIMK.S	3 Oxidation (M)	15.19		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P42766	8%	52	1	14543	11	P42766|RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2												41	1
							57	66	572.25	1142.48	1142.67	-0.19	0	52	5.50E-04	R.VLTVINQTQK.E		14.63		
BCG (3 days, b), [ST7]	P42766	8%	47	1	14543	11	P42766|RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2												35	1
							57	66	572.31	1142.61	1142.67	-0.06	0	47	1.50E-03	R.VLTVINQTQK.E		15.96		
BCG (5 days), [ST8]	P42766	8%	42	1	14543	11	P42766|RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2												26	1
							57	66	572.34	1142.66	1142.67	-0.01	0	42	4.70E-03	R.VLTVINQTQK.E		16.85		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P62917	4%	42	1	28235	11	P62917|RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2												23	1
							164	174	471.31	940.61	940.55	0.06	0	43	3.30E-03	R.AVVGVVAGGGR.I		22.05		
BCG (3 days, b), [ST7]	P62917	4%	61	1	28235	11	P62917|RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2												21	1
							164	174	471.26	940.51	940.55	-0.03	0	40	7.60E-03	R.AVVGVVAGGGR.I		13.9		
BCG (5 days), [ST8]	P62917	4%	38	1	28235	11	P62917|RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2												18	1
							164	174	471.27	940.53	940.55	-0.02	0	38	1.20E-02	R.AVVGVVAGGGR.I		14.43		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P24539	3%	50	1	28947	9.4	P24539|AT5F1_HUMAN ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2												37	1
							132	139	451.17	900.33	900.49	-0.16	0	52	6.30E-04	K.LAQLEEAK.Q		13.14		
BCG (3 days, a), [ST6]	P24539	3%	92	1	28947	9.4	P24539|AT5F1_HUMAN ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2												25	2
							132	139	451.28	900.54	900.49	0.05	0	38	1.40E-02	K.LAQLEEAK.Q		20.07		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P16070	2%	123	1	82017	5.1	P16070|CD44_HUMAN CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2												21	1
							682	694	672.25	1342.48	1342.68	-0.2	0	85	2.10E-07	K.LVINSGNGAVEDR.K		14.93		
BCG (3 days, a), [ST6]	P16070	2%	132	1	82017	5.1	P16070|CD44_HUMAN CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2												7	5
							682	694	672.38	1342.74	1342.68	0.06	0	95	2.30E-08	K.LVINSGNGAVEDR.K		25.29		
BCG (3 days, b), [ST7]	P16070	2%	70	1	82017	5.1	P16070|CD44_HUMAN CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2												7	2
							682	694	672.33	1342.64	1342.68	-0.05	0	70	8.00E-06	K.LVINSGNGAVEDR.K		16.33		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P00918	4%	91	1	29285	6.9	P00918|CAH2_HUMAN Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2												35	1
							172	181	585.18	1168.35	1168.51	-0.17	0	40	5.30E-03	K.SADFTNFDPR.G		19.39		
BCG (3 days, b), [ST7]	P00918	3%	129	1	29285	6.9	P00918|CAH2_HUMAN Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2												22	4
							159	167	494.28	986.55	986.56	-0.02	0	57	1.60E-04	K.VVDVLDSIK.T		20.5		
BCG (5 days), [ST8]	P00918	3%	63	1	29285	6.9	P00918|CAH2_HUMAN Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2												19	1
							159	167	494.28	986.54	986.56	-0.03	0	47	1.70E-03	K.VVDVLDSIK.T		20.73		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	O75955	2%	83	1	47554	7.1	O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3												29	1
							254	261	478.7	955.39	955.55	-0.16	0	45	2.50E-03	R.VQVQVVER.A		13.44		
BCG (3 days, b), [ST7]	O75955	3%	45	1	47554	7.1	O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3												14	1
							41	51	608.36	1214.71	1214.72	-0.01	0	45	2.90E-03	R.ISLNTLTLNVK.S		20.39		
BCG (5 days), [ST8]	O75955	3%	65	1	47554	7.1	O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3												11	1
							393	403	608.35	1214.69	1214.69	0	0	65	2.90E-05	K.VTGEVLDILTR.L		21.82		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q16836	3%	53	1	34313	8.9	Q16836|HCDH_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=2												15	1
							88	95	447.72	893.42	893.41	0.01	0	45	2.30E-03	K.AGDEFVEK.T		14.47		
BCG (3 days, a), [ST6]	Q16836	3%	40	1	34313	8.9	Q16836|HCDH_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=2												20	1
							88	95	447.77	893.53	893.41	0.12	0	35	1.90E-02	K.AGDEFVEK.T		20.7		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P14174	10%	67	1	12639	7.7	P14174|MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4												43	1
							2	12	652.23	1302.45	1302.68	-0.23	0	67	1.30E-05	M.PMFIVNTNVPR.A	Oxidation (M)	19.23		
BCG (3 days, a), [ST6]	P14174	10%	47	1	12639	7.7	P14174|MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4												36	1
							2	12	652.36	1302.7	1302.68	0.02	0	47	1.40E-03	M.PMFIVNTNVPR.A	Oxidation (M)	26.48		
BCG (3 days, b), [ST7]	P14174	10%	44	1	12639	7.7	P14174|MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4												46	1
							2	12	652.3	1302.59	1302.68	-0.09	0	44	2.90E-03	M.PMFIVNTNVPR.A	Oxidation (M)	19.66		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P43307	3%	40	1	32215	4.4	P43307|SSRA_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3												14	1
							103	110	463.27	924.53	924.51	0.02	0	42	4.00E-03	K.FLVGFTNK.G		21.01		
BCG (3 days, a), [ST6]	P43307	3%	66	1	32215	4.4	P43307|SSRA_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3												19	3
							103	110	463.31	924.61	924.51	0.11	0	35	1.90E-02	K.FLVGFTNK.G		30.21		
BCG (5 days), [ST8]	P43307	3%	68	1	32215	4.4	P43307|SSRA_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3												16	1
							103	110	463.24	924.47	924.51	-0.03	0	42	3.80E-03	K.FLVGFTNK.G		20.55		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q9BVK6	5%	69	1	25203	6.7	Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=1												37	1
							149	159	671.27	1340.53	1340.73	-0.2	0	48	1.00E-03	R.QLVEQVEQIQK.E		18.83		
BCG (3 days, a), [ST6]	Q9BVK6	5%	103	1	25203	6.7	Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=1												25	2
							149	159	671.4	1340.78	1340.73	0.05	0	55	2.40E-04	R.QLVEQVEQIQK.E		25.88		
BCG (5 days), [ST8]	Q9BVK6	5%	148	1	25203	6.7	Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=1												22	3
							149	159	671.37	1340.73	1340.73	0	0	90	7.50E-08	R.QLVEQVEQIQK.E		19.82		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

BCG (3 days, a), [ST6]	P35268	10%	61	1	14835	9.2	P35268|RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2												33	1
							53	65	621.85	1241.69	1241.67	0.02	0	61	6.60E-05	K.AGNLGGGVVTIER.S		25.91		
BCG (3 days, b), [ST7]	P35268	10%	51	1	14835	9.2	P35268|RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2												37	1
							53	65	621.81	1241.6	1241.67	-0.07	0	51	6.70E-04	K.AGNLGGGVVTIER.S		19.27		
beads (3 hours), [ST9]	P35268	10%	56	1	14835	9.2	P35268|RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2												32	2
							53	65	621.74	1241.47	1241.67	-0.2	0	56	2.00E-04	K.AGNLGGGVVTIER.S		20.77		
beads (3 days), [ST10]	P35268	10%	76	1	14835	9.2	P35268|RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2												31	1
							53	65	621.89	1241.76	1241.67	0.08	0	55	2.70E-04	K.AGNLGGGVVTIER.S		25.66		
beads (5 days), [ST11]	P35268	10%	57	1	14835	9.2	P35268|RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2												28	1
							53	65	621.82	1241.62	1241.67	-0.06	0	57	1.50E-04	K.AGNLGGGVVTIER.S		20.3		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P36542	3%	66	1	33032	9.2	P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1												16	1
							127	136	538.8	1075.58	1075.56	0.02	0	38	1.20E-02	K.EVMLVGIGDK.I	Oxidation (M)	20.23		
BCG (3 days, b), [ST7]	P36542	4%	62	1	33032	9.2	P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1												20	1
							116	126	524.28	1046.54	1046.56	-0.02	0	42	5.10E-03	K.SEVATLTAAGK.E		14.93		
beads (3 hours), [ST9]	P36542	3%	58	1	33032	9.2	P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1												18	1
							127	136	538.77	1075.53	1075.56	-0.02	0	40	8.00E-03	K.EVMLVGIGDK.I	Oxidation (M)	20.45		
beads (3 days), [ST10]	P36542	3%	59	1	33032	9.2	P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1												20	1
							127	136	538.8	1075.58	1075.56	0.02	0	34	2.80E-02	K.EVMLVGIGDK.I	Oxidation (M)	33.12		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P27824	2%	89	1	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												4	2
							574	582	544.77	1087.53	1087.51	0.01	0	59	1.20E-04	K.AEEDEILNR.S		18.43		
BCG (3 days, b), [ST7]	P27824	2%	100	1	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												7	1
							574	582	544.75	1087.48	1087.51	-0.04	0	49	9.90E-04	K.AEEDEILNR.S		16.98		
beads (3 hours), [ST9]	P27824	2%	149	1	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												5	2
							574	582	544.77	1087.53	1087.51	0.01	0	57	1.80E-04	K.AEEDEILNR.S		16.59		
beads (3 days), [ST10]	P27824	2%	97	1	67982	4.5	P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2												6	1
							574	582	544.78	1087.55	1087.51	0.04	0	55	2.60E-04	K.AEEDEILNR.S		32.56		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P00403	3%	61	1	25719	4.7	P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1												23	1
							135	141	422.69	843.37	843.45	-0.08	0	34	3.90E-02	R.LLDVDNR.V		17.79		
BCG (3 days, a), [ST6]	P00403	3%	47	1	25719	4.7	P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1												29	1
							172	178	365.23	728.45	728.38	0.07	0	41	6.80E-03	K.TDAIPGR.L		18.25		
beads (3 hours), [ST9]	P00403	3%	89	1	25719	4.7	P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1												26	1
							172	178	365.17	728.33	728.38	-0.05	0	36	2.20E-02	K.TDAIPGR.L		14.18		
beads (3 days), [ST10]	P00403	3%	68	1	25719	4.7	P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1												29	1
							172	178	365.22	728.42	728.38	0.04	0	42	5.80E-03	K.TDAIPGR.L		17.04		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9UEU0	4%	79	1	26672	9	Q9UEU0|VTI1B_HUMAN Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=2 SV=3												18	1
							181	190	552.8	1103.58	1103.58	0	0	57	1.50E-04	R.LVNTSENLSK.S		13.85		
BCG (3 days, b), [ST7]	Q9UEU0	4%	39	1	26672	9	Q9UEU0|VTI1B_HUMAN Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=2 SV=3												40	1
							181	190	552.76	1103.5	1103.58	-0.08	0	39	9.90E-03	R.LVNTSENLSK.S		13.07		
beads (3 hours), [ST9]	Q9UEU0	4%	44	1	26672	9	Q9UEU0|VTI1B_HUMAN Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=2 SV=3												32	1
							181	190	552.75	1103.48	1103.58	-0.1	0	44	3.50E-03	R.LVNTSENLSK.S		14.54		
beads (3 days), [ST10]	Q9UEU0	4%	74	1	26672	9	Q9UEU0|VTI1B_HUMAN Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=2 SV=3												23	1
							181	190	552.83	1103.65	1103.58	0.06	0	47	1.50E-03	R.LVNTSENLSK.S		18.18		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P63220	12%	53	1	9220	8.7	P63220|RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1												43	1
							62	71	569.66	1137.31	1137.5	-0.19	0	43	1.70E-03	R.MGESDDSILR.L	Oxidation (M)	14.64		
BCG (3 days, b), [ST7]	P63220	12%	81	1	9220	8.7	P63220|RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1												43	2
							62	71	569.7	1137.39	1137.5	-0.1	0	81	4.40E-07	R.MGESDDSILR.L	Oxidation (M)	15.35		
beads (3 days), [ST10]	P63220	12%	60	1	9220	8.7	P63220|RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1												35	1
							62	71	569.78	1137.55	1137.5	0.05	0	60	6.10E-05	R.MGESDDSILR.L	Oxidation (M)	24.56		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P63010	1%	72	1	105398	5.2	P63010|AP2B1_HUMAN AP-2 complex subunit beta-1 OS=Homo sapiens GN=AP2B1 PE=1 SV=1												5	1
							868	878	639.36	1276.71	1276.68	0.03	0	36	1.70E-02	K.LQNNNVYTIAK.R		26.26		
BCG (5 days), [ST8]	P63010	1%	54	1	105398	5.2	P63010|AP2B1_HUMAN AP-2 complex subunit beta-1 OS=Homo sapiens GN=AP2B1 PE=1 SV=1												5	1
							868	878	639.32	1276.64	1276.68	-0.04	0	54	3.10E-04	K.LQNNNVYTIAK.R		17.05		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P30049	5%	51	1	17479	5.4	P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2												28	1
							157	165	493.72	985.43	985.54	-0.11	0	51	6.50E-04	R.IEANEALVK.A		17.06		
BCG (3 days, b), [ST7]	P30049	8%	66	1	17479	5.4	P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2												37	1
							137	150	716.32	1430.63	1430.7	-0.07	0	59	9.00E-05	K.AQAELVGTADEATR.A		16.07		
beads (3 days), [ST10]	P30049	5%	46	1	17479	5.4	P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2												32	1
							157	165	493.8	985.59	985.54	0.05	0	46	1.90E-03	R.IEANEALVK.A		22.7		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P61160	3%	37	1	45017	6.3	P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1												31	1
							107	118	685.27	1368.52	1368.73	-0.22	0	34	2.40E-02	K.ILLTEPPMNPTK.N	Oxidation (M)	18.86		
BCG (5 days), [ST8]	P61160	2%	45	1	45017	6.3	P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1												13	1
							47	53	386.71	771.41	771.45	-0.03	0	40	1.00E-02	K.VGNIEIK.D		14.61		
beads (3 days), [ST10]	P61160	3%	124	1	45017	6.3	P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1												15	1
							107	118	685.48	1368.95	1368.73	0.22	0	34	2.30E-02	K.ILLTEPPMNPTK.N	Oxidation (M)	31.14		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	O15511	8%	68	1	16367	5.5	O15511|ARPC5_HUMAN Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3												26	1
							132	143	535.82	1069.62	1069.62	0	0	68	1.30E-05	K.ALAAGGVGSIVR.V		19.9		
beads (5 days), [ST11]	O15511	8%	47	1	16367	5.5	O15511|ARPC5_HUMAN Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3												27	1
							132	143	535.8	1069.58	1069.62	-0.04	0	47	1.50E-03	K.ALAAGGVGSIVR.V		20.37		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P08758	3%	56	1	35971	4.9	P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2												15	1
							109	117	501.32	1000.62	1000.59	0.03	0	33	4.00E-02	K.VLTEIIASR.T		20.29		

BCG (3 days, a), [ST6]	P08758	3%	56	1	35971	4.9	P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2												19	3
							51	58	447.32	892.63	892.47	0.16	0	56	1.70E-04	R.QEISAAFK.T		26.2		
beads (5 days), [ST11]	P08758	3%	50	1	35971	4.9	P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2												18	1
							109	117	501.3	1000.58	1000.59	-0.02	0	50	8.60E-04	K.VLTEIIASR.T		20.22		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P35613	2%	41	1	42573	5.4	P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2												28	1
							274	282	507.67	1013.33	1013.49	-0.17	0	41	4.50E-03	R.FFVSSSQGR.S		15.09		
BCG (3 days, b), [ST7]	P35613	2%	60	1	42573	5.4	P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2												12	3
							274	282	507.75	1013.48	1013.49	-0.01	0	60	8.60E-05	R.FFVSSSQGR.S		16.18		
beads (5 days), [ST11]	P35613	2%	41	1	42573	5.4	P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2												11	1
							274	282	507.75	1013.49	1013.49	0	0	41	6.40E-03	R.FFVSSSQGR.S		16.69		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P25774	3%	60	1	38099	8.6	P25774|CATS_HUMAN Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3												25	1
							246	255	478.78	955.55	955.51	0.04	0	36	1.70E-02	K.GPVSVGVDAR.H		22.29		
BCG (5 days), [ST8]	P25774	3%	58	1	38099	8.6	P25774|CATS_HUMAN Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3												20	2
							246	255	478.76	955.5	955.51	-0.01	0	58	1.00E-04	K.GPVSVGVDAR.H		14.67		
beads (3 hours), [ST9]	P25774	3%	53	1	38099	8.6	P25774|CATS_HUMAN Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3												22	3
							197	207	608.25	1214.49	1214.55	-0.06	0	54	3.20E-04	K.GIDSDASYPYK.A		19.65		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q9Y678	1%	112	1	98967	5.3	Q9Y678|COPG_HUMAN Coatomer subunit gamma OS=Homo sapiens GN=COPG PE=1 SV=1												18	1
							33	42	593.73	1185.44	1185.61	-0.18	0	61	5.70E-05	R.VFNETPINPR.K		18.18		
BCG (5 days), [ST8]	Q9Y678	1%	63	1	98967	5.3	Q9Y678|COPG_HUMAN Coatomer subunit gamma OS=Homo sapiens GN=COPG PE=1 SV=1												5	1
							33	42	593.79	1185.57	1185.61	-0.04	0	63	3.80E-05	R.VFNETPINPR.K		19.26		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	O00299	5%	52	1	27248	5.1	O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4												21	1
							120	131	664.9	1327.79	1327.64	0.16	0	52	0.0004348	K.NSNPALNDNLEK.G		22.55		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P23528	7%	98	1	18719	8.2	P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3												25	1
							2	13	572.76	1143.51	1143.61	-0.1	0	88	1.40E-07	M.ASGVAVSDGVIK.V	Acetyl (Protein N-term)	21.59		
BCG (5 days), [ST8]	P23528	7%	72	1	18719	8.2	P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3												26	1
							2	13	572.81	1143.6	1143.61	-0.01	0	72	4.70E-06	M.ASGVAVSDGVIK.V	Acetyl (Protein N-term)	20.55		
beads (3 hours), [ST9]	P23528	7%	51	1	18719	8.2	P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3												29	1
							2	13	572.78	1143.55	1143.61	-0.06	0	48	1.30E-03	M.ASGVAVSDGVIK.V	Acetyl (Protein N-term)	21.57		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9NX63	4%	67	1	26421	8.5	Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1												18	1
							28	35	473.24	944.47	944.49	-0.02	0	48	1.40E-03	R.LSENVIDR.M		15.66		
BCG (5 days), [ST8]	Q9NX63	4%	45	1	26421	8.5	Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1												20	1
							96	104	487.25	972.49	972.5	-0.01	0	42	6.10E-03	R.AAANEQLTR.A		12.84		
beads (3 days), [ST10]	Q9NX63	4%	85	1	26421	8.5	Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1												23	1
							96	104	487.28	972.55	972.5	0.05	0	67	1.70E-05	R.AAANEQLTR.A		16.62		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P22695	4%	86	1	48584	8.7	P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3												14	1
							360	375	816.02	1630.02	1629.83	0.19	0	55	1.90E-04	K.TIAQGNLSNTDVQAAK.N		25.19		
BCG (5 days), [ST8]	P22695	4%	122	1	48584	8.7	P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3												12	1
							360	375	815.89	1629.77	1629.83	-0.07	0	122	4.30E-11	K.TIAQGNLSNTDVQAAK.N		15.78		
beads (3 days), [ST10]	P22695	4%	151	1	48584	8.7	P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3												14	1
							360	375	815.98	1629.95	1629.83	0.12	0	99	8.40E-09	K.TIAQGNLSNTDVQAAK.N		28.8		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	O15372	5%	46	1	40076	6.1	O15372|EIF3H_HUMAN Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1												16	1
							6	24	814.36	1626.71	1626.73	-0.02	0	46	1.80E-03	K.EGTGSTATSSSSTAGAAGK.G		11.96		
BCG (5 days), [ST8]	O15372	5%	95	1	40076	6.1	O15372|EIF3H_HUMAN Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1												14	1
							6	24	814.37	1626.73	1626.73	0	0	79	8.70E-07	K.EGTGSTATSSSSTAGAAGK.G		12.28		
beads (5 days), [ST11]	O15372	5%	41	1	40076	6.1	O15372|EIF3H_HUMAN Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1												15	1
							6	24	814.4	1626.79	1626.73	0.06	0	41	5.90E-03	K.EGTGSTATSSSSTAGAAGK.G		12.31		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q9H3U5	3%	48	1	51973	6.3	Q9H3U5|MFSD1_HUMAN Major facilitator superfamily domain-containing protein 1 OS=Homo sapiens GN=MFSD1 PE=2 SV=2												1	1
							10	21	592.79	1183.57	1183.58	-0.02	0	48	1.10E-03	R.ALLAGGPDEADR.G		18.07		
BCG (5 days), [ST8]	Q9H3U5	3%	38	1	51973	6.3	Q9H3U5|MFSD1_HUMAN Major facilitator superfamily domain-containing protein 1 OS=Homo sapiens GN=MFSD1 PE=2 SV=2												1	1
							10	21	592.79	1183.56	1183.58	-0.02	0	38	1.00E-02	R.ALLAGGPDEADR.G		17.72		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	O15427	3%	71	1	50064	8.2	O15427|MOT4_HUMAN Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1												2	2
							2	14	593.33	1184.65	1184.6	0.05	0	50	7.40E-04	M.GGAVVDEGPTGVK.A		19.97		
BCG (3 days, b), [ST7]	O15427	3%	86	1	50064	8.2	O15427|MOT4_HUMAN Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1												1	2
							2	14	593.31	1184.6	1184.6	-0.01	0	39	9.50E-03	M.GGAVVDEGPTGVK.A		13.91		
beads (3 days), [ST10]	O15427	3%	70	1	50064	8.2	O15427|MOT4_HUMAN Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1												1	1
							2	14	593.38	1184.74	1184.6	0.14	0	48	1.40E-03	M.GGAVVDEGPTGVK.A		21.44		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q16718	8%	69	1	13507	5.8	Q16718|NDUA5_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3												30	1
							47	55	563.22	1124.42	1124.53	-0.12	0	54	2.50E-04	K.YTEQITNEK.L		14.51		
BCG (3 days, a), [ST6]	Q16718	8%	51	1	13507	5.8	Q16718|NDUA5_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3												35	1
							47	55	563.31	1124.6	1124.53	0.07	0	51	4.80E-04	K.YTEQITNEK.L		18.59		
beads (3 days), [ST10]	Q16718	8%	54	1	13507	5.8	Q16718|NDUA5_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3												34	1
							47	55	563.32	1124.63	1124.53	0.1	0	54	2.50E-04	K.YTEQITNEK.L		18.71		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P16671	2%	82	1	53589	8.2	P16671|CD36_HUMAN Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2												4	2
							224	231	461.76	921.51	921.52	0	0	47	1.20E-03	K.VAIIDTYK.G		20.13		
BCG (3 days, b), [ST7]	P16671	2%	57	1	53589	8.2	P16671|CD36_HUMAN Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2												7	1

							224	231	461.75	921.49	921.52	-0.02	0	34	2.90E-02	K.VAIIDTYK.G		19.37		
beads (3 hours), [ST9]	P16671	2%	104	1	53589	8.2	P16671|CD36_HUMAN Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2												5	1
							224	231	461.75	921.49	921.52	-0.03	0	48	1.20E-03	K.VAIIDTYK.G		19.7		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P25788	5%	70	1	28643	5.2	P25788|PSA3_HUMAN Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2												23	4
							30	41	609.31	1216.61	1216.64	-0.03	0	62	4.90E-05	K.AVENSSTAIGIR.C		15.5		
BCG (5 days), [ST8]	P25788	5%	105	1	28643	5.2	P25788|PSA3_HUMAN Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2												19	1
							30	41	609.34	1216.66	1216.64	0.02	0	57	1.50E-04	K.AVENSSTAIGIR.C		15.6		
beads (5 days), [ST11]	P25788	5%	80	1	28643	5.2	P25788|PSA3_HUMAN Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2												20	1
							30	41	609.33	1216.65	1216.64	0.01	0	50	7.50E-04	K.AVENSSTAIGIR.C		17.15		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P28072	5%	52	1	25570	4.8	P28072|PSB6_HUMAN Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4												28	1
							210	220	558.28	1114.55	1114.6	-0.05	0	52	4.90E-04	R.LAAIAESGVER.Q		16.49		
BCG (5 days), [ST8]	P28072	5%	46	1	25570	4.8	P28072|PSB6_HUMAN Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4												22	1
							210	220	558.3	1114.59	1114.6	-0.01	0	45	2.30E-03	R.LAAIAESGVER.Q		17.16		
beads (5 days), [ST11]	P28072	5%	70	1	25570	4.8	P28072|PSB6_HUMAN Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4												23	1
							210	220	558.32	1114.63	1114.6	0.03	0	70	7.10E-06	R.LAAIAESGVER.Q		17.64		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9UL25	7%	110	1	24731	8.1	Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3												20	1
							2	16	557.3	1112.58	1112.53	0.05	0	110	7.30E-10	M.AAAGGGGGGAAAAGR.A	Acetyl (Protein N-term)	13.26		
BCG (5 days), [ST8]	Q9UL25	7%	94	1	24731	8.1	Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3												20	1
							2	16	557.27	1112.53	1112.53	0	0	94	3.00E-08	M.AAAGGGGGGAAAAGR.A	Acetyl (Protein N-term)	12.97		
beads (3 hours), [ST9]	Q9UL25	4%	55	1	24731	8.1	Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3												23	1
							180	189	604.27	1206.52	1206.56	-0.03	0	55	2.40E-04	R.MIETAQVDER.A	Oxidation (M)	14.57		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q04837	5%	101	1	17249	9.6	Q04837|SSB_HUMAN Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1												28	1
							39	46	442.2	882.39	882.49	-0.11	0	49	7.80E-04	R.VGQDPVLR.Q		15.35		
BCG (3 days, b), [ST7]	Q04837	5%	38	1	17249	9.6	Q04837|SSB_HUMAN Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1												37	1
							39	46	442.22	882.42	882.49	-0.08	0	38	9.90E-03	R.VGQDPVLR.Q		13.76		
beads (3 hours), [ST9]	Q04837	5%	45	1	17249	9.6	Q04837|SSB_HUMAN Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1												31	1
							39	46	442.2	882.38	882.49	-0.11	0	45	1.90E-03	R.VGQDPVLR.Q		15.26		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q8TED4	2%	38	1	55256	6.4	Q8TED4|SPX2_HUMAN Sugar phosphate exchanger 2 OS=Homo sapiens GN=SLC37A2 PE=2 SV=2												1	1
							266	274	467.28	932.54	932.48	0.06	0	38	1.20E-02	R.ESGLETVAK.C		20.15		
BCG (3 days, b), [ST7]	Q8TED4	2%	52	1	55256	6.4	Q8TED4|SPX2_HUMAN Sugar phosphate exchanger 2 OS=Homo sapiens GN=SLC37A2 PE=2 SV=2												1	1
							266	274	467.23	932.45	932.48	-0.03	0	52	5.80E-04	R.ESGLETVAK.C		13.7		
beads (3 hours), [ST9]	Q8TED4	2%	60	1	55256	6.4	Q8TED4|SPX2_HUMAN Sugar phosphate exchanger 2 OS=Homo sapiens GN=SLC37A2 PE=2 SV=2												1	2
							266	274	467.24	932.47	932.48	-0.01	0	60	9.60E-05	R.ESGLETVAK.C		14.26		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9H3N1	4%	64	1	32170	4.9	Q9H3N1|TXND1_HUMAN Thioredoxin domain-containing protein 1 OS=Homo sapiens GN=TXNDC1 PE=1 SV=1												28	3
							83	94	629.35	1256.69	1256.64	0.06	0	64	3.10E-05	K.VDVTEQPGLSGR.F		24.73		
BCG (5 days), [ST8]	Q9H3N1	4%	54	1	32170	4.9	Q9H3N1|TXND1_HUMAN Thioredoxin domain-containing protein 1 OS=Homo sapiens GN=TXNDC1 PE=1 SV=1												17	1
							83	94	629.32	1256.63	1256.64	-0.01	0	54	3.20E-04	K.VDVTEQPGLSGR.F		15.82		
beads (3 days), [ST10]	Q9H3N1	4%	47	1	32170	4.9	Q9H3N1|TXND1_HUMAN Thioredoxin domain-containing protein 1 OS=Homo sapiens GN=TXNDC1 PE=1 SV=1												29	1
							83	94	629.36	1256.7	1256.64	0.07	0	47	1.70E-03	K.VDVTEQPGLSGR.F		23.21		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P29144	1%	45	1	139745	5.9	P29144|TPP2_HUMAN Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4												13	1
							629	638	491.74	981.46	981.62	-0.16	0	35	2.00E-02	R.VPITAVIAAK.V		19.39		
beads (5 days), [ST11]	P29144	1%	38	1	139745	5.9	P29144|TPP2_HUMAN Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4												2	1
							629	638	491.8	981.59	981.62	-0.03	0	38	1.00E-02	R.VPITAVIAAK.V		20.3		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P23381	4%	120	1	53474	5.8	P23381|SYWC_HUMAN Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2												12	1
							350	366	900.91	1799.8	1799.82	-0.02	0	99	8.50E-09	K.MSASDPNSSIFLTDTAK.Q	Oxidation (M)	20.11		
BCG (5 days), [ST8]	P23381	4%	92	1	53474	5.8	P23381|SYWC_HUMAN Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2												10	1
							350	366	900.89	1799.77	1799.82	-0.06	0	77	1.40E-06	K.MSASDPNSSIFLTDTAK.Q	Oxidation (M)	20.48		
beads (5 days), [ST11]	P23381	4%	87	1	53474	5.8	P23381|SYWC_HUMAN Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2												10	1
							350	366	900.91	1799.8	1799.82	-0.02	0	76	1.40E-06	K.MSASDPNSSIFLTDTAK.Q	Oxidation (M)	20.4		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9BV40	9%	56	1	11488	6.7	Q9BV40|VAMP8_HUMAN Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1												34	1
							25	33	560.79	1119.57	1119.53	0.03	0	35	2.50E-02	K.NIMTQNVER.I	Oxidation (M)	17.55		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P21796	4%	73	1	30868	8.6	P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2												21	3
							164	174	607.35	1212.68	1212.61	0.07	0	73	3.75E-06	R.VTQSNFAVGYK.T		27.57		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9Y277	4%	70	1	30981	8.8	Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1												17	1
							164	174	627.84	1253.67	1253.64	0.03	0	70	7.20E-06	K.LSQNNFALGYK.A		20.28		
BCG (3 days, b), [ST7]	Q9Y277	4%	62	1	30981	8.8	Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1												21	2
							164	174	627.82	1253.63	1253.64	-0.01	0	46	1.80E-03	K.LSQNNFALGYK.A		19.6		
beads (5 days), [ST11]	Q9Y277	4%	56	1	30981	8.8	Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1												19	1
							164	174	627.79	1253.57	1253.64	-0.07	0	56	1.80E-04	K.LSQNNFALGYK.A		20.8		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P30050	5%	110	1	17979	9.5	P30050|RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1												30	1
							32	40	441.3	880.59	880.54	0.05	0	34	2.00E-02	K.IGPLGLSPK.K		26.49		
BCG (3 days, b), [ST7]	P30050	5%	44	1	17979	9.5	P30050|RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1												35	2
							32	40	441.25	880.48	880.54	-0.06	0	44	2.40E-03	K.IGPLGLSPK.K		19.79		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P61313	4%	44	1	24245	11.6	P61313|RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2												37	1

							97	105	509.67	1017.32	1017.51	-0.19	0	44	3.10E-03	R.SLQSVAEER.A		13.73		
BCG (5 days), [ST8]	P61313	4%	47	1	24245	11.6	P61313|RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2												21	1
							97	105	509.76	1017.5	1017.51	-0.01	0	47	1.60E-03	R.SLQSVAEER.A		15.24		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P46776	7%	44	1	16665	11	P46776|RL27A_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2												41	1
							95	105	556.23	1110.45	1110.64	-0.19	0	44	2.50E-03	K.TGAAPIIDVVR.S		19.54		
BCG (5 days), [ST8]	P46776	7%	56	1	16665	11	P46776|RL27A_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2												26	1
							95	105	556.33	1110.64	1110.64	0	0	57	1.50E-04	K.TGAAPIIDVVR.S		20.73		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P05141	3%	66	1	33102	9.8	P05141|ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=6												21	1
							2	10	476.28	950.54	950.47	0.07	0	47	1.30E-03	M.TDAAVSFAK.D	Acetyl (Protein N-term)	29.95		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P05090	6%	85	1	21547	5.1	P05090|APOD_HUMAN Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1												26	2
							177	187	654.84	1307.67	1307.58	0.09	0	55	2.40E-04	K.MTVTDQVNCPK.L	Oxidation (M)	18.63		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9Y2J2	1%	85	1	121458	5.1	Q9Y2J2|E41L3_HUMAN Band 4.1-like protein 3 OS=Homo sapiens GN=EPB41L3 PE=1 SV=2												4	1
							912	924	687.9	1373.79	1373.68	0.11	0	75	2.10E-06	K.AVLEQEETAAASR.E		24.22		
BCG (3 days, b), [ST7]	Q9Y2J2	1%	75	1	121458	5.1	Q9Y2J2|E41L3_HUMAN Band 4.1-like protein 3 OS=Homo sapiens GN=EPB41L3 PE=1 SV=2												5	1
							912	924	687.84	1373.66	1373.68	-0.02	0	75	2.10E-06	K.AVLEQEETAAASR.E		14.92		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P61769	8%	61	1	13820	6.1	P61769|B2MG_HUMAN Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1												36	1
							102	111	374.89	1121.66	1121.62	0.04	0	39	9.50E-03	R.VNHVTLSQPK.I		17.77		
BCG (3 days, b), [ST7]	P61769	8%	62	1	13820	6.1	P61769|B2MG_HUMAN Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1												46	3
							102	111	374.85	1121.53	1121.62	-0.09	0	39	8.60E-03	R.VNHVTLSQPK.I		12.55		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q10589	6%	45	1	20041	5.4	Q10589|BST2_HUMAN Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1												23	2
							127	136	559.32	1116.63	1116.54	0.09	0	39	1.20E-02	K.LQDASAEVER.L		18.85		
BCG (5 days), [ST8]	Q10589	6%	49	1	20041	5.4	Q10589|BST2_HUMAN Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1												17	1
							127	136	559.26	1116.51	1116.54	-0.03	0	49	1.10E-03	K.LQDASAEVER.L		13.38		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P10606	5%	70	1	13915	9.1	P10606|COX5B_HUMAN Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2												30	1
							50	56	396.17	790.33	790.43	-0.1	0	40	9.40E-03	R.EIMLAAK.K	Oxidation (M)	15.63		
BCG (3 days, a), [ST6]	P10606	5%	67	1	13915	9.1	P10606|COX5B_HUMAN Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2												35	1
							50	56	396.23	790.45	790.43	0.02	0	39	1.00E-02	R.EIMLAAK.K	Oxidation (M)	20.9		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P28838	3%	78	1	56530	8	P28838|AMPL_HUMAN Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3												12	1
							268	282	763.39	1524.76	1524.79	-0.04	0	52	4.70E-04	K.GSPNANEPPLVFVGK.G		20.51		
BCG (5 days), [ST8]	P28838	3%	66	1	56530	8	P28838|AMPL_HUMAN Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3												10	1
							268	282	763.38	1524.75	1524.79	-0.05	0	49	8.70E-04	K.GSPNANEPPLVFVGK.G		20.79		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9UHL4	2%	84	1	54749	5.9	Q9UHL4|DPP2_HUMAN Dipeptidyl-peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=2												12	1
							113	123	596.34	1190.67	1190.6	0.07	0	36	1.80E-02	K.SLPFGAQSTQR.G		28.32		
BCG (3 days, b), [ST7]	Q9UHL4	3%	94	1	54749	5.9	Q9UHL4|DPP2_HUMAN Dipeptidyl-peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=2												12	2
							449	462	488.88	1463.63	1463.7	-0.07	0	52	3.70E-04	R.ASHPEDPASVVEAR.K		14.83		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q96C19	5%	66	1	26794	5.2	Q96C19|EFHD2_HUMAN EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1												20	1
							177	188	631.83	1261.64	1261.64	0	0	55	2.20E-04	R.LSEIDVSSEGVK.G		19.12		
BCG (5 days), [ST8]	Q96C19	5%	63	1	26794	5.2	Q96C19|EFHD2_HUMAN EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1												17	1
							177	188	631.8	1261.58	1261.64	-0.06	0	63	3.60E-05	R.LSEIDVSSEGVK.G		19.35		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q96HE7	3%	38	1	55213	5.5	Q96HE7|ERO1A_HUMAN ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2												10	1
							137	150	753.37	1504.73	1504.73	0.01	0	38	1.10E-02	R.LGAVDESLSEETQK.A		18.91		
BCG (5 days), [ST8]	Q96HE7	3%	119	1	55213	5.5	Q96HE7|ERO1A_HUMAN ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2												9	1
							137	150	753.34	1504.67	1504.73	-0.05	0	119	7.90E-11	R.LGAVDESLSEETQK.A		19.25		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P07954	2%	53	1	54773	8.8	P07954|FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3												9	1
							161	172	610.83	1219.64	1219.61	0.03	0	53	3.90E-04	R.AIEMLGGELGSK.I	Oxidation (M)	15.72		
BCG (5 days), [ST8]	P07954	2%	142	1	54773	8.8	P07954|FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3												12	1
							161	172	610.79	1219.57	1219.61	-0.04	0	72	5.00E-06	R.AIEMLGGELGSK.I	Oxidation (M)	19.65		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P63218	16%	96	1	7428	9.9	P63218|GBG5_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3												32	1
							2	12	555.7	1109.39	1109.54	-0.15	1	49	7.50E-04	M.SGSSSVAAMKK.V	Acetyl (Protein N-term); Oxidation (M)	12.91		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9H4G4	8%	48	1	17322	9.4	Q9H4G4|GAPR1_HUMAN Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3												26	1
							120	132	627.28	1252.54	1252.6	-0.06	0	48	1.20E-03	K.ASASDGSSFVVAR.Y		19.92		
BCG (3 days, b), [ST7]	Q9H4G4	8%	98	1	17322	9.4	Q9H4G4|GAPR1_HUMAN Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3												35	1
							120	132	627.3	1252.59	1252.6	-0.01	0	98	1.00E-08	K.ASASDGSSFVVAR.Y		17.35		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P08648	1%	43	1	115605	5.5	P08648|ITA5_HUMAN Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2												13	1
							695	708	744.92	1487.82	1487.76	0.06	0	43	3.50E-03	R.VTAPPEAEYSGLVR.H		20.48		
BCG (3 days, a), [ST6]	P08648	1%	58	1	115605	5.5	P08648|ITA5_HUMAN Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2												3	2
							728	738	638.43	1274.84	1274.64	0.21	0	39	9.30E-03	R.LLVCDLGNPMK.A	Oxidation (M)	27.99		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P05362	2%	53	1	58587	8.3	P05362|ICAM1_HUMAN Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=1 SV=2												18	1

							135	143	487.15	972.28	972.44	-0.17	0	38	6.20E-03	R.CQVEGGAPR.A		12.12		
BCG (5 days), [ST8]	P05362	2%	39	1	58587	8.3	P05362|ICAM1_HUMAN Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=1 SV=2												5	1
							135	143	487.2	972.38	972.44	-0.06	0	34	3.70E-02	R.CQVEGGAPR.A		12.64		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	O95202	2%	74	1	83986	6.3	O95202|LETM1_HUMAN LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1												4	1
							452	463	658.8	1315.59	1315.63	-0.04	0	56	2.00E-04	K.VAEVEGEQVDNK.A		13.95		
BCG (3 days, a), [ST6]	O95202	2%	62	1	83986	6.3	O95202|LETM1_HUMAN LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1												7	1
							452	463	658.85	1315.68	1315.63	0.06	0	62	5.60E-05	K.VAEVEGEQVDNK.A		19.23		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P36776	1%	48	1	106936	6	P36776|LONM_HUMAN Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=2 SV=2												6	1
							473	482	597.78	1193.54	1193.57	-0.03	0	48	1.20E-03	K.YSNENLDLAR.A		18.2		
BCG (5 days), [ST8]	P36776	1%	50	1	106936	6	P36776|LONM_HUMAN Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=2 SV=2												5	1
							473	482	597.76	1193.5	1193.57	-0.06	0	50	7.60E-04	K.YSNENLDLAR.A		18.48		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P11117	2%	38	1	48713	6.3	P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3												24	1
							357	364	441.69	881.36	881.52	-0.16	0	38	9.50E-03	R.LTEPVVPK.D		14.34		
BCG (3 days, b), [ST7]	P11117	2%	124	1	48713	6.3	P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3												9	2
							35	41	456.24	910.47	910.53	-0.05	0	42	4.20E-03	R.FVTLLYR.H		20.64		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P10253	1%	80	1	106126	5.6	P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=2												35	2
							892	903	615.81	1229.6	1229.66	-0.07	0	80	8.10E-07	R.VTSEGAGLQLQK.V		15.38		
BCG (5 days), [ST8]	P10253	1%	50	1	106126	5.6	P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=2												4	2
							892	903	615.82	1229.63	1229.66	-0.04	0	50	7.30E-04	R.VTSEGAGLQLQK.V		15.9		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q8TCT9	3%	65	1	41747	6	Q8TCT9|HM13_HUMAN Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1												1	1
							62	73	669.29	1336.56	1336.59	-0.04	0	44	2.60E-03	K.NASDMPETITSR.D	Oxidation (M)	13.52		
BCG (5 days), [ST8]	Q8TCT9	3%	68	1	41747	6	Q8TCT9|HM13_HUMAN Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1												1	1
							62	73	669.29	1336.56	1336.59	-0.03	0	68	1.10E-05	K.NASDMPETITSR.D	Oxidation (M)	13.68		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9NS69	8%	56	1	15512	4.3	Q9NS69|TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3												25	1
							106	117	787.33	1572.64	1572.77	-0.12	0	56	1.70E-04	K.LQMEQQQQLQQR.Q	Oxidation (M)	14.09		
BCG (3 days, a), [ST6]	Q9NS69	8%	84	1	15512	4.3	Q9NS69|TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3												31	2
							106	117	787.4	1572.79	1572.77	0.03	0	84	2.80E-07	K.LQMEQQQQLQQR.Q	Oxidation (M)	17.91		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q16891	1%	87	1	84026	6.1	Q16891|IMMT_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1												4	1
							507	516	605.79	1209.56	1209.55	0.01	0	35	2.40E-02	K.SEFEQNLSEK.L		16.95		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P15586	2%	92	1	62840	8.6	P15586|GNS_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3												22	1
							247	255	525.19	1048.36	1048.55	-0.18	0	33	3.60E-02	K.AFQNVFAPR.N		19.79		
BCG (3 days, a), [ST6]	P15586	2%	73	1	62840	8.6	P15586|GNS_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3												7	1
							247	255	525.34	1048.66	1048.55	0.11	0	37	1.40E-02	K.AFQNVFAPR.N		29.59		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P07602	2%	152	1	59899	5.1	P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2												43	1
							430	438	507.71	1013.41	1013.58	-0.16	0	83	3.80E-07	K.QEILAALEK.G		19.63		
BCG (5 days), [ST8]	P07602	2%	38	1	59899	5.1	P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2												8	1
							233	242	539.24	1076.47	1076.5	-0.03	0	38	1.30E-02	R.LGPGMADICK.N	Oxidation (M)	14.96		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q6P4E1	3%	49	1	48949	5.5	Q6P4E1|CASC4_HUMAN Protein CASC4 OS=Homo sapiens GN=CASC4 PE=2 SV=1												9	1
							324	335	649.31	1296.61	1296.67	-0.05	0	51	5.70E-04	R.LIPGSNLDSEPR.I		19.02		
BCG (5 days), [ST8]	Q6P4E1	3%	47	1	48949	5.5	Q6P4E1|CASC4_HUMAN Protein CASC4 OS=Homo sapiens GN=CASC4 PE=2 SV=1												8	1
							324	335	649.33	1296.64	1296.67	-0.03	0	47	1.40E-03	R.LIPGSNLDSEPR.I		19.3		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q99497	4%	55	1	20050	6.3	Q99497|PARK7_HUMAN Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2												37	1
							183	189	378.17	754.33	754.46	-0.13	1	37	1.10E-02	K.APLVLKD.-		14.77		
BCG (3 days, b), [ST7]	Q99497	4%	59	1	20050	6.3	Q99497|PARK7_HUMAN Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2												27	1
							183	189	378.22	754.44	754.46	-0.02	1	39	6.10E-03	K.APLVLKD.-		16.12		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P60059	18%	51	1	7793	10	P60059|SC61G_HUMAN Protein transport protein Sec61 subunit gamma OS=Homo sapiens GN=SEC61G PE=2 SV=1												36	1
							1	12	770.87	1539.73	1539.67	0.06	0	51	5.60E-04	-.MDQVMQFVEPSR.Q	Acetyl (Protein N-term); 2 Oxidation (M)	27.13		
BCG (3 days, b), [ST7]	P60059	18%	63	1	7793	10	P60059|SC61G_HUMAN Protein transport protein Sec61 subunit gamma OS=Homo sapiens GN=SEC61G PE=2 SV=1												47	2
							1	12	770.79	1539.57	1539.67	-0.1	0	63	3.50E-05	-.MDQVMQFVEPSR.Q	Acetyl (Protein N-term); 2 Oxidation (M)	20.21		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P15498	1%	54	1	99677	6.2	P15498|VAV_HUMAN Proto-oncogene vav OS=Homo sapiens GN=VAV1 PE=1 SV=4												6	1
							679	688	501.25	1000.49	1000.53	-0.04	0	54	3.40E-04	R.AGAESILANR.S		17.81		
BCG (5 days), [ST8]	P15498	1%	47	1	99677	6.2	P15498|VAV_HUMAN Proto-oncogene vav OS=Homo sapiens GN=VAV1 PE=1 SV=4												5	1
							679	688	501.26	1000.5	1000.53	-0.03	0	47	1.70E-03	R.AGAESILANR.S		18.26		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P61106	4%	79	1	24110	5.8	P61106|RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4												37	1
							52	59	437.18	872.35	872.5	-0.15	0	35	3.60E-02	R.IIEVSGQK.I		12.96		
BCG (3 days, a), [ST6]	P61106	4%	105	1	24110	5.8	P61106|RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4												26	1
							52	59	437.29	872.56	872.5	0.07	0	40	1.10E-02	R.IIEVSGQK.I		19.12		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P52566	6%	60	1	23031	5.1	P52566|GDIR2_HUMAN Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3												25	1
							51	63	656.39	1310.77	1310.71	0.06	0	36	1.90E-02	K.TLLGDGPVVTDPK.A		26.71		
BCG (3 days, b), [ST7]	P52566	6%	117	1	23031	5.1	P52566|GDIR2_HUMAN Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3												26	1

							51	63	656.33	1310.65	1310.71	-0.06	0	86	1.70E-07	K.TLLGDGPVVTDPK.A		19.83		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q9H299	11%	67	1	10488	4.8	Q9H299|SH3L3_HUMAN SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1												43	1
							6	15	528.68	1055.34	1055.52	-0.18	0	67	1.30E-05	R.VYSTSVTGSR.E		12.64		
BCG (3 days, b), [ST7]	Q9H299	11%	53	1	10488	4.8	Q9H299|SH3L3_HUMAN SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1												43	2
							6	15	528.73	1055.45	1055.52	-0.08	0	53	4.30E-04	R.VYSTSVTGSR.E		12.9		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P16949	7%	41	1	17292	5.8	P16949|STMN1_HUMAN Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3												41	1
							86	95	583.19	1164.36	1164.54	-0.18	0	41	5.00E-03	K.AIEENNNFSK.M		12.96		
BCG (5 days), [ST8]	P16949	7%	50	1	17292	5.8	P16949|STMN1_HUMAN Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3												26	1
							86	95	583.27	1164.53	1164.54	-0.01	0	50	6.90E-04	K.AIEENNNFSK.M		13.86		
other possible isoforms		Q93045 STMN2_HUMAN Stathmin-2																		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q13277	3%	45	1	33134	5.3	Q13277|STX3_HUMAN Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3												14	1
							189	197	501.8	1001.59	1001.51	0.08	0	34	4.10E-02	K.QALSEIEGR.H		17.02		
BCG (5 days), [ST8]	Q13277	3%	38	1	33134	5.3	Q13277|STX3_HUMAN Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3												16	1
							189	197	501.74	1001.46	1001.51	-0.05	0	38	1.60E-02	K.QALSEIEGR.H		15.94		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P37837	3%	45	1	37688	6.4	P37837|TALDO_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2												18	1
							259	269	607.35	1212.68	1212.67	0.01	0	45	2.60E-03	K.LLGELLQDNAK.L		20.46		
BCG (5 days), [ST8]	P37837	3%	55	1	37688	6.4	P37837|TALDO_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2												15	1
							259	269	607.32	1212.63	1212.67	-0.04	0	55	2.10E-04	K.LLGELLQDNAK.L		20.86		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q15582	2%	146	1	75261	7.6	Q15582|BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1												9	1
							643	655	704.33	1406.65	1406.69	-0.05	0	63	3.30E-05	R.GDELADSALEIFK.Q		22.25		
BCG (5 days), [ST8]	Q15582	2%	71	1	75261	7.6	Q15582|BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1												8	1
							643	655	704.33	1406.65	1406.69	-0.04	0	71	6.00E-06	R.GDELADSALEIFK.Q		22.69		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P51571	8%	80	1	19158	5.8	P51571|SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1												31	1
							61	73	691.37	1380.73	1380.67	0.05	0	67	1.30E-05	R.VQNMALYADVGGK.Q	Oxidation (M)	25.34		
BCG (3 days, b), [ST7]	P51571	8%	41	1	19158	5.8	P51571|SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1												35	1
							61	73	691.29	1380.57	1380.67	-0.1	0	41	6.30E-03	R.VQNMALYADVGGK.Q	Oxidation (M)	18.79		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	O43399	7%	47	1	22281	5.3	O43399|TPD54_HUMAN Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2												37	1
							140	153	660.75	1319.48	1319.7	-0.22	0	48	1.10E-03	K.TSAALSTVGSAISR.K		19.07		
BCG (5 days), [ST8]	O43399	7%	73	1	22281	5.3	O43399|TPD54_HUMAN Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2												20	1
							140	153	660.85	1319.69	1319.7	-0.01	0	73	3.70E-06	K.TSAALSTVGSAISR.K		19.73		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q0VGL1	10%	66	1	10792	6.1	Q0VGL1|CG059_HUMAN UPF0539 protein C7orf59 OS=Homo sapiens GN=C7orf59 PE=3 SV=1												36	1
							2	11	559.31	1116.61	1116.58	0.03	0	47	1.70E-03	M.TSALTQGLER.I	Acetyl (Protein N-term)	27.48		
BCG (3 days, b), [ST7]	Q0VGL1	10%	73	1	10792	6.1	Q0VGL1|CG059_HUMAN UPF0539 protein C7orf59 OS=Homo sapiens GN=C7orf59 PE=3 SV=1												46	1
							2	11	559.26	1116.51	1116.58	-0.07	0	62	4.80E-05	M.TSALTQGLER.I	Acetyl (Protein N-term)	20.4		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	O95766	3%	76	1	56286	6.1	O95766|CG028_HUMAN UPF0550 protein C7orf28 OS=Homo sapiens GN=C7orf28A PE=1 SV=1												27	1
							282	295	757.78	1513.55	1513.78	-0.23	0	56	1.60E-04	R.FLTGPLNLNDPDAK.C		20.4		
BCG (3 days, b), [ST7]	O95766	3%	59	1	56286	6.1	O95766|CG028_HUMAN UPF0550 protein C7orf28 OS=Homo sapiens GN=C7orf28A PE=1 SV=1												12	1
							282	295	757.88	1513.75	1513.78	-0.02	0	59	7.60E-05	R.FLTGPLNLNDPDAK.C		20.96		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P21283	3%	124	1	44085	7	P21283|VATC1_HUMAN Vacuolar proton pump subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4												16	1
							128	137	551.78	1101.55	1101.57	-0.02	0	44	3.40E-03	K.GVTQIDNDLK.S		17.28		
BCG (5 days), [ST8]	P21283	3%	52	1	44085	7	P21283|VATC1_HUMAN Vacuolar proton pump subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4												13	1
							128	137	551.77	1101.52	1101.57	-0.04	0	33	3.90E-02	K.GVTQIDNDLK.S		17.07		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9Y5K8	4%	52	1	28245	9.4	Q9Y5K8|VATD_HUMAN Vacuolar proton pump subunit D OS=Homo sapiens GN=ATP6V1D PE=1 SV=1												15	1
							64	73	518.78	1035.55	1035.52	0.03	0	37	1.50E-02	R.EAAFSLAEAK.F		20.16		
BCG (3 days, b), [ST7]	Q9Y5K8	4%	62	1	28245	9.4	Q9Y5K8|VATD_HUMAN Vacuolar proton pump subunit D OS=Homo sapiens GN=ATP6V1D PE=1 SV=1												20	1
							64	73	518.76	1035.52	1035.52	-0.01	0	52	4.60E-04	R.EAAFSLAEAK.F		19.51		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q9Y2Q5	10%	78	1	13613	5.3	Q9Y2Q5|MAPIP_HUMAN Mitogen-activated protein-binding protein-interacting protein OS=Homo sapiens GN=MAPBPIP PE=2 SV=1												31	1
							59	70	682.22	1362.42	1362.62	-0.19	0	45	1.90E-03	R.NGNQAFNEDNLK.F		17.83		
beads (3 hours), [ST9]	Q9Y2Q5	10%	74	1	13613	5.3	Q9Y2Q5|MAPIP_HUMAN Mitogen-activated protein-binding protein-interacting protein OS=Homo sapiens GN=MAPBPIP PE=2 SV=1												34	1
							59	70	682.29	1362.56	1362.62	-0.06	0	45	1.90E-03	R.NGNQAFNEDNLK.F		18.3		
beads (3 days), [ST10]	Q9Y2Q5	10%	92	1	13613	5.3	Q9Y2Q5|MAPIP_HUMAN Mitogen-activated protein-binding protein-interacting protein OS=Homo sapiens GN=MAPBPIP PE=2 SV=1												34	1
							59	70	682.37	1362.73	1362.62	0.11	0	48	1.00E-03	R.NGNQAFNEDNLK.F		24.35		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P13667	2%	108	1	73229	5	P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2												22	1
							120	131	595.75	1189.48	1189.63	-0.15	0	81	6.00E-07	K.IDATSASVLASR.F		18.93		
beads (3 days), [ST10]	P13667	2%	61	1	73229	5	P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2												8	1
							350	362	729.94	1457.87	1457.75	0.11	0	39	8.10E-03	K.VSQGQLVVMQPEK.F	Oxidation (M)	28.96		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	O43760	4%	92	1	25079	4.8	O43760|SNG2_HUMAN Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1												25	1
							20	29	579.87	1157.73	1157.66	0.08	0	42	4.90E-03	R.FLTQPQVVAR.A		25.84		
beads (3 hours), [ST9]	O43760	4%	44	1	25079	4.8	O43760|SNG2_HUMAN Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1												30	1
							20	29	579.78	1157.55	1157.66	-0.11	0	44	3.20E-03	R.FLTQPQVVAR.A		20.64		
beads (3 days), [ST10]	O43760	4%	54	1	25079	4.8	O43760|SNG2_HUMAN Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1												29	1
							20	29	579.86	1157.7	1157.66	0.05	0	34	3.60E-02	R.FLTQPQVVAR.A		24.39		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P39019	6%	102	1	16051	10.3	P39019|RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2												37	1
							103	111	485.76	969.51	969.59	-0.07	0	44	2.80E-03	R.VLQALEGLK.M		20.1		
beads (5 days), [ST11]	P39019	6%	100	1	16051	10.3	P39019|RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2												28	1
							103	111	485.77	969.52	969.59	-0.06	0	49	9.30E-04	R.VLQALEGLK.M		21.13		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P08865	4%	74	1	32947	4.8	P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4												31	1
							90	102	602.25	1202.49	1202.64	-0.16	0	52	5.30E-04	K.FAAATGATPIAGR.F		15.09		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P08865	4%	65	1	32947	4.8	P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4												18	2
							90	102	602.41	1202.81	1202.64	0.17	0	65	2.28E-05	K.FAAATGATPIAGR.F		26.07		
beads (3 days), [ST10]	P08865	4%	46	1	32947	4.8	P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4												23	1
							90	102	602.36	1202.7	1202.64	0.06	0	46	2.20E-03	K.FAAATGATPIAGR.F		23.74		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P18124	4%	83	1	29264	10.7	P18124|RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1												18	1
							167	177	585.83	1169.64	1169.68	-0.03	0	76	1.80E-06	R.IALTDNALIAR.S		20.42		
beads (5 days), [ST11]	P18124	4%	203	1	29264	10.7	P18124|RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1												19	1
							167	177	585.82	1169.63	1169.68	-0.05	0	73	3.50E-06	R.IALTDNALIAR.S		21.41		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	O75947	6%	69	1	18537	5.2	O75947|ATP5H_HUMAN ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3												22	1
							64	72	497.2	992.39	992.48	-0.09	0	38	1.10E-02	K.AGLVDDFEK.K		21.56		
beads (3 hours), [ST9]	O75947	6%	78	1	18537	5.2	O75947|ATP5H_HUMAN ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3												25	1
							64	72	497.23	992.44	992.48	-0.04	0	40	7.30E-03	K.AGLVDDFEK.K		21.57		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P59998	7%	128	1	19768	8.5	P59998|ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3												30	1
							61	71	593.88	1185.74	1185.67	0.07	0	35	2.70E-02	K.VLIEGSINSVR.V		26.23		
beads (5 days), [ST11]	P59998	7%	54	1	19768	8.5	P59998|ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3												25	1
							61	71	593.82	1185.62	1185.67	-0.05	0	54	2.90E-04	K.VLIEGSINSVR.V		20.59		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P06733	2%	66	1	47481	7	P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2												29	2
							413	420	452.66	903.3	903.45	-0.15	0	42	5.00E-03	R.IEEELGSK.A		12.87		
beads (3 hours), [ST9]	P06733	2%	70	1	47481	7	P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2												11	1
							222	228	401.23	800.44	800.46	-0.02	0	35	3.50E-02	K.EGLELLK.T		21.17		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P50995	2%	53	1	54697	7.5	P50995|ANX11_HUMAN Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1												10	1
							462	470	531.26	1060.51	1060.54	-0.03	0	41	7.20E-03	R.SETDLLDIR.S		21.01		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P27797	3%	123	1	48283	4.3	P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1												10	2
							74	87	804.38	1606.75	1606.77	-0.02	0	66	1.60E-05	R.FYALSASFEPFSNK.G		22.14		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P23786	2%	44	1	74244	8.4	P23786|CPT2_HUMAN Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2												24	1
							152	161	540.19	1078.37	1078.54	-0.17	0	37	1.40E-02	R.ATNMTVSAIR.F	Oxidation (M)	12.87		
beads (3 hours), [ST9]	P23786	2%	43	1	74244	8.4	P23786|CPT2_HUMAN Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2												7	1
							152	161	540.29	1078.56	1078.54	0.01	0	39	9.60E-03	R.ATNMTVSAIR.F	Oxidation (M)	14.23		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	Q9H444	6%	57	1	24935	4.8	Q9H444|CHM4B_HUMAN Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1												17	1
							94	107	773.35	1544.69	1544.77	-0.08	0	57	1.40E-04	R.EALENANTNTEVLK.N		17.61		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P09496	4%	44	1	27174	4.4	P09496|CLCA_HUMAN Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1												21	1
							121	129	494.74	987.47	987.5	-0.02	0	44	3.90E-03	R.LEALDANSR.K		13.99		
beads (5 days), [ST11]	P09496	4%	49	1	27174	4.4	P09496|CLCA_HUMAN Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1												19	1
							121	129	494.72	987.43	987.5	-0.07	0	49	1.30E-03	R.LEALDANSR.K		15.68		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P04839	2%	75	1	66206	8.9	P04839|CY24B_HUMAN Cytochrome b-245 heavy chain OS=Homo sapiens GN=CYBB PE=1 SV=2												1	2
							549	559	581.27	1160.52	1160.54	-0.02	0	77	1.70E-06	K.QSISNSESGPR.G		12.64		
beads (3 days), [ST10]	P04839	2%	56	1	66206	8.9	P04839|CY24B_HUMAN Cytochrome b-245 heavy chain OS=Homo sapiens GN=CYBB PE=1 SV=2												1	1
							549	559	581.35	1160.69	1160.54	0.14	0	56	2.10E-04	K.QSISNSESGPR.G		18.36		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P99999	13%	88	1	11855	9.6	P99999|CYC_HUMAN Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2												30	1
							41	54	714.75	1427.49	1427.67	-0.18	0	37	1.50E-02	K.TGQAPGYSYTAANK.N		15.33		
beads (3 days), [ST10]	P99999	13%	44	1	11855	9.6	P99999|CYC_HUMAN Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2												33	1
							41	54	714.87	1427.72	1427.67	0.05	0	33	3.70E-02	K.TGQAPGYSYTAANK.N		21.08		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q14204	0%	138	1	534809	6	Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5												2	1
							2350	2358	491.27	980.52	980.53	0	0	39	7.70E-03	K.YATLATVSR.C		16.07		
beads (5 days), [ST11]	Q14204	0%	119	1	534809	6	Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5												1	1
							2350	2358	491.25	980.49	980.53	-0.04	0	42	4.10E-03	K.YATLATVSR.C		16.62		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q9P2X0	11%	53	1	10258	5.7	Q9P2X0|DPM3_HUMAN Dolichol-phosphate mannosyltransferase subunit 3 OS=Homo sapiens GN=DPM3 PE=1 SV=2												45	1
							73	82	601.27	1200.52	1200.61	-0.09	0	53	3.90E-04	R.ELQSQIQEAR.A		13.74		
beads (3 days), [ST10]	Q9P2X0	11%	55	1	10258	5.7	Q9P2X0|DPM3_HUMAN Dolichol-phosphate mannosyltransferase subunit 3 OS=Homo sapiens GN=DPM3 PE=1 SV=2												36	1
							73	82	601.33	1200.64	1200.61	0.03	0	55	2.40E-04	R.ELQSQIQEAR.A		21.37		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P13804	5%	127	1	35400	8.6	P13804|ETFA_HUMAN Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1												16	1
							170	187	815.87	1629.72	1629.71	0.01	0	46	1.60E-03	R.GTSFDAAATSGGSASSEK.A		14.54		
beads (3 days), [ST10]	P13804	5%	56	1	35400	8.6	P13804|ETFA_HUMAN Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1												20	1
							170	187	815.91	1629.81	1629.71	0.1	0	46	1.50E-03	R.GTSFDAAATSGGSASSEK.A		24.5		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P49411	2%	107	1	49852	7.3	P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2												14	1
							71	79	460.31	918.6	918.54	0.07	0	38	1.20E-02	K.TTLTAAITK.I		27.19		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P30040	4%	69	1	29032	6.8	P30040|ERP29_HUMAN Endoplasmic reticulum protein ERp29 OS=Homo sapiens GN=ERP29 PE=1 SV=4												23	1
							183	192	538.29	1074.57	1074.53	0.04	0	69	9.30E-06	K.QGQDNLSSVK.E		18.16		
beads (3 days), [ST10]	P30040	4%	60	1	29032	6.8	P30040|ERP29_HUMAN Endoplasmic reticulum protein ERp29 OS=Homo sapiens GN=ERP29 PE=1 SV=4												23	1
							183	192	538.3	1074.58	1074.53	0.05	0	60	8.50E-05	K.QGQDNLSSVK.E		17.32		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P62826	5%	69	1	24579	7	P62826|RAN_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3												26	1
							13	23	508.27	1014.52	1014.57	-0.05	0	41	7.20E-03	K.LVLVGDGGTGK.T		18.52		
beads (5 days), [ST11]	P62826	5%	48	1	24579	7	P62826|RAN_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3												22	1
							13	23	508.27	1014.52	1014.57	-0.05	0	45	2.80E-03	K.LVLVGDGGTGK.T		19.78		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P06396	1%	97	1	86043	5.9	P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1												19	1
							361	368	441.66	881.31	881.45	-0.14	0	31	4.40E-02	K.TASDFITK.M		14.66		
beads (3 hours), [ST9]	P06396	1%	55	1	86043	5.9	P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1												5	1
							616	623	444.25	886.49	886.49	0.01	0	39	1.20E-02	K.TGAQELLR.V		15.98		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q9UBI6	15%	49	1	8115	9.1	Q9UBI6|GBG12_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3												45	1
							5	15	573.76	1145.5	1145.58	-0.08	0	49	9.40E-04	K.TASTNNIAQAR.R		12.57		
beads (3 days), [ST10]	Q9UBI6	15%	85	1	8115	9.1	Q9UBI6|GBG12_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3												36	1
							5	15	573.82	1145.63	1145.58	0.05	0	69	9.50E-06	K.TASTNNIAQAR.R		17.18		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q92598	1%	61	1	97716	5.3	Q92598|HS105_HUMAN Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1												6	2
							462	471	560.3	1118.59	1118.61	-0.02	0	33	3.90E-02	R.FVVQNVSAQK.D		15.34		
beads (5 days), [ST11]	Q92598	1%	101	1	97716	5.3	Q92598|HS105_HUMAN Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1												3	1
							462	471	560.3	1118.6	1118.61	-0.01	0	44	3.00E-03	R.FVVQNVSAQK.D		16.3		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q16543	2%	39	1	44953	5.2	Q16543|CDC37_HUMAN Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1												13	1
							84	92	528.77	1055.52	1055.57	-0.05	0	39	1.10E-02	R.LQAEAQQLR.K		13.3		
beads (5 days), [ST11]	Q16543	2%	45	1	44953	5.2	Q16543|CDC37_HUMAN Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1												11	1
							84	92	528.79	1055.56	1055.57	-0.01	0	42	4.70E-03	R.LQAEAQQLR.K		13.79		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9Y4L1	1%	159	1	111494	5.2	Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1												3	2
							283	291	524.33	1046.65	1046.55	0.09	0	46	2.30E-03	R.LAGLFNEQR.K		28.21		
beads (3 hours), [ST9]	Q9Y4L1	1%	145	1	111494	5.2	Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1												2	2
							283	291	524.27	1046.52	1046.55	-0.03	0	49	9.20E-04	R.LAGLFNEQR.K		20.48		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	Q04760	5%	77	1	20992	5.1	Q04760|LGUL_HUMAN Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4												22	1
							29	38	640.84	1279.66	1279.66	0	0	37	1.50E-02	K.DFLLQQTMLR.V	Oxidation (M)	21.55		
beads (5 days), [ST11]	Q04760	5%	69	1	20992	5.1	Q04760|LGUL_HUMAN Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4												23	1
							29	38	640.86	1279.7	1279.66	0.04	0	68	1.00E-05	K.DFLLQQTMLR.V	Oxidation (M)	21.47		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P13473	2%	105	1	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												16	3
							153	161	526.17	1050.32	1050.5	-0.18	0	58	7.40E-05	R.CNSLSTLEK.N		14.22		
beads (5 days), [ST11]	P13473	2%	87	1	45503	5.3	P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2												2	1
							153	161	526.26	1050.5	1050.5	0	0	55	2.10E-04	R.CNSLSTLEK.N		15.64		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	Q99571	5%	136	1	44139	8.3	Q99571|P2RX4_HUMAN P2X purinoceptor 4 OS=Homo sapiens GN=P2RX4 PE=2 SV=2												1	2
							128	148	660.67	1978.98	1978.84	0.14	0	89	7.30E-08	K.SDASCTAGSAGTHSNGVSTGR.C		18.18		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q06830	4%	78	1	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												21	1
							121	128	447.69	893.37	893.42	-0.06	0	53	3.30E-04	K.ADEGISFR.G		20.53		
beads (3 days), [ST10]	Q06830	6%	82	1	22324	8.3	Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1												27	2
							17	27	590.8	1179.59	1179.56	0.03	0	46	1.70E-03	K.ATAVMPDGQFK.D	Oxidation (M)	22		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q8NC51	4%	50	1	44995	8.7	Q8NC51|PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2												12	1
							53	68	730.85	1459.69	1459.7	-0.01	0	51	6.10E-04	K.SAAQAAAQTNSNAAGK.Q		12.12		
beads (5 days), [ST11]	Q8NC51	4%	106	1	44995	8.7	Q8NC51|PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2												10	1
							53	68	730.83	1459.65	1459.7	-0.05	0	81	5.80E-07	K.SAAQAAAQTNSNAAGK.Q		12.34		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q06323	6%	139	1	28876	5.8	Q06323|PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1												25	1
							142	155	760.35	1518.69	1518.73	-0.04	0	95	2.40E-08	R.IEDGNNFGVAVQEK.V		19.29		
beads (5 days), [ST11]	Q06323	6%	90	1	28876	5.8	Q06323|PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1												19	1
							142	155	760.32	1518.62	1518.73	-0.11	0	72	4.60E-06	R.IEDGNNFGVAVQEK.V		20.27		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P25789	3%	62	1	29750	7.6	P25789|PSA4_HUMAN Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1												25	1
							9	17	504.25	1006.48	1006.51	-0.03	0	33	4.10E-02	R.TTIFSPEGR.L		19.12		

beads (5 days), [ST11]	P25789	3%	73	1	29750	7.6	P25789|PSA4_HUMAN Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1												19	1
							9	17	504.24	1006.46	1006.51	-0.05	0	44	2.90E-03	R.TTIFSPEGR.L		20.41		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P49721	5%	51	1	22993	6.5	P49721|PSB2_HUMAN Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1												28	1
							20	29	538.77	1075.52	1075.57	-0.05	0	51	6.40E-04	R.VAASNIVQMK.D	Oxidation (M)	13.38		
beads (5 days), [ST11]	P49721	5%	71	1	22993	6.5	P49721|PSB2_HUMAN Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1												23	1
							20	29	538.81	1075.6	1075.57	0.03	0	71	5.60E-06	R.VAASNIVQMK.D	Oxidation (M)	14.02		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q15084	4%	45	1	48490	5	Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1												13	1
							393	409	808.53	1615.05	1614.84	0.21	0	37	1.50E-02	R.GSTAPVGGGAFPTIVER.E		30.79		
beads (3 hours), [ST9]	Q15084	4%	78	1	48490	5	Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1												11	1
							393	409	808.41	1614.81	1614.84	-0.03	0	48	9.50E-04	R.GSTAPVGGGAFPTIVER.E		21.22		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P50454	3%	81	1	46525	8.8	P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2												12	1
							394	405	647.32	1292.62	1292.67	-0.05	0	81	6.00E-07	R.DTQSGSLLFIGR.L		21.68		
beads (3 days), [ST10]	P50454	3%	41	1	46525	8.8	P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2												13	1
							394	405	647.44	1292.87	1292.67	0.2	0	41	6.00E-03	R.DTQSGSLLFIGR.L		35.45		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9H9B4	4%	50	1	35881	9.2	Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4												20	1
							203	214	635.95	1269.89	1269.63	0.26	0	50	6.00E-04	K.VGIPVTDENGNR.L		24.87		
beads (3 hours), [ST9]	Q9H9B4	4%	49	1	35881	9.2	Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4												18	1
							203	214	635.79	1269.57	1269.63	-0.06	0	49	8.70E-04	K.VGIPVTDENGNR.L		17.28		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q86Y82	3%	80	1	31736	5.5	Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1												18	1
							36	44	480.33	958.65	958.54	0.11	0	44	3.30E-03	R.ISQATAQIK.N		18.82		
beads (3 days), [ST10]	Q86Y82	3%	58	1	31736	5.5	Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1												18	1
							36	44	480.3	958.59	958.54	0.05	0	35	3.10E-02	R.ISQATAQIK.N		21.93		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q14956	2%	40	1	64623	6.2	Q14956|GPNMB_HUMAN Transmembrane glycoprotein NMB OS=Homo sapiens GN=GPNMB PE=1 SV=2												10	2
							219	227	494.8	987.59	987.58	0.02	0	40	9.40E-03	R.AYVPIAQVK.D		19.69		
beads (3 hours), [ST9]	Q14956	2%	40	1	64623	6.2	Q14956|GPNMB_HUMAN Transmembrane glycoprotein NMB OS=Homo sapiens GN=GPNMB PE=1 SV=2												17	3
							219	227	494.78	987.56	987.58	-0.02	0	40	9.00E-03	R.AYVPIAQVK.D		19.79		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P38606	2%	45	1	68660	5.3	P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2												9	2
							309	323	766.48	1530.95	1530.78	0.17	0	38	9.90E-03	R.TALVANTSNMPVAAR.E	Oxidation (M)	21.77		
beads (5 days), [ST11]	P38606	2%	160	1	68660	5.3	P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2												7	1
							309	323	766.38	1530.75	1530.78	-0.03	0	86	1.70E-07	R.TALVANTSNMPVAAR.E	Oxidation (M)	14.65		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P12955	2%	41	1	55311	5.6	P12955|PEPD_HUMAN Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3												12	1
							18	27	557.35	1112.68	1112.67	0.01	0	43	4.00E-03	K.VPLALFALNR.Q		22.1		
beads (5 days), [ST11]	P12955	2%	46	1	55311	5.6	P12955|PEPD_HUMAN Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3												10	1
							18	27	557.33	1112.66	1112.67	-0.02	0	47	1.50E-03	K.VPLALFALNR.Q		22.32		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q16698	4%	65	1	36330	9.3	Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1												20	1
							61	73	589.34	1176.67	1176.65	0.02	0	33	4.20E-02	K.VAFITGGGTGLGK.G		19.81		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	Q99714	5%	37	1	27134	7.7	Q99714|HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3												20	1
							173	184	600.84	1199.67	1199.67	0	0	37	1.40E-02	K.GGIVGMTLPIAR.D	Oxidation (M)	20.22		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P62851	8%	67	1	13791	10.1	P62851|RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1												31	1
							67	76	542.83	1083.65	1083.63	0.02	0	36	1.80E-02	K.LITPAVVSER.L		26.12		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P62701	3%	61	1	29807	10.2	P62701|RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2												18	1
							222	230	495.79	989.56	989.59	-0.03	0	61	7.40E-05	R.LSNIFVIGK.G		21.08		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P05388	4%	46	1	34423	5.7	P05388|RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1												13	1
							135	146	657.36	1312.7	1312.7	0	0	43	3.50E-03	K.TSFFQALGITTK.I		22.86		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P56385	14%	47	1	7928	9.3	P56385|ATP5I_HUMAN ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=2 SV=2												45	1
							60	69	566.75	1131.49	1131.57	-0.08	0	47	1.50E-03	R.ELAEDDSILK.-		19.41		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q13510	3%	40	1	45077	7.5	Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4												43	1
							82	92	612.2	1222.39	1222.6	-0.22	0	40	6.40E-03	K.NMINTFVPSGK.V	Oxidation (M)	18.38		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P14868	2%	52	1	57499	6.1	P14868|SYDC_HUMAN Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2												12	1
							321	330	604.31	1206.6	1206.62	-0.02	0	33	3.50E-02	R.FQTEIQTVNK.Q		16.09		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q13884	2%	46	1	58367	8.8	Q13884|SNTB1_HUMAN Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3												10	1
							254	263	560.31	1118.6	1118.5	0.1	0	46	2.20E-03	R.SMALADPENR.Q	Oxidation (M)	19.72		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P07858	2%	51	1	38766	5.9	P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3												19	2
							238	245	499.73	997.44	997.48	-0.04	0	36	2.00E-02	K.DIMAEIYK.N	Oxidation (M)	19.42		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9UBR2	3%	67	1	34530	6.7	Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1												19	1
							190	199	505.79	1009.56	1009.48	0.08	0	55	1.80E-04	R.VGDYGSLSGR.E		22.63		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	P31146	2%	79	1	51678	6.3	P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4												25	1
							440	449	579.22	1156.43	1156.65	-0.21	0	57	1.60E-04	K.LQATVQELQK.R		14.69		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q16555	2%	105	1	62711	6	Q16555|DPYL2_HUMAN Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1												24	1
							259	268	516.2	1030.39	1030.54	-0.15	0	36	2.30E-02	K.SSAEVIAQAR.K		13.12		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	O94905	4%	76	1	38044	5.5	O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1												15	1
							221	232	653.84	1305.66	1305.69	-0.03	0	76	1.60E-06	K.VAQVAEITYGQK.V		18.68		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P27105	4%	122	1	31882	7.7	P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3												16	4
							221	232	632.3	1262.59	1262.59	0	0	60	8.10E-05	K.VIAAEGEMNASR.A	Oxidation (M)	13.25		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P15311	1%	85	1	69484	5.9	P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4												4	1
							364	371	501.76	1001.51	1001.51	-0.01	0	39	1.20E-02	R.ELSEQIQR.A		14.66		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P09382	6%	78	1	15048	5.3	P09382|LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2												35	1
							101	108	484.75	967.49	967.47	0.03	0	39	8.70E-03	K.LPDGYEFK.F		26.19		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P78417	6%	45	1	27833	6.2	P78417|GSTO1_HUMAN Glutathione transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2												19	1
							12	25	660.84	1319.66	1319.68	-0.02	0	32	4.90E-02	K.GSAPPGPVPEGSIR.I		16.03		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	O00461	2%	58	1	81888	4.7	O00461|GOLI4_HUMAN Golgi integral membrane protein 4 OS=Homo sapiens GN=GOLIM4 PE=1 SV=1												4	1
							416	428	756.39	1510.76	1510.81	-0.05	0	58	1.10E-04	R.LAVQQVEEAQQLR.E		20.08		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q14789	0%	46	1	377215	5	Q14789|GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2												6	1
							2082	2093	659.3	1316.59	1316.66	-0.06	0	44	3.30E-03	K.VLLDDTQSEAAR.V		16.29		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P34932	1%	50	1	95127	5.1	P34932|HSP74_HUMAN Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4												6	1
							755	764	567.28	1132.55	1132.58	-0.03	0	42	5.60E-03	K.QSLTMDPVVK.S	Oxidation (M)	14.6		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P04792	5%	84	1	22826	6	P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2												24	1
							80	89	538.32	1074.63	1074.57	0.06	0	62	5.50E-05	R.QLSSGVSEIR.H		24.28		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q7LGA3	3%	124	1	42140	8.8	Q7LGA3|HS2ST_HUMAN Heparan sulfate 2-O-sulfotransferase 1 OS=Homo sapiens GN=HS2ST1 PE=2 SV=1												13	2
							112	123	708.84	1415.66	1415.68	-0.02	0	58	1.00E-04	K.NNPVMSLQDQVR.F	Oxidation (M)	19.48		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q14974	1%	100	1	98420	4.7	Q14974|IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2												19	1
							43	54	613.25	1224.48	1224.66	-0.18	0	61	5.50E-05	R.VLANPGNSQVAR.V		12.96		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P05556	2%	52	1	91714	5.3	P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=1												4	1
							191	202	662.82	1323.63	1323.67	-0.04	0	48	1.20E-03	K.TVMPYISTTPAK.L	Oxidation (M)	17.04		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P40121	3%	81	1	38779	5.9	P40121|CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=1												16	1
							254	265	640.88	1279.75	1279.61	0.14	0	69	8.80E-06	K.VSDATGQMNLTK.V	Oxidation (M)	19.51		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P40925	3%	43	1	36631	6.9	P40925|MDHC_HUMAN Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4												19	1
							171	179	458.76	915.51	915.5	0	0	38	1.50E-02	K.LGVTANDVK.N		13.74		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q14697	1%	153	1	107263	5.7	Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3												6	1
							158	164	437.22	872.43	872.46	-0.03	0	36	2.40E-02	R.LDLLEDR.S		20.08		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q92542	2%	114	1	79103	5.7	Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2												13	1
							486	496	543.24	1084.46	1084.62	-0.16	0	37	1.70E-02	K.ALADVATVLGR.A		20.47		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	P00558	2%	52	1	44985	8.3	P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3												14	1
							354	361	460.75	919.48	919.47	0.02	0	38	1.20E-02	K.ALMDEVVK.A	Oxidation (M)	22.37		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	Q8WUM4	1%	49	1	96590	6.1	Q8WUM4|PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1												5	1
							340	350	585.31	1168.61	1168.65	-0.04	0	39	8.40E-03	K.STPVNVPISQK.F		16.09		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P35232	4%	62	1	29843	5.6	P35232|PHB_HUMAN Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1												25	1
							134	143	575.27	1148.53	1148.58	-0.05	0	39	9.40E-03	R.FDAGELITQR.E		20.39		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found

BCG (5 days), [ST8]	Q99623	3%	69	1	33276	9.8	Q99623|PHB2_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2												16	1
							148	157	589.31	1176.6	1176.63	-0.03	0	69	1.00E-05	K.FNASQLITQR.A		20.28		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	P30101	3%	63	1	57146	6	P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4												7	1
							367	379	684.88	1367.74	1367.66	0.08	0	32	4.30E-02	K.SEPIPESNDGPVK.V		15.81		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P61019	7%	154	1	23702	6.1	P61019|RAB2A_HUMAN Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1												22	1
							152	165	747.88	1493.75	1493.74	0.01	0	66	1.70E-05	K.TASNVEEAFINTAK.E		20.8		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P34897	2%	62	1	56414	8.8	P34897|GLYM_HUMAN Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3												10	1
							360	368	503.24	1004.46	1004.5	-0.03	0	36	2.30E-02	R.AMADALLER.G	Oxidation (M)	18.14		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, a), [ST6]	Q9UJZ1	4%	38	2	38624	6.9	Q9UJZ1|STML2_HUMAN Stomatin-like protein 2 OS=Homo sapiens GN=STOML2 PE=1 SV=1												16	1
							322	337	757.97	1513.92	1513.74	0.18	0	38	9.90E-03	K.APVPGTPDSLSSGSSR.D		27.35		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P04179	6%	103	1	24878	8.3	P04179|SODM_HUMAN Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2												28	1
							76	89	712.87	1423.73	1423.8	-0.08	0	66	1.60E-05	K.GDVTAQIALQPALK.F		20.21		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	Q99536	4%	38	1	42122	5.9	Q99536|VAT1_HUMAN Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2												14	1
							256	271	795.85	1589.69	1589.76	-0.07	0	32	4.20E-02	K.GVDIVMDPLGGSDTAK.G	Oxidation (M)	18.63		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P06753	5%	83	1	32856	4.7	P06753|TPM3_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1												21	1
							78	90	658.8	1315.58	1315.64	-0.06	0	33	3.70E-02	K.AADAEAEVASLNR.R		16.9		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P54577	2%	64	1	59448	6.6	P54577|SYYC_HUMAN Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4												9	1
							392	400	493.24	984.46	984.49	-0.03	0	35	2.40E-02	K.IDVGEAEPR.T		14.87		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 hours), [ST4]	Q6IAA8	7%	43	1	17848	5	Q6IAA8|CK059_HUMAN UPF0404 protein C11orf59 OS=Homo sapiens GN=C11orf59 PE=1 SV=2												26	1
							21	31	584.29	1166.56	1166.65	-0.09	0	43	3.10E-03	K.LLLDPSSPPTK.A		21.23		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P53990	2%	56	1	39897	5.2	P53990|K0174_HUMAN Uncharacterized protein KIAA0174 OS=Homo sapiens GN=KIAA0174 PE=1 SV=1												12	1
							110	118	508.76	1015.51	1015.55	-0.04	0	56	2.30E-04	R.LQSEVAELK.I		15.99		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (1 day), [ST5]	Q8IYS2	1%	48	1	69684	8.4	Q8IYS2|K2013_HUMAN Uncharacterized protein KIAA2013 OS=Homo sapiens GN=KIAA2013 PE=2 SV=1												24	1
							206	214	542.71	1083.4	1083.57	-0.17	0	48	1.20E-03	R.IQLNNPTER.V		14.26		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	P61421	4%	69	1	40759	4.9	P61421|VA0D1_HUMAN Vacuolar proton pump subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1												15	1
							276	288	652.81	1303.6	1303.64	-0.05	0	60	7.90E-05	K.LLFEGAGSNPGDK.T		19.97		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	P49748	2%	75	1	70745	8.9	P49748|ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1												10	1
							460	469	589.28	1176.55	1176.61	-0.07	0	36	1.90E-02	R.IFEGTNDILR.L		20.31		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (3 days, b), [ST7]	O75083	2%	55	1	66836	6.2	O75083|WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4												10	1
							29	38	564.25	1126.49	1126.54	-0.05	0	34	2.70E-02	K.GNNFLYTNGK.C		18.56		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
BCG (5 days), [ST8]	Q15942	2%	47	1	62436	6.2	Q15942|ZYX_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1												7	1
							254	265	538.77	1075.53	1075.57	-0.04	0	47	1.50E-03	R.GPPASSPAPAPK.F		12.81		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 hours), [ST9]	P62263	7%	80	1	16434	10.1	P62263|RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3												31	1
							107	117	527.72	1053.43	1053.56	-0.13	0	80	5.90E-07	K.TPGPGAQSALR.A		14.48		
beads (3 days), [ST10]	P62263	7%	49	1	16434	10.1	P62263|RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3												31	1
							107	117	527.82	1053.62	1053.56	0.06	0	49	8.00E-04	K.TPGPGAQSALR.A		19.2		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 hours), [ST9]	P02649	5%	41	1	36246	5.7	P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1												17	1
							210	224	749.4	1496.79	1496.79	-0.01	0	34	2.50E-02	R.AATVGSLAGQPLQER.A		20.13		
beads (5 days), [ST11]	P02649	3%	59	1	36246	5.7	P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1												16	2
							199	207	484.74	967.47	967.55	-0.08	0	45	2.00E-03	R.LGPLVEQGR.V		19.33		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 hours), [ST9]	P16278	2%	37	1	76499	6.1	P16278|BGAL_HUMAN Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=1												8	1
							286	299	754.9	1507.78	1507.79	-0.01	0	37	1.50E-02	K.TEAVASSLYDILAR.G		23.37		
beads (3 days), [ST10]	P16278	2%	108	1	76499	6.1	P16278|BGAL_HUMAN Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=1												9	1
							286	299	754.93	1507.85	1507.79	0.06	0	60	6.70E-05	K.TEAVASSLYDILAR.G		39.02		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P07686	2%	82	1	63527	6.3	P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3												20	1
							391	400	550.34	1098.66	1098.66	0	0	56	1.90E-04	K.VLDIIATINK.G		21.55		
Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	P39656	3%	138	1	48893	5.4	P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2												13	1
							61	71	580.36	1158.71	1158.61	0.1	0	43	4.00E-03	K.TADDPSLSLIK.Y		32.58		
beads (5 days), [ST11]	P39656	1%	45	1	48893	5.4	P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2												10	2
							343	348	373.71	745.4	745.41	-0.01	0	41	7.90E-03	R.IDPFVR.T		19.99		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 hours), [ST9]	Q9HAT2	2%	57	1	58961	6.9	Q9HAT2|SIAE_HUMAN Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=2 SV=1												21	1
							142	153	669.77	1337.53	1337.66	-0.13	0	57	1.30E-04	R.ELSNTAAYQSVR.I		17.14		
beads (3 days), [ST10]	Q9HAT2	2%	63	1	58961	6.9	Q9HAT2|SIAE_HUMAN Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=2 SV=1												23	1
							142	153	669.87	1337.72	1337.66	0.06	0	63	3.80E-05	R.ELSNTAAYQSVR.I		23.31		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 hours), [ST9]	P40939	1%	71	1	83688	9.2	P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2												6	1
							561	569	499.79	997.57	997.54	0.03	0	50	6.70E-04	R.ILQEGVDPK.K		14.88		
beads (3 days), [ST10]	P40939	2%	146	1	83688	9.2	P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2												7	1
							520	531	559.84	1117.66	1117.6	0.07	0	47	1.50E-03	K.DTSASAVAVGLK.Q		33.29		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P62241	6%	74	1	24475	10.3	P62241|RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2												20	1
							158	170	753.9	1505.79	1505.77	0.02	0	74	3.00E-06	K.ISSLLEEQFQQGK.L		20.85		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P46781	4%	51	1	22635	10.7	P46781|RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3												23	1
							84	91	415.74	829.47	829.45	0.01	0	47	1.90E-03	R.IGVLDEGK.M		17.37		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 hours), [ST9]	P48047	5%	81	1	23377	10	P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1												24	1
							74	84	580.8	1159.58	1159.66	-0.08	0	32	4.60E-02	K.VAASVLNPYVK.R		21.39		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P80723	6%	44	1	22680	4.6	P80723|BASP_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2												10	2
							185	198	693.82	1385.63	1385.67	-0.04	0	44	3.00E-03	K.ETPAATEAPSSTPK.A		13.25		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	P31930	3%	68	1	53297	5.9	P31930|QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3												13	1
							379	390	662.35	1322.69	1322.61	0.07	0	55	2.20E-04	R.LCTSATESEVAR.G		23.06		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	P09622	2%	112	1	54686	7.6	P09622|DLDH_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=1												11	1
							167	177	552.82	1103.63	1103.55	0.08	0	75	2.50E-06	K.ADGGTQVIDTK.N		22.32		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P49327	0%	124	1	275850	6	P49327|FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=2												1	1
							1073	1082	522.3	1042.58	1042.58	0	0	32	4.70E-02	K.AQVADVVVSR.W		16.41		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	P00338	3%	52	1	36950	8.4	P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2												19	1
							306	315	567.8	1133.59	1133.56	0.04	0	34	2.90E-02	K.VTLTSEEEAR.L		25.29		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P08575	1%	89	1	148644	5.8	P08575|CD45_HUMAN Leukocyte common antigen OS=Homo sapiens GN=PTPRC PE=1 SV=2												1	1
							1134	1143	588.33	1174.65	1174.66	-0.01	0	57	1.50E-04	K.ELISMIQVVK.Q	Oxidation (M)	20.68		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	O60488	2%	62	1	80220	8.7	O60488|ACSL4_HUMAN Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2												7	1
							100	113	817.41	1632.8	1632.73	0.07	0	34	2.60E-02	R.EILSEENEMQPNGK.V	Oxidation (M)	25.73		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P61626	8%	107	1	16982	9.4	P61626|LYSC_HUMAN Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1												6	1
							69	80	700.84	1399.67	1399.67	0	0	51	5.30E-04	R.STDYGIFQINSR.Y		21.3		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 hours), [ST9]	P22307	2%	74	1	59640	6.4	P22307|NLTP_HUMAN Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2												34	1
							512	522	635.76	1269.5	1269.58	-0.08	0	58	1.10E-04	K.MNPQSAFFQGK.L	Oxidation (M)	20.85		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P50897	3%	40	1	34627	6.1	P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1												18	1
							166	174	462.74	923.46	923.47	-0.01	0	40	6.10E-03	K.TLNAGAYSK.V		13.63		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P28070	4%	62	1	29242	5.7	P28070|PSB4_HUMAN Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4												22	1
							202	211	564.77	1127.52	1127.59	-0.08	0	61	6.20E-05	K.QPVLSQTEAR.D		14.44		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P51148	6%	68	1	23696	8.6	P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2												22	2
							185	196	606.26	1210.5	1210.57	-0.07	0	39	8.00E-03	K.NEPQNATGAPGR.N		12.83		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	P55084	2%	104	1	51547	9.4	P55084|ECHB_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3												13	1
							62	72	607.37	1212.72	1212.64	0.08	0	52	4.90E-04	R.TPFLLSGTSYK.D		34.11		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (5 days), [ST11]	P08670	2%	39	1	53676	5.1	P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4												9	1
							295	304	547.26	1092.51	1092.52	-0.01	0	39	8.10E-03	K.FADLSEAANR.N		18.55		

Experiment [Suppl. Table #]	accession #	coverage	score	distinct peptides	mass	pI	start AA	end AA	m/z obs	M obs	M calc	delta	miss	pept score	exp val	peptide	modifications	retent time	Strongest gel slice	# gel slices found
beads (3 days), [ST10]	P45880	3%	111	1	32060	7.5	P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2												20	1
							268	277	508.82	1015.63	1015.59	0.04	0	62	5.30E-05	K.LTLSALVDGK.S		35.85		

Footnotes to Supplemental Table 12:

* All single-peptide based protein assignments underwent a BLAST Search (www.expasy.org) to check for a unique peptide sequences; in a few cases another possible protein isoform is indicated (protein homolog)

Data sets were searched with the Mascot search engine (see Perkins et al. (1999) *Electrophoresis* **20**, 3551-3567).
Detailed are the SwissProt accession number, the number of distinct proteolytic peptides (in all cases "1"), and the sequence coverage of the protein (%).

Listed is the Mascot protein score as well as the score and expectation value for the individual peptide.
Further columns indicate the position of the protein in the 1D-SDS PAGE gel (strongest lane in which the protein was identified, and the total # of adjacent gel lanes in which the protein was found)

Supplemental Document: MS/MS spectra of all single-peptide based protein assignments and fragment ion mass table extracted from the MASCOT search engine results reports.

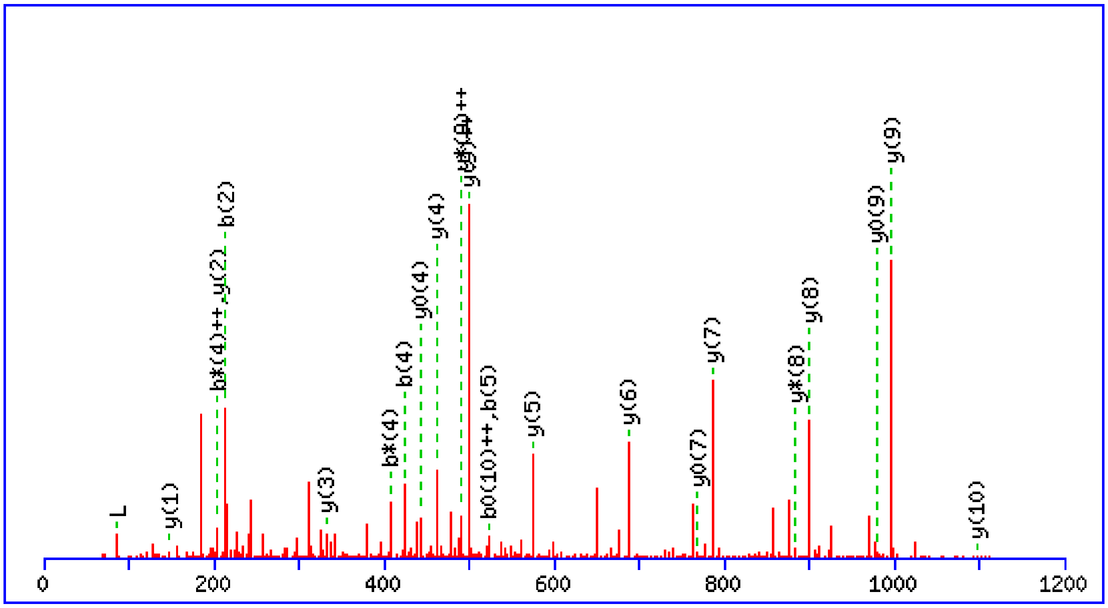
Additional Information and mass spectrometric details can be found in Supplemental Table 12.

For single-peptide based protein assignment criteria see the “Methods” section of the main manuscript. As additional criteria, we required that each specific protein identified by a single-peptide based protein assignment be observed in more than one independent biological experiment either as part of a regular protein assignment observed together with multiple other peptides for that specific protein, or as another single-peptide based protein assignment.

MS/MS Fragmentation of **IVPNVLLEQGK**

Found in **O75390**, O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2

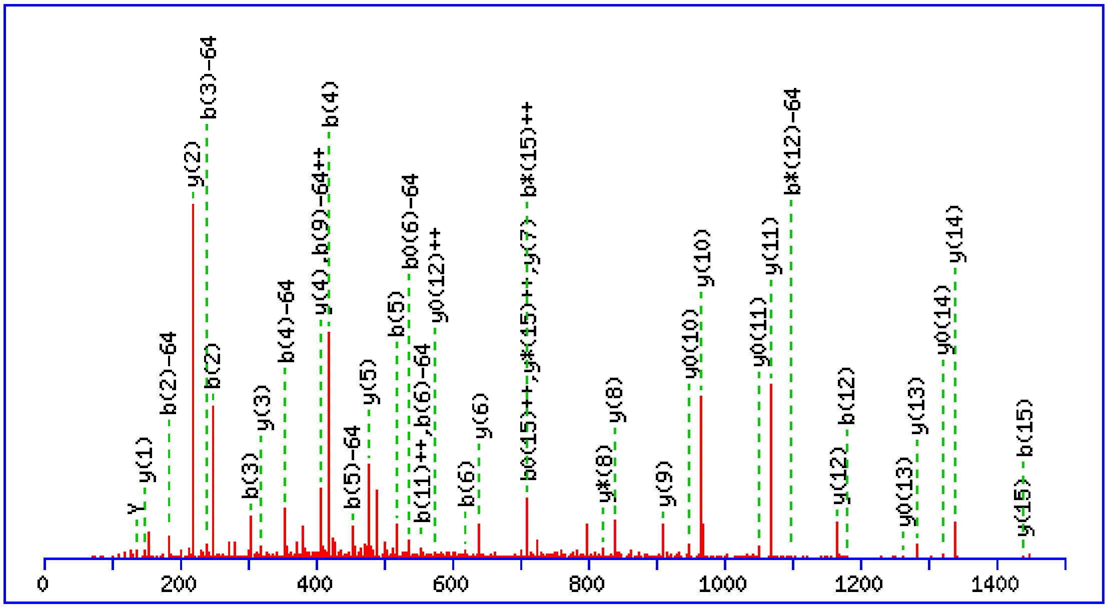
Match to Query 482: 1208.698618 from(605.356585,2+)



Monoisotopic mass of neutral peptide Mr(calc): 1208.7129
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.00068
Matches (Bold Red): 25/105 fragment ions using 76 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							11
2	72.0808	**213.1598**	107.0835					V	**1096.6361**	548.8217	1079.6095	540.3084	1078.6255	539.8164	10
3	70.0651	310.2125	155.6099					P	**997.5677**	**499.2875**	980.5411	**490.7742**	**979.5571**	490.2822	9
4	87.0553	**424.2554**	212.6314	**407.2289**	**204.1181**			N	**900.5149**	450.7611	**883.4884**	442.2478	882.5043	441.7558	8
5	72.0808	**523.3239**	262.1656	506.2973	253.6523			V	**786.4720**	393.7396	769.4454	385.2264	**768.4614**	384.7343	7
6	**86.0964**	636.4079	318.7076	619.3814	310.1943			L	**687.4036**	344.2054	670.3770	335.6921	669.3930	335.2001	6
7	**86.0964**	749.4920	375.2496	732.4654	366.7364			L	**574.3195**	287.6634	557.2930	279.1501	556.3089	278.6581	5
8	102.0550	878.5346	439.7709	861.5080	431.2577	860.5240	430.7656	E	**461.2354**	231.1214	444.2089	222.6081	**443.2249**	222.1161	4
9	101.0709	1006.5932	503.8002	989.5666	495.2869	988.5826	494.7949	Q	**332.1928**	166.6001	315.1663	158.0868			3
10	30.0338	1063.6146	532.3109	1046.5881	523.7977	1045.6041	**523.3057**	G	**204.1343**	102.5708	187.1077	94.0575			2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **MVGDVTGAQAYASTAK**
Found in **Q01628**, Q01628|IFM3_HUMAN Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2
Match to Query 384: 1584.576544 from(793.295548,2+)



Monoisotopic mass of neutral peptide Mr(calc): 1584.7454

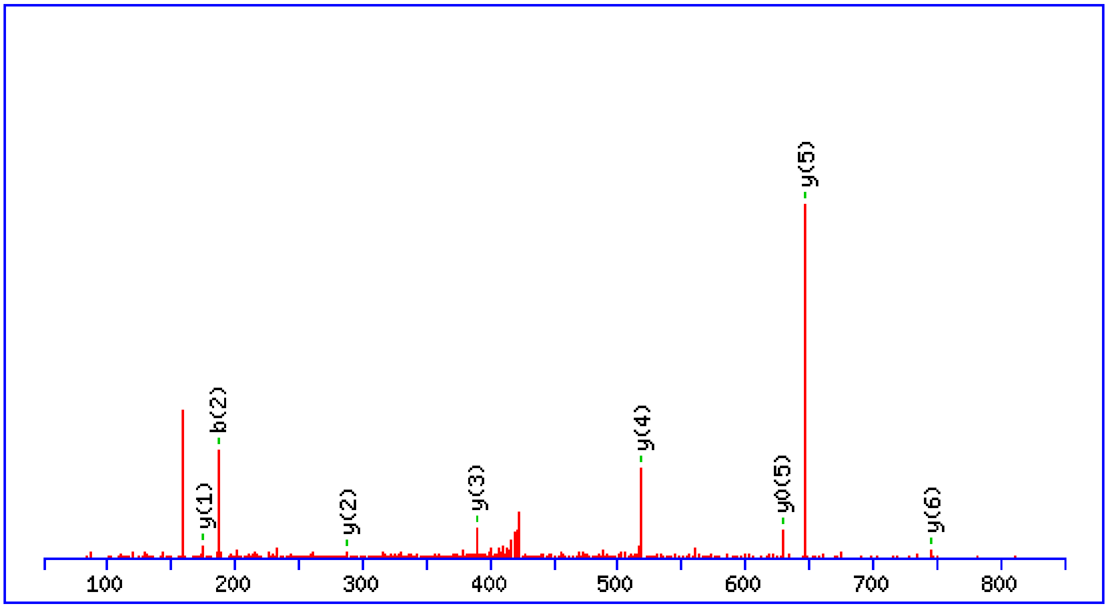
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 116 **Expect:** 1.5e-010
Matches (Bold Red): 41/239 fragment ions using 72 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	56.0495	84.0444	42.5258					M							16
2	72.0808	**183.1128**	92.0600					V	**1438.7173**	719.8623	1421.6907	**711.3490**	1420.7067	710.8570	15
3	30.0338	**240.1343**	120.5708					G	**1339.6488**	670.3281	1322.6223	661.8148	**1321.6383**	661.3228	14
4	88.0393	**355.1612**	178.0842			337.1507	169.0790	D	**1282.6274**	641.8173	1265.6008	633.3041	**1264.6168**	632.8120	13
5	72.0808	**454.2296**	227.6185			436.2191	218.6132	V	**1167.6004**	584.3039	1150.5739	575.7906	1149.5899	**575.2986**	12
6	74.0600	**555.2773**	278.1423			**537.2667**	269.1370	T	**1068.5320**	534.7696	1051.5055	526.2564	**1050.5215**	525.7644	11
7	30.0338	612.2988	306.6530			594.2882	297.6477	G	**967.4843**	484.2458	950.4578	475.7325	**949.4738**	475.2405	10
8	44.0495	683.3359	342.1716			665.3253	333.1663	A	**910.4629**	455.7351	893.4363	447.2218	892.4523	446.7298	9
9	101.0709	811.3945	**406.2009**	794.3679	397.6876	793.3839	397.1956	Q	**839.4258**	420.2165	**822.3992**	411.7032	821.4152	411.2112	8
10	44.0495	882.4316	441.7194	865.4050	433.2062	864.4210	432.7141	A	**711.3672**	356.1872	694.3406	347.6740	693.3566	347.1819	7
11	**136.0757**	1045.4949	523.2511	1028.4684	514.7378	1027.4843	514.2458	Y	**640.3301**	320.6687	623.3035	312.1554	622.3195	311.6634	6
12	44.0495	1116.5320	558.7696	**1099.5055**	550.2564	1098.5215	549.7644	A	**477.2667**	239.1370	460.2402	230.6237	459.2562	230.1317	5
13	60.0444	1203.5641	602.2857	1186.5375	593.7724	1185.5535	593.2804	S	**406.2296**	203.6185	389.2031	195.1052	388.2191	194.6132	4
14	74.0600	1304.6117	652.8095	1287.5852	644.2962	1286.6012	643.8042	T	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	3
15	44.0495	1375.6488	688.3281	1358.6223	679.8148	1357.6383	679.3228	A	**218.1499**	109.5786	201.1234	101.0653			2
16	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

Interferon-induced transmembrane protein 3 (Q01628): single-peptide could possibly also be assigned to
IFM1_HUMAN Interferon-induced transmembrane protein 1 (P13164) or
IFM2_HUMAN Interferon-induced transmembrane protein 2 (Q01629)

MS/MS Fragmentation of **SVEETLR**
Found in **P30048**, P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3

Match to Query 165: 832.414152 from(417.214352,2+)

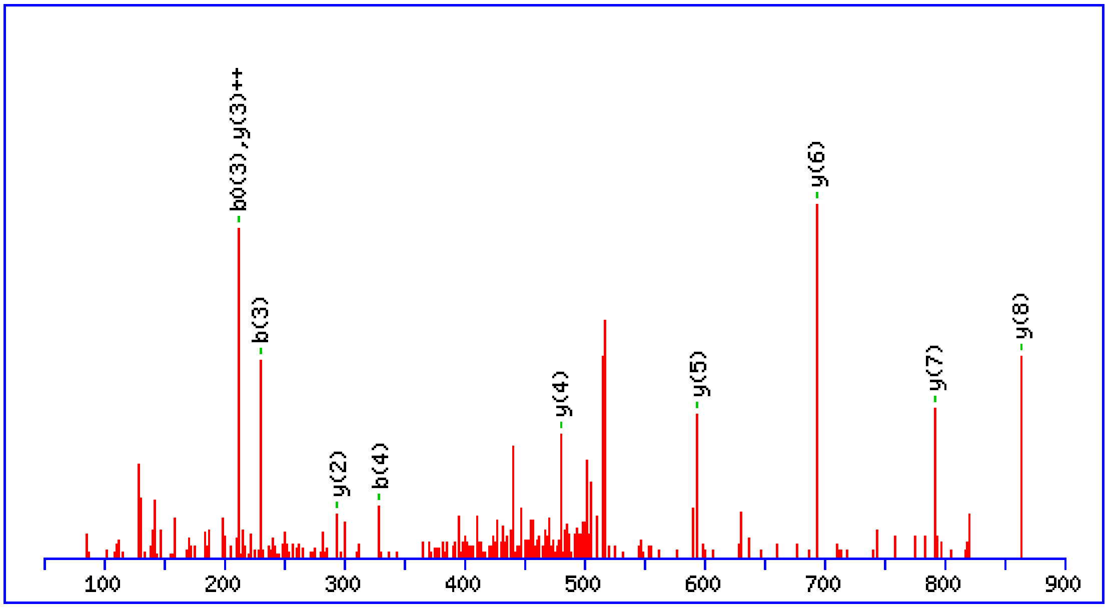


Monoisotopic mass of neutral peptide Mr(calc): 832.4290
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 **Expect:** 0.0055
Matches (Bold Red): 8/63 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233	70.0287	35.5180	S							7
2	72.0808	**187.1077**	94.0575	169.0972	85.0522	V	**746.4043**	373.7058	729.3777	365.1925	728.3937	364.7005	6
3	102.0550	316.1503	158.5788	298.1397	149.5735	E	**647.3359**	324.1716	630.3093	315.6583	**629.3253**	315.1663	5
4	102.0550	445.1929	223.1001	427.1823	214.0948	E	**518.2933**	259.6503	501.2667	251.1370	500.2827	250.6450	4
5	74.0600	546.2406	273.6239	528.2300	264.6186	T	**389.2507**	195.1290	372.2241	186.6157	371.2401	186.1237	3
6	86.0964	659.3246	330.1660	641.3141	321.1607	L	**288.2030**	144.6051	271.1765	136.0919			2
7	129.1135					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GTAVVNGEFK**
Found in **P30048**, P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3

Match to Query 218: 1020.450338 from(511.232445,2+)

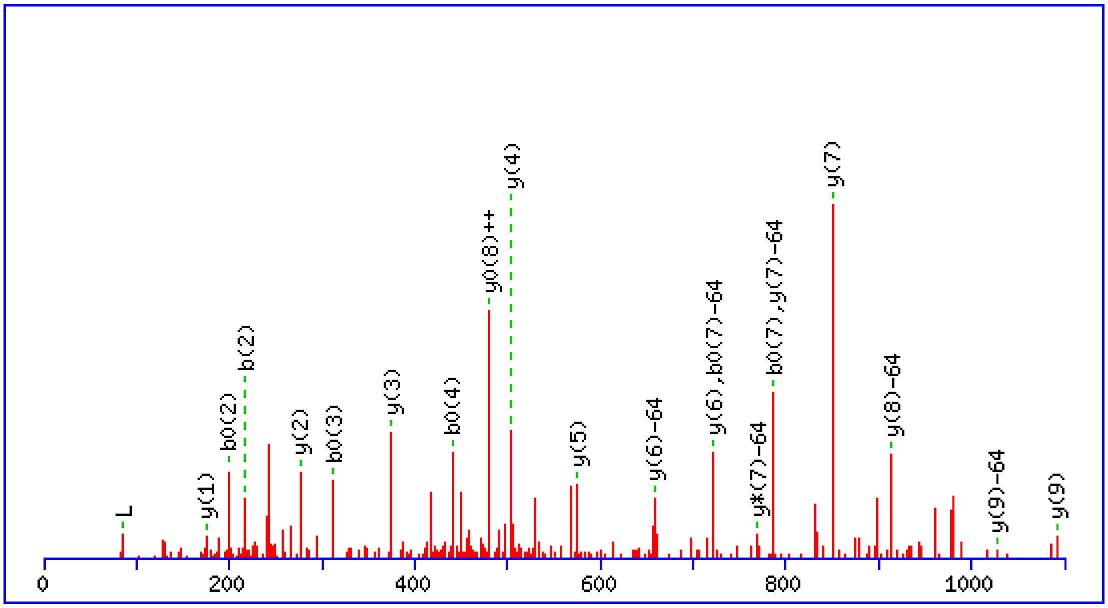


Monoisotopic mass of neutral peptide Mr(calc): 1020.5240
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 **Expect:** 0.0073
Matches (Bold Red): 10/102 fragment ions using 16 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180					G							10
2	74.0600	159.0764	80.0418			141.0659	71.0366	T	964.5098	482.7585	947.4833	474.2453	946.4993	473.7533	9
3	44.0495	**230.1135**	115.5604			**212.1030**	106.5551	A	**863.4621**	432.2347	846.4356	423.7214	845.4516	423.2294	8
4	72.0808	**329.1819**	165.0946			311.1714	156.0893	V	**792.4250**	396.7162	775.3985	388.2029	774.4145	387.7109	7
5	72.0808	428.2504	214.6288			410.2398	205.6235	V	**693.3566**	347.1819	676.3301	338.6687	675.3461	338.1767	6
6	87.0553	542.2933	271.6503	525.2667	263.1370	524.2827	262.6450	N	**594.2882**	297.6477	577.2617	289.1345	576.2776	288.6425	5
7	30.0338	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	G	**480.2453**	240.6263	463.2187	232.1130	462.2347	231.6210	4
8	102.0550	728.3573	364.6823	711.3308	356.1690	710.3468	355.6770	E	423.2238	**212.1155**	406.1973	203.6023	405.2132	203.1103	3
9	120.0808	875.4258	438.2165	858.3992	429.7032	857.4152	429.2112	F	**294.1812**	147.5942	277.1547	139.0810			2
10	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ESLQQMAEVTR**
Found in **P14314**, P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2

Match to Query 530: 1306.557494 from(654.286023,2+)

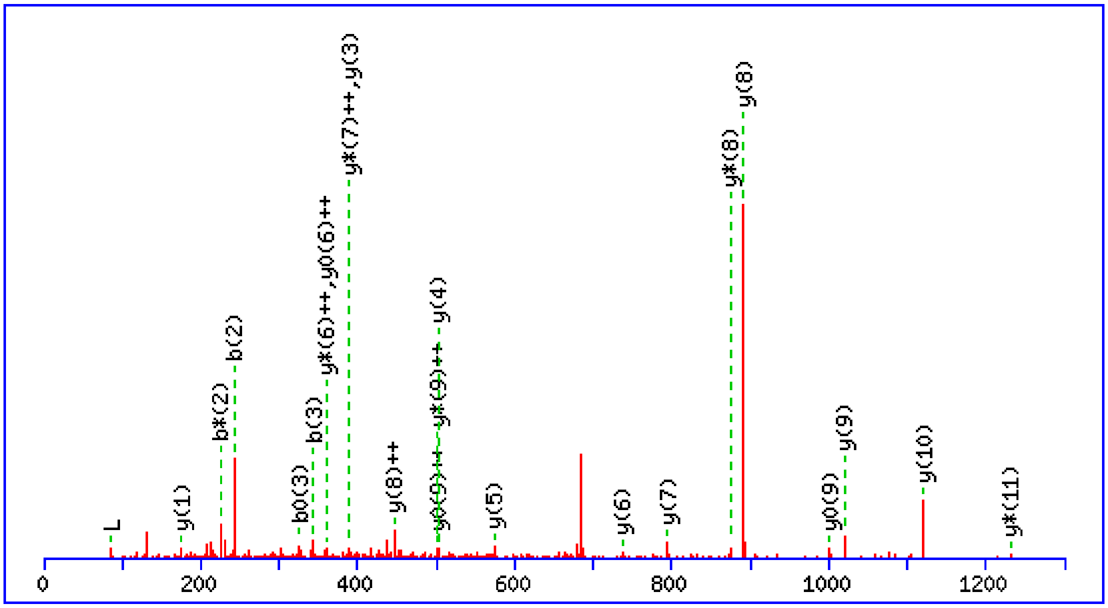


Monoisotopic mass of neutral peptide Mr(calc): 1306.6187
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 72 **Expect:** 4.5e-006
Matches (Bold Red): 21/184 fragment ions using 25 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286			112.0393	56.5233	E							11
2	60.0444	**217.0819**	109.0446			**199.0713**	100.0393	S	1114.5851	557.7962	1097.5586	549.2829	1096.5746	548.7909	10
3	**86.0964**	330.1660	165.5866			**312.1554**	156.5813	L	**1027.5531**	514.2802	1010.5265	505.7669	1009.5425	505.2749	9
4	101.0709	458.2245	229.6159	441.1980	221.1026	**440.2140**	220.6106	Q	**914.4690**	457.7382	897.4425	449.2249	896.4585	448.7329	8
5	101.0709	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	Q	**786.4104**	393.7089	**769.3839**	385.1956	768.3999	384.7036	7
6	56.0495	669.3202	335.1638	652.2937	326.6505	651.3097	326.1585	M	**658.3519**	329.6796	641.3253	321.1663	640.3413	320.6743	6
7	44.0495	740.3574	370.6823	723.3308	362.1690	**722.3468**	361.6770	A	**575.3148**	288.1610	558.2882	279.6477	557.3042	279.1557	5
8	102.0550	869.3999	435.2036	852.3734	426.6903	851.3894	426.1983	E	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	4
9	72.0808	968.4684	484.7378	951.4418	476.2245	950.4578	475.7325	V	**375.2350**	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	74.0600	1069.5160	535.2617	1052.4895	526.7484	1051.5055	526.2564	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
11	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IQTQPGYANTLR**
Found in **Q00325**, Q00325|MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2

Match to Query 378: 1360.875740 from(681.445146,2+)

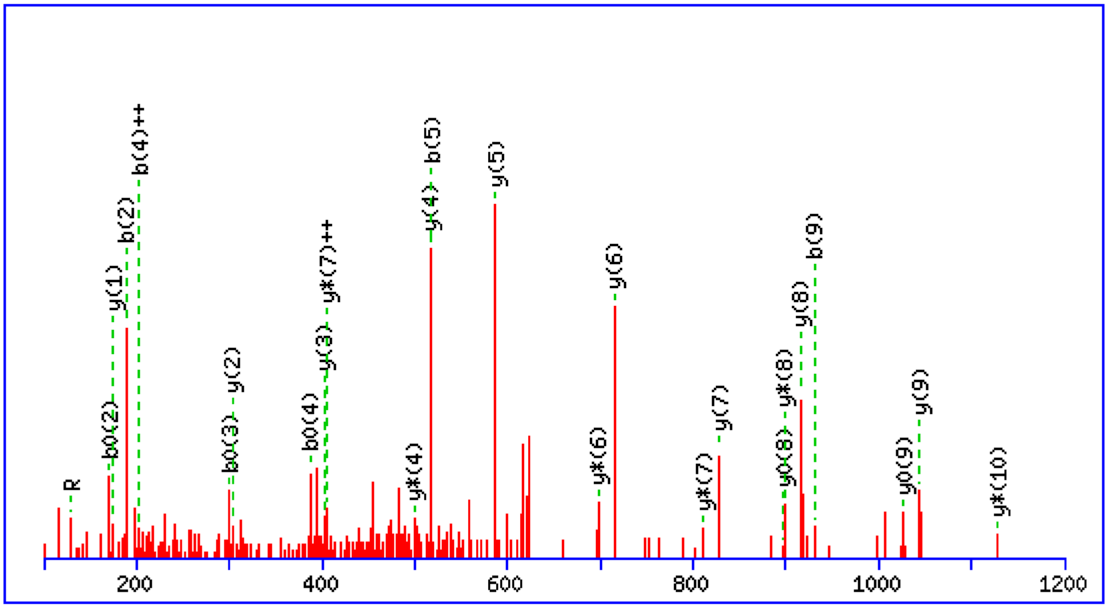


Monoisotopic mass of neutral peptide Mr(calc): 1360.7099
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00052
Matches (Bold Red): 24/134 fragment ions using 49 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**I**							**12**
2	101.0709	**242.1499**	121.5786	**225.1234**	113.0653			**Q**	1248.6331	624.8202	**1231.6066**	616.3069	1230.6226	615.8149	**11**
3	74.0600	**343.1976**	172.1024	326.1710	163.5892	**325.1870**	163.0972	**T**	**1120.5746**	560.7909	1103.5480	552.2776	1102.5640	551.7856	**10**
4	101.0709	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	**Q**	**1019.5269**	510.2671	1002.5003	**501.7538**	**1001.5163**	**501.2618**	**9**
5	70.0651	568.3089	284.6581	551.2824	276.1448	550.2984	275.6528	**P**	**891.4683**	**446.2378**	**874.4417**	437.7245	873.4577	437.2325	**8**
6	30.0338	625.3304	313.1688	608.3039	304.6556	607.3198	304.1636	**G**	**794.4155**	397.7114	777.3890	**389.1981**	776.4050	388.7061	**7**
7	136.0757	788.3937	394.7005	771.3672	386.1872	770.3832	385.6952	**Y**	**737.3941**	369.2007	720.3675	**360.6874**	719.3835	**360.1954**	**6**
8	44.0495	859.4308	430.2191	842.4043	421.7058	841.4203	421.2138	**A**	**574.3307**	287.6690	557.3042	279.1557	556.3202	278.6637	**5**
9	87.0553	973.4738	487.2405	956.4472	478.7273	955.4632	478.2352	**N**	**503.2936**	252.1504	486.2671	243.6372	485.2831	243.1452	**4**
10	74.0600	1074.5215	537.7644	1057.4949	529.2511	1056.5109	528.7591	**T**	**389.2507**	195.1290	372.2241	186.6157	371.2401	186.1237	**3**
11	**86.0964**	1187.6055	594.3064	1170.5790	585.7931	1169.5950	585.3011	**L**	288.2030	144.6051	271.1765	136.0919			**2**
12	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **STESLQANVQR**
Found in **P26373**, P26373|RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4

Match to Query 410: 1231.650074 from(616.832313,2+)

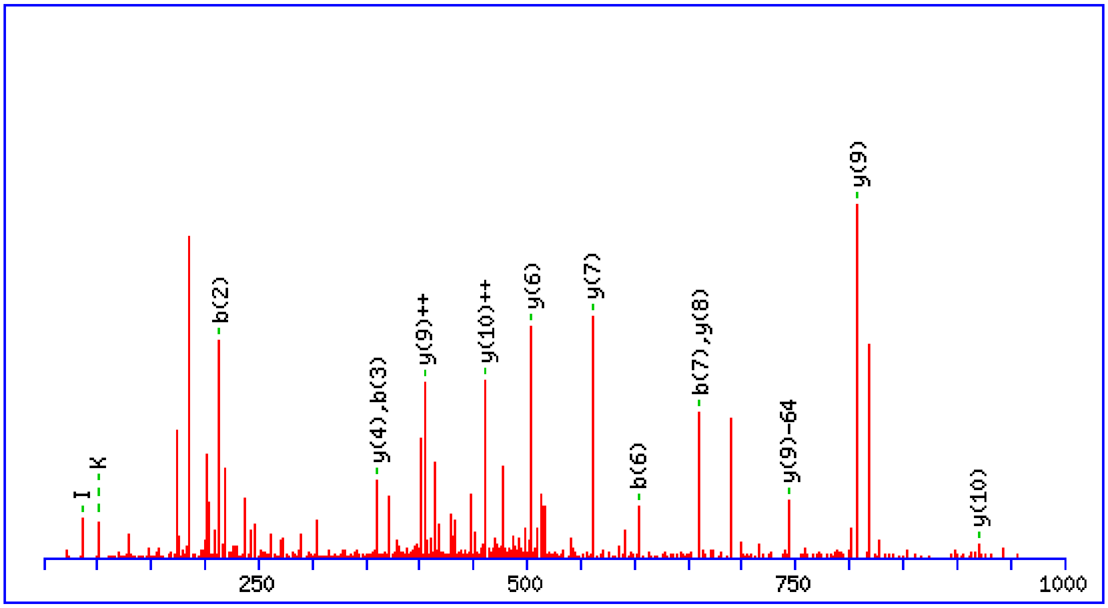


Monoisotopic mass of neutral peptide Mr(calc): 1231.6157
Fixed modifications: Carbamidomethyl (C)
Ions Score: 46 **Expect:** 0.0019
Matches (Bold Red): 25/107 fragment ions using 63 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							11
2	74.0600	**189.0870**	95.0471			**171.0764**	86.0418	T	1145.5909	573.2991	**1128.5644**	564.7858	1127.5804	564.2938	10
3	102.0550	318.1296	159.5684			**300.1190**	150.5631	E	**1044.5432**	522.7753	1027.5167	514.2620	**1026.5327**	513.7700	9
4	60.0444	405.1616	**203.0844**			**387.1510**	194.0792	S	**915.5007**	458.2540	**898.4741**	449.7407	**897.4901**	449.2487	8
5	86.0964	**518.2457**	259.6265			500.2351	250.6212	L	**828.4686**	414.7380	**811.4421**	**406.2247**			7
6	101.0709	646.3042	323.6558	629.2777	315.1425	628.2937	314.6505	Q	**715.3846**	358.1959	**698.3580**	349.6826			6
7	44.0495	717.3414	359.1743	700.3148	350.6610	699.3308	350.1690	A	**587.3260**	294.1666	570.2994	285.6534			5
8	87.0553	831.3843	416.1958	814.3577	407.6825	813.3737	407.1905	N	**516.2889**	258.6481	**499.2623**	250.1348			4
9	72.0808	**930.4527**	465.7300	913.4262	457.2167	912.4421	456.7247	V	**402.2459**	201.6266	385.2194	193.1133			3
10	101.0709	1058.5113	529.7593	1041.4847	521.2460	1040.5007	520.7540	Q	**303.1775**	152.0924	286.1510	143.5791			2
11	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VIMVGSGGVGK**
Found in **P11234**, P11234|RALB_HUMAN Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1

Match to Query 219: 1018.492938 from(510.253745,2+)



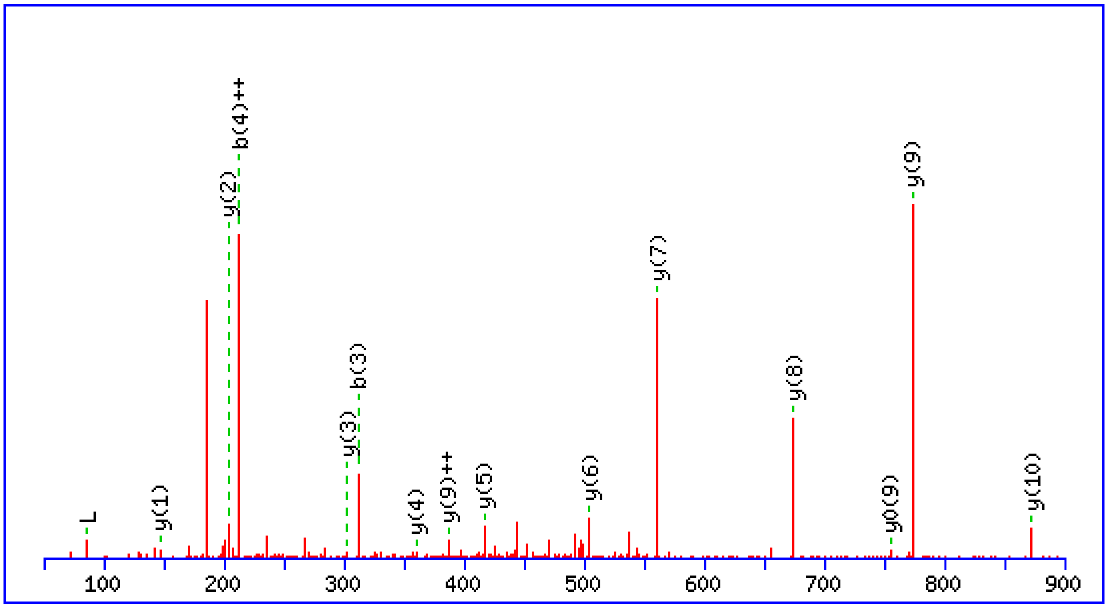
Monoisotopic mass of neutral peptide Mr(calc): 1018.5481
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 **Expect:** 0.0056
Matches (Bold Red): 15/130 fragment ions using 23 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			**V**							**11**
2	**86.0964**	**213.1598**	107.0835			**I**	**920.4870**	**460.7471**	903.4604	452.2339	902.4764	451.7418	**10**
3	120.0478	**360.1952**	180.6012			**M**	**807.4029**	**404.2051**	790.3764	395.6918	789.3924	395.1998	**9**
4	72.0808	459.2636	230.1354			**V**	**660.3675**	330.6874	643.3410	322.1741	642.3570	321.6821	**8**
5	30.0338	516.2850	258.6462			**G**	**561.2991**	281.1532	544.2726	272.6399	543.2885	272.1479	**7**
6	60.0444	**603.3171**	302.1622	585.3065	293.1569	**S**	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	**6**
7	30.0338	**660.3385**	330.6729	642.3280	321.6676	**G**	417.2456	209.1264	400.2191	200.6132			**5**
8	30.0338	717.3600	359.1836	699.3494	350.1784	**G**	**360.2241**	180.6157	343.1976	172.1024			**4**
9	72.0808	816.4284	408.7178	798.4178	399.7126	**V**	303.2027	152.1050	286.1761	143.5917			**3**
10	30.0338	873.4499	437.2286	855.4393	428.2233	**G**	204.1343	102.5708	187.1077	94.0575			**2**
11	**101.1073**					**K**	147.1128	74.0600	130.0863	65.5468			**1**

Ras-related protein Ral-B (P11234): single-peptide based protein identification could possibly also be assigned to RALA_HUMAN Ras-related protein Ral-A precursor (P11233)

MS/MS Fragmentation of **LVVLGSGGVGK**
Found in **P61224**, P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1

Match to Query 349: 984.634244 from(493.324398,2+)



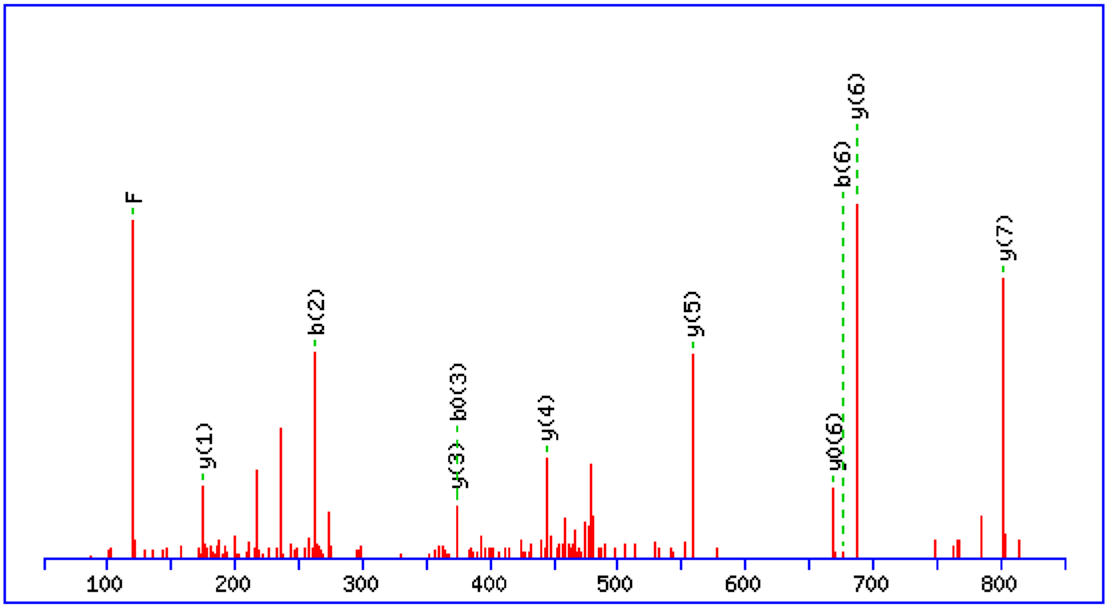
Monoisotopic mass of neutral peptide Mr(calc): 984.5968
Fixed modifications: Carbamidomethyl (C)
Ions Score: 66 **Expect:** 2e-005
Matches (Bold Red): 17/91 fragment ions using 38 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			L							11
2	72.0808	**213.1598**	107.0835			V	**872.5200**	436.7636	855.4934	428.2504	854.5094	427.7584	10
3	72.0808	**312.2282**	156.6177			V	**773.4516**	**387.2294**	756.4250	378.7162	**755.4410**	378.2241	9
4	**86.0964**	425.3122	**213.1598**			L	**674.3832**	337.6952	657.3566	329.1819	656.3726	328.6899	8
5	30.0338	482.3337	241.6705			G	**561.2991**	281.1532	544.2726	272.6399	543.2885	272.1479	7
6	60.0444	569.3657	285.1865	551.3552	276.1812	S	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	6
7	30.0338	626.3872	313.6972	608.3766	304.6919	G	**417.2456**	209.1264	400.2191	200.6132			5
8	30.0338	683.4087	342.2080	665.3981	333.2027	G	**360.2241**	180.6157	343.1976	172.1024			4
9	72.0808	782.4771	391.7422	764.4665	382.7369	V	**303.2027**	152.1050	286.1761	143.5917			3
10	30.0338	839.4985	420.2529	821.4880	411.2476	G	**204.1343**	102.5708	187.1077	94.0575			2
11	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

Ras-related protein Rap-1b (P61224): single-peptide based protein identification could possibly also be assigned to RAP1A_HUMAN Ras-related protein Rap-1A precursor (P62834)

MS/MS Fragmentation of **FDENAVVR**
Found in **Q3B8N2**, Q3B8N2|LEG9B_HUMAN Galectin-9B OS=Homo sapiens GN=LGALS9B PE=2 SV=3

Match to Query 140: 948.545162 from(475.279857,2+)



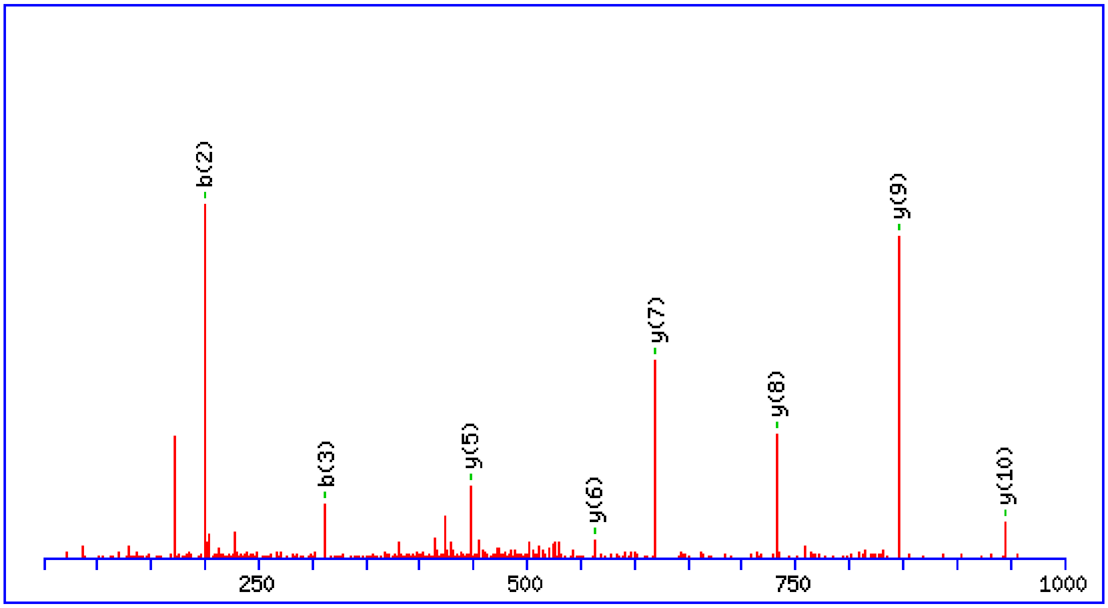
Monoisotopic mass of neutral peptide Mr(calc): 948.4665
Fixed modifications: Carbamidomethyl (C)
Ions Score: 49 **Expect:** 0.0011
Matches (Bold Red): 11/74 fragment ions using 21 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					**F**							**8**
2	88.0393	**263.1026**	132.0550			245.0921	123.0497	**D**	**802.4054**	401.7063	785.3788	393.1930	784.3948	392.7010	**7**
3	102.0550	392.1452	196.5763			**374.1347**	187.5710	**E**	**687.3784**	344.1928	670.3519	335.6796	**669.3678**	335.1876	**6**
4	87.0553	506.1882	253.5977	489.1616	245.0844	488.1776	244.5924	**N**	**558.3358**	279.6715	541.3093	271.1583			**5**
5	44.0495	577.2253	289.1163	560.1987	280.6030	559.2147	280.1110	**A**	**444.2929**	222.6501	427.2663	214.1368			**4**
6	72.0808	**676.2937**	338.6505	659.2671	330.1372	658.2831	329.6452	**V**	**373.2558**	187.1315	356.2292	178.6183			**3**
7	72.0808	775.3621	388.1847	758.3355	379.6714	757.3515	379.1794	**V**	274.1874	137.5973	257.1608	129.0840			**2**
8	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

Galectin-9B (Q3B8N2): single-peptide based protein identification could possibly also be assigned to LEG9C_HUMAN Galectin-9C (Galectin-9-like protein B) (Q6DKI2)

MS/MS Fragmentation of **VVLIGDSGVGK**
Found in **Q15907**, Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4

Match to Query 298: 1042.564002 from(522.289277,2+)



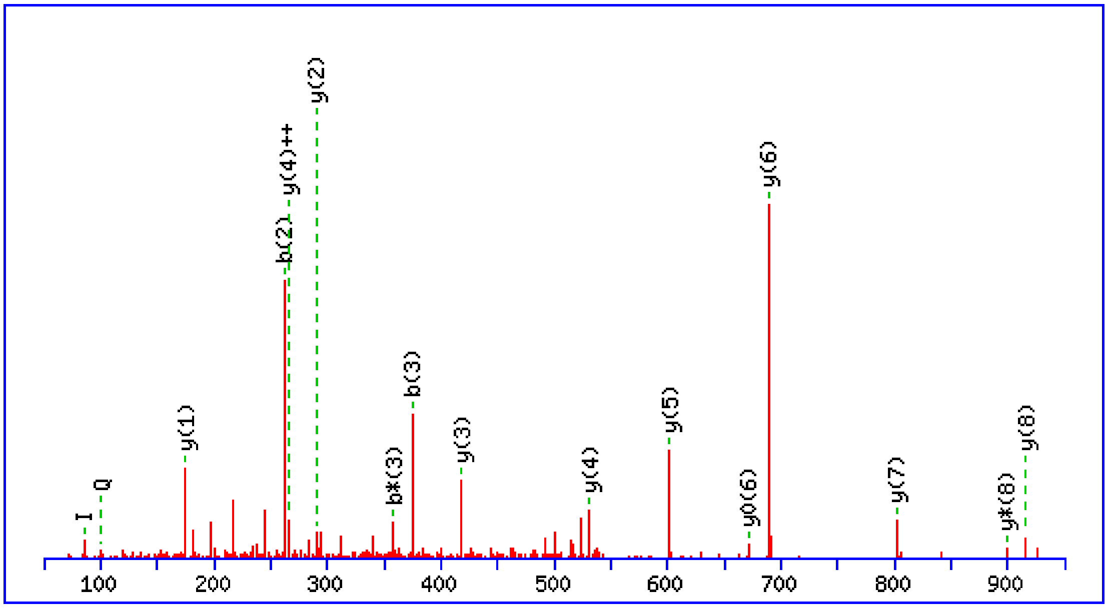
Monoisotopic mass of neutral peptide Mr(calc): 1042.6023
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 **Expect:** 0.00015
Matches (Bold Red): 8/93 fragment ions using 10 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			V							11
2	72.0808	**199.1441**	100.0757			V	**944.5411**	472.7742	927.5146	464.2609	926.5306	463.7689	10
3	86.0964	**312.2282**	156.6177			L	**845.4727**	423.2400	828.4462	414.7267	827.4621	414.2347	9
4	86.0964	425.3122	213.1598			I	**732.3886**	366.6980	715.3621	358.1847	714.3781	357.6927	8
5	30.0338	482.3337	241.6705			G	**619.3046**	310.1559	602.2780	301.6427	601.2940	301.1506	7
6	88.0393	597.3606	299.1840	579.3501	290.1787	D	**562.2831**	281.6452	545.2566	273.1319	544.2726	272.6399	6
7	60.0444	684.3927	342.7000	666.3821	333.6947	S	**447.2562**	224.1317	430.2296	215.6185	429.2456	215.1264	5
8	30.0338	741.4141	371.2107	723.4036	362.2054	G	360.2241	180.6157	343.1976	172.1024			4
9	72.0808	840.4825	420.7449	822.4720	411.7396	V	303.2027	152.1050	286.1761	143.5917			3
10	30.0338	897.5040	449.2556	879.4934	440.2504	G	204.1343	102.5708	187.1077	94.0575			2
11	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

Ras-related protein Rab-11B (Q15907): single-peptide based protein identification could possibly also be assigned to RB11A_HUMAN Ras-related protein Rab-11A (Rab-11) (P62491)

MS/MS Fragmentation of **MNLSAIQDR**
Found in **Q9NVJ2**, Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1

Match to Query 102: 1062.333098 from(532.173825,2+)



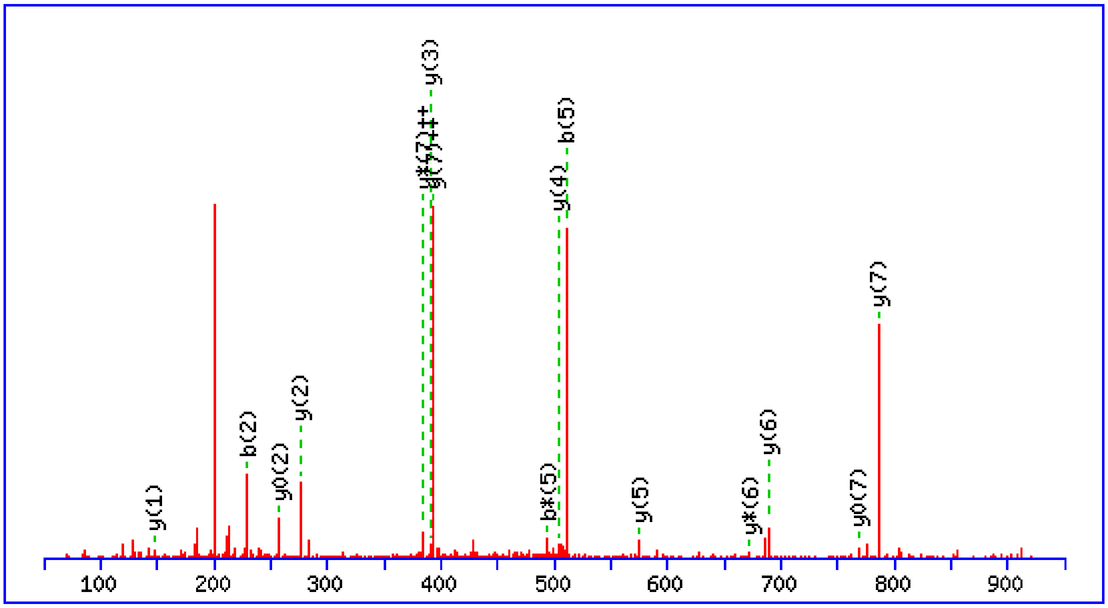
Monoisotopic mass of neutral peptide Mr(calc): 1062.5128
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 84 **Expect:** 2.7e-007
Matches (Bold Red): 17/136 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	120.0478	148.0427	74.5250					**M**							**9**
2	87.0553	**262.0856**	131.5464	245.0591	123.0332			**N**	**916.4847**	458.7460	**899.4581**	450.2327	898.4741	449.7407	**8**
3	**86.0964**	**375.1697**	188.0885	**358.1431**	179.5752			**L**	**802.4417**	401.7245	785.4152	393.2112	784.4312	392.7192	**7**
4	60.0444	462.2017	231.6045	445.1752	223.0912	444.1911	222.5992	**S**	**689.3577**	345.1825	672.3311	336.6692	**671.3471**	336.1772	**6**
5	44.0495	533.2388	267.1230	516.2123	258.6098	515.2282	258.1178	**A**	**602.3257**	301.6665	585.2991	293.1532	584.3151	292.6612	**5**
6	**86.0964**	646.3229	323.6651	629.2963	315.1518	628.3123	314.6598	**I**	**531.2885**	**266.1479**	514.2620	257.6346	513.2780	257.1426	**4**
7	**101.0709**	774.3815	387.6944	757.3549	379.1811	756.3709	378.6891	**Q**	**418.2045**	209.6059	401.1779	201.0926	400.1939	200.6006	**3**
8	88.0393	889.4084	445.2078	872.3818	436.6946	871.3978	436.2026	**D**	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
9	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

ADP-ribosylation factor-like protein 8B (Q9NVJ2): single-peptide based protein identification could possibly also be assigned to ARL8A_HUMAN ADP-ribosylation factor-like protein 8A (Q96BM9)

MS/MS Fragmentation of **DLPNALDEK**
Found in **Q9NVJ2**, Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1

Match to Query 366: 1013.545718 from(507.780135,2+)

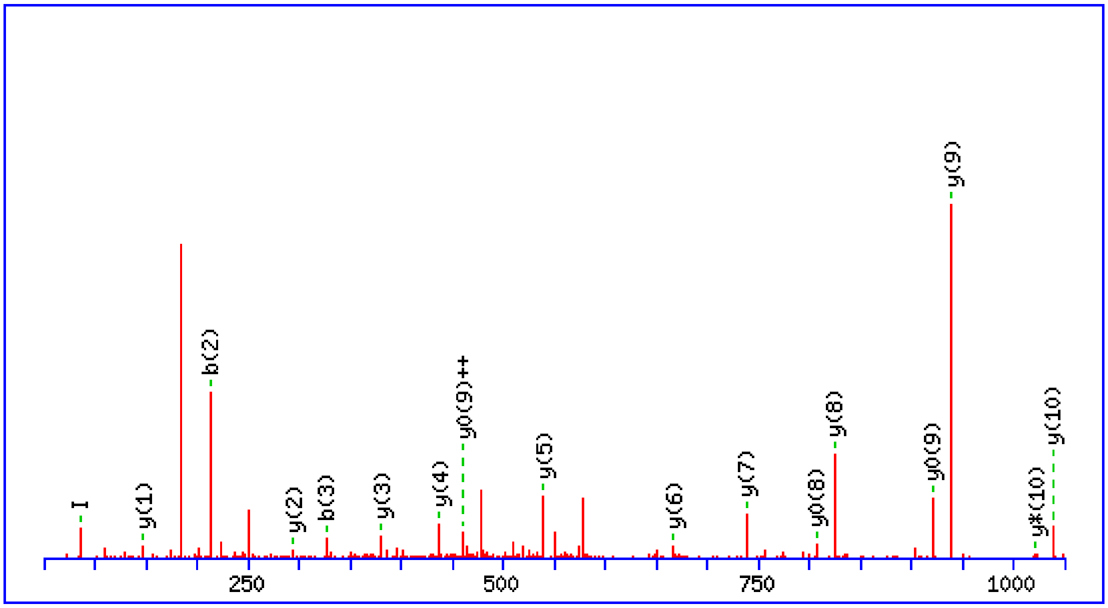


Monoisotopic mass of neutral peptide Mr(calc): 1013.5029
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 **Expect:** 0.02
Matches (Bold Red): 15/97 fragment ions using 41 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	116.0342	58.5207			98.0237	49.5155	D							9
2	86.0964	**229.1183**	115.0628			211.1077	106.0575	L	899.4833	450.2453	882.4567	441.7320	881.4727	441.2400	8
3	70.0651	326.1710	163.5892			308.1605	154.5839	P	**786.3992**	**393.7032**	769.3727	**385.1900**	**768.3886**	384.6980	7
4	87.0553	440.2140	220.6106	423.1874	212.0974	422.2034	211.6053	N	**689.3464**	345.1769	**672.3199**	336.6636	671.3359	336.1716	6
5	44.0495	**511.2511**	256.1292	**494.2245**	247.6159	493.2405	247.1239	A	**575.3035**	288.1554	558.2770	279.6421	557.2930	279.1501	5
6	86.0964	624.3352	312.6712	607.3086	304.1579	606.3246	303.6659	L	**504.2664**	252.6368	487.2399	244.1236	486.2558	243.6316	4
7	88.0393	739.3621	370.1847	722.3355	361.6714	721.3515	361.1794	D	**391.1823**	196.0948	374.1558	187.5815	373.1718	187.0895	3
8	102.0550	868.4047	434.7060	851.3781	426.1927	850.3941	425.7007	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
9	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IVNSAQTGSFK**
Found in **O75964**, O75964|ATP5L_HUMAN ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3

Match to Query 153: 1150.445704 from(576.230128,2+)

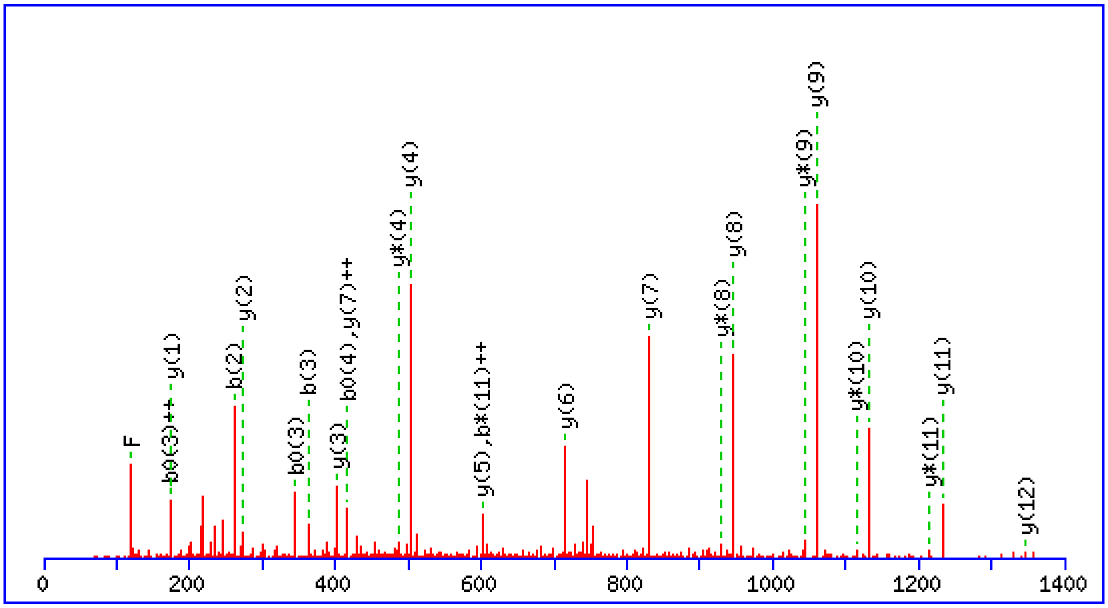


Monoisotopic mass of neutral peptide Mr(calc): 1150.5982
Fixed modifications: Carbamidomethyl (C)
Ions Score: 88 **Expect:** 1.1e-007
Matches (Bold Red): 17/117 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**I**							**11**
2	72.0808	**213.1598**	107.0835					**V**	**1038.5215**	519.7644	**1021.4949**	511.2511	1020.5109	510.7591	**10**
3	87.0553	**327.2027**	164.1050	310.1761	155.5917			**N**	**939.4530**	470.2302	922.4265	461.7169	**921.4425**	**461.2249**	**9**
4	60.0444	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	**S**	**825.4101**	413.2087	808.3836	404.6954	**807.3995**	404.2034	**8**
5	44.0495	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	**A**	**738.3781**	369.6927	721.3515	361.1794	720.3675	360.6874	**7**
6	101.0709	613.3304	307.1688	596.3039	298.6556	595.3198	298.1636	**Q**	**667.3410**	334.1741	650.3144	325.6608	649.3304	325.1688	**6**
7	74.0600	714.3781	357.6927	697.3515	349.1794	696.3675	348.6874	**T**	**539.2824**	270.1448	522.2558	261.6316	521.2718	261.1396	**5**
8	30.0338	771.3995	386.2034	754.3730	377.6901	753.3890	377.1981	**G**	**438.2347**	219.6210	421.2082	211.1077	420.2241	210.6157	**4**
9	60.0444	858.4316	429.7194	841.4050	421.2061	840.4210	420.7141	**S**	**381.2132**	191.1103	364.1867	182.5970	363.2027	182.1050	**3**
10	120.0808	1005.5000	503.2536	988.4734	494.7404	987.4894	494.2483	**F**	**294.1812**	147.5942	277.1547	139.0810			**2**
11	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **FNTANDDNVTQVR**
Found in **P04040**, P04040|CATA_HUMAN Catalase OS=Homo sapiens GN=CAT PE=1 SV=3

Match to Query 637: 1492.647104 from(747.330828,2+)

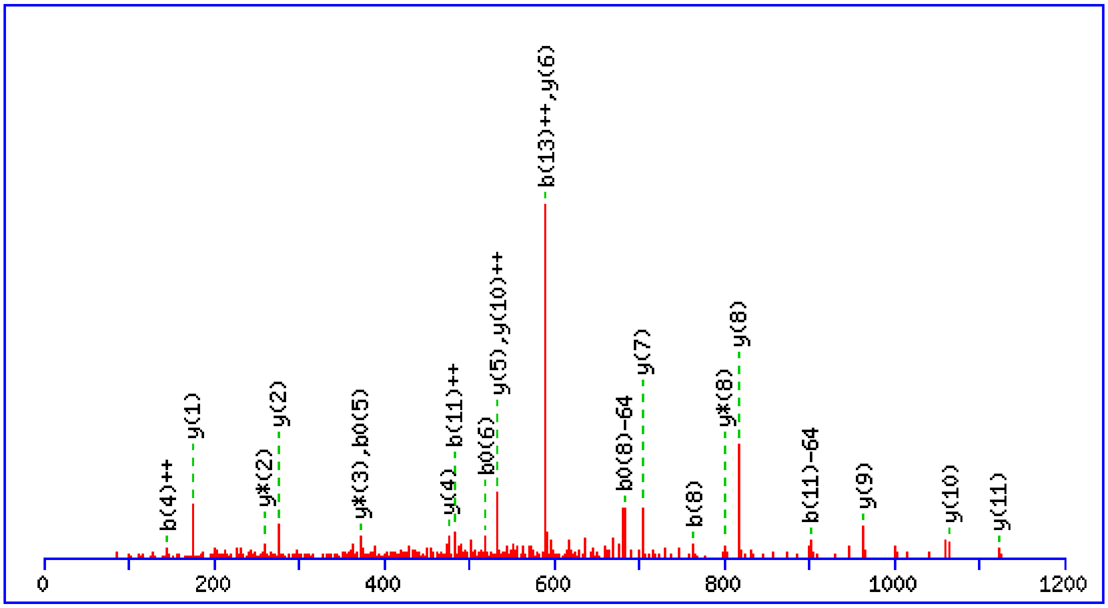


Monoisotopic mass of neutral peptide Mr(calc): 1492.6906
Fixed modifications: Carbamidomethyl (C)
Ions Score: 93 **Expect:** 3.7e-008
Matches (Bold Red): 25/145 fragment ions using 44 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							13
2	87.0553	**262.1186**	131.5629	245.0921	123.0497			N	**1346.6295**	673.8184	1329.6029	665.3051	1328.6189	664.8131	12
3	74.0600	**363.1663**	182.0868	346.1397	173.5735	**345.1557**	**173.0815**	T	**1232.5866**	616.7969	**1215.5600**	608.2836	1214.5760	607.7916	11
4	44.0495	434.2034	217.6053	417.1769	209.0921	**416.1928**	208.6001	A	**1131.5389**	566.2731	**1114.5123**	557.7598	1113.5283	557.2678	10
5	87.0553	548.2463	274.6268	531.2198	266.1135	530.2358	265.6215	N	**1060.5018**	530.7545	**1043.4752**	522.2413	1042.4912	521.7492	9
6	88.0393	663.2733	332.1403	646.2467	323.6270	645.2627	323.1350	D	**946.4588**	473.7331	**929.4323**	465.2198	928.4483	464.7278	8
7	88.0393	778.3002	389.6537	761.2737	381.1405	760.2897	380.6485	D	**831.4319**	**416.2196**	814.4054	407.7063	813.4213	407.2143	7
8	87.0553	892.3431	446.6752	875.3166	438.1619	874.3326	437.6699	N	**716.4050**	358.7061	699.3784	350.1928	698.3944	349.7008	6
9	72.0808	991.4116	496.2094	974.3850	487.6961	973.4010	487.2041	V	**602.3620**	301.6847	585.3355	293.1714	584.3515	292.6794	5
10	74.0600	1092.4592	546.7333	1075.4327	538.2200	1074.4487	537.7280	T	**503.2936**	252.1504	**486.2671**	243.6372	485.2831	243.1452	4
11	101.0709	1220.5178	610.7625	1203.4913	**602.2493**	1202.5073	601.7573	Q	**402.2459**	201.6266	385.2194	193.1133			3
12	72.0808	1319.5862	660.2968	1302.5597	651.7835	1301.5757	651.2915	V	**274.1874**	137.5973	257.1608	129.0840			2
13	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SGSGTMNLGGSLTR**
Found in **P47756**, P47756|CAPZB_HUMAN F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4

Match to Query 321: 1352.660978 from(677.337765,2+)

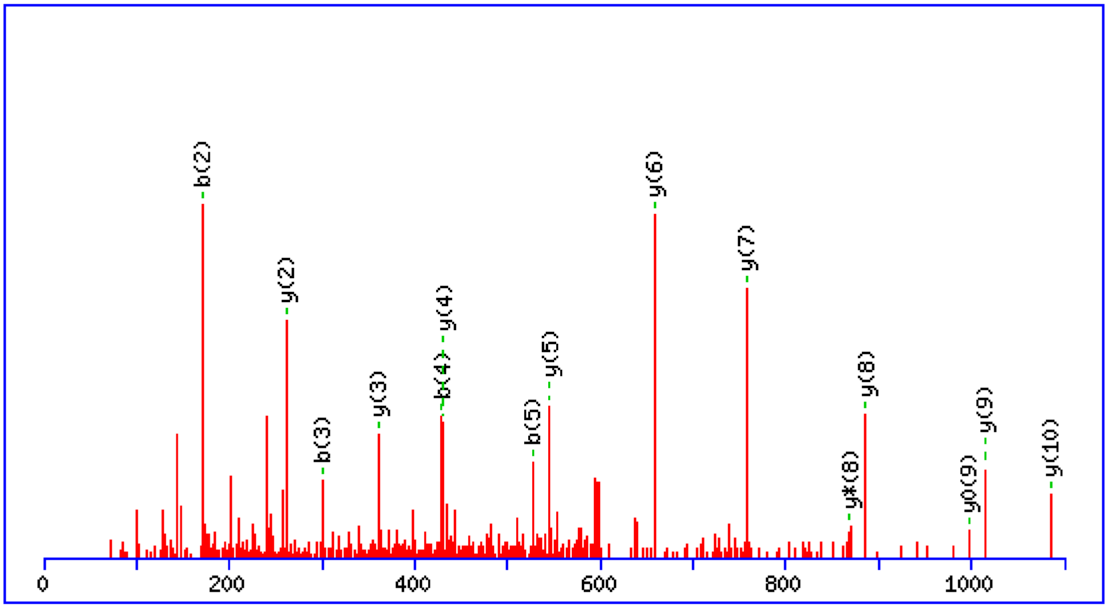


Monoisotopic mass of neutral peptide Mr(calc): 1352.6354
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 90 **Expect:** 6.6e-008
Matches (Bold Red): 23/233 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	**S**							**14**
2	30.0338	**145.0608**	73.0340			127.0502	64.0287	**G**	1266.6107	633.8090	1249.5841	625.2957	1248.6001	624.8037	**13**
3	60.0444	232.0928	116.5500			214.0822	107.5448	**S**	1209.5892	605.2982	1192.5627	596.7850	1191.5787	596.2930	**12**
4	30.0338	289.1143	**145.0608**			271.1037	136.0555	**G**	**1122.5572**	561.7822	1105.5306	553.2690	1104.5466	552.7769	**11**
5	74.0600	390.1619	195.5846			**372.1514**	186.5793	**T**	**1065.5357**	**533.2715**	1048.5092	524.7582	1047.5252	524.2662	**10**
6	120.0478	537.1973	269.1023			**519.1868**	260.0970	**M**	**964.4880**	482.7477	947.4615	474.2344	946.4775	473.7424	**9**
7	87.0553	651.2403	326.1238	634.2137	317.6105	633.2297	317.1185	**N**	**817.4526**	409.2300	**800.4261**	400.7167	799.4421	400.2247	**8**
8	86.0964	**764.3243**	382.6658	747.2978	374.1525	746.3138	373.6605	**L**	**703.4097**	352.2085	686.3832	343.6952	685.3991	343.2032	**7**
9	30.0338	821.3458	411.1765	804.3192	402.6633	803.3352	402.1713	**G**	**590.3257**	295.6665	573.2991	287.1532	572.3151	286.6612	**6**
10	30.0338	878.3673	439.6873	861.3407	431.1740	860.3567	430.6820	**G**	**533.3042**	267.1557	516.2776	258.6425	515.2936	258.1504	**5**
11	60.0444	965.3993	**483.2033**	948.3727	474.6900	947.3887	474.1980	**S**	**476.2827**	238.6450	459.2562	230.1317	458.2722	229.6397	**4**
12	86.0964	1078.4834	539.7453	1061.4568	531.2320	1060.4728	530.7400	**L**	389.2507	195.1290	**372.2241**	186.6157	371.2401	186.1237	**3**
13	74.0600	1179.5310	**590.2692**	1162.5045	581.7559	1161.5205	581.2639	**T**	**276.1666**	138.5870	**259.1401**	130.0737	258.1561	129.5817	**2**
14	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VAEQVLNAVNK**
Found in **Q9HB40**, Q9HB40|RISC_HUMAN Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1

Match to Query 156: 1183.533408 from(592.773980,2+)

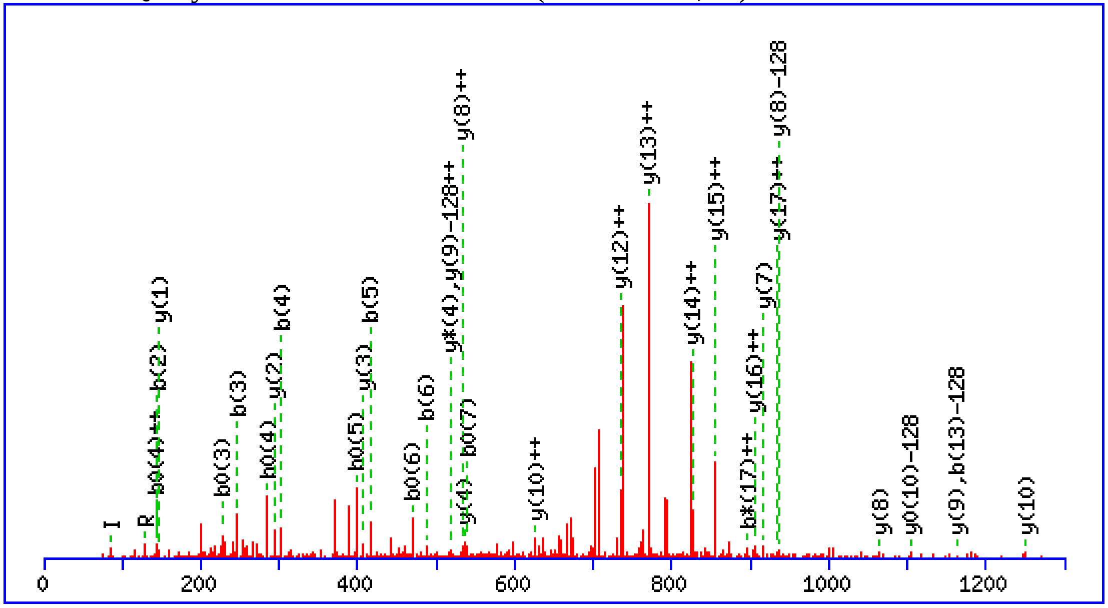


Monoisotopic mass of neutral peptide Mr(calc): 1183.6561
Fixed modifications: Carbamidomethyl (C)
Ions Score: 84 **Expect:** 2.7e-007
Matches (Bold Red): 15/105 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							11
2	44.0495	**171.1128**	86.0600					A	**1085.5949**	543.3011	1068.5684	534.7878	1067.5844	534.2958	10
3	102.0550	**300.1554**	150.5813			282.1448	141.5761	E	**1014.5578**	507.7826	997.5313	499.2693	**996.5473**	498.7773	9
4	101.0709	**428.2140**	214.6106	411.1874	206.0974	410.2034	205.6053	Q	**885.5152**	443.2613	**868.4887**	434.7480			8
5	72.0808	**527.2824**	264.1448	510.2558	255.6316	509.2718	255.1396	V	**757.4567**	379.2320	740.4301	370.7187			7
6	86.0964	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	L	**658.3883**	329.6978	641.3617	321.1845			6
7	87.0553	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	N	**545.3042**	273.1557	528.2776	264.6425			5
8	44.0495	825.4465	413.2269	808.4199	404.7136	807.4359	404.2216	A	**431.2613**	216.1343	414.2347	207.6210			4
9	72.0808	924.5149	462.7611	907.4884	454.2478	906.5043	453.7558	V	**360.2241**	180.6157	343.1976	172.1024			3
10	87.0553	1038.5578	519.7826	1021.5313	511.2693	1020.5473	510.7773	N	**261.1557**	131.0815	244.1292	122.5682			2
11	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **SGTGIAAMSVMRPEQIMK**
Found in **P27449**, P27449|VATL_HUMAN Vacuolar ATP synthase 16 kDa proteolipid subunit OS=Homo sapiens GN=ATP6V0C PE=1 SV=1

Match to Query 1004: 1953.904956 from(652.308928,3+)

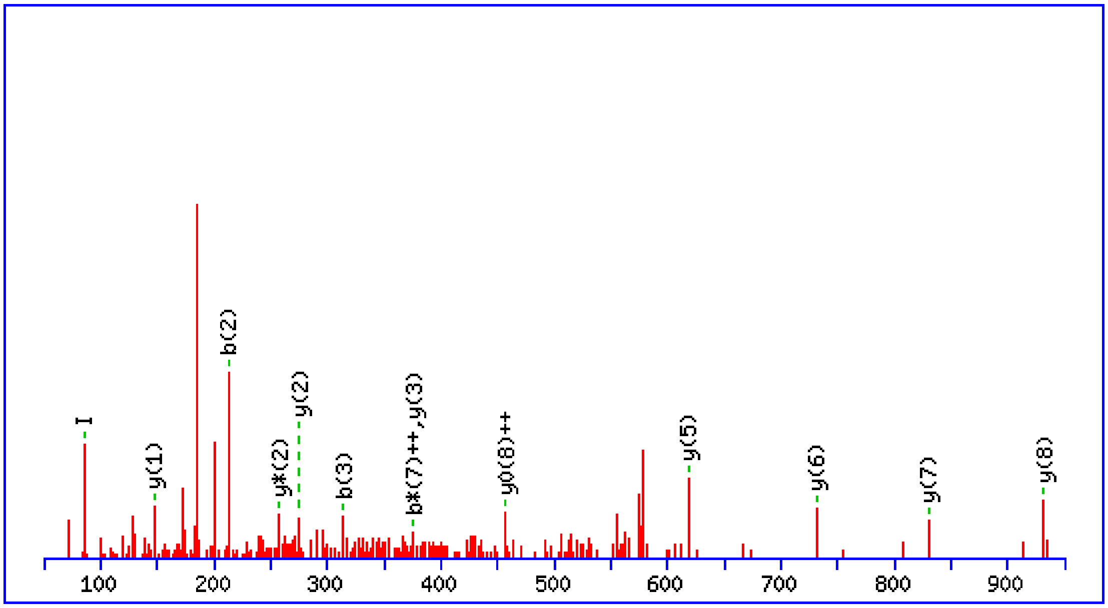


Monoisotopic mass of neutral peptide Mr(calc): 1953.9322
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M17 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 **Expect:** 0.0014
Matches (Bold Red): 36/337 fragment ions using 75 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							18
2	30.0338	**145.0608**	73.0340			127.0502	64.0287	G	1867.9075	**934.4574**	1850.8809	925.9441	1849.8969	925.4521	17
3	74.0600	**246.1084**	123.5579			**228.0979**	114.5526	T	1810.8860	**905.9466**	1793.8595	897.4334	1792.8754	896.9414	16
4	30.0338	**303.1299**	152.0686			**285.1193**	**143.0633**	G	1709.8383	**855.4228**	1692.8118	846.9095	1691.8278	846.4175	15
5	**86.0964**	**416.2140**	208.6106			**398.2034**	199.6053	I	1652.8169	**826.9121**	1635.7903	818.3988	1634.8063	817.9068	14
6	44.0495	**487.2511**	244.1292			**469.2405**	235.1239	A	1539.7328	**770.3700**	1522.7062	761.8568	1521.7222	761.3648	13
7	44.0495	558.2882	279.6477			**540.2776**	270.6425	A	1468.6957	**734.8515**	1451.6691	726.3382	1450.6851	725.8462	12
8	120.0478	705.3236	353.1654			687.3130	344.1602	M	1397.6586	699.3329	1380.6320	690.8196	1379.6480	690.3276	11
9	60.0444	792.3556	396.6815			774.3451	387.6762	S	**1250.6232**	**625.8152**	1233.5966	617.3019	1232.6126	616.8099	10
10	72.0808	891.4240	446.2157			873.4135	437.2104	V	**1163.5911**	582.2992	1146.5646	573.7859	1145.5806	573.2939	9
11	120.0478	1038.4595	519.7334			1020.4489	510.7281	M	**1064.5227**	**532.7650**	1047.4962	524.2517	1046.5122	523.7597	8
12	**129.1135**	1194.5606	597.7839	1177.5340	589.2706	1176.5500	588.7786	R	**917.4873**	459.2473	900.4608	450.7340	899.4768	450.2420	7
13	70.0651	1291.6133	646.3103	1274.5868	637.7970	1273.6028	637.3050	P	761.3862	381.1967	744.3597	372.6835	743.3756	372.1915	6
14	102.0550	1420.6559	710.8316	1403.6294	702.3183	1402.6454	701.8263	E	664.3334	332.6704	647.3069	324.1571	646.3229	323.6651	5
15	101.0709	1548.7145	774.8609	1531.6880	766.3476	1530.7039	765.8556	Q	**535.2909**	268.1491	**518.2643**	259.6358			4
16	**86.0964**	1661.7986	831.4029	1644.7720	822.8896	1643.7880	822.3976	I	**407.2323**	204.1198	390.2057	195.6065			3
17	120.0478	1808.8340	904.9206	1791.8074	**896.4073**	1790.8234	895.9153	M	**294.1482**	147.5777	277.1217	139.0645			2
18	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VLTVINQTQK**
Found in **P42766**, P42766|RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2

Match to Query 159: 1142.477962 from(572.246257,2+)

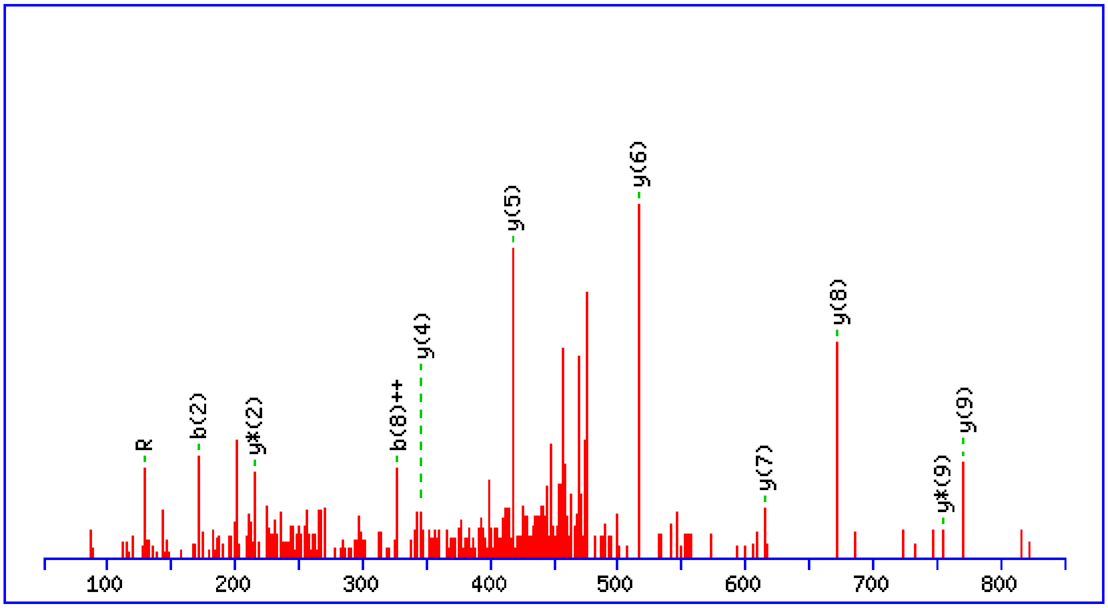


Monoisotopic mass of neutral peptide Mr(calc): 1142.6659
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00055
Matches (Bold Red): 14/100 fragment ions using 25 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							10
2	**86.0964**	**213.1598**	107.0835					L	1044.6048	522.8060	1027.5782	514.2928	1026.5942	513.8007	9
3	74.0600	**314.2074**	157.6074			296.1969	148.6021	T	**931.5207**	466.2640	914.4942	457.7507	913.5102	**457.2587**	8
4	72.0808	413.2758	207.1416			395.2653	198.1363	V	**830.4730**	415.7402	813.4465	407.2269	812.4625	406.7349	7
5	**86.0964**	526.3599	263.6836			508.3493	254.6783	I	**731.4046**	366.2060	714.3781	357.6927	713.3941	357.2007	6
6	87.0553	640.4028	320.7051	623.3763	312.1918	622.3923	311.6998	N	**618.3206**	309.6639	601.2940	301.1506	600.3100	300.6586	5
7	101.0709	768.4614	384.7343	751.4349	**376.2211**	750.4509	375.7291	Q	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
8	74.0600	869.5091	435.2582	852.4825	426.7449	851.4985	426.2529	T	**376.2191**	188.6132	359.1925	180.0999	358.2085	179.6079	3
9	101.0709	997.5677	499.2875	980.5411	490.7742	979.5571	490.2822	Q	**275.1714**	138.0893	**258.1448**	129.5761			2
10	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AVVGVVAGGGR**
Found in **P62917**, P62917|RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2

Match to Query 255: 940.606620 from(471.310586,2+)

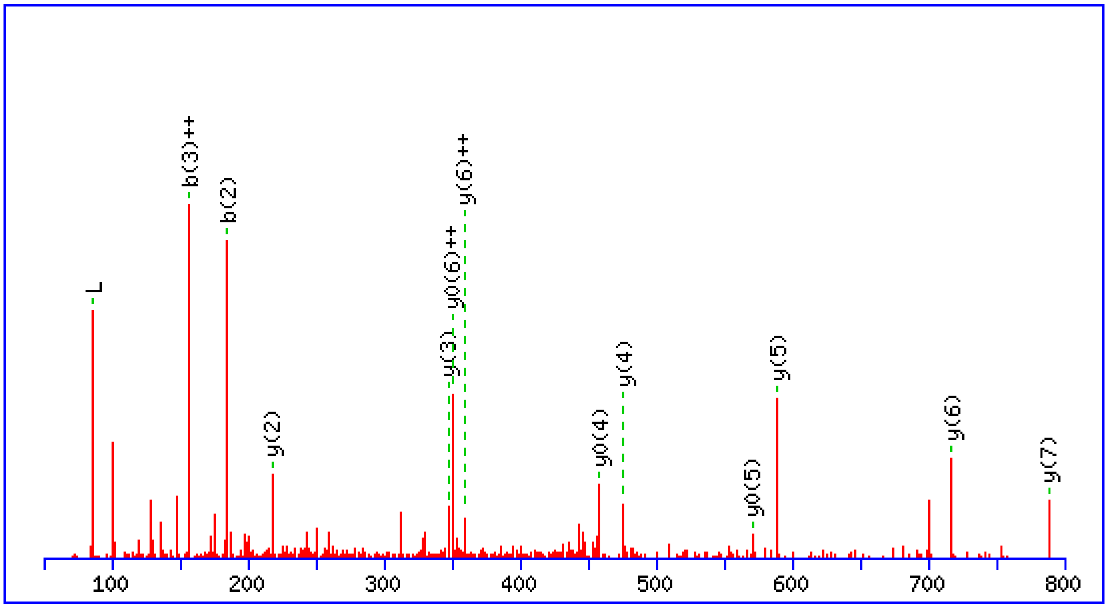


Monoisotopic mass of neutral peptide Mr(calc): 940.5454
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 **Expect:** 0.0033
Matches (Bold Red): 12/71 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	44.0495	72.0444	36.5258	**A**					**11**
2	72.0808	**171.1128**	86.0600	**V**	870.5156	435.7614	853.4890	427.2482	**10**
3	72.0808	270.1812	135.5942	**V**	**771.4472**	386.2272	**754.4206**	377.7139	**9**
4	30.0338	**327.2027**	164.1050	**G**	**672.3788**	336.6930	655.3522	328.1797	**8**
5	72.0808	426.2711	213.6392	**V**	**615.3573**	308.1823	598.3307	299.6690	**7**
6	72.0808	525.3395	263.1734	**V**	**516.2889**	258.6481	499.2623	250.1348	**6**
7	44.0495	596.3766	298.6920	**A**	**417.2205**	209.1139	400.1939	200.6006	**5**
8	30.0338	653.3981	**327.2027**	**G**	**346.1833**	173.5953	329.1568	165.0820	**4**
9	30.0338	710.4196	355.7134	**G**	289.1619	145.0846	272.1353	136.5713	**3**
10	30.0338	767.4410	384.2241	**G**	232.1404	116.5738	**215.1139**	108.0606	**2**
11	**129.1135**			**R**	175.1190	88.0631	158.0924	79.5498	**1**

MS/MS Fragmentation of **LAQLEEAK**
Found in **P24539**, P24539|AT5F1_HUMAN ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2

Match to Query 108: 900.328958 from(451.171755,2+)

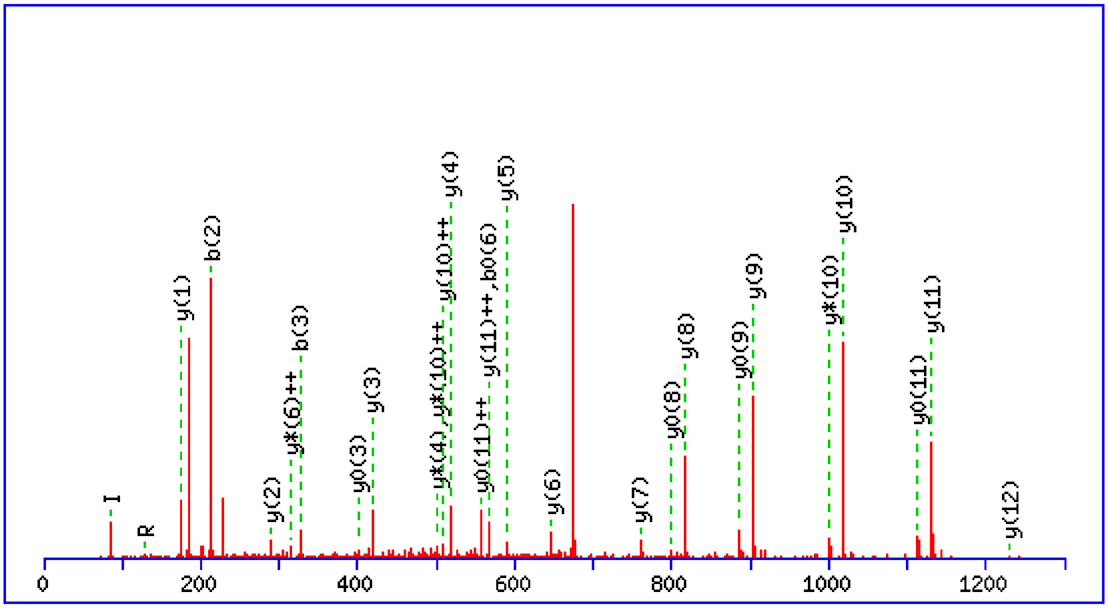


Monoisotopic mass of neutral peptide Mr(calc): 900.4916
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00063
Matches (Bold Red): 14/76 fragment ions using 17 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**8**
2	44.0495	**185.1285**	93.0679					**A**	**788.4149**	394.7111	771.3883	386.1978	770.4043	385.7058	**7**
3	101.0709	313.1870	**157.0972**	296.1605	148.5839			**Q**	**717.3777**	**359.1925**	700.3512	350.6792	699.3672	**350.1872**	**6**
4	**86.0964**	426.2711	213.6392	409.2445	205.1259			**L**	**589.3192**	295.1632	572.2926	286.6499	**571.3086**	286.1579	**5**
5	102.0550	555.3137	278.1605	538.2871	269.6472	537.3031	269.1552	**E**	**476.2351**	238.6212	459.2086	230.1079	**458.2245**	229.6159	**4**
6	102.0550	684.3563	342.6818	667.3297	334.1685	666.3457	333.6765	**E**	**347.1925**	174.0999	330.1660	165.5866	329.1819	165.0946	**3**
7	44.0495	755.3934	378.2003	738.3668	369.6871	737.3828	369.1951	**A**	**218.1499**	109.5786	201.1234	101.0653			**2**
8	101.1073							**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **LVINSGNGAVEDR**
Found in **P16070**, P16070|CD44_HUMAN CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=2

Match to Query 401: 1342.744584 from(672.379568,2+)

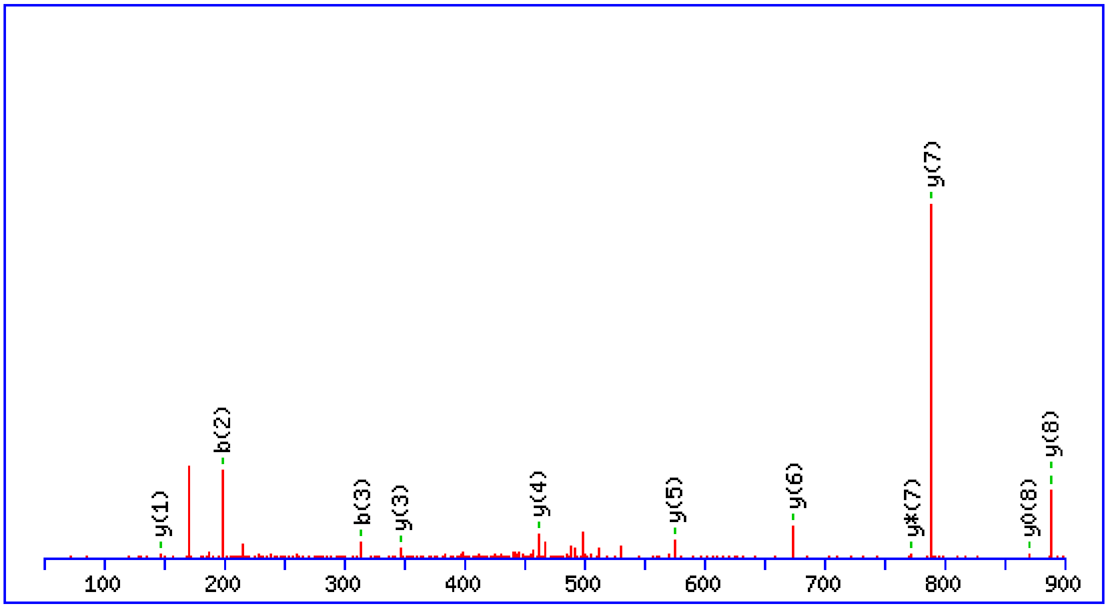


Monoisotopic mass of neutral peptide Mr(calc): 1342.6841
Fixed modifications: Carbamidomethyl (C)
Ions Score: 95 **Expect:** 2.3e-008
Matches (Bold Red): 29/141 fragment ions using 51 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**13**
2	72.0808	**213.1598**	107.0835					**V**	**1230.6073**	615.8073	1213.5808	607.2940	1212.5967	606.8020	**12**
3	**86.0964**	**326.2438**	163.6255					**I**	**1131.5389**	**566.2731**	1114.5123	557.7598	**1113.5283**	**557.2678**	**11**
4	87.0553	440.2867	220.6470	423.2602	212.1337			**N**	**1018.4548**	**509.7311**	**1001.4283**	**501.2178**	1000.4443	500.7258	**10**
5	60.0444	527.3188	264.1630	510.2922	255.6498	509.3082	255.1577	**S**	**904.4119**	452.7096	887.3854	444.1963	**886.4013**	443.7043	**9**
6	30.0338	584.3402	292.6738	567.3137	284.1605	**566.3297**	283.6685	**G**	**817.3799**	409.1936	800.3533	400.6803	**799.3693**	400.1883	**8**
7	87.0553	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	**N**	**760.3584**	380.6828	743.3319	372.1696	742.3478	371.6776	**7**
8	30.0338	755.4046	378.2060	738.3781	369.6927	737.3941	369.2007	**G**	**646.3155**	323.6614	629.2889	**315.1481**	628.3049	314.6561	**6**
9	44.0495	826.4417	413.7245	809.4152	405.2112	808.4312	404.7192	**A**	**589.2940**	295.1506	572.2675	286.6374	571.2835	286.1454	**5**
10	72.0808	925.5102	463.2587	908.4836	454.7454	907.4996	454.2534	**V**	**518.2569**	259.6321	**501.2304**	251.1188	500.2463	250.6268	**4**
11	102.0550	1054.5527	527.7800	1037.5262	519.2667	1036.5422	518.7747	**E**	**419.1885**	210.0979	402.1619	201.5846	**401.1779**	201.0926	**3**
12	88.0393	1169.5797	585.2935	1152.5531	576.7802	1151.5691	576.2882	**D**	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	**2**
13	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VVDVLDSIK**
Found in **P00918**, P00918|CAH2_HUMAN Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2

Match to Query 212: 986.546988 from(494.280770,2+)

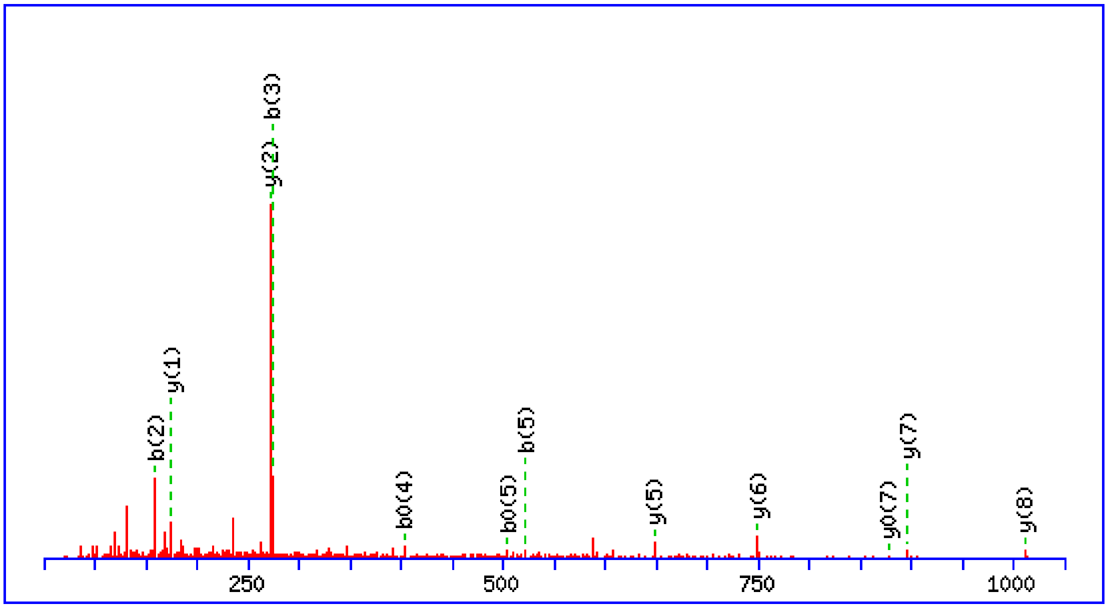


Monoisotopic mass of neutral peptide Mr(calc): 986.5648
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 **Expect:** 0.00016
Matches (Bold Red): 11/81 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			V							9
2	72.0808	**199.1441**	100.0757			V	**888.5037**	444.7555	871.4771	436.2422	**870.4931**	435.7502	8
3	88.0393	**314.1710**	157.5892	296.1605	148.5839	D	**789.4353**	395.2213	**772.4087**	386.7080	771.4247	386.2160	7
4	72.0808	413.2395	207.1234	395.2289	198.1181	V	**674.4083**	337.7078	657.3818	329.1945	656.3978	328.7025	6
5	86.0964	526.3235	263.6654	508.3130	254.6601	L	**575.3399**	288.1736	558.3134	279.6603	557.3293	279.1683	5
6	88.0393	641.3505	321.1789	623.3399	312.1736	D	**462.2558**	231.6316	445.2293	223.1183	444.2453	222.6263	4
7	60.0444	728.3825	364.6949	710.3719	355.6896	S	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	3
8	86.0964	841.4666	421.2369	823.4560	412.2316	I	260.1969	130.6021	243.1703	122.0888			2
9	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **SADFTNFDPR**
Found in **P00918**, P00918|CAH2_HUMAN Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2

Match to Query 172: 1168.348294 from(585.181423,2+)

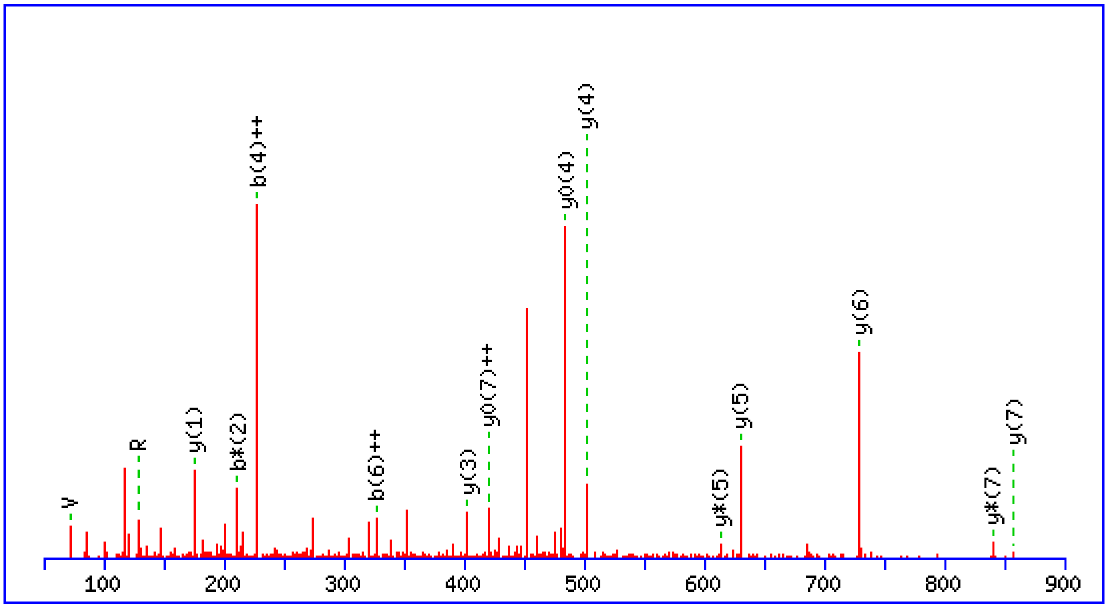


Monoisotopic mass of neutral peptide Mr(calc): 1168.5149
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 **Expect:** 0.0053
Matches (Bold Red): 12/104 fragment ions using 23 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	**S**							**10**
2	44.0495	**159.0764**	80.0418			141.0659	71.0366	**A**	1082.4901	541.7487	1065.4636	533.2354	1064.4796	532.7434	**9**
3	88.0393	**274.1034**	137.5553			256.0928	128.5500	**D**	**1011.4530**	506.2302	994.4265	497.7169	993.4425	497.2249	**8**
4	120.0808	421.1718	211.0895			**403.1612**	202.0842	**F**	**896.4261**	448.7167	879.3995	440.2034	**878.4155**	439.7114	**7**
5	74.0600	**522.2195**	261.6134			**504.2089**	252.6081	**T**	**749.3577**	375.1825	732.3311	366.6692	731.3471	366.1772	**6**
6	87.0553	636.2624	318.6348	619.2358	310.1216	618.2518	309.6295	**N**	**648.3100**	324.6586	631.2835	316.1454	630.2994	315.6534	**5**
7	120.0808	783.3308	392.1690	766.3042	383.6558	765.3202	383.1638	**F**	534.2671	267.6372	517.2405	259.1239	516.2565	258.6319	**4**
8	88.0393	898.3577	449.6825	881.3312	441.1692	880.3472	440.6772	**D**	387.1987	194.1030	370.1721	185.5897	369.1881	185.0977	**3**
9	70.0651	995.4105	498.2089	978.3840	489.6956	977.3999	489.2036	**P**	**272.1717**	136.5895	255.1452	128.0762			**2**
10	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VQVQVVER**
Found in **O75955**, O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3

Match to Query 42: 955.386216 from(478.700384,2+)

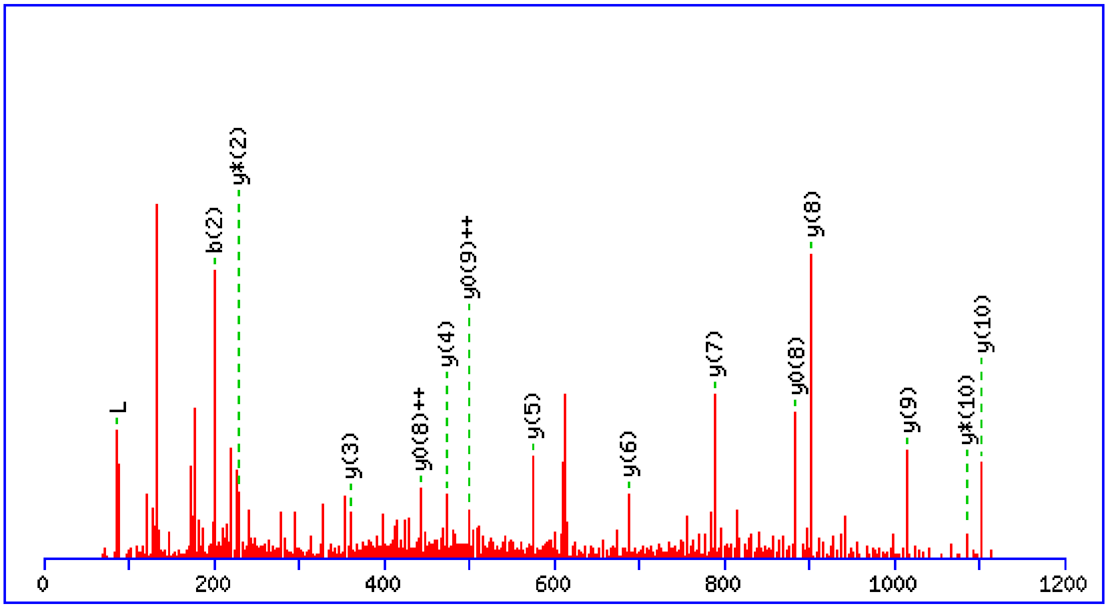


Monoisotopic mass of neutral peptide Mr(calc): 955.5451
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 **Expect:** 0.0025
Matches (Bold Red): 20/76 fragment ions using 27 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**72.0808**	100.0757	50.5415					**V**							**8**
2	101.0709	**228.1343**	114.5708	**211.1077**	106.0575			**Q**	**857.4839**	429.2456	**840.4574**	420.7323	839.4734	**420.2403**	**7**
3	**72.0808**	**327.2027**	164.1050	310.1761	155.5917			**V**	**729.4254**	365.2163	712.3988	356.7030	711.4148	356.2110	**6**
4	101.0709	455.2613	**228.1343**	438.2347	219.6210			**Q**	**630.3570**	315.6821	**613.3304**	307.1688	612.3464	306.6768	**5**
5	**72.0808**	554.3297	277.6685	537.3031	269.1552			**V**	**502.2984**	251.6528	485.2718	243.1395	**484.2878**	242.6475	**4**
6	**72.0808**	653.3981	**327.2027**	636.3715	318.6894			**V**	**403.2300**	202.1186	386.2034	193.6053	385.2194	193.1133	**3**
7	102.0550	782.4407	391.7240	765.4141	383.2107	764.4301	382.7187	**E**	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
8	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **ISLNTLTLNVK**
Found in **O75955**, O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3

Match to Query 399: 1214.709068 from(608.361810,2+)

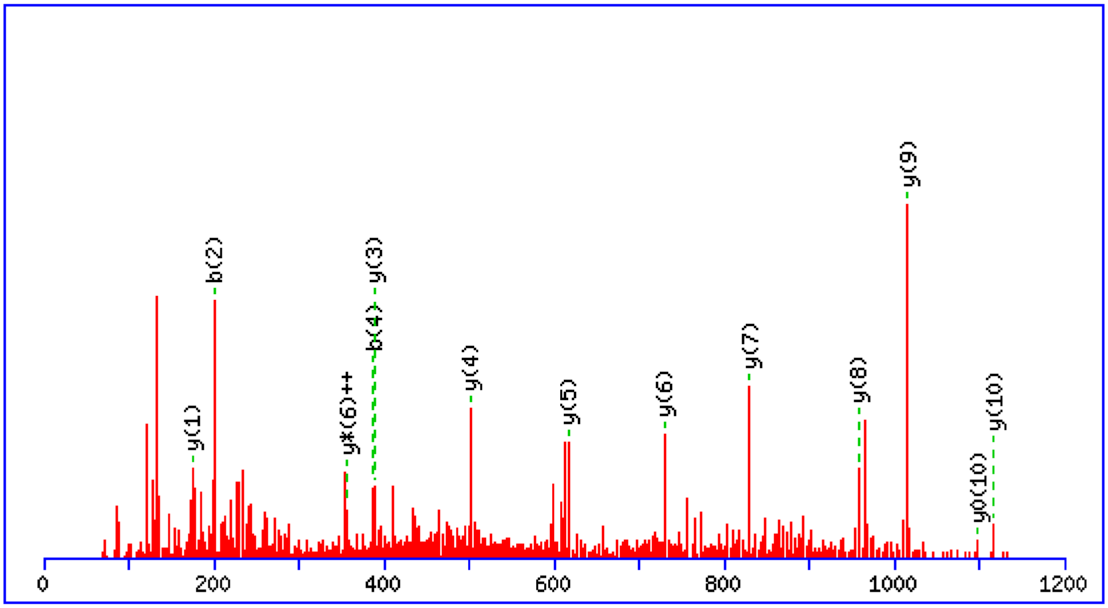


Monoisotopic mass of neutral peptide Mr(calc): 1214.7234
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 **Expect:** 0.0029
Matches (Bold Red): 18/115 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							11
2	60.0444	**201.1234**	101.0653			183.1128	92.0600	S	**1102.6467**	551.8270	**1085.6201**	543.3137	1084.6361	542.8217	10
3	**86.0964**	314.2074	157.6074			296.1969	148.6021	L	**1015.6146**	508.3109	998.5881	499.7977	997.6041	**499.3057**	9
4	87.0553	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	N	**902.5306**	451.7689	885.5040	443.2556	**884.5200**	**442.7636**	8
5	74.0600	529.2980	265.1527	512.2715	256.6394	511.2875	256.1474	T	**788.4876**	394.7475	771.4611	386.2342	770.4771	385.7422	7
6	**86.0964**	642.3821	321.6947	625.3556	313.1814	624.3715	312.6894	L	**687.4400**	344.2236	670.4134	335.7103	669.4294	335.2183	6
7	74.0600	743.4298	372.2185	726.4032	363.7053	725.4192	363.2132	T	**574.3559**	287.6816	557.3293	279.1683	556.3453	278.6763	5
8	**86.0964**	856.5138	428.7606	839.4873	420.2473	838.5033	419.7553	L	**473.3082**	237.1577	456.2817	228.6445			4
9	87.0553	970.5568	485.7820	953.5302	477.2687	952.5462	476.7767	N	**360.2241**	180.6157	343.1976	172.1024			3
10	72.0808	1069.6252	535.3162	1052.5986	526.8030	1051.6146	526.3109	V	246.1812	123.5942	**229.1547**	115.0810			2
11	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VTGEVLDILTR**
Found in **O75955**, O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3

Match to Query 504: 1214.688006 from(608.351279,2+)

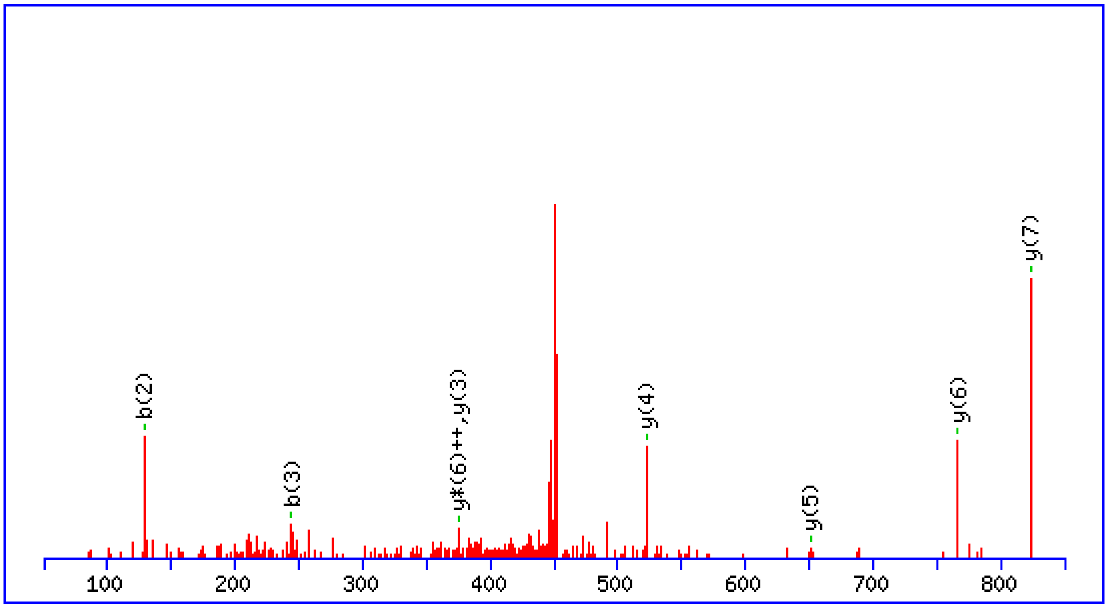


Monoisotopic mass of neutral peptide Mr(calc): 1214.6871
Fixed modifications: Carbamidomethyl (C)
Ions Score: 65 **Expect:** 2.9e-005
Matches (Bold Red): 13/107 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			**V**							**11**
2	74.0600	**201.1234**	101.0653	183.1128	92.0600	**T**	**1116.6259**	558.8166	1099.5994	550.3033	**1098.6154**	549.8113	**10**
3	30.0338	258.1448	129.5761	240.1343	120.5708	**G**	**1015.5782**	508.2928	998.5517	499.7795	997.5677	499.2875	**9**
4	102.0550	**387.1874**	194.0974	369.1769	185.0921	**E**	**958.5568**	479.7820	941.5302	471.2688	940.5462	470.7767	**8**
5	72.0808	486.2558	243.6316	468.2453	234.6263	**V**	**829.5142**	415.2607	812.4876	406.7475	811.5036	406.2554	**7**
6	86.0964	599.3399	300.1736	581.3293	291.1683	**L**	**730.4458**	365.7265	713.4192	**357.2132**	712.4352	356.7212	**6**
7	88.0393	714.3668	357.6871	696.3563	348.6818	**D**	**617.3617**	309.1845	600.3352	300.6712	599.3511	300.1792	**5**
8	86.0964	827.4509	414.2291	809.4403	405.2238	**I**	**502.3348**	251.6710	485.3082	243.1577	484.3242	242.6657	**4**
9	86.0964	940.5350	470.7711	922.5244	461.7658	**L**	**389.2507**	195.1290	372.2241	186.6157	371.2401	186.1237	**3**
10	74.0600	1041.5827	521.2950	1023.5721	512.2897	**T**	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	**2**
11	129.1135					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **AGDEFVEK**
Found in **Q16836**, Q16836|HCDH_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=2

Match to Query 212: 893.420562 from(447.717557,2+)

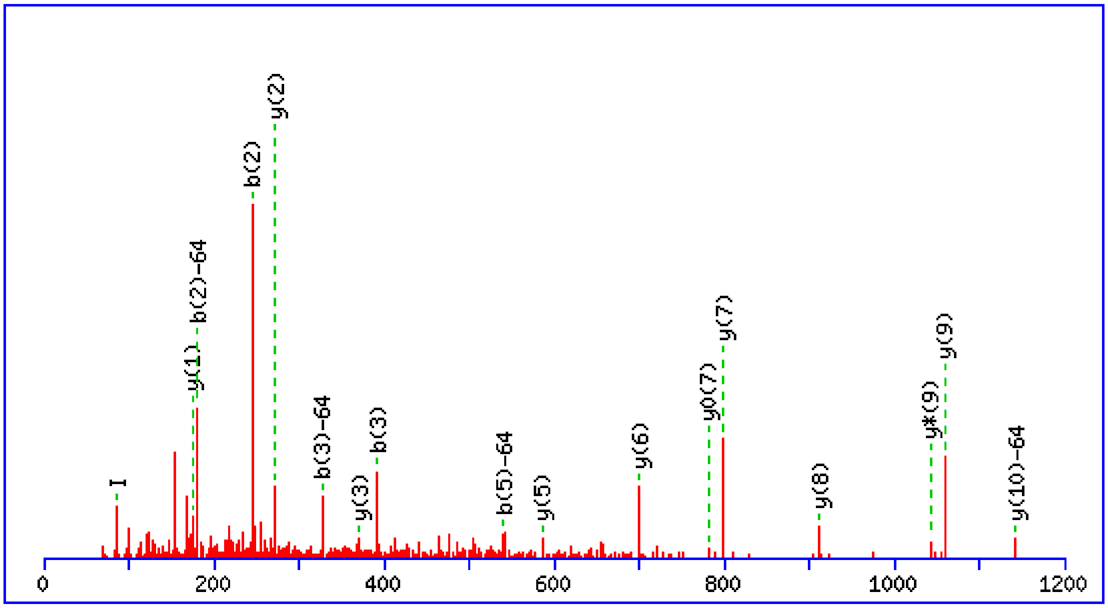


Monoisotopic mass of neutral peptide Mr(calc): 893.4131
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 **Expect:** 0.0023
Matches (Bold Red): 8/72 fragment ions using 18 most intense peaks

#	Immon.	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	44.0495	72.0444	36.5258			A							8
2	30.0338	**129.0659**	65.0366			G	**823.3832**	412.1953	806.3567	403.6820	805.3727	403.1900	7
3	88.0393	**244.0928**	122.5500	226.0822	113.5448	D	**766.3618**	383.6845	749.3352	**375.1712**	748.3512	374.6792	6
4	102.0550	373.1354	187.0713	355.1248	178.0661	E	**651.3348**	326.1710	634.3083	317.6578	633.3243	317.1658	5
5	120.0808	520.2038	260.6055	502.1932	251.6003	F	**522.2922**	261.6498	505.2657	253.1365	504.2817	252.6445	4
6	72.0808	619.2722	310.1397	601.2617	301.1345	V	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
7	102.0550	748.3148	374.6610	730.3042	365.6558	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
8	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **PMFIVNTNVPR**
Found in **P14174**, P14174|MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4

Match to Query 226: 1302.446554 from(652.230553,2+)

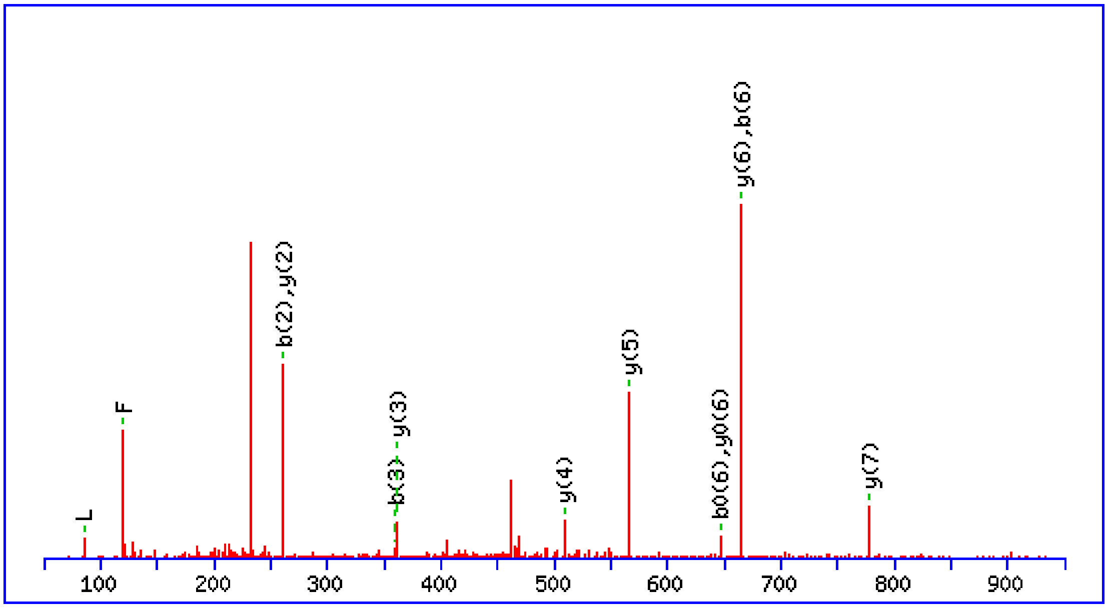


Monoisotopic mass of neutral peptide Mr(calc): 1302.6754
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 67 **Expect:** 1.3e-005
Matches (Bold Red): 17/144 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	70.0651	98.0600	49.5337					P							11
2	56.0495	**181.0972**	91.0522					M	**1142.6317**	571.8195	1125.6051	563.3062	1124.6211	562.8142	10
3	120.0808	**328.1656**	164.5864					F	**1059.5946**	530.3009	**1042.5680**	521.7876	1041.5840	521.2956	9
4	**86.0964**	441.2496	221.1285					I	**912.5261**	456.7667	895.4996	448.2534	894.5156	447.7614	8
5	72.0808	**540.3181**	270.6627					V	**799.4421**	400.2247	782.4155	391.7114	**781.4315**	391.2194	7
6	87.0553	654.3610	327.6841	637.3344	319.1709			N	**700.3737**	350.6905	683.3471	342.1772	682.3631	341.6852	6
7	74.0600	755.4087	378.2080	738.3821	369.6947	737.3981	369.2027	T	**586.3307**	293.6690	569.3042	285.1557	568.3202	284.6637	5
8	87.0553	869.4516	435.2294	852.4250	426.7162	851.4410	426.2241	N	485.2831	243.1452	468.2565	234.6319			4
9	72.0808	968.5200	484.7636	951.4934	476.2504	950.5094	475.7584	V	**371.2401**	186.1237	354.2136	177.6104			3
10	70.0651	1065.5728	533.2900	1048.5462	524.7767	1047.5622	524.2847	P	**272.1717**	136.5895	255.1452	128.0762			2
11	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FLVGFTNK**
Found in **P43307**, P43307|SSRA_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3

Match to Query 260: 924.472170 from(463.243361,2+)

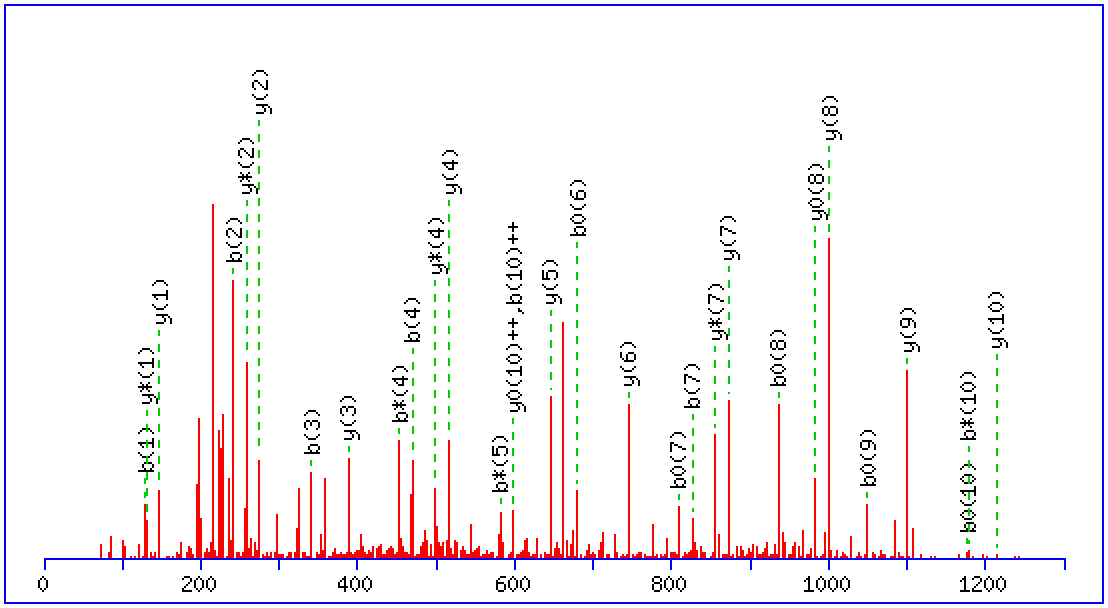


Monoisotopic mass of neutral peptide Mr(calc): 924.5069
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 **Expect:** 0.0038
Matches (Bold Red): 14/66 fragment ions using 18 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							8
2	**86.0964**	**261.1598**	131.0835					L	**778.4458**	389.7265	761.4192	381.2132	760.4352	380.7212	7
3	72.0808	**360.2282**	180.6177					V	**665.3617**	333.1845	648.3352	324.6712	**647.3511**	324.1792	6
4	30.0338	417.2496	209.1285					G	**566.2933**	283.6503	549.2667	275.1370	548.2827	274.6450	5
5	**120.0808**	564.3180	282.6627					F	**509.2718**	255.1395	492.2453	246.6263	491.2613	246.1343	4
6	74.0600	**665.3657**	333.1865			**647.3552**	324.1812	T	**362.2034**	181.6053	345.1769	173.0921	344.1928	172.6001	3
7	87.0553	779.4087	390.2080	762.3821	381.6947	761.3981	381.2027	N	**261.1557**	131.0815	244.1292	122.5682			2
8	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **QLVEQVEQIQK**
Found in **Q9BVK6**, Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=1

Match to Query 589: 1340.728280 from(671.371416,2+)

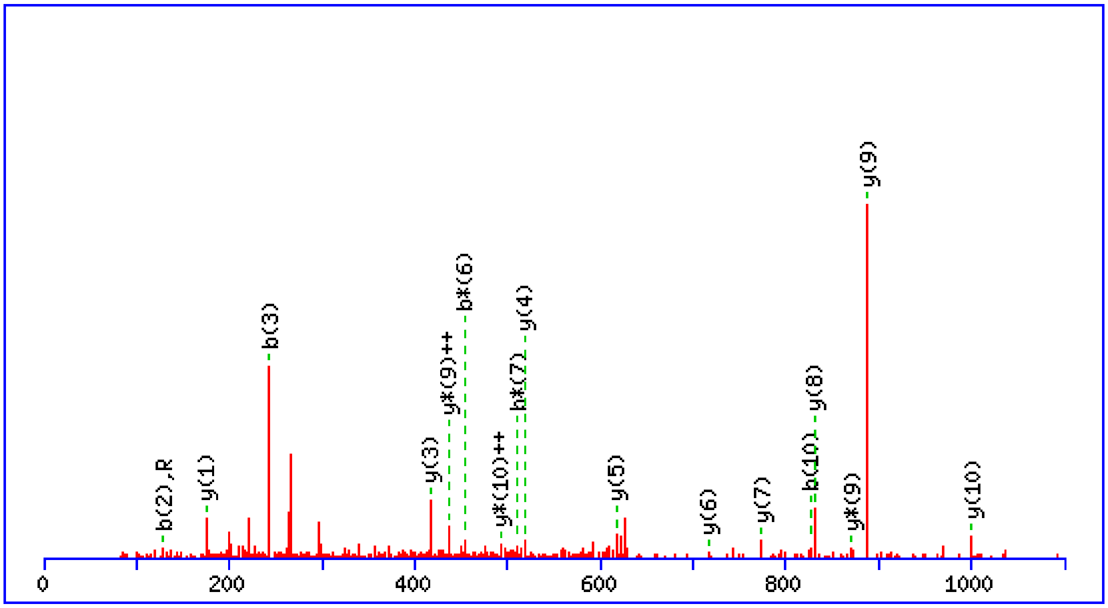


Monoisotopic mass of neutral peptide Mr(calc): 1340.7300
Fixed modifications: Carbamidomethyl (C)
Ions Score: 90 **Expect:** 7.5e-008
Matches (Bold Red): 31/117 fragment ions using 39 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0709	**129.0659**	65.0366	112.0393	56.5233			Q							11
2	86.0964	**242.1499**	121.5786	225.1234	113.0653			L	**1213.6787**	607.3430	1196.6521	598.8297	1195.6681	**598.3377**	10
3	72.0808	**341.2183**	171.1128	324.1918	162.5995			V	**1100.5946**	550.8009	1083.5681	542.2877	1082.5841	541.7957	9
4	102.0550	**470.2609**	235.6341	**453.2344**	227.1208	452.2504	226.6288	E	**1001.5262**	501.2667	984.4997	492.7535	**983.5156**	492.2615	8
5	101.0709	**598.3195**	299.6634	**581.2930**	291.1501	580.3089	290.6581	Q	**872.4836**	436.7454	**855.4571**	428.2322	854.4730	427.7402	7
6	72.0808	697.3879	349.1976	680.3614	340.6843	**679.3774**	340.1923	V	**744.4250**	372.7162	727.3985	364.2029	726.4145	363.7109	6
7	102.0550	**826.4305**	413.7189	809.4040	405.2056	**808.4199**	404.7136	E	**645.3566**	323.1819	628.3301	314.6687	627.3461	314.1767	5
8	101.0709	954.4891	477.7482	937.4625	469.2349	**936.4785**	468.7429	Q	**516.3140**	258.6607	**499.2875**	250.1474			4
9	86.0964	1067.5732	534.2902	1050.5466	525.7769	**1049.5626**	525.2849	I	**388.2554**	194.6314	371.2289	186.1181			3
10	101.0709	1195.6317	**598.3195**	**1178.6052**	589.8062	**1177.6212**	589.3142	Q	**275.1714**	138.0893	**258.1448**	129.5761			2
11	101.1073							K	**147.1128**	74.0600	**130.0863**	65.5468			1

MS/MS Fragmentation of **AGNLGGGVVTIER**
Found in **P35268**, P35268|RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2

Match to Query 439: 1241.694936 from(621.854744,2+)

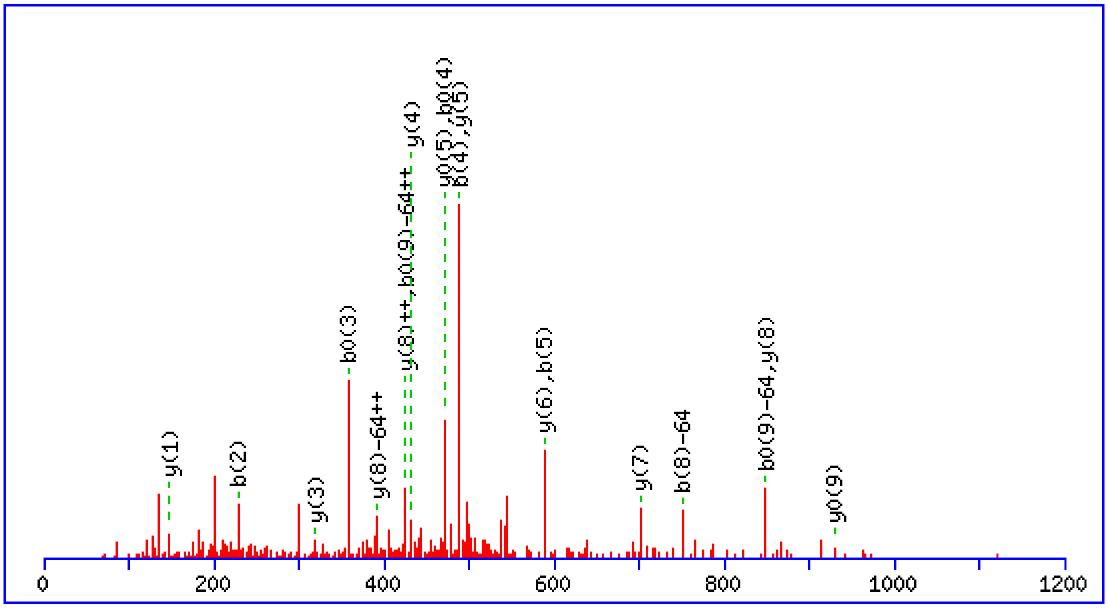


Monoisotopic mass of neutral peptide Mr(calc): 1241.6728
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 **Expect:** 6.6e-005
Matches (Bold Red): 18/133 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	44.0495	72.0444	36.5258					A							13
2	30.0338	**129.0659**	65.0366					G	1171.6430	586.3251	1154.6164	577.8118	1153.6324	577.3198	12
3	87.0553	**243.1088**	122.0580	226.0822	113.5448			N	1114.6215	557.8144	1097.5950	549.3011	1096.6109	548.8091	11
4	86.0964	356.1928	178.6001	339.1663	170.0868			L	**1000.5786**	500.7929	983.5520	**492.2796**	982.5680	491.7876	10
5	30.0338	413.2143	207.1108	396.1878	198.5975			G	**887.4945**	444.2509	**870.4680**	**435.7376**	869.4839	435.2456	9
6	30.0338	470.2358	235.6215	**453.2092**	227.1083			G	**830.4730**	415.7402	813.4465	407.2269	812.4625	406.7349	8
7	30.0338	527.2572	264.1323	**510.2307**	255.6190			G	**773.4516**	387.2294	756.4250	378.7162	755.4410	378.2241	7
8	72.0808	626.3257	313.6665	609.2991	305.1532			V	**716.4301**	358.7187	699.4036	350.2054	698.4196	349.7134	6
9	72.0808	725.3941	363.2007	708.3675	354.6874			V	**617.3617**	309.1845	600.3352	300.6712	599.3511	300.1792	5
10	74.0600	**826.4417**	413.7245	809.4152	405.2112	808.4312	404.7192	T	**518.2933**	259.6503	501.2667	251.1370	500.2827	250.6450	4
11	86.0964	939.5258	470.2665	922.4993	461.7533	921.5152	461.2613	I	**417.2456**	209.1264	400.2191	200.6132	399.2350	200.1212	3
12	102.0550	1068.5684	534.7878	1051.5419	526.2746	1050.5578	525.7826	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **EVMLVGIGDK**
Found in **P36542**, P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1

Match to Query 261: 1075.533962 from(538.774257,2+)

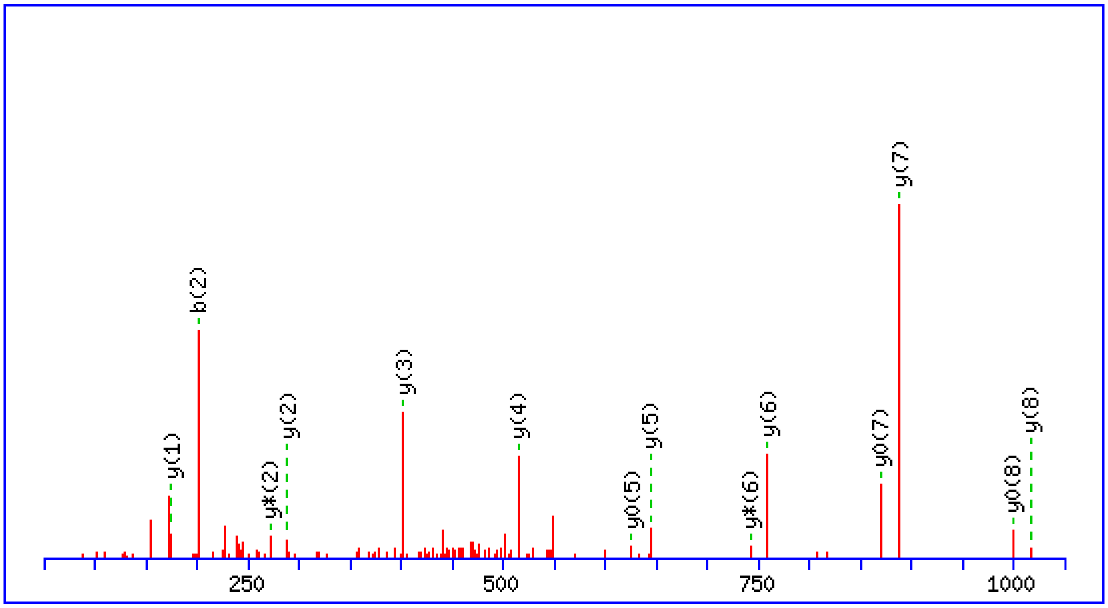


Monoisotopic mass of neutral peptide Mr(calc): 1075.5584
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 **Expect:** 0.008
Matches (Bold Red): 19/139 fragment ions using 29 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286	112.0393	56.5233	E							10
2	72.0808	**229.1183**	115.0628	211.1077	106.0575	V	947.5230	474.2652	930.4965	465.7519	**929.5125**	465.2599	9
3	120.0478	376.1537	188.5805	**358.1431**	179.5752	M	**848.4546**	**424.7309**	831.4281	416.2177	830.4441	415.7257	8
4	86.0964	**489.2378**	245.1225	**471.2272**	236.1172	L	**701.4192**	351.2132	684.3927	342.7000	683.4087	342.2080	7
5	72.0808	**588.3062**	294.6567	570.2956	285.6514	V	**588.3352**	294.6712	571.3086	286.1579	570.3246	285.6659	6
6	30.0338	645.3276	323.1675	627.3171	314.1622	G	**489.2667**	245.1370	472.2402	236.6237	**471.2562**	236.1317	5
7	86.0964	758.4117	379.7095	740.4011	370.7042	I	**432.2453**	216.6263	415.2187	208.1130	414.2347	207.6210	4
8	30.0338	815.4332	408.2202	797.4226	399.2149	G	**319.1612**	160.0842	302.1347	151.5710	301.1506	151.0790	3
9	88.0393	930.4601	465.7337	912.4495	456.7284	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
10	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AEEDEILNR**
Found in **P27824**, P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2

Match to Query 347: 1087.528544 from(544.771548,2+)

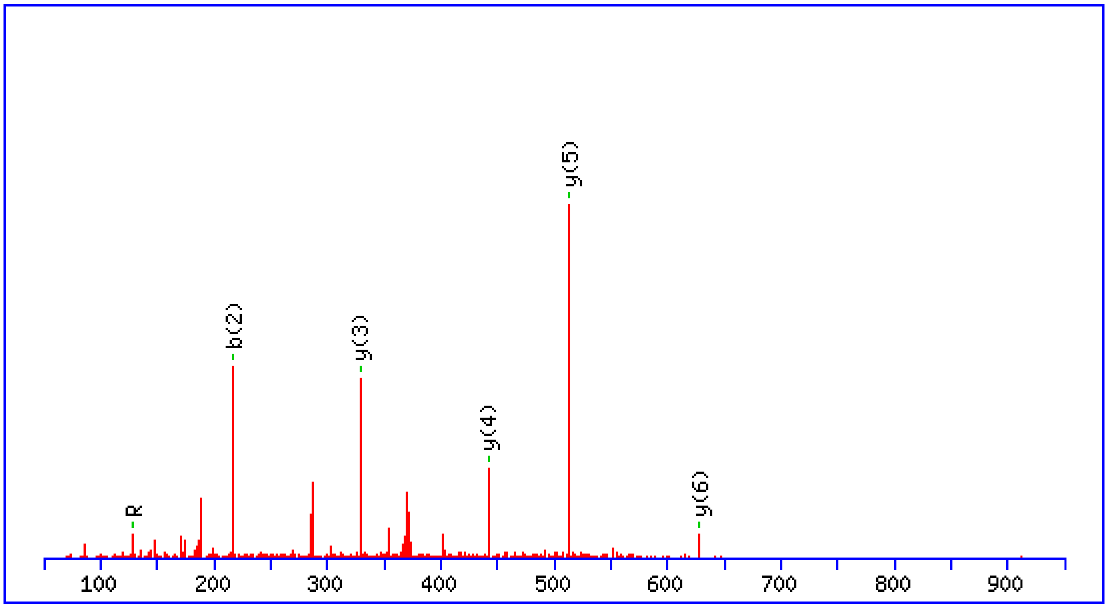


Monoisotopic mass of neutral peptide Mr(calc): 1087.5145
Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 **Expect:** 0.00012
Matches (Bold Red): 14/81 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					**A**							9
2	102.0550	**201.0870**	101.0471			183.0764	92.0418	**E**	**1017.4847**	509.2460	1000.4582	500.7327	**999.4742**	500.2407	8
3	102.0550	330.1296	165.5684			312.1190	156.5631	**E**	**888.4421**	444.7247	871.4156	436.2114	**870.4316**	435.7194	7
4	88.0393	445.1565	223.0819			427.1460	214.0766	**D**	**759.3995**	380.2034	**742.3730**	371.6901	741.3890	371.1981	6
5	102.0550	574.1991	287.6032			556.1885	278.5979	**E**	**644.3726**	322.6899	627.3461	314.1767	**626.3620**	313.6847	5
6	86.0964	687.2832	344.1452			669.2726	335.1399	**I**	**515.3300**	258.1686	498.3035	249.6554			4
7	86.0964	800.3672	400.6873			782.3567	391.6820	**L**	**402.2459**	201.6266	385.2194	193.1133			3
8	87.0553	914.4102	457.7087	897.3836	449.1954	896.3996	448.7034	**N**	**289.1619**	145.0846	**272.1353**	136.5713			2
9	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TDAIPGR**
Found in **P00403**, P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1

Match to Query 52: 728.417890 from(365.216221,2+)

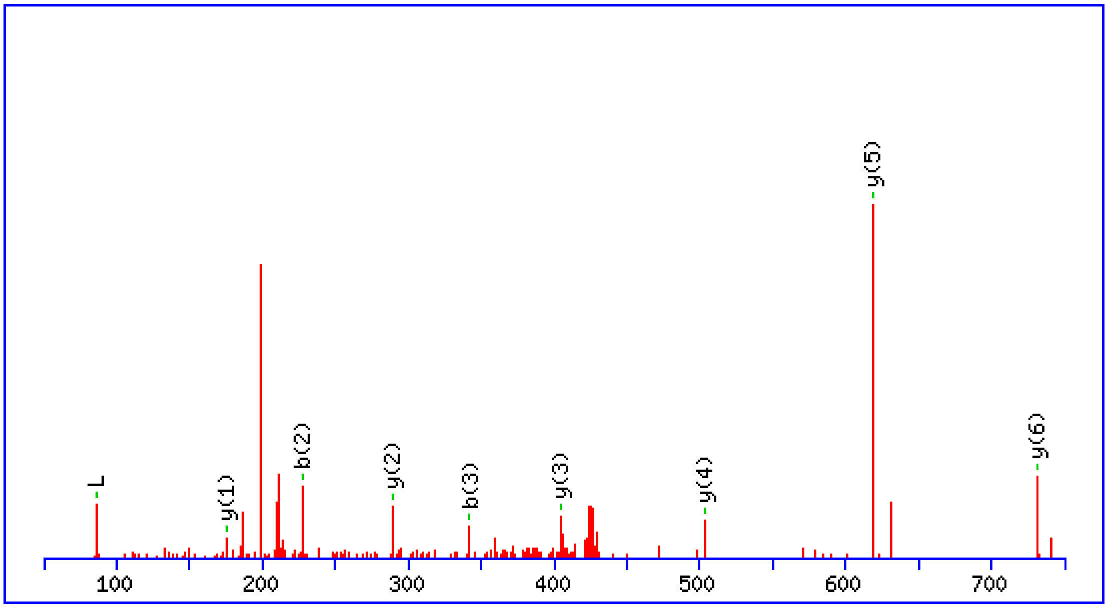


Monoisotopic mass of neutral peptide Mr(calc): 728.3817
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 **Expect:** 0.0058
Matches (Bold Red): 6/57 fragment ions using 7 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	**T**							**7**
2	88.0393	**217.0819**	109.0446	199.0713	100.0393	**D**	**628.3413**	314.6743	611.3148	306.1610	610.3307	305.6690	**6**
3	44.0495	288.1190	144.5631	270.1084	135.5579	**A**	**513.3144**	257.1608	496.2878	248.6475			**5**
4	86.0964	401.2031	201.1052	383.1925	192.0999	**I**	**442.2772**	221.6423	425.2507	213.1290			**4**
5	70.0651	498.2558	249.6316	480.2453	240.6263	**P**	**329.1932**	165.1002	312.1666	156.5870			**3**
6	30.0338	555.2773	278.1423	537.2667	269.1370	**G**	232.1404	116.5738	215.1139	108.0606			**2**
7	**129.1135**					**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LLDVDNR**
Found in **P00403**, P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1

Match to Query 47: 843.368168 from(422.691360,2+)

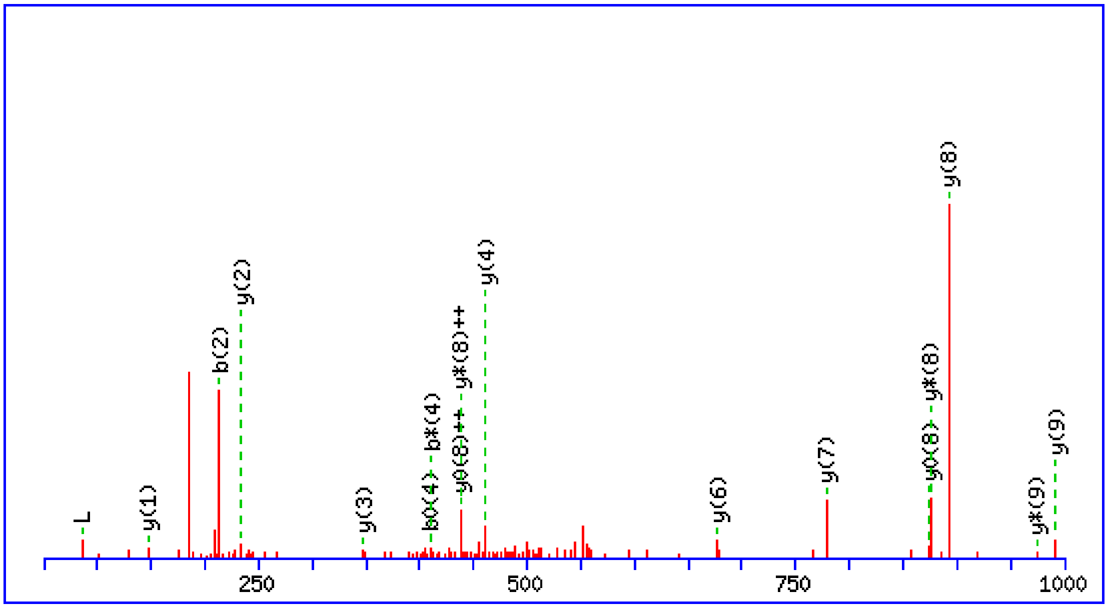


Monoisotopic mass of neutral peptide Mr(calc): 843.4450
Fixed modifications: Carbamidomethyl (C)
Ions Score: 34 **Expect:** 0.039
Matches (Bold Red): 10/61 fragment ions using 29 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**7**
2	**86.0964**	**227.1754**	114.0913					**L**	**731.3682**	366.1878	714.3417	357.6745	713.3577	357.1825	**6**
3	88.0393	**342.2023**	171.6048			324.1918	162.5995	**D**	**618.2842**	309.6457	601.2576	301.1325	600.2736	300.6404	**5**
4	72.0808	441.2708	221.1390			423.2602	212.1337	**V**	**503.2572**	252.1323	486.2307	243.6190	485.2467	243.1270	**4**
5	88.0393	556.2977	278.6525			538.2871	269.6472	**D**	**404.1888**	202.5980	387.1623	194.0848	386.1783	193.5928	**3**
6	87.0553	670.3406	335.6740	653.3141	327.1607	652.3301	326.6687	**N**	**289.1619**	145.0846	272.1353	136.5713			**2**
7	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LVNTSENLSK**
Found in **Q9UEU0**, Q9UEU0|VTI1B_HUMAN Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=2 SV=3

Match to Query 301: 1103.582372 from(552.798462,2+)

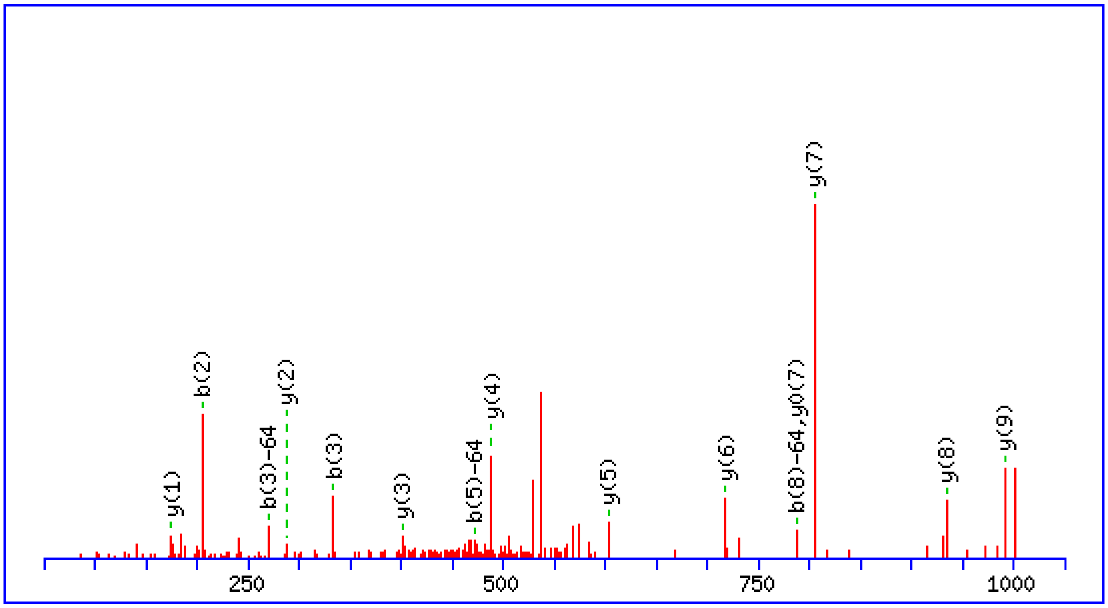


Monoisotopic mass of neutral peptide Mr(calc): 1103.5822
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 **Expect:** 0.00015
Matches (Bold Red): 18/106 fragment ions using 42 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**10**
2	72.0808	**213.1598**	107.0835					**V**	**991.5055**	496.2564	**974.4789**	487.7431	973.4949	487.2511	**9**
3	87.0553	327.2027	164.1050	310.1761	155.5917			**N**	**892.4371**	446.7222	**875.4105**	**438.2089**	**874.4265**	**437.7169**	**8**
4	74.0600	428.2504	214.6288	**411.2238**	206.1155	**410.2398**	205.6235	**T**	**778.3941**	389.7007	761.3676	381.1874	760.3836	380.6954	**7**
5	60.0444	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	**S**	**677.3464**	339.1769	660.3199	330.6636	659.3359	330.1716	**6**
6	102.0550	644.3250	322.6661	627.2984	314.1529	626.3144	313.6608	**E**	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	**5**
7	87.0553	758.3679	379.6876	741.3414	371.1743	740.3573	370.6823	**N**	**461.2718**	231.1395	444.2453	222.6263	443.2613	222.1343	**4**
8	**86.0964**	871.4520	436.2296	854.4254	427.7163	853.4414	427.2243	**L**	**347.2289**	174.1181	330.2023	165.6048	329.2183	165.1128	**3**
9	60.0444	958.4840	479.7456	941.4575	471.2324	940.4734	470.7404	**S**	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	**2**
10	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **MGESDDSILR**
Found in **P63220**, P63220|RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1

Match to Query 256: 1137.393458 from(569.704005,2+)

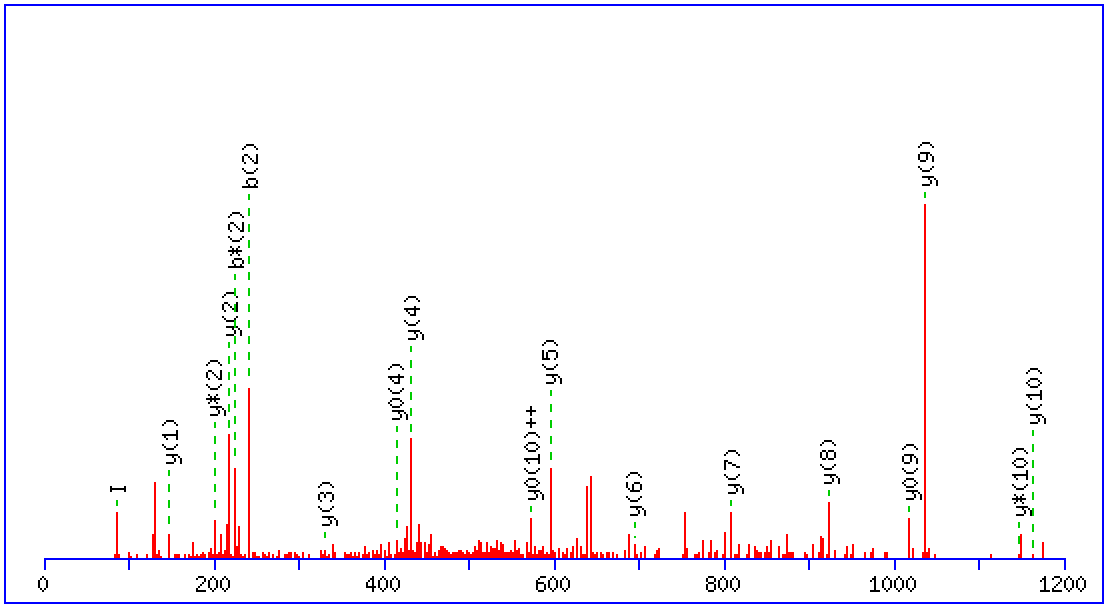


Monoisotopic mass of neutral peptide Mr(calc): 1137.4972
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 81 **Expect:** 4.4e-007
Matches (Bold Red): 15/123 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	56.0495	84.0444	42.5258			M							10
2	30.0338	141.0659	71.0366			G	**991.4691**	496.2382	974.4425	487.7249	973.4585	487.2329	9
3	102.0550	**270.1085**	135.5579	252.0979	126.5526	E	**934.4476**	467.7274	917.4211	459.2142	916.4370	458.7222	8
4	60.0444	357.1405	179.0739	339.1299	170.0686	S	**805.4050**	403.2061	788.3785	394.6929	**787.3945**	394.2009	7
5	88.0393	**472.1674**	236.5873	454.1569	227.5821	D	**718.3730**	359.6901	701.3464	351.1769	700.3624	350.6849	6
6	88.0393	587.1944	294.1008	569.1838	285.0955	D	**603.3461**	302.1767	586.3195	293.6634	585.3355	293.1714	5
7	60.0444	674.2264	337.6168	656.2158	328.6116	S	**488.3191**	244.6632	471.2926	236.1499	470.3085	235.6579	4
8	86.0964	**787.3105**	394.1589	769.2999	385.1536	I	**401.2871**	201.1472	384.2605	192.6339			3
9	86.0964	900.3945	450.7009	882.3840	441.6956	L	**288.2030**	144.6051	271.1765	136.0919			2
10	129.1135					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LQNNNVYTIAK**
Found in **P63010**, P63010|AP2B1_HUMAN AP-2 complex subunit beta-1 OS=Homo sapiens GN=AP2B1 PE=1 SV=1

Match to Query 588: 1276.635040 from(639.324796,2+)

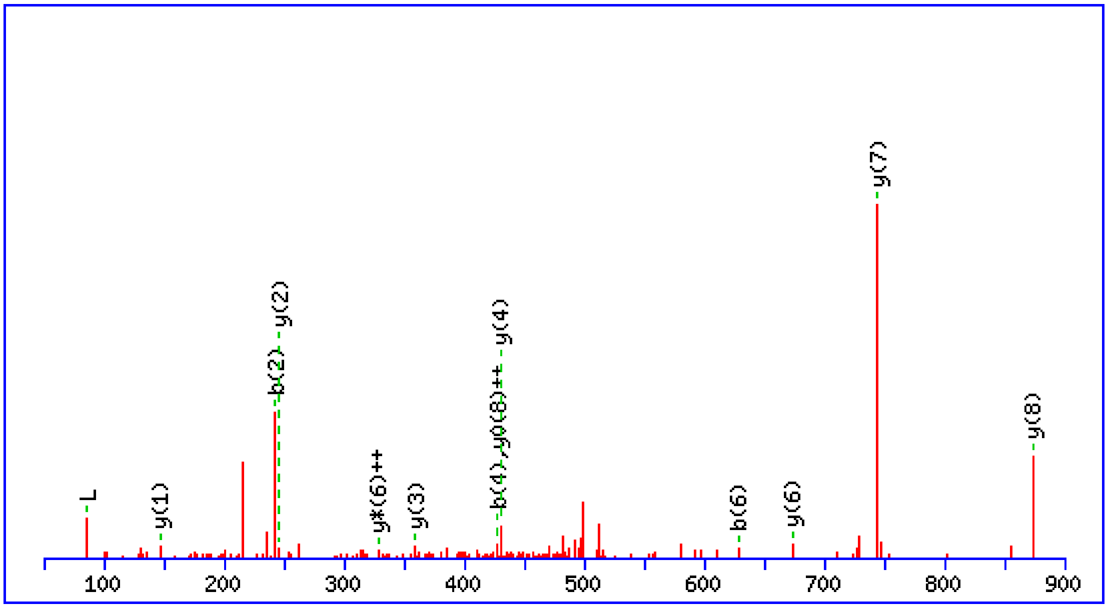


Monoisotopic mass of neutral peptide Mr(calc): 1276.6775
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00031
Matches (Bold Red): 19/109 fragment ions using 49 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							11
2	101.0709	**242.1499**	121.5786	**225.1234**	113.0653			Q	**1164.6008**	582.8040	**1147.5742**	574.2907	1146.5902	**573.7987**	10
3	87.0553	356.1928	178.6001	339.1663	170.0868			N	**1036.5422**	518.7747	1019.5156	510.2615	**1018.5316**	509.7694	9
4	87.0553	470.2358	235.6215	453.2092	227.1082			N	**922.4993**	461.7533	905.4727	453.2400	904.4887	452.7480	8
5	87.0553	584.2787	292.6430	567.2522	284.1297			N	**808.4563**	404.7318	791.4298	396.2185	790.4458	395.7265	7
6	72.0808	683.3471	342.1772	666.3206	333.6639			V	**694.4134**	347.7103	677.3869	339.1971	676.4028	338.7051	6
7	136.0757	846.4104	423.7089	829.3839	415.1956			Y	**595.3450**	298.1761	578.3184	289.6629	577.3344	289.1709	5
8	74.0600	947.4581	474.2327	930.4316	465.7194	929.4476	465.2274	T	**432.2817**	216.6445	415.2551	208.1312	**414.2711**	207.6392	4
9	**86.0964**	1060.5422	530.7747	1043.5156	522.2615	1042.5316	521.7694	I	**331.2340**	166.1206	314.2074	157.6074			3
10	44.0495	1131.5793	566.2933	1114.5528	557.7800	1113.5687	557.2880	A	**218.1499**	109.5786	**201.1234**	101.0653			2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IEANEALVK**
Found in **P30049**, P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2

Match to Query 96: 985.432808 from(493.723680,2+)

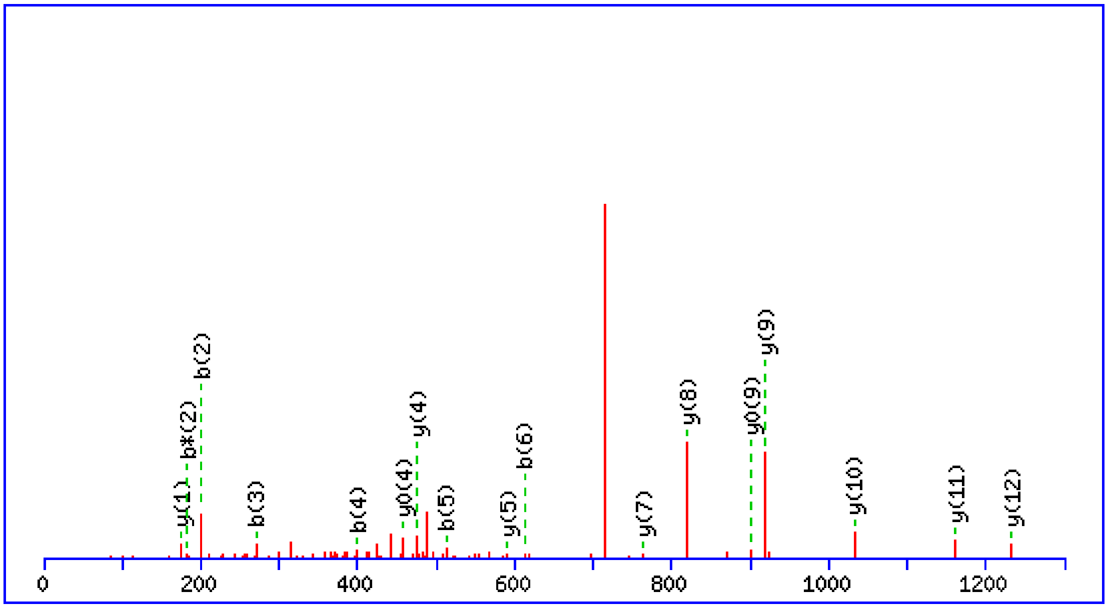


Monoisotopic mass of neutral peptide Mr(calc): 985.5444
Fixed modifications: Carbamidomethyl (C)
Ions Score: 51 **Expect:** 0.00065
Matches (Bold Red): 14/89 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**I**							9
2	102.0550	**243.1339**	122.0706			225.1234	113.0653	**E**	**873.4676**	437.2374	856.4411	428.7242	855.4571	**428.2322**	8
3	44.0495	314.1710	157.5892			296.1605	148.5839	**A**	**744.4250**	372.7162	727.3985	364.2029	726.4145	363.7109	7
4	87.0553	**428.2140**	214.6106	411.1874	206.0974	410.2034	205.6053	**N**	**673.3879**	337.1976	656.3614	**328.6843**	655.3774	328.1923	6
5	102.0550	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	**E**	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
6	44.0495	**628.2937**	314.6505	611.2671	306.1372	610.2831	305.6452	**A**	**430.3024**	215.6548	413.2758	207.1416			4
7	**86.0964**	741.3777	371.1925	724.3512	362.6792	723.3672	362.1872	**L**	**359.2653**	180.1363	342.2387	171.6230			3
8	72.0808	840.4462	420.7267	823.4196	412.2134	822.4356	411.7214	**V**	**246.1812**	123.5942	229.1547	115.0810			2
9	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AQAELVGTADEATR**
Found in **P30049**, P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2

Match to Query 368: 1430.626790 from(716.320671,2+)

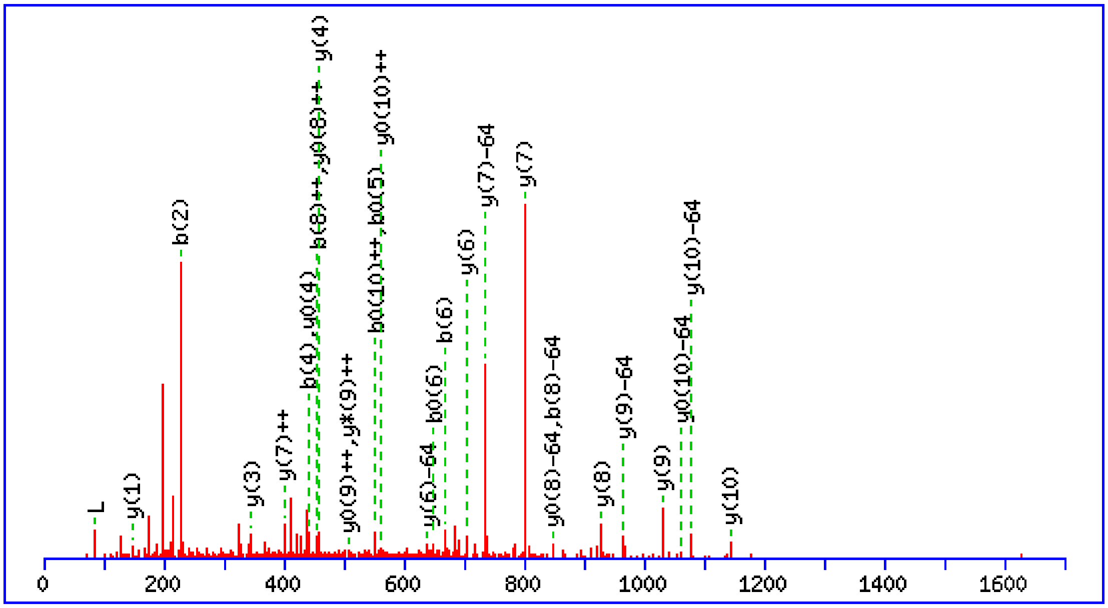


Monoisotopic mass of neutral peptide Mr(calc): 1430.7001
Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 **Expect:** 9e-005
Matches (Bold Red): 17/160 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							14
2	101.0709	**200.1030**	100.5551	**183.0764**	92.0418			Q	1360.6703	680.8388	1343.6438	672.3255	1342.6597	671.8335	13
3	44.0495	**271.1401**	136.0737	254.1135	127.5604			A	**1232.6117**	616.8095	1215.5852	608.2962	1214.6012	607.8042	12
4	102.0550	**400.1827**	200.5950	383.1561	192.0817	382.1721	191.5897	E	**1161.5746**	581.2909	1144.5481	572.7777	1143.5640	572.2857	11
5	86.0964	**513.2667**	257.1370	496.2402	248.6237	495.2562	248.1317	L	**1032.5320**	516.7696	1015.5055	508.2564	1014.5215	507.7644	10
6	72.0808	**612.3352**	306.6712	595.3086	298.1579	594.3246	297.6659	V	**919.4480**	460.2276	902.4214	451.7143	**901.4374**	451.2223	9
7	30.0338	669.3566	335.1819	652.3301	326.6687	651.3461	326.1767	G	**820.3795**	410.6934	803.3530	402.1801	802.3690	401.6881	8
8	74.0600	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	T	**763.3581**	382.1827	746.3315	373.6694	745.3475	373.1774	7
9	44.0495	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	A	662.3104	331.6588	645.2838	323.1456	644.2998	322.6536	6
10	88.0393	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	D	**591.2733**	296.1403	574.2467	287.6270	573.2627	287.1350	5
11	102.0550	1085.5109	543.2591	1068.4844	534.7458	1067.5004	534.2538	E	**476.2463**	238.6268	459.2198	230.1135	**458.2358**	229.6215	4
12	44.0495	1156.5481	578.7777	1139.5215	570.2644	1138.5375	569.7724	A	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
13	74.0600	1257.5957	629.3015	1240.5692	620.7882	1239.5852	620.2962	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
14	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ILLTEPPMNPTK**
Found in **P61160**, P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1

Match to Query 327: 1368.953878 from(685.484215,2+)

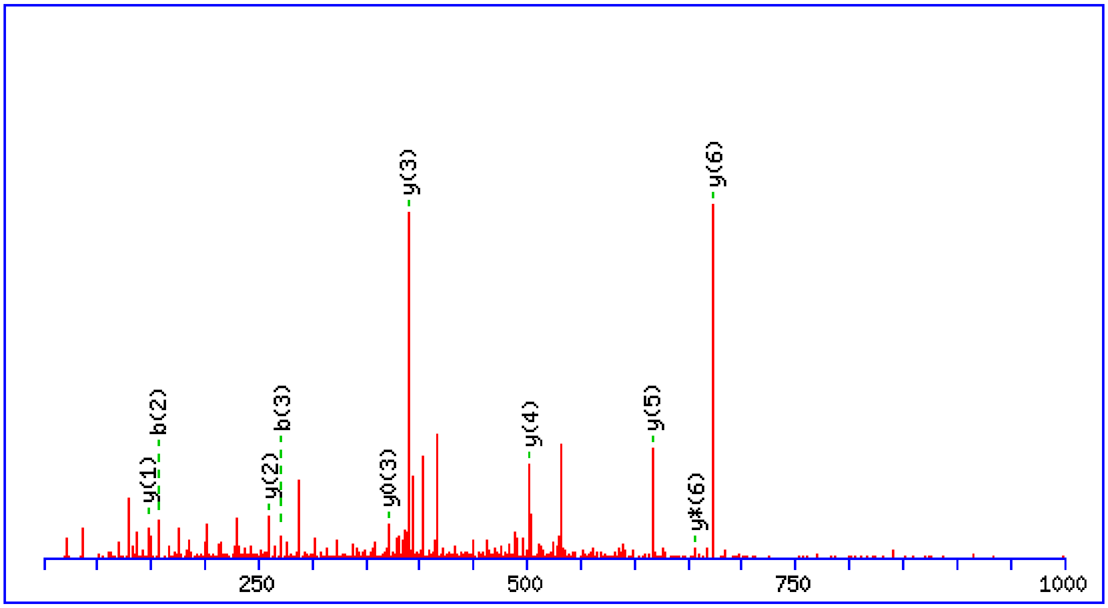


Monoisotopic mass of neutral peptide Mr(calc): 1368.7323
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 34 **Expect:** 0.023
Matches (Bold Red): 31/185 fragment ions using 44 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							12
2	**86.0964**	**227.1754**	114.0913					L	1256.6555	628.8314	1239.6290	620.3181	1238.6449	619.8261	11
3	**86.0964**	340.2595	170.6334					L	**1143.5714**	572.2894	1126.5449	563.7761	1125.5609	**563.2841**	10
4	74.0600	**441.3071**	221.1572			423.2966	212.1519	T	**1030.4874**	515.7473	1013.4608	**507.2341**	1012.4768	**506.7420**	9
5	102.0550	570.3497	285.6785			**552.3392**	276.6732	E	**929.4397**	465.2235	912.4132	456.7102	911.4291	**456.2182**	8
6	70.0651	**667.4025**	334.2049			**649.3919**	325.1996	P	**800.3971**	**400.7022**	783.3706	392.1889	782.3865	391.6969	7
7	70.0651	764.4553	382.7313			746.4447	373.7260	P	**703.3443**	352.1758	686.3178	343.6625	685.3338	343.1705	6
8	120.0478	911.4907	**456.2490**			893.4801	447.2437	M	606.2916	303.6494	589.2650	295.1362	588.2810	294.6441	5
9	87.0553	1025.5336	513.2704	1008.5071	504.7572	1007.5230	504.2652	N	**459.2562**	230.1317	442.2296	221.6185	**441.2456**	221.1264	4
10	70.0651	1122.5864	561.7968	1105.5598	553.2835	1104.5758	**552.7915**	P	**345.2132**	173.1103	328.1867	164.5970	327.2027	164.1050	3
11	74.0600	1223.6340	612.3207	1206.6075	603.8074	1205.6235	603.3154	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
12	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VGNIEIK**
Found in **P61160**, P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1

Match to Query 66: 771.414454 from(386.714503,2+)

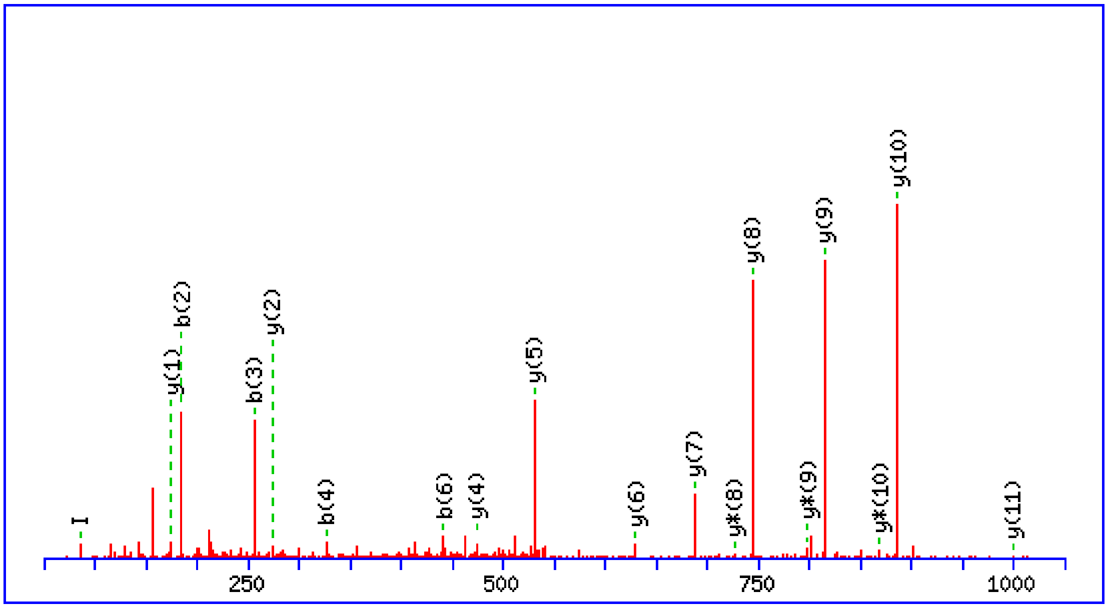


Monoisotopic mass of neutral peptide Mr(calc): 771.4490
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 **Expect:** 0.01
Matches (Bold Red): 10/63 fragment ions using 30 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							7
2	30.0338	**157.0972**	79.0522					G	**673.3879**	337.1976	**656.3614**	328.6843	655.3774	328.1923	6
3	87.0553	**271.1401**	136.0737	254.1135	127.5604			N	**616.3665**	308.6869	599.3399	300.1736	598.3559	299.6816	5
4	86.0964	384.2241	192.6157	367.1976	184.1024			I	**502.3235**	251.6654	485.2970	243.1521	484.3130	242.6601	4
5	102.0550	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	E	**389.2395**	195.1234	372.2129	186.6101	**371.2289**	186.1181	3
6	86.0964	626.3508	313.6790	609.3243	305.1658	608.3402	304.6738	I	**260.1969**	130.6021	243.1703	122.0888			2
7	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ALAAGGVGSIVR**
Found in **O15511**, O15511|ARPC5_HUMAN Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3

Match to Query 377: 1069.622170 from(535.818361,2+)

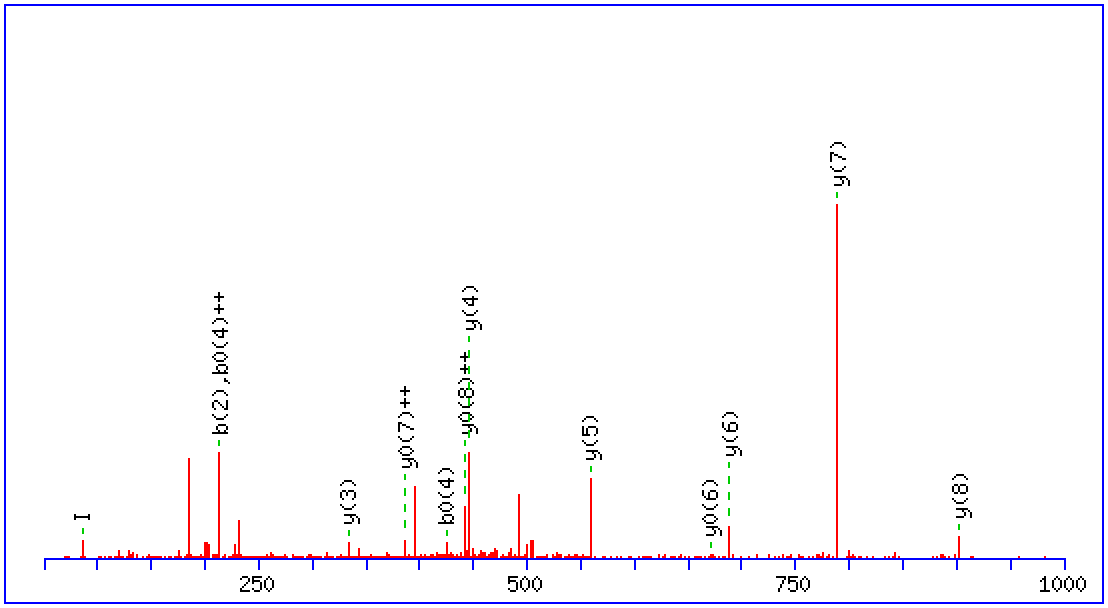


Monoisotopic mass of neutral peptide Mr(calc): 1069.6244
Fixed modifications: Carbamidomethyl (C)
Ions Score: 68 **Expect:** 1.3e-005
Matches (Bold Red): 19/100 fragment ions using 43 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							12
2	**86.0964**	**185.1285**	93.0679			L	**999.5946**	500.3009	982.5680	491.7876	981.5840	491.2956	11
3	44.0495	**256.1656**	128.5864			A	**886.5105**	443.7589	**869.4839**	435.2456	868.4999	434.7536	10
4	44.0495	**327.2027**	164.1050			A	**815.4734**	408.2403	**798.4468**	399.7271	797.4628	399.2350	9
5	30.0338	384.2241	192.6157			G	**744.4363**	372.7218	**727.4097**	364.2085	726.4257	363.7165	8
6	30.0338	**441.2456**	221.1264			G	**687.4148**	344.2110	670.3883	335.6978	669.4042	335.2058	7
7	72.0808	540.3140	270.6607			V	**630.3933**	315.7003	613.3668	307.1870	612.3828	306.6950	6
8	30.0338	597.3355	299.1714			G	**531.3249**	266.1661	514.2984	257.6528	513.3144	257.1608	5
9	60.0444	684.3675	342.6874	666.3570	333.6821	S	**474.3035**	237.6554	457.2769	229.1421	456.2929	228.6501	4
10	**86.0964**	797.4516	399.2294	779.4410	390.2241	I	387.2714	194.1394	370.2449	185.6261			3
11	72.0808	896.5200	448.7636	878.5094	439.7584	V	**274.1874**	137.5973	257.1608	129.0840			2
12	129.1135					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VLTEIIASR**
Found in **P08758**, P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2

Match to Query 377: 1000.576104 from(501.295328,2+)

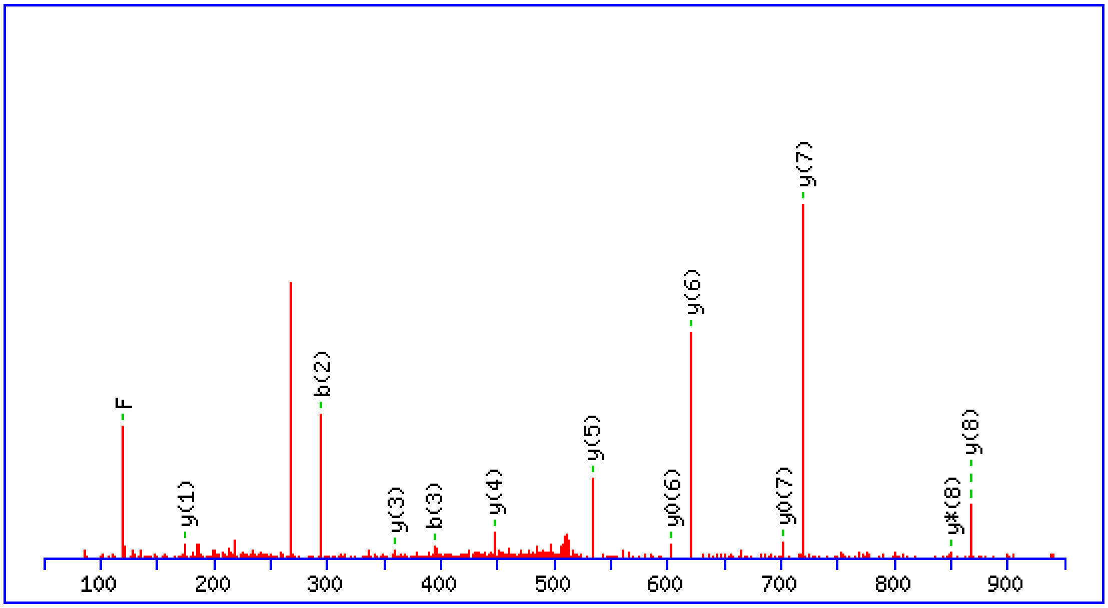


Monoisotopic mass of neutral peptide Mr(calc): 1000.5917
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.00086
Matches (Bold Red): 15/83 fragment ions using 18 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0808	100.0757	50.5415			V							9
2	**86.0964**	**213.1598**	107.0835			L	**902.5306**	451.7689	885.5040	443.2556	884.5200	**442.7636**	8
3	74.0600	314.2074	157.6074	296.1969	148.6021	T	**789.4465**	395.2269	772.4199	386.7136	771.4359	**386.2216**	7
4	102.0550	443.2500	222.1287	**425.2395**	**213.1234**	E	**688.3988**	344.7030	671.3723	336.1898	**670.3882**	335.6978	6
5	**86.0964**	556.3341	278.6707	538.3235	269.6654	I	**559.3562**	280.1817	542.3297	271.6685	541.3457	271.1765	5
6	**86.0964**	669.4182	335.2127	651.4076	326.2074	I	**446.2722**	223.6397	429.2456	215.1264	428.2616	214.6344	4
7	44.0495	740.4553	370.7313	722.4447	361.7260	A	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	3
8	60.0444	827.4873	414.2473	809.4767	405.2420	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FFVSSSQGR**
Found in **P35613**, P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2

Match to Query 226: 1013.484538 from(507.749545,2+)

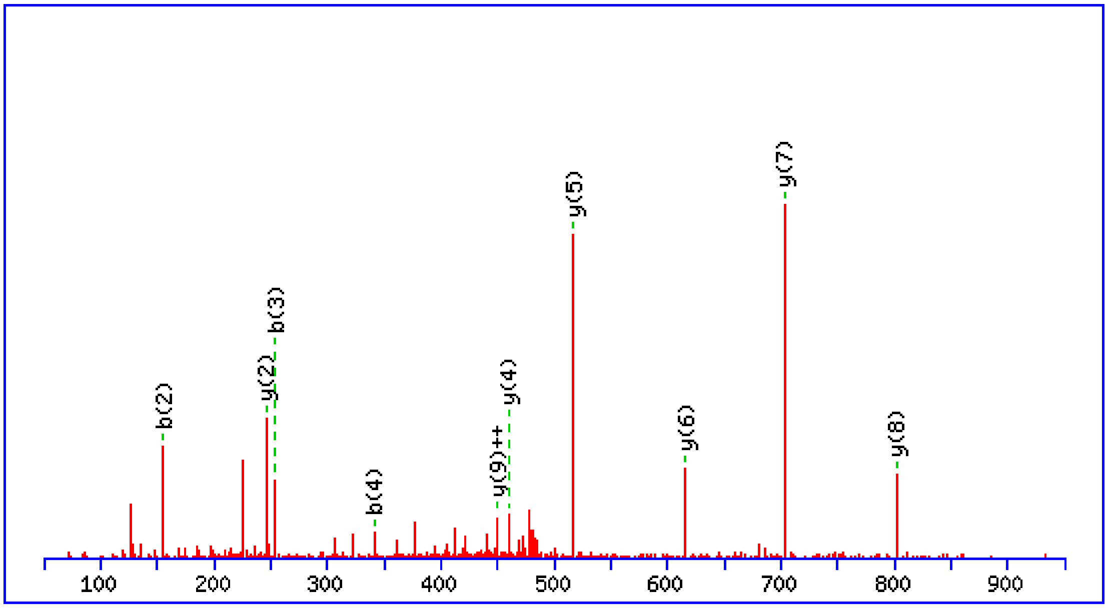


Monoisotopic mass of neutral peptide Mr(calc): 1013.4931
Fixed modifications: Carbamidomethyl (C)
Ions Score: 60 **Expect:** 8.6e-005
Matches (Bold Red): 14/81 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							9
2	**120.0808**	**295.1441**	148.0757					F	**867.4319**	434.2196	**850.4054**	425.7063	849.4213	425.2143	8
3	72.0808	**394.2125**	197.6099					V	**720.3635**	360.6854	703.3369	352.1721	**702.3529**	351.6801	7
4	60.0444	481.2445	241.1259			463.2340	232.1206	S	**621.2951**	311.1512	604.2685	302.6379	**603.2845**	302.1459	6
5	60.0444	568.2766	284.6419			550.2660	275.6366	S	**534.2631**	267.6352	517.2365	259.1219	516.2525	258.6299	5
6	60.0444	655.3086	328.1579			637.2980	319.1527	S	**447.2310**	224.1191	430.2045	215.6059	429.2205	215.1139	4
7	101.0709	783.3672	392.1872	766.3406	383.6740	765.3566	383.1819	Q	**360.1990**	180.6031	343.1724	172.0899			3
8	30.0338	840.3886	420.6980	823.3621	412.1847	822.3781	411.6927	G	232.1404	116.5738	215.1139	108.0606			2
9	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GPVSVGVDAR**
Found in **P25774**, P25774|CATS_HUMAN Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3

Match to Query 280: 955.497060 from(478.755806,2+)

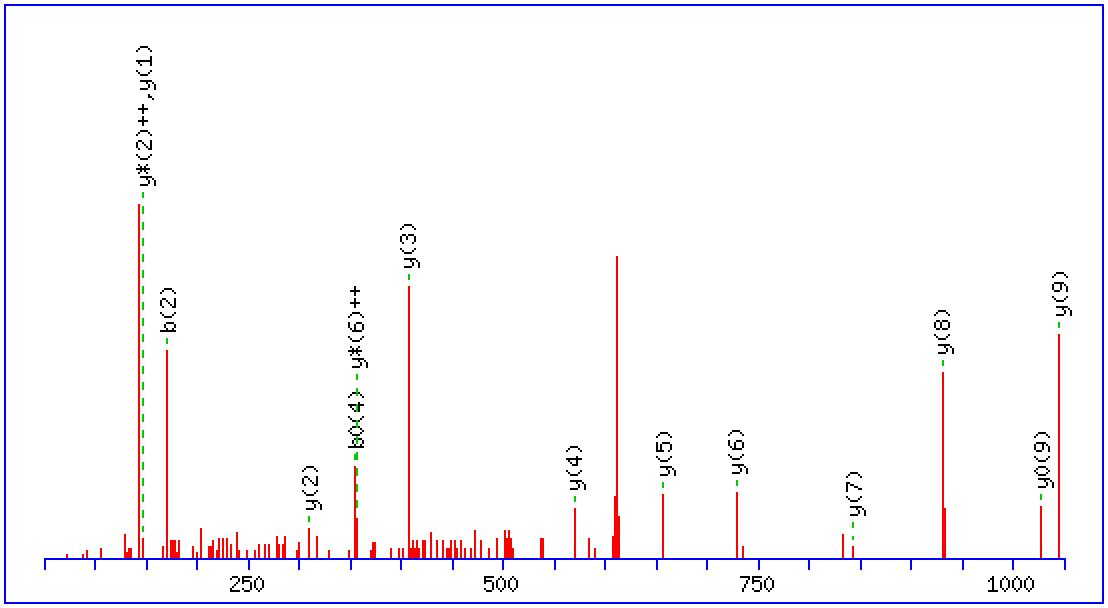


Monoisotopic mass of neutral peptide Mr(calc): 955.5087
Fixed modifications: Carbamidomethyl (C)
Ions Score: 58 **Expect:** 0.0001
Matches (Bold Red): 10/90 fragment ions using 17 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			G							10
2	70.0651	**155.0815**	78.0444			P	899.4945	**450.2509**	882.4680	441.7376	881.4839	441.2456	9
3	72.0808	**254.1499**	127.5786			V	**802.4417**	401.7245	785.4152	393.2112	784.4312	392.7192	8
4	60.0444	**341.1819**	171.0946	323.1714	162.0893	S	**703.3733**	352.1903	686.3468	343.6770	685.3628	343.1850	7
5	72.0808	440.2504	220.6288	422.2398	211.6235	V	**616.3413**	308.6743	599.3148	300.1610	598.3307	299.6690	6
6	30.0338	497.2718	249.1395	479.2613	240.1343	G	**517.2729**	259.1401	500.2463	250.6268	499.2623	250.1348	5
7	72.0808	596.3402	298.6738	578.3297	289.6685	V	**460.2514**	230.6293	443.2249	222.1161	442.2409	221.6241	4
8	88.0393	711.3672	356.1872	693.3566	347.1819	D	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
9	44.0495	782.4043	391.7058	764.3937	382.7005	A	**246.1561**	123.5817	229.1295	115.0684			2
10	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GIDSDASYPYK**
Found in **P25774**, P25774|CATS_HUMAN Cathepsin S OS=Homo sapiens GN=CTSS PE=1 SV=3

Match to Query 152: 1214.490102 from(608.252327,2+)

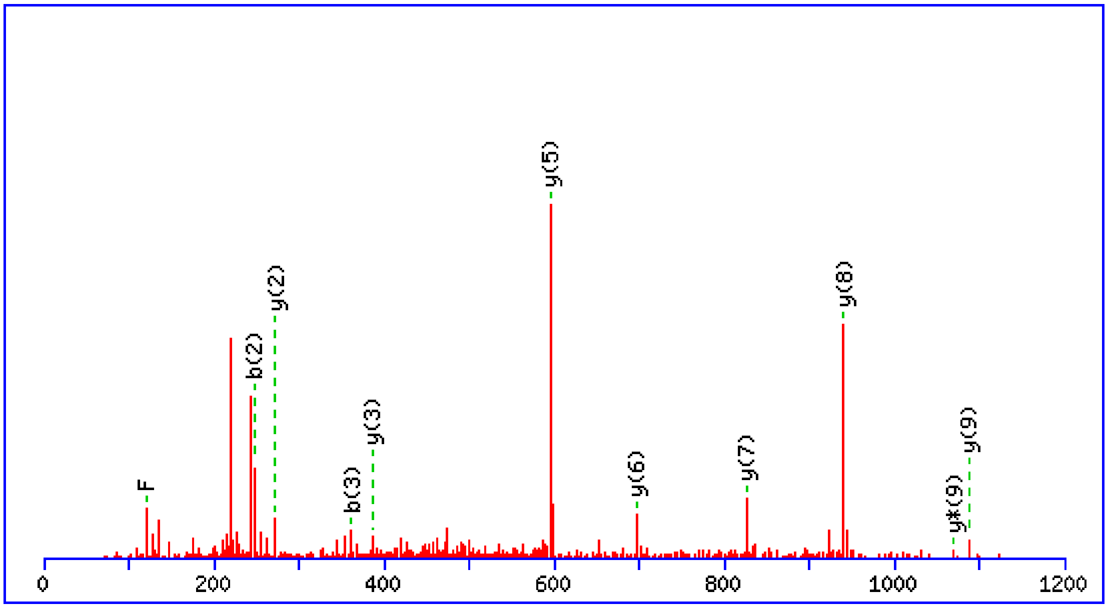


Monoisotopic mass of neutral peptide Mr(calc): 1214.5455
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00032
Matches (Bold Red): 14/99 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			G							11
2	86.0964	**171.1128**	86.0600			I	1158.5313	579.7693	1141.5048	571.2560	1140.5208	570.7640	10
3	88.0393	286.1397	143.5735	268.1292	134.5682	D	**1045.4473**	523.2273	1028.4207	514.7140	**1027.4367**	514.2220	9
4	60.0444	373.1718	187.0895	**355.1612**	178.0842	S	**930.4203**	465.7138	913.3938	457.2005	912.4098	456.7085	8
5	88.0393	488.1987	244.6030	470.1882	235.5977	D	**843.3883**	422.1978	826.3618	413.6845	825.3777	413.1925	7
6	44.0495	559.2358	280.1216	541.2253	271.1163	A	**728.3614**	364.6843	711.3348	**356.1710**	710.3508	355.6790	6
7	60.0444	646.2679	323.6376	628.2573	314.6323	S	**657.3243**	329.1658	640.2977	320.6525	639.3137	320.1605	5
8	136.0757	809.3312	405.1692	791.3206	396.1640	Y	**570.2922**	285.6498	553.2657	277.1365			4
9	70.0651	906.3840	453.6956	888.3734	444.6903	P	**407.2289**	204.1181	390.2023	195.6048			3
10	136.0757	1069.4473	535.2273	1051.4367	526.2220	Y	**310.1761**	155.5917	293.1496	**147.0784**			2
11	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VFNETPINPR**
Found in **Q9Y678**, Q9Y678|COPG_HUMAN Coatomer subunit gamma OS=Homo sapiens GN=COPG PE=1 SV=1

Match to Query 536: 1185.573906 from(593.794229,2+)

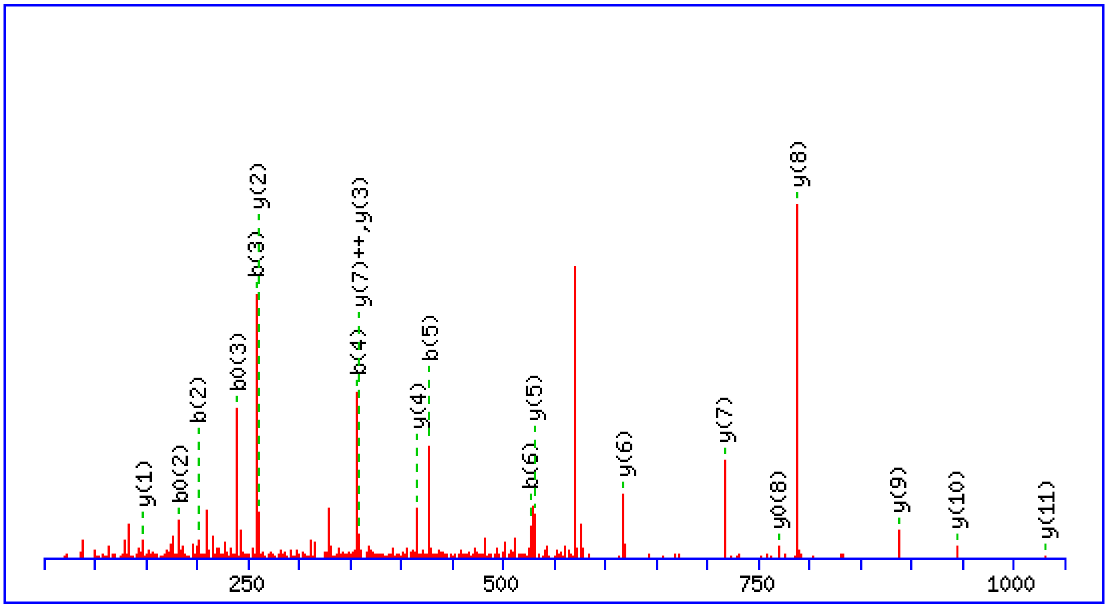


Monoisotopic mass of neutral peptide Mr(calc): 1185.6142
Fixed modifications: Carbamidomethyl (C)
Ions Score: 63 **Expect:** 3.8e-005
Matches (Bold Red): 11/98 fragment ions using 18 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							10
2	**120.0808**	**247.1441**	124.0757					F	**1087.5531**	544.2802	**1070.5265**	535.7669	1069.5425	535.2749	9
3	87.0553	**361.1870**	181.0972	344.1605	172.5839			N	**940.4847**	470.7460	923.4581	462.2327	922.4741	461.7407	8
4	102.0550	490.2296	245.6185	473.2031	237.1052	472.2191	236.6132	E	**826.4417**	413.7245	809.4152	405.2112	808.4312	404.7192	7
5	74.0600	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	T	**697.3992**	349.2032	680.3726	340.6899	679.3886	340.1979	6
6	70.0651	688.3301	344.6687	671.3035	336.1554	670.3195	335.6634	P	**596.3515**	298.6794	579.3249	290.1661			5
7	86.0964	801.4141	401.2107	784.3876	392.6974	783.4036	392.2054	I	499.2987	250.1530	482.2722	241.6397			4
8	87.0553	915.4571	458.2322	898.4305	449.7189	897.4465	449.2269	N	**386.2146**	193.6110	369.1881	185.0977			3
9	70.0651	1012.5098	506.7585	995.4833	498.2453	994.4993	497.7533	P	**272.1717**	136.5895	255.1452	128.0762			2
10	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ASGVAVSDGVIK**
Found in **P23528**, P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3

Match to Query 156: 1143.510576 from(572.762564,2+)

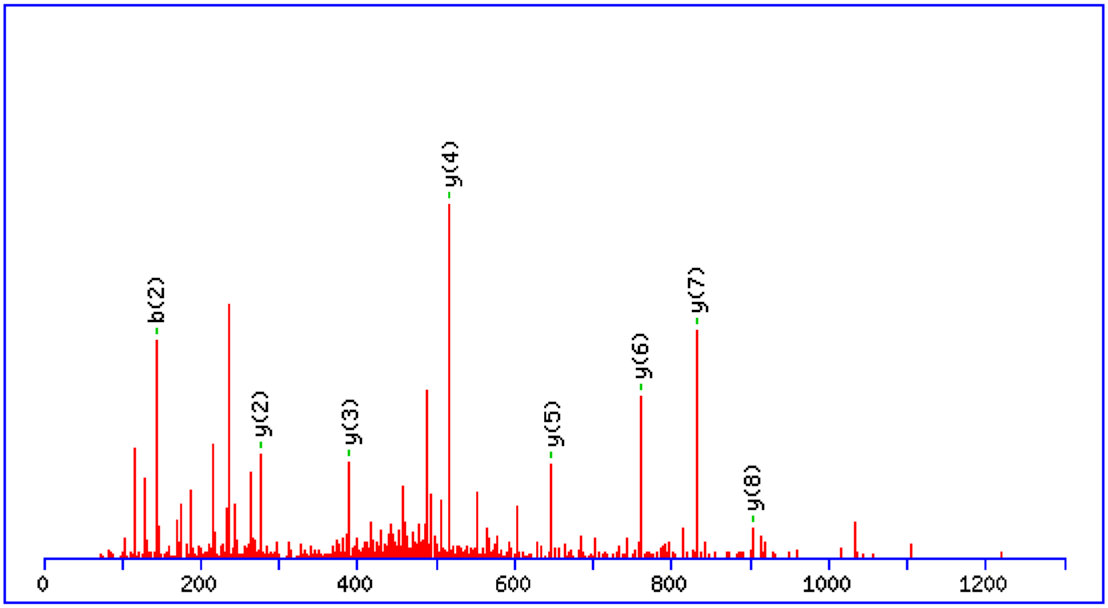


Monoisotopic mass of neutral peptide Mr(calc): 1143.6136
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
N-term : Acetyl (Protein N-term)
Ions Score: 88 **Expect:** 1.4e-007
Matches (Bold Red): 20/112 fragment ions using 44 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	114.0549	57.5311			**A**							**12**
2	60.0444	**201.0870**	101.0471	**183.0764**	92.0418	**S**	**1031.5732**	516.2902	1014.5466	507.7769	1013.5626	507.2849	**11**
3	30.0338	**258.1084**	129.5579	**240.0979**	120.5526	**G**	**944.5411**	472.7742	927.5146	464.2609	926.5306	463.7689	**10**
4	72.0808	**357.1769**	179.0921	339.1663	170.0868	**V**	**887.5197**	444.2635	870.4931	435.7502	869.5091	435.2582	**9**
5	44.0495	**428.2140**	214.6106	410.2034	205.6053	**A**	**788.4512**	394.7293	771.4247	386.2160	**770.4407**	385.7240	**8**
6	72.0808	**527.2824**	264.1448	509.2718	255.1395	**V**	**717.4141**	**359.2107**	700.3876	350.6974	699.4036	350.2054	**7**
7	60.0444	614.3144	307.6608	596.3038	298.6556	**S**	**618.3457**	309.6765	601.3192	301.1632	600.3352	300.6712	**6**
8	88.0393	729.3414	365.1743	711.3308	356.1690	**D**	**531.3137**	266.1605	514.2871	257.6472	513.3031	257.1552	**5**
9	30.0338	786.3628	393.6850	768.3523	384.6798	**G**	**416.2867**	208.6470	399.2602	200.1337			**4**
10	72.0808	885.4312	443.2193	867.4207	434.2140	**V**	**359.2653**	180.1363	342.2387	171.6230			**3**
11	86.0964	998.5153	499.7613	980.5047	490.7560	**I**	**260.1969**	130.6021	243.1703	122.0888			**2**
12	101.1073					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **AAANEQLTR**
Found in **Q9NX63**, Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1

Match to Query 266: 972.547446 from(487.280999,2+)

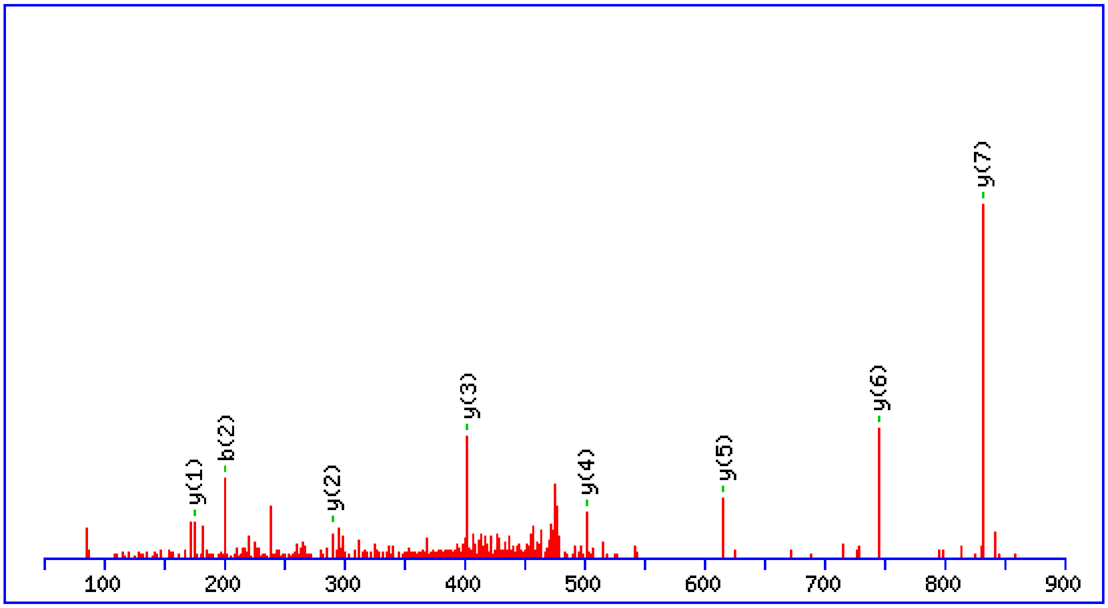


Monoisotopic mass of neutral peptide Mr(calc): 972.4988
Fixed modifications: Carbamidomethyl (C)
Ions Score: 67 **Expect:** 1.7e-005
Matches (Bold Red): 8/89 fragment ions using 11 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							9
2	44.0495	**143.0815**	72.0444					A	**902.4690**	451.7381	885.4425	443.2249	884.4585	442.7329	8
3	44.0495	214.1186	107.5629					A	**831.4319**	416.2196	814.4054	407.7063	813.4213	407.2143	7
4	87.0553	328.1615	164.5844	311.1350	156.0711			N	**760.3948**	380.7010	743.3682	372.1878	742.3842	371.6958	6
5	102.0550	457.2041	229.1057	440.1776	220.5924	439.1936	220.1004	E	**646.3519**	323.6796	629.3253	315.1663	628.3413	314.6743	5
6	101.0709	585.2627	293.1350	568.2362	284.6217	567.2522	284.1297	Q	**517.3093**	259.1583	500.2827	250.6450	499.2987	250.1530	4
7	86.0964	698.3468	349.6770	681.3202	341.1638	680.3362	340.6717	L	**389.2507**	195.1290	372.2241	186.6157	371.2401	186.1237	3
8	74.0600	799.3945	400.2009	782.3679	391.6876	781.3839	391.1956	T	**276.1666**	138.5870	259.1401	130.0737	258.1561	129.5817	2
9	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LSENVIDR**
Found in **Q9NX63**, Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1

Match to Query 230: 944.470694 from(473.242623,2+)

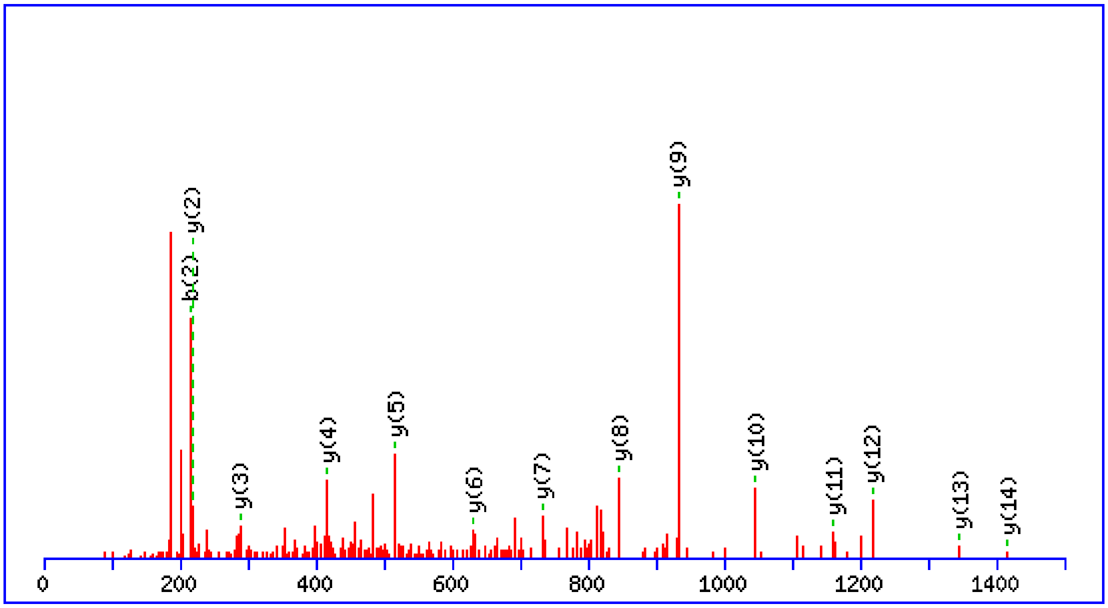


Monoisotopic mass of neutral peptide Mr(calc): 944.4927
Fixed modifications: Carbamidomethyl (C)
Ions Score: 48 **Expect:** 0.0014
Matches (Bold Red): 8/82 fragment ions using 17 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	86.0964	114.0913	57.5493					L							8
2	60.0444	**201.1234**	101.0653			183.1128	92.0600	S	**832.4159**	416.7116	815.3894	408.1983	814.4054	407.7063	7
3	102.0550	330.1660	165.5866			312.1554	156.5813	E	**745.3839**	373.1956	728.3573	364.6823	727.3733	364.1903	6
4	87.0553	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	N	**616.3413**	308.6743	599.3148	300.1610	598.3307	299.6690	5
5	72.0808	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	V	**502.2984**	251.6528	485.2718	243.1396	484.2878	242.6475	4
6	86.0964	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	I	**403.2300**	202.1186	386.2034	193.6053	385.2194	193.1133	3
7	88.0393	771.3883	386.1978	754.3618	377.6845	753.3777	377.1925	D	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	2
8	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TIAQGNLSNTDVQAAK**
Found in **P22695**, P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3

Match to Query 703: 1629.766122 from(815.890337,2+)

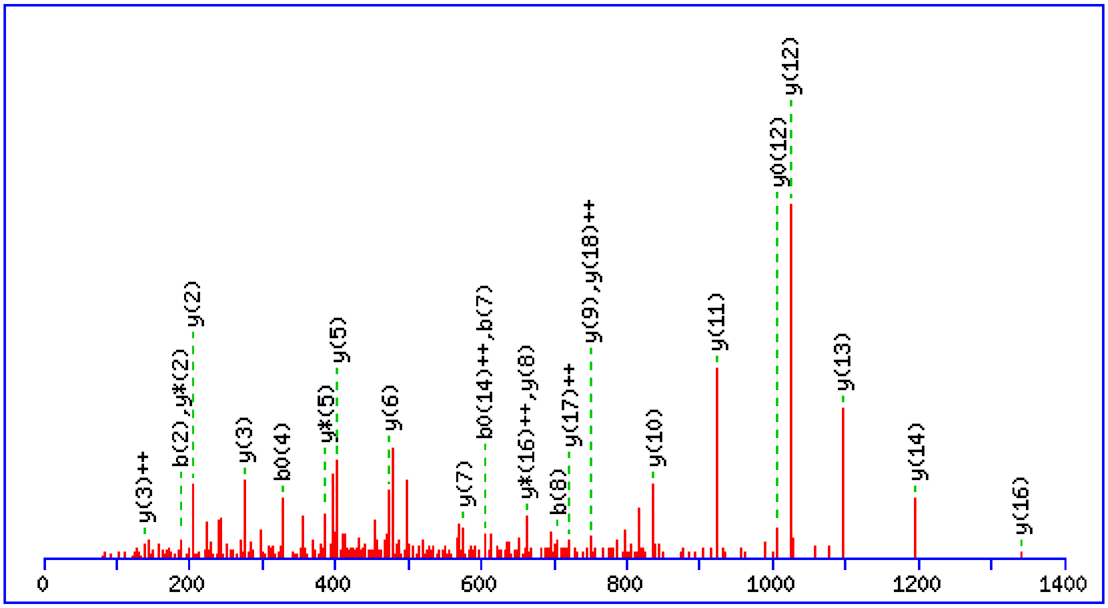


Monoisotopic mass of neutral peptide Mr(calc): 1629.8322
Fixed modifications: Carbamidomethyl (C)
Ions Score: 122 **Expect:** 4.3e-011
Matches (Bold Red): 14/180 fragment ions using 18 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	T							16
2	86.0964	**215.1390**	108.0731			197.1285	99.0679	I	1529.7918	765.3995	1512.7653	756.8863	1511.7812	756.3943	15
3	44.0495	286.1761	143.5917			268.1656	134.5864	A	**1416.7077**	708.8575	1399.6812	700.3442	1398.6972	699.8522	14
4	101.0709	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	Q	**1345.6706**	673.3390	1328.6441	664.8257	1327.6601	664.3337	13
5	30.0338	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	G	**1217.6121**	609.3097	1200.5855	600.7964	1199.6015	600.3044	12
6	87.0553	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	N	**1160.5906**	580.7989	1143.5640	572.2857	1142.5800	571.7937	11
7	86.0964	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	L	**1046.5477**	523.7775	1029.5211	515.2642	1028.5371	514.7722	10
8	60.0444	785.4152	393.2112	768.3886	384.6980	767.4046	384.2060	S	**933.4636**	467.2354	916.4371	458.7222	915.4530	458.2302	9
9	87.0553	899.4581	450.2327	882.4316	441.7194	881.4476	441.2274	N	**846.4316**	423.7194	829.4050	415.2061	828.4210	414.7141	8
10	74.0600	1000.5058	500.7565	983.4793	492.2433	982.4952	491.7513	T	**732.3886**	366.6980	715.3621	358.1847	714.3781	357.6927	7
11	88.0393	1115.5327	558.2700	1098.5062	549.7567	1097.5222	549.2647	D	**631.3410**	316.1741	614.3144	307.6608	613.3304	307.1688	6
12	72.0808	1214.6012	607.8042	1197.5746	599.2909	1196.5906	598.7989	V	**516.3140**	258.6607	499.2875	250.1474			5
13	101.0709	1342.6597	671.8335	1325.6332	663.3202	1324.6492	662.8282	Q	**417.2456**	209.1264	400.2191	200.6132			4
14	44.0495	1413.6968	707.3521	1396.6703	698.8388	1395.6863	698.3468	A	**289.1870**	145.0972	272.1605	136.5839			3
15	44.0495	1484.7340	742.8706	1467.7074	734.3573	1466.7234	733.8653	A	**218.1499**	109.5786	201.1234	101.0653			2
16	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **EGTGSTATSSSSTAGAAGK**
Found in **O15372**, O15372|EIF3H_HUMAN Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1

Match to Query 745: 1626.730688 from(814.372620,2+)

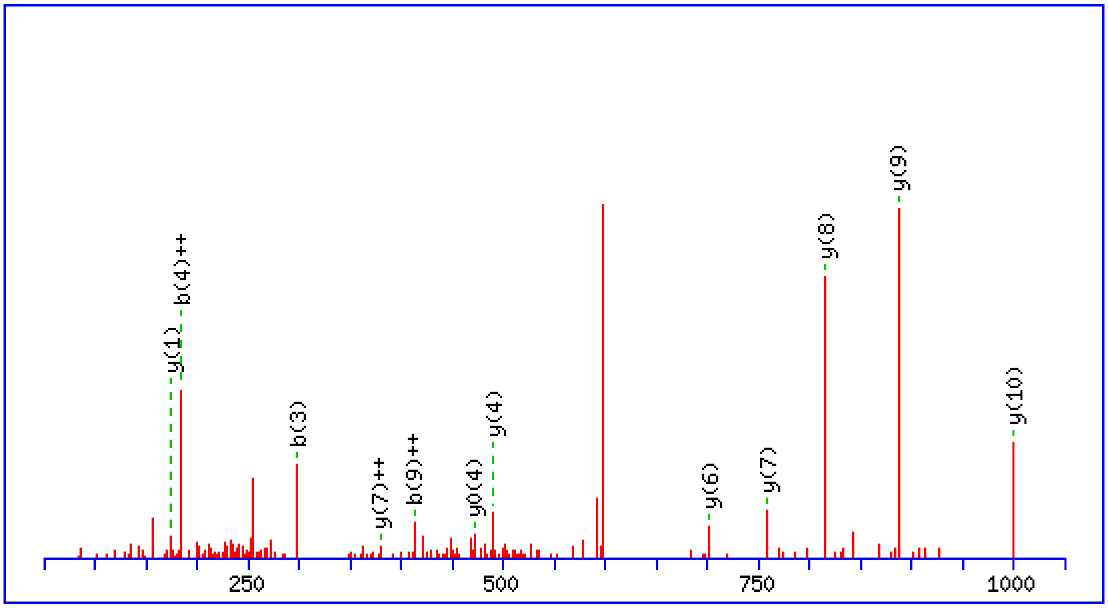


Monoisotopic mass of neutral peptide Mr(calc): 1626.7333
Fixed modifications: Carbamidomethyl (C)
Ions Score: 79 **Expect:** 8.7e-007
Matches (Bold Red): 25/187 fragment ions using 47 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286	112.0393	56.5233	E							19
2	30.0338	**187.0713**	94.0393	169.0608	85.0340	G	1498.6980	**749.8526**	1481.6714	741.3393	1480.6874	740.8473	18
3	74.0600	288.1190	144.5631	270.1084	135.5579	T	1441.6765	**721.3419**	1424.6500	712.8286	1423.6659	712.3366	17
4	30.0338	345.1405	173.0739	**327.1299**	164.0686	G	**1340.6288**	670.8181	1323.6023	**662.3048**	1322.6183	661.8128	16
5	60.0444	432.1725	216.5899	414.1619	207.5846	S	1283.6074	642.3073	1266.5808	633.7940	1265.5968	633.3020	15
6	74.0600	533.2202	267.1137	515.2096	258.1084	T	**1196.5753**	598.7913	1179.5488	590.2780	1178.5648	589.7860	14
7	44.0495	**604.2573**	302.6323	586.2467	293.6270	A	**1095.5277**	548.2675	1078.5011	539.7542	1077.5171	539.2622	13
8	74.0600	**705.3050**	353.1561	687.2944	344.1508	T	**1024.4905**	512.7489	1007.4640	504.2356	**1006.4800**	503.7436	12
9	60.0444	792.3370	396.6721	774.3264	387.6669	S	**923.4429**	462.2251	906.4163	453.7118	905.4323	453.2198	11
10	60.0444	879.3690	440.1882	861.3585	431.1829	S	**836.4108**	418.7091	819.3843	410.1958	818.4003	409.7038	10
11	60.0444	966.4011	483.7042	948.3905	474.6989	S	**749.3788**	375.1930	732.3523	366.6798	731.3682	366.1878	9
12	60.0444	1053.4331	527.2202	1035.4225	518.2149	S	**662.3468**	331.6770	645.3202	323.1638	644.3362	322.6717	8
13	74.0600	1154.4808	577.7440	1136.4702	568.7387	T	**575.3148**	288.1610	558.2882	279.6477	557.3042	279.1557	7
14	44.0495	1225.5179	613.2626	1207.5073	**604.2573**	A	**474.2671**	237.6372	457.2405	229.1239			6
15	30.0338	1282.5393	641.7733	1264.5288	632.7680	G	**403.2300**	202.1186	**386.2034**	193.6053			5
16	44.0495	1353.5765	677.2919	1335.5659	668.2866	A	346.2085	173.6079	329.1819	165.0946			4
17	44.0495	1424.6136	712.8104	1406.6030	703.8051	A	**275.1714**	**138.0893**	258.1448	129.5761			3
18	30.0338	1481.6350	741.3212	1463.6245	732.3159	G	**204.1343**	102.5708	**187.1077**	94.0575			2
19	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ALLAGGPDEADR**
Found in **Q9H3U5**, Q9H3U5|MFSD1_HUMAN Major facilitator superfamily domain-containing protein 1 OS=Homo sapiens GN=MFSD1 PE=2 SV=2

Match to Query 285: 1183.567142 from(592.790847,2+)

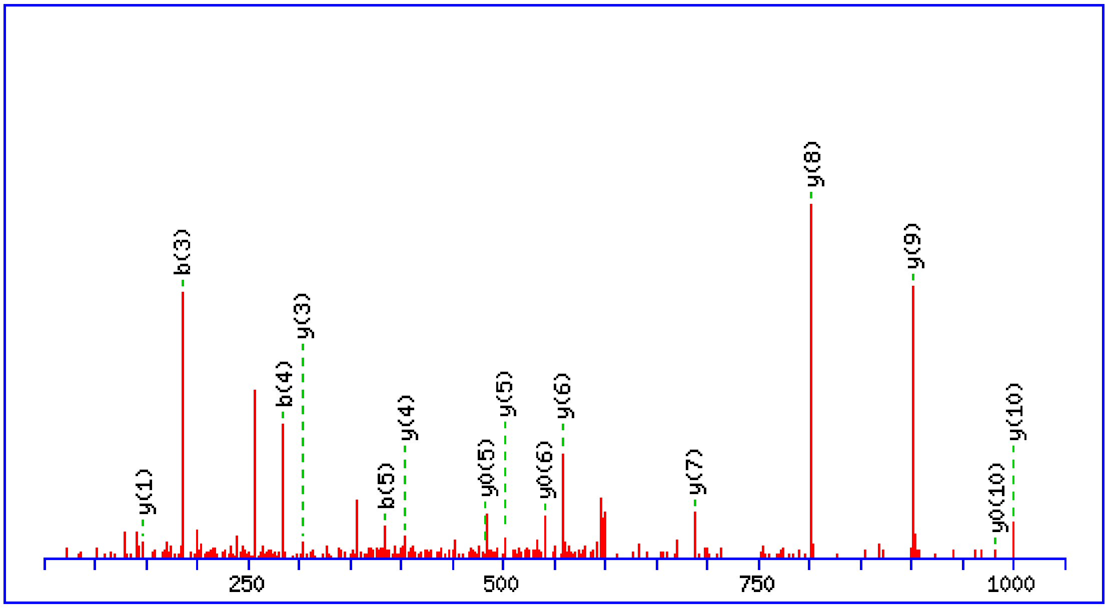


Monoisotopic mass of neutral peptide Mr(calc): 1183.5833
Fixed modifications: Carbamidomethyl (C)
Ions Score: 48 **Expect:** 0.0011
Matches (Bold Red): 13/106 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			**A**							12
2	86.0964	**185.1285**	93.0679			**L**	1113.5535	557.2804	1096.5269	548.7671	1095.5429	548.2751	11
3	86.0964	**298.2125**	149.6099			**L**	**1000.4694**	500.7383	983.4429	492.2251	982.4588	491.7331	10
4	44.0495	369.2496	**185.1285**			**A**	**887.3854**	444.1963	870.3588	435.6830	869.3748	435.1910	9
5	30.0338	426.2711	213.6392			**G**	**816.3482**	408.6778	799.3217	400.1645	798.3377	399.6725	8
6	30.0338	483.2926	242.1499			**G**	**759.3268**	**380.1670**	742.3002	371.6538	741.3162	371.1617	7
7	70.0651	580.3453	290.6763			**P**	**702.3053**	351.6563	685.2788	343.1430	684.2947	342.6510	6
8	88.0393	695.3723	348.1898	677.3617	339.1845	**D**	605.2525	303.1299	588.2260	294.6166	587.2420	294.1246	5
9	102.0550	824.4149	**412.7111**	806.4043	403.7058	**E**	**490.2256**	245.6164	473.1991	237.1032	**472.2150**	236.6112	4
10	44.0495	895.4520	448.2296	877.4414	439.2243	**A**	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
11	88.0393	1010.4789	505.7431	992.4684	496.7378	**D**	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
12	129.1135					**R**	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GGAVVDEGPTGVK**
Found in **O15427**, O15427|MOT4_HUMAN Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1

Match to Query 336: 1184.650720 from(593.332636,2+)

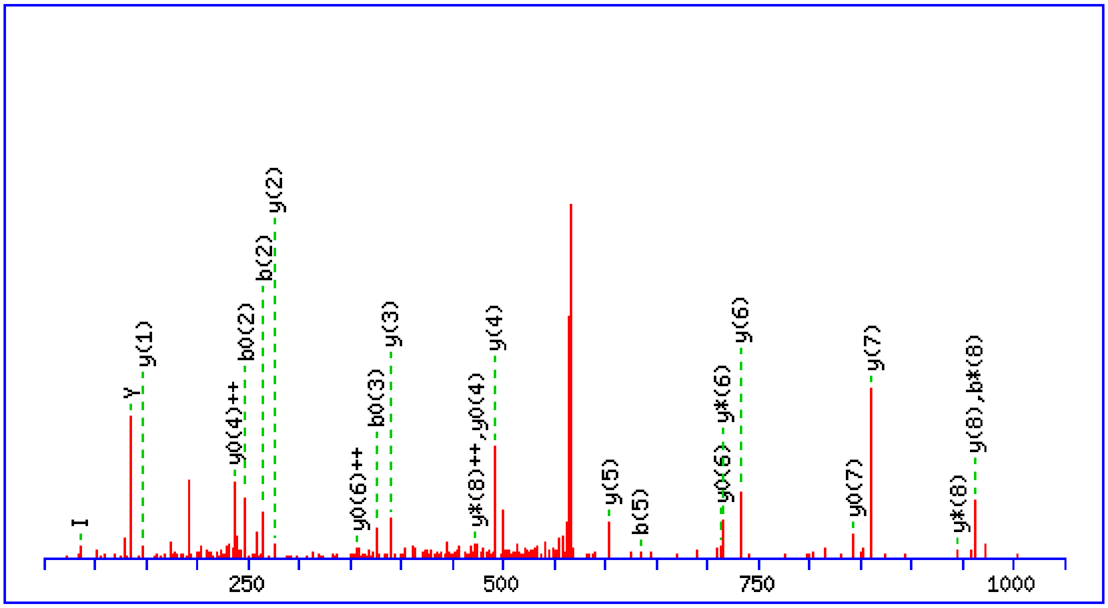


Monoisotopic mass of neutral peptide Mr(calc): 1184.6037
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.00074
Matches (Bold Red): 15/117 fragment ions using 39 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			**G**							**13**
2	30.0338	115.0502	58.0287			**G**	1128.5895	564.7984	1111.5630	556.2851	1110.5790	555.7931	**12**
3	44.0495	**186.0873**	93.5473			**A**	1071.5681	536.2877	1054.5415	527.7744	1053.5575	527.2824	**11**
4	72.0808	**285.1557**	143.0815			**V**	**1000.5310**	500.7691	983.5044	492.2558	**982.5204**	491.7638	**10**
5	72.0808	**384.2241**	192.6157			**V**	**901.4625**	451.2349	884.4360	442.7216	883.4520	442.2296	**9**
6	88.0393	499.2511	250.1292	481.2405	241.1239	**D**	**802.3941**	401.7007	785.3676	393.1874	784.3836	392.6954	**8**
7	102.0550	628.2937	314.6505	610.2831	305.6452	**E**	**687.3672**	344.1872	670.3406	335.6740	669.3566	335.1819	**7**
8	30.0338	685.3151	343.1612	667.3046	334.1559	**G**	**558.3246**	279.6659	541.2980	271.1527	**540.3140**	270.6607	**6**
9	70.0651	782.3679	391.6876	764.3573	382.6823	**P**	**501.3031**	251.1552	484.2766	242.6419	**483.2926**	242.1499	**5**
10	74.0600	883.4156	442.2114	865.4050	433.2062	**T**	**404.2504**	202.6288	387.2238	194.1155	386.2398	193.6235	**4**
11	30.0338	940.4371	470.7222	922.4265	461.7169	**G**	**303.2027**	152.1050	286.1761	143.5917			**3**
12	72.0808	1039.5055	520.2564	1021.4949	511.2511	**V**	246.1812	123.5942	229.1547	115.0810			**2**
13	101.1073					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **YTEQITNEK**
Found in **Q16718**, Q16718|NDUA5_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3

Match to Query 146: 1124.418462 from(563.216507,2+)

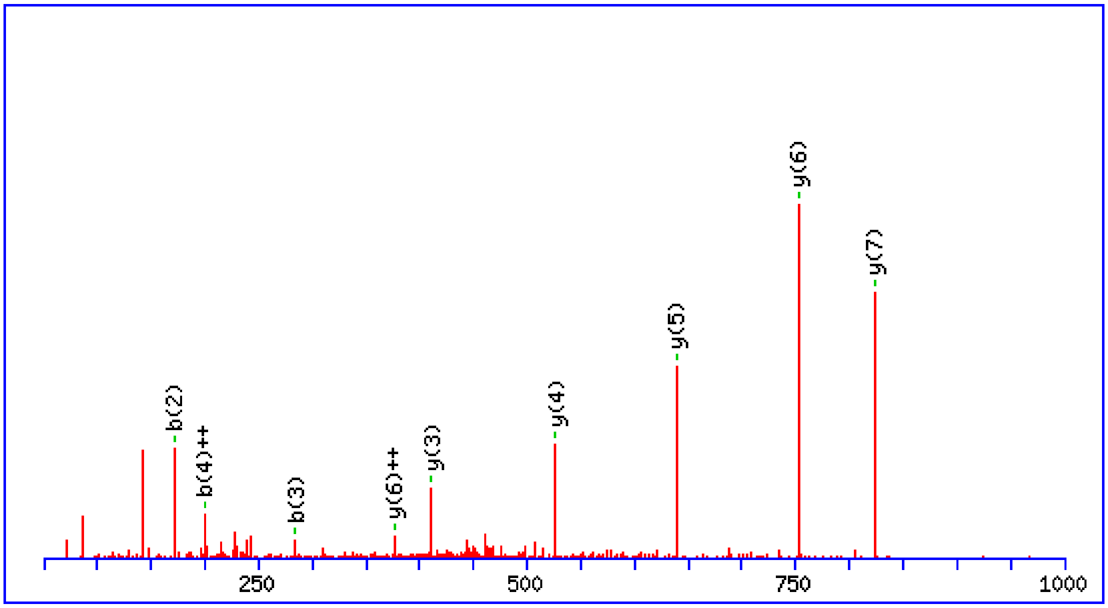


Monoisotopic mass of neutral peptide Mr(calc): 1124.5349
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00025
Matches (Bold Red): 23/95 fragment ions using 43 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**136.0757**	164.0706	82.5389					Y							9
2	74.0600	**265.1183**	133.0628			**247.1077**	124.0575	T	**962.4789**	481.7431	**945.4524**	**473.2298**	944.4684	472.7378	8
3	102.0550	394.1609	197.5841			**376.1503**	188.5788	E	**861.4312**	431.2193	844.4047	422.7060	**843.4207**	422.2140	7
4	101.0709	522.2195	261.6134	505.1929	253.1001	504.2089	252.6081	Q	**732.3886**	366.6980	**715.3621**	358.1847	**714.3781**	**357.6927**	6
5	**86.0964**	**635.3035**	318.1554	618.2770	309.6421	617.2930	309.1501	I	**604.3301**	302.6687	587.3035	294.1554	586.3195	293.6634	5
6	74.0600	736.3512	368.6792	719.3246	360.1660	718.3406	359.6740	T	**491.2460**	246.1266	474.2195	237.6134	**473.2354**	**237.1214**	4
7	87.0553	850.3941	425.7007	833.3676	417.1874	832.3836	416.6954	N	**390.1983**	195.6028	373.1718	187.0895	372.1878	186.5975	3
8	102.0550	979.4367	490.2220	**962.4102**	481.7087	961.4262	481.2167	E	**276.1554**	138.5813	259.1288	130.0681	258.1448	129.5761	2
9	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VAIIDTYK**
Found in **P16671**, P16671|CD36_HUMAN Platelet glycoprotein 4 OS=Homo sapiens GN=CD36 PE=1 SV=2

Match to Query 207: 921.490600 from(461.752576,2+)

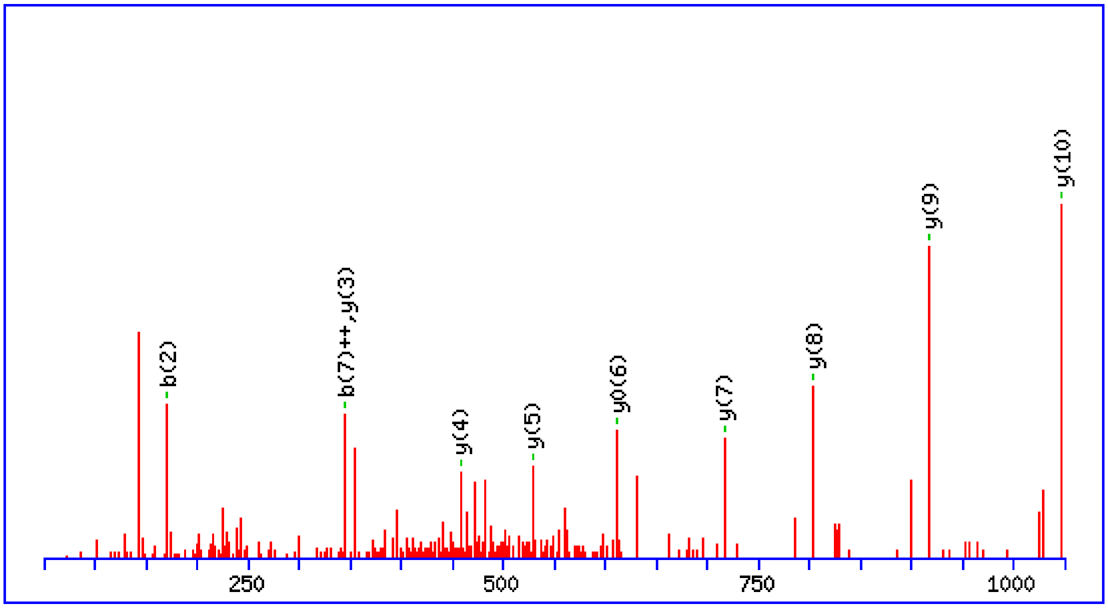


Monoisotopic mass of neutral peptide Mr(calc): 921.5171
Fixed modifications: Carbamidomethyl (C)
Ions Score: 48 **Expect:** 0.0012
Matches (Bold Red): 9/66 fragment ions using 11 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			V							8
2	44.0495	**171.1128**	86.0600			A	**823.4560**	412.2316	806.4294	403.7184	805.4454	403.2264	7
3	86.0964	**284.1969**	142.6021			I	**752.4189**	**376.7131**	735.3923	368.1998	734.4083	367.7078	6
4	86.0964	397.2809	**199.1441**			I	**639.3348**	320.1710	622.3083	311.6578	621.3243	311.1658	5
5	88.0393	512.3079	256.6576	494.2973	247.6523	D	**526.2508**	263.6290	509.2242	255.1157	508.2402	254.6237	4
6	74.0600	613.3556	307.1814	595.3450	298.1761	T	**411.2238**	206.1155	394.1973	197.6023	393.2132	197.1103	3
7	136.0757	776.4189	388.7131	758.4083	379.7078	Y	310.1761	155.5917	293.1496	147.0784			2
8	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AVENSSTAIGIR**
Found in **P25788**, P25788|PSA3_HUMAN Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2

Match to Query 284: 1216.611298 from(609.312925,2+)

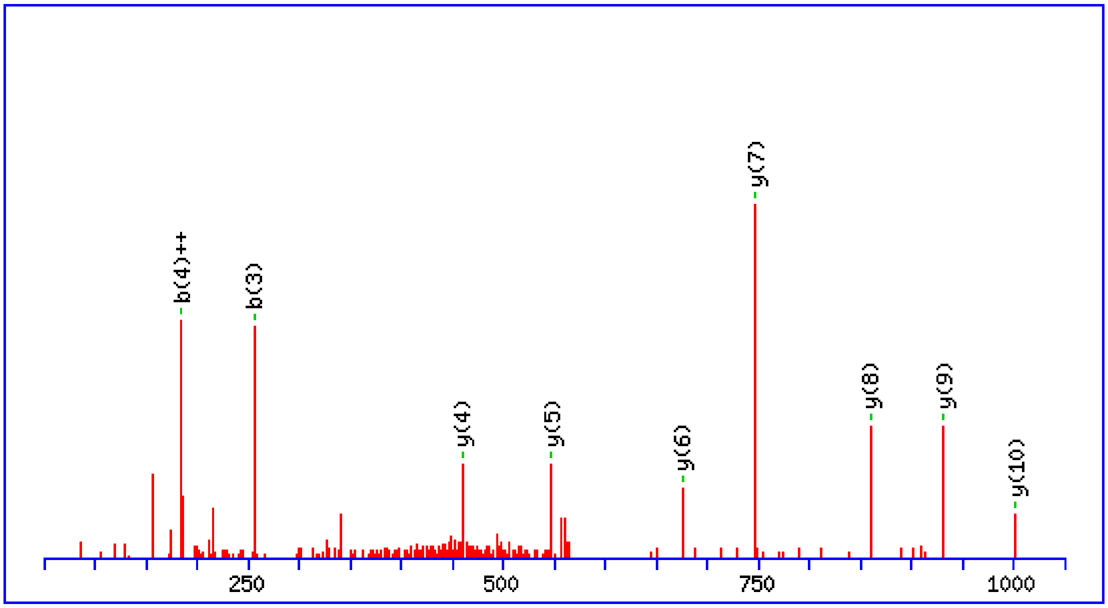


Monoisotopic mass of neutral peptide Mr(calc): 1216.6411
Fixed modifications: Carbamidomethyl (C)
Ions Score: 62 **Expect:** 4.9e-005
Matches (Bold Red): 10/124 fragment ions using 12 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					**A**							**12**
2	72.0808	**171.1128**	86.0600					**V**	1146.6113	573.8093	1129.5848	565.2960	1128.6008	564.8040	**11**
3	102.0550	300.1554	150.5813			282.1448	141.5761	**E**	**1047.5429**	524.2751	1030.5164	515.7618	1029.5323	515.2698	**10**
4	87.0553	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	**N**	**918.5003**	459.7538	901.4738	451.2405	900.4898	450.7485	**9**
5	60.0444	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	**S**	**804.4574**	402.7323	787.4308	394.2191	786.4468	393.7271	**8**
6	60.0444	588.2624	294.6348	571.2358	286.1216	570.2518	285.6295	**S**	**717.4254**	359.2163	700.3988	350.7030	699.4148	350.2110	**7**
7	74.0600	689.3101	**345.1587**	672.2835	336.6454	671.2995	336.1534	**T**	630.3933	315.7003	613.3668	307.1870	**612.3828**	306.6950	**6**
8	44.0495	760.3472	380.6772	743.3206	372.1640	742.3366	371.6719	**A**	**529.3457**	265.1765	512.3191	256.6632			**5**
9	86.0964	873.4312	437.2193	856.4047	428.7060	855.4207	428.2140	**I**	**458.3085**	229.6579	441.2820	221.1446			**4**
10	30.0338	930.4527	465.7300	913.4262	457.2167	912.4421	456.7247	**G**	**345.2245**	173.1159	328.1979	164.6026			**3**
11	86.0964	1043.5368	522.2720	1026.5102	513.7587	1025.5262	513.2667	**I**	288.2030	144.6051	271.1765	136.0919			**2**
12	129.1135							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LAAIAESGVER**
Found in **P28072**, P28072|PSB6_HUMAN Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4

Match to Query 405: 1114.625244 from(558.319898,2+)

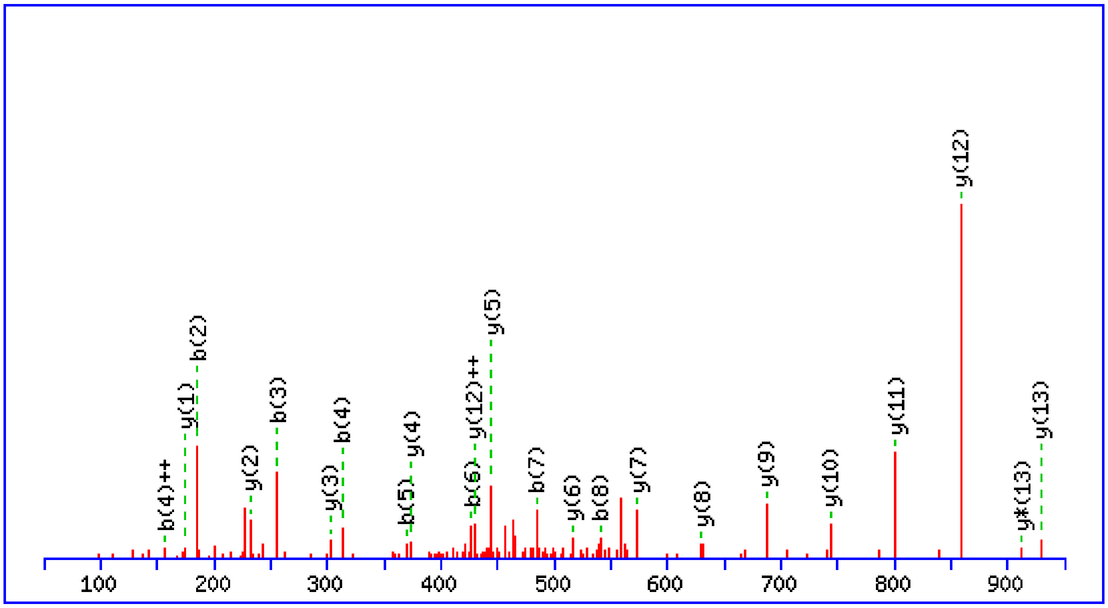


Monoisotopic mass of neutral peptide Mr(calc): 1114.5982
Fixed modifications: Carbamidomethyl (C)
Ions Score: 70 **Expect:** 7.1e-006
Matches (Bold Red): 10/99 fragment ions using 10 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	86.0964	114.0913	57.5493			L							11
2	44.0495	**185.1285**	93.0679			A	**1002.5215**	501.7644	985.4949	493.2511	984.5109	492.7591	10
3	44.0495	**256.1656**	128.5864			A	**931.4843**	466.2458	914.4578	457.7325	913.4738	457.2405	9
4	86.0964	369.2496	**185.1285**			I	**860.4472**	430.7272	843.4207	422.2140	842.4367	421.7220	8
5	44.0495	440.2867	220.6470			A	**747.3632**	374.1852	730.3366	365.6719	729.3526	365.1799	7
6	102.0550	569.3293	285.1683	551.3188	276.1630	E	**676.3260**	338.6667	659.2995	330.1534	658.3155	329.6614	6
7	60.0444	656.3614	328.6843	638.3508	319.6790	S	**547.2835**	274.1454	530.2569	265.6321	529.2729	265.1401	5
8	30.0338	713.3828	357.1951	695.3723	348.1898	G	**460.2514**	230.6293	443.2249	222.1161	442.2409	221.6241	4
9	72.0808	812.4512	406.7293	794.4407	397.7240	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
10	102.0550	941.4938	471.2506	923.4833	462.2453	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AAAGGGGGGAAAAGR**
Found in **Q9UL25**, Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3

Match to Query 355: 1112.583686 from(557.299119,2+)

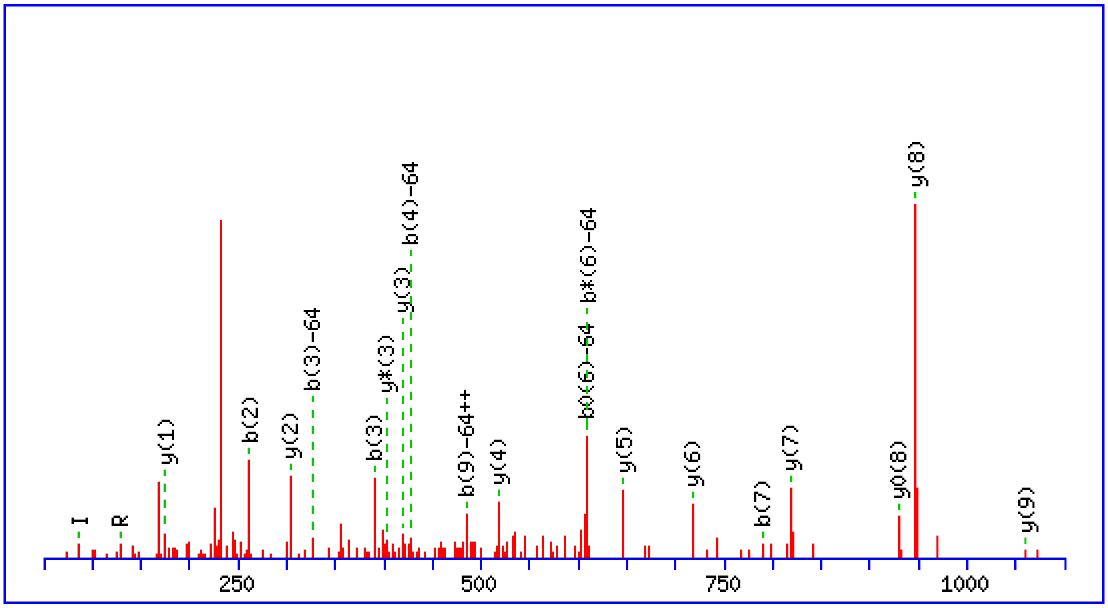


Monoisotopic mass of neutral peptide Mr(calc): 1112.5323
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
N-term : Acetyl (Protein N-term)
Ions Score: 110 **Expect:** 7.3e-010
Matches (Bold Red): 23/99 fragment ions using 36 most intense peaks

#	Immon.	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	44.0495	114.0549	57.5311	A					15
2	44.0495	**185.0921**	93.0497	A	1000.4919	500.7496	983.4653	492.2363	14
3	44.0495	**256.1292**	128.5682	A	**929.4548**	465.2310	**912.4282**	456.7177	13
4	30.0338	**313.1506**	**157.0790**	G	**858.4177**	**429.7125**	841.3911	421.1992	12
5	30.0338	**370.1721**	185.5897	G	**801.3962**	401.2017	784.3696	392.6885	11
6	30.0338	**427.1936**	214.1004	G	**744.3747**	372.6910	727.3482	364.1777	10
7	30.0338	**484.2150**	242.6112	G	**687.3533**	344.1803	670.3267	335.6670	9
8	30.0338	**541.2365**	271.1219	G	**630.3318**	315.6695	613.3053	307.1563	8
9	30.0338	598.2580	299.6326	G	**573.3103**	287.1588	556.2838	278.6455	7
10	44.0495	669.2951	335.1512	A	**516.2889**	258.6481	499.2623	250.1348	6
11	44.0495	740.3322	370.6697	A	**445.2518**	223.1295	428.2252	214.6162	5
12	44.0495	811.3693	406.1883	A	**374.2146**	187.6110	357.1881	179.0977	4
13	44.0495	882.4064	441.7068	A	**303.1775**	152.0924	286.1510	143.5791	3
14	30.0338	939.4279	470.2176	G	**232.1404**	116.5738	215.1139	108.0606	2
15	129.1135			R	**175.1190**	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **MIETAQVDER**
Found in **Q9UL25**, Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=3

Match to Query 192: 1206.520130 from(604.267341,2+)

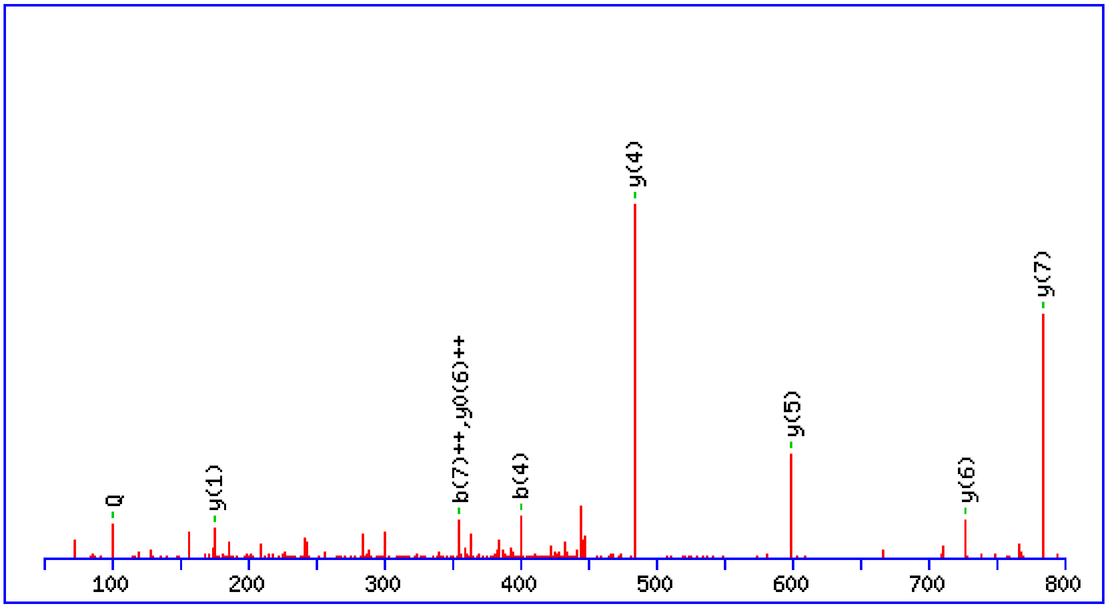


Monoisotopic mass of neutral peptide Mr(calc): 1206.5550
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 55 **Expect:** 0.00024
Matches (Bold Red): 21/143 fragment ions using 53 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	56.0495	84.0444	42.5258					**M**							**10**
2	**86.0964**	197.1285	99.0679					**I**	**1060.5269**	530.7671	1043.5004	522.2538	1042.5164	521.7618	**9**
3	102.0550	**326.1711**	163.5892			308.1605	154.5839	**E**	**947.4429**	474.2251	930.4163	465.7118	**929.4323**	465.2198	**8**
4	74.0600	**427.2187**	214.1130			409.2082	205.1077	**T**	**818.4003**	409.7038	801.3737	401.1905	800.3897	400.6985	**7**
5	44.0495	498.2558	249.6316			480.2453	240.6263	**A**	**717.3526**	359.1799	700.3260	350.6667	699.3420	350.1747	**6**
6	101.0709	626.3144	313.6608	**609.2879**	305.1476	**608.3039**	304.6556	**Q**	**646.3155**	323.6614	629.2889	315.1481	628.3049	314.6561	**5**
7	72.0808	725.3828	363.1951	708.3563	354.6818	707.3723	354.1898	**V**	**518.2569**	259.6321	501.2304	251.1188	500.2463	250.6268	**4**
8	88.0393	840.4098	420.7085	823.3832	412.1953	822.3992	411.7032	**D**	**419.1885**	210.0979	**402.1619**	201.5846	401.1779	201.0926	**3**
9	102.0550	969.4524	**485.2298**	952.4258	476.7165	951.4418	476.2245	**E**	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
10	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VGQDPVLR**
Found in **Q04837**, Q04837|SSB_HUMAN Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1

Match to Query 73: 882.385506 from(442.200029,2+)

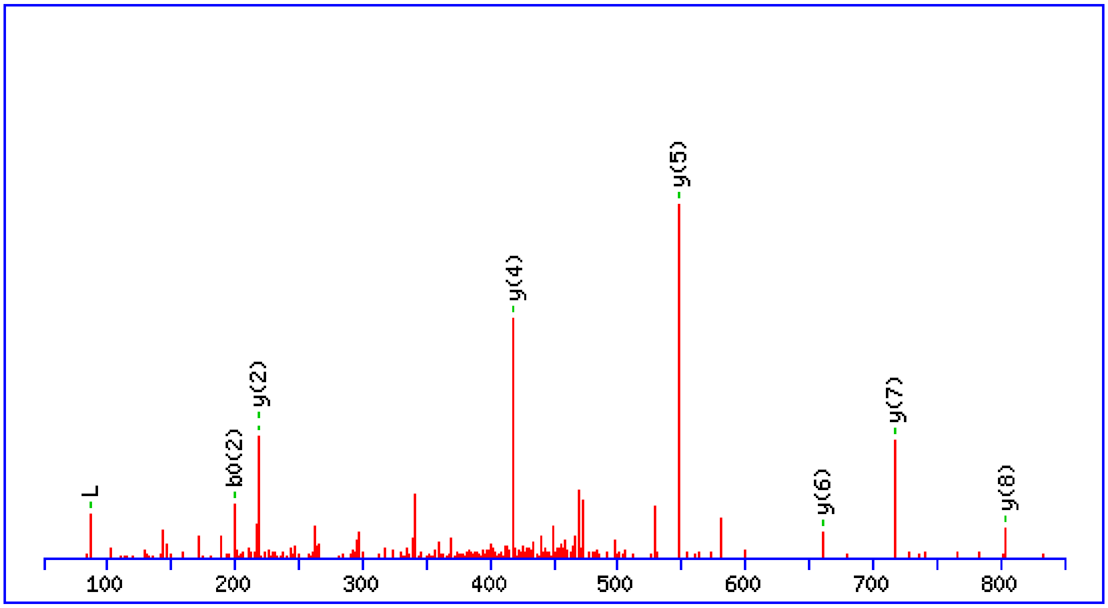


Monoisotopic mass of neutral peptide Mr(calc): 882.4923
Fixed modifications: Carbamidomethyl (C)
Ions Score: 49 **Expect:** 0.00078
Matches (Bold Red): 9/74 fragment ions using 9 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							8
2	30.0338	157.0972	79.0522					G	**784.4312**	392.7192	767.4046	384.2060	766.4206	383.7139	7
3	**101.0709**	285.1557	143.0815	268.1292	134.5682			Q	**727.4097**	364.2085	710.3832	355.6952	709.3991	**355.2032**	6
4	88.0393	**400.1827**	200.5950	383.1561	192.0817	382.1721	191.5897	D	**599.3511**	300.1792	582.3246	291.6659	581.3406	291.1739	5
5	70.0651	497.2354	249.1214	480.2089	240.6081	479.2249	240.1161	P	**484.3242**	242.6657	467.2976	234.1525			4
6	72.0808	596.3039	298.6556	579.2773	290.1423	578.2933	289.6503	V	387.2714	194.1394	370.2449	185.6261			3
7	86.0964	709.3879	**355.1976**	692.3614	346.6843	691.3774	346.1923	L	288.2030	144.6051	271.1765	136.0919			2
8	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ESGLETVAK**
Found in **Q8TED4**, Q8TED4|SPX2_HUMAN Sugar phosphate exchanger 2 OS=Homo sapiens GN=SLC37A2 PE=2 SV=2

Match to Query 193: 932.472836 from(467.243694,2+)

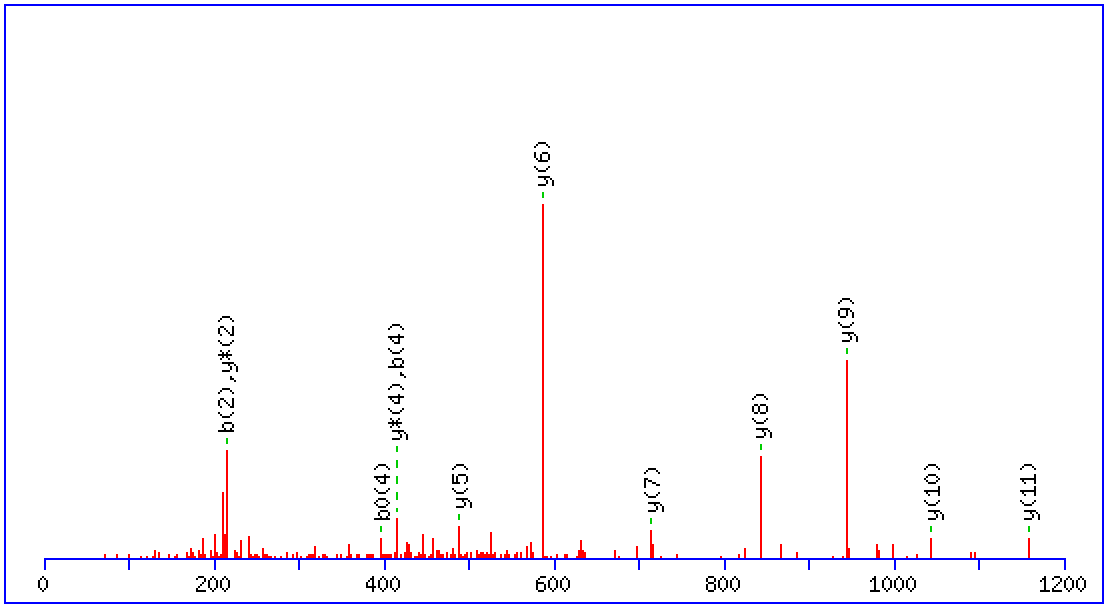


Monoisotopic mass of neutral peptide Mr(calc): 932.4815
Fixed modifications: Carbamidomethyl (C)
Ions Score: 60 **Expect:** 9.6e-005
Matches (Bold Red): 8/83 fragment ions using 10 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286	112.0393	56.5233	E							9
2	60.0444	217.0819	109.0446	**199.0713**	100.0393	S	**804.4462**	402.7267	787.4196	394.2134	786.4356	393.7214	8
3	30.0338	274.1034	137.5553	256.0928	128.5500	G	**717.4141**	359.2107	700.3876	350.6974	699.4036	350.2054	7
4	**86.0964**	387.1874	194.0974	369.1769	185.0921	L	**660.3927**	330.7000	643.3661	322.1867	642.3821	321.6947	6
5	102.0550	516.2300	258.6186	498.2195	249.6134	E	**547.3086**	274.1579	530.2821	265.6447	529.2980	265.1527	5
6	74.0600	617.2777	309.1425	599.2671	300.1372	T	**418.2660**	209.6366	401.2395	201.1234	400.2554	200.6314	4
7	72.0808	716.3461	358.6767	698.3355	349.6714	V	317.2183	159.1128	300.1918	150.5995			3
8	44.0495	787.3832	394.1953	769.3727	385.1900	A	**218.1499**	109.5786	201.1234	101.0653			2
9	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VDVTEQPGLSGR**
Found in **Q9H3N1**, Q9H3N1|TXND1_HUMAN Thioredoxin domain-containing protein 1 OS=Homo sapiens GN=TXNDC1 PE=1 SV=1

Match to Query 388: 1256.691118 from(629.352835,2+)

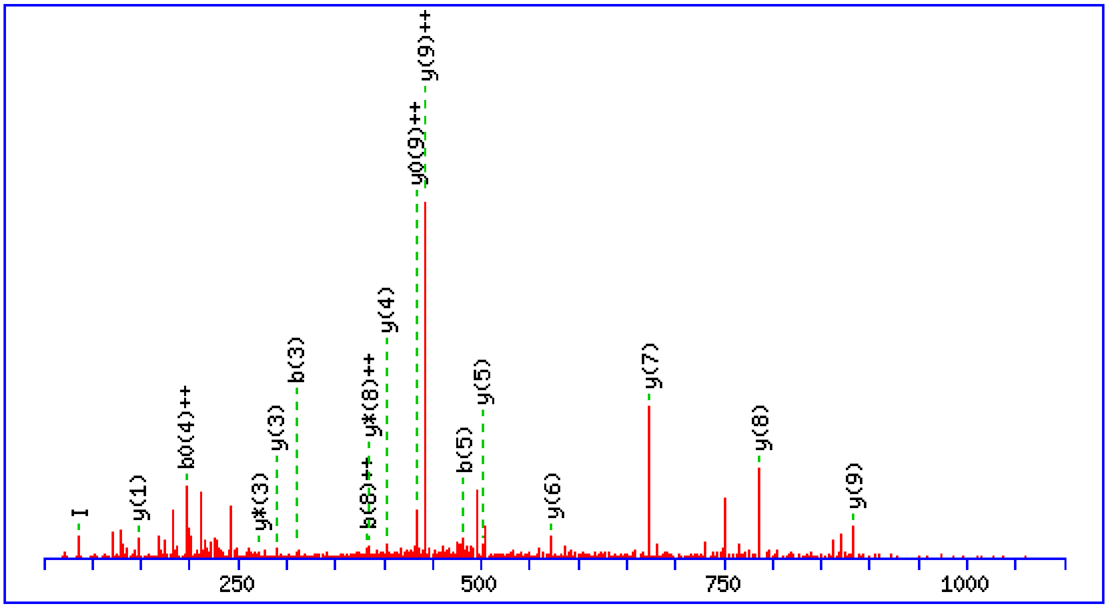


Monoisotopic mass of neutral peptide Mr(calc): 1256.6361
Fixed modifications: Carbamidomethyl (C)
Ions Score: 64 **Expect:** 3.1e-005
Matches (Bold Red): 12/128 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					**V**							**12**
2	88.0393	**215.1026**	108.0550			197.0921	99.0497	**D**	**1158.5749**	579.7911	1141.5484	571.2778	1140.5644	570.7858	**11**
3	72.0808	314.1710	157.5892			296.1605	148.5839	**V**	**1043.5480**	522.2776	1026.5215	513.7644	1025.5374	513.2724	**10**
4	74.0600	**415.2187**	208.1130			**397.2082**	199.1077	**T**	**944.4796**	472.7434	927.4530	464.2302	926.4690	463.7381	**9**
5	102.0550	544.2613	272.6343			526.2508	263.6290	**E**	**843.4319**	422.2196	826.4054	413.7063	825.4213	413.2143	**8**
6	101.0709	672.3199	336.6636	655.2933	328.1503	654.3093	327.6583	**Q**	**714.3893**	357.6983	697.3628	349.1850	696.3787	348.6930	**7**
7	70.0651	769.3727	385.1900	752.3461	376.6767	751.3621	376.1847	**P**	**586.3307**	293.6690	569.3042	285.1557	568.3202	284.6637	**6**
8	30.0338	826.3941	413.7007	809.3676	405.1874	808.3836	404.6954	**G**	**489.2780**	245.1426	472.2514	236.6293	471.2674	236.1373	**5**
9	86.0964	939.4782	470.2427	922.4516	461.7295	921.4676	461.2375	**L**	432.2565	216.6319	**415.2300**	208.1186	414.2459	207.6266	**4**
10	60.0444	1026.5102	513.7587	1009.4837	505.2455	1008.4997	504.7535	**S**	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	**3**
11	30.0338	1083.5317	542.2695	1066.5051	533.7562	1065.5211	533.2642	**G**	232.1404	116.5738	**215.1139**	108.0606			**2**
12	129.1135							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VPITAVIAAK**
Found in **P29144**, P29144|TPP2_HUMAN Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4

Match to Query 322: 981.593466 from(491.804009,2+)

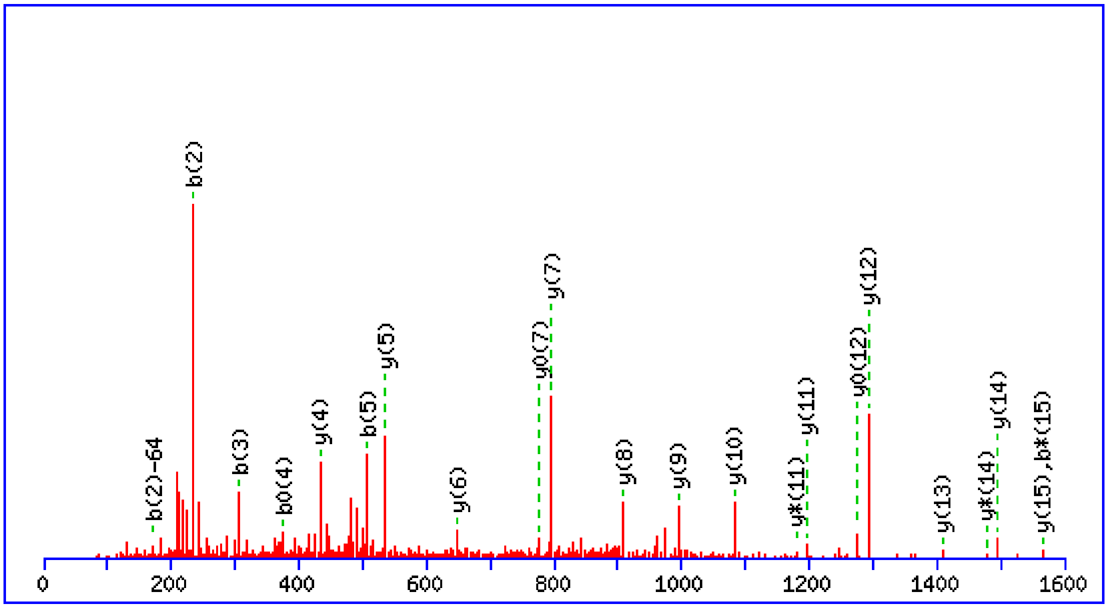


Monoisotopic mass of neutral peptide Mr(calc): 981.6223
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 **Expect:** 0.01
Matches (Bold Red): 20/82 fragment ions using 52 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			V							10
2	70.0651	**197.1285**	99.0679			P	**883.5611**	**442.2842**	866.5346	433.7709	865.5506	**433.2789**	9
3	**86.0964**	**310.2125**	155.6099			I	**786.5084**	393.7578	769.4818	**385.2445**	768.4978	384.7525	8
4	74.0600	411.2602	206.1337	393.2496	**197.1285**	T	**673.4243**	337.2158	656.3978	328.7025	655.4137	328.2105	7
5	44.0495	**482.2973**	241.6523	464.2867	232.6470	A	**572.3766**	286.6920	555.3501	278.1787			6
6	72.0808	581.3657	291.1865	563.3552	282.1812	V	**501.3395**	251.1734	484.3130	242.6601			5
7	**86.0964**	694.4498	347.7285	676.4392	338.7233	I	**402.2711**	201.6392	**385.2445**	193.1259			4
8	44.0495	765.4869	**383.2471**	747.4763	374.2418	A	**289.1870**	145.0972	**272.1605**	136.5839			3
9	44.0495	836.5240	418.7656	818.5135	409.7604	A	218.1499	109.5786	201.1234	101.0653			2
10	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **MSASDPNSSIFLTDTAK**
Found in **P23381**, P23381|SYWC_HUMAN Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2

Match to Query 515: 1799.802566 from(900.908559,2+)

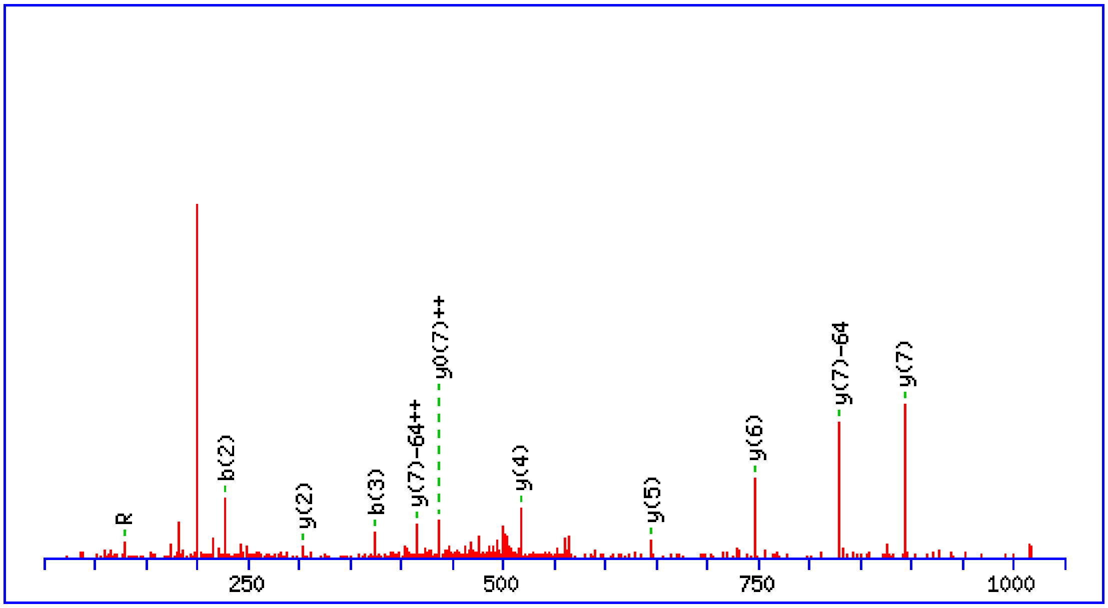


Monoisotopic mass of neutral peptide Mr(calc): 1799.8247
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 99 **Expect:** 8.5e-009
Matches (Bold Red): 22/274 fragment ions using 31 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	120.0478	148.0427	74.5250					M							17
2	60.0444	**235.0747**	118.0410			217.0641	109.0357	S	1653.7966	827.4019	1636.7701	818.8887	1635.7861	818.3967	16
3	44.0495	**306.1118**	153.5595			288.1013	144.5543	A	**1566.7646**	783.8859	1549.7380	775.3727	1548.7540	774.8807	15
4	60.0444	393.1438	197.0756			**375.1333**	188.0703	S	**1495.7275**	748.3674	**1478.7009**	739.8541	1477.7169	739.3621	14
5	88.0393	**508.1708**	254.5890			490.1602	245.5838	D	**1408.6955**	704.8514	1391.6689	696.3381	1390.6849	695.8461	13
6	70.0651	605.2236	303.1154			587.2130	294.1101	P	**1293.6685**	647.3379	1276.6420	638.8246	**1275.6579**	638.3326	12
7	87.0553	719.2665	360.1369	702.2399	351.6236	701.2559	351.1316	N	**1196.6157**	598.8115	**1179.5892**	590.2982	1178.6052	589.8062	11
8	60.0444	806.2985	403.6529	789.2720	395.1396	788.2879	394.6476	S	**1082.5728**	541.7900	1065.5463	533.2768	1064.5623	532.7848	10
9	60.0444	893.3305	447.1689	876.3040	438.6556	875.3200	438.1636	S	**995.5408**	498.2740	978.5142	489.7608	977.5302	489.2688	9
10	86.0964	1006.4146	503.7109	989.3881	495.1977	988.4040	494.7057	I	**908.5088**	454.7580	891.4822	446.2447	890.4982	445.7527	8
11	120.0808	1153.4830	577.2451	1136.4565	568.7319	1135.4725	568.2399	F	**795.4247**	398.2160	778.3981	389.7027	**777.4141**	389.2107	7
12	86.0964	1266.5671	633.7872	1249.5405	625.2739	1248.5565	624.7819	L	**648.3563**	324.6818	631.3297	316.1685	630.3457	315.6765	6
13	74.0600	1367.6148	684.3110	1350.5882	675.7977	1349.6042	675.3057	T	**535.2722**	268.1397	518.2457	259.6265	517.2617	259.1345	5
14	88.0393	1482.6417	741.8245	1465.6152	733.3112	1464.6311	732.8192	D	**434.2245**	217.6159	417.1980	209.1026	416.2140	208.6106	4
15	74.0600	1583.6894	792.3483	**1566.6628**	783.8351	1565.6788	783.3430	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
16	44.0495	1654.7265	827.8669	1637.6999	819.3536	1636.7159	818.8616	A	218.1499	109.5786	201.1234	101.0653			2
17	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **NIMTQNVER**
Found in **Q9BV40**, Q9BV40|VAMP8_HUMAN Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1

Match to Query 360: 1119.566328 from(560.790440,2+)

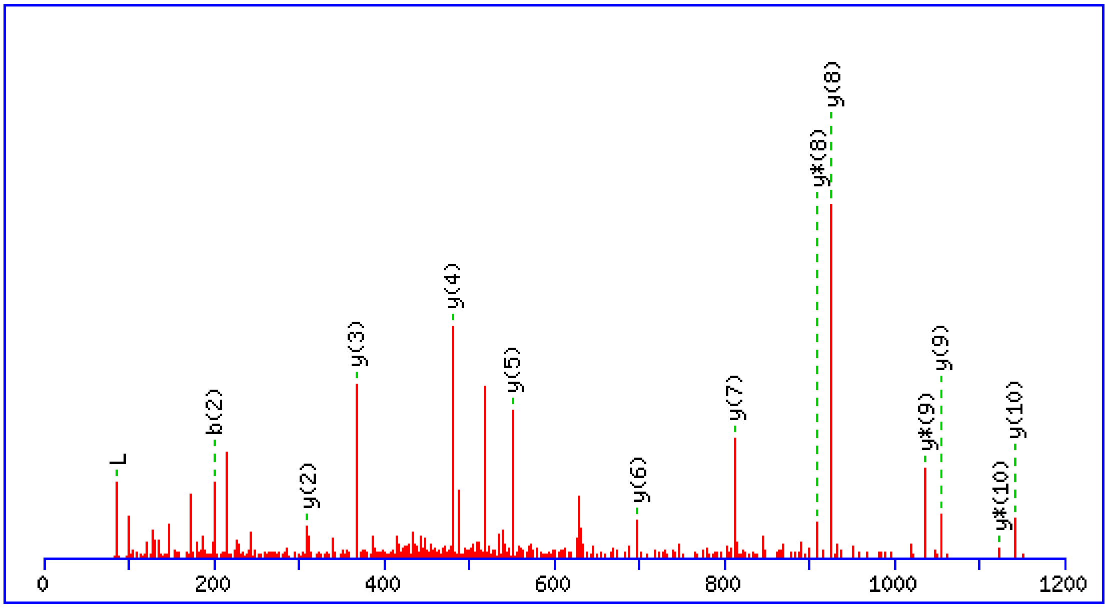


Monoisotopic mass of neutral peptide Mr(calc): 1119.5342
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.025
Matches (Bold Red): 11/144 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	87.0553	115.0502	58.0287	98.0237	49.5155			**N**							**9**
2	86.0964	**228.1343**	114.5708	211.1077	106.0575			**I**	942.5003	471.7538	925.4738	463.2405	924.4898	462.7485	**8**
3	56.0495	311.1714	156.0893	294.1448	147.5761			**M**	**829.4163**	**415.2118**	812.3897	406.6985	811.4057	406.2065	**7**
4	74.0600	412.2191	206.6132	395.1925	198.0999	394.2085	197.6079	**T**	**746.3791**	373.6932	729.3526	365.1799	728.3686	364.6879	**6**
5	101.0709	540.2776	270.6425	523.2511	262.1292	522.2671	261.6372	**Q**	**645.3315**	323.1694	628.3049	314.6561	627.3209	314.1641	**5**
6	87.0553	654.3206	327.6639	637.2940	319.1506	636.3100	318.6586	**N**	**517.2729**	259.1401	500.2463	250.6268	499.2623	250.1348	**4**
7	72.0808	753.3890	377.1981	736.3624	368.6849	735.3784	368.1928	**V**	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	**3**
8	102.0550	882.4316	441.7194	865.4050	433.2062	864.4210	432.7141	**E**	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
9	**129.1135**							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LSQNNFALGYK**
Found in **Q9Y277**, Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1

Match to Query 384: 1253.670776 from(627.842664,2+)

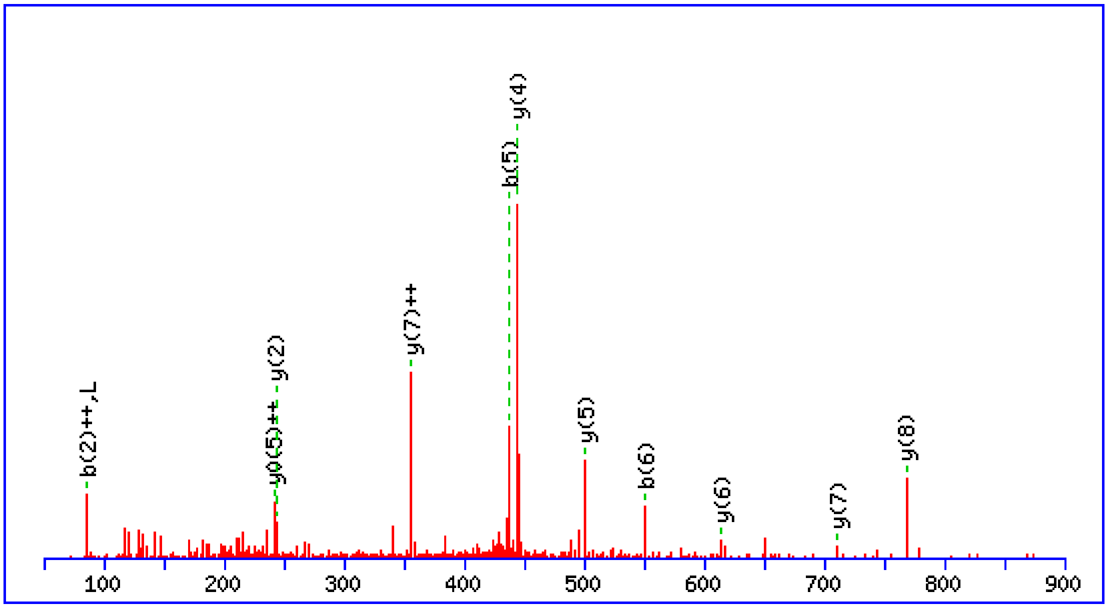


Monoisotopic mass of neutral peptide Mr(calc): 1253.6404
Fixed modifications: Carbamidomethyl (C)
Ions Score: 70 **Expect:** 7.2e-006
Matches (Bold Red): 15/107 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							11
2	60.0444	**201.1234**	101.0653			183.1128	92.0600	S	**1141.5636**	571.2855	**1124.5371**	562.7722	1123.5531	562.2802	10
3	101.0709	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	**1054.5316**	527.7694	**1037.5051**	519.2562			9
4	87.0553	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	N	**926.4730**	463.7402	**909.4465**	455.2269			8
5	87.0553	557.2678	279.1375	540.2413	270.6243	539.2572	270.1323	N	**812.4301**	406.7187	795.4036	398.2054			7
6	120.0808	704.3362	352.6717	687.3097	344.1585	686.3256	343.6665	F	**698.3872**	349.6972	681.3606	341.1840			6
7	44.0495	775.3733	388.1903	758.3468	379.6770	757.3628	379.1850	A	**551.3188**	276.1630	534.2922	267.6498			5
8	**86.0964**	888.4574	444.7323	871.4308	436.2191	870.4468	435.7271	L	**480.2817**	240.6445	463.2551	232.1312			4
9	30.0338	945.4789	473.2431	928.4523	464.7298	927.4683	464.2378	G	**367.1976**	184.1024	350.1710	175.5892			3
10	136.0757	1108.5422	554.7747	1091.5156	546.2615	1090.5316	545.7694	Y	**310.1761**	155.5917	293.1496	147.0784			2
11	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IGPLGLSPK**
Found in **P30050**, P30050|RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1

Match to Query 170: 880.481382 from(441.247967,2+)

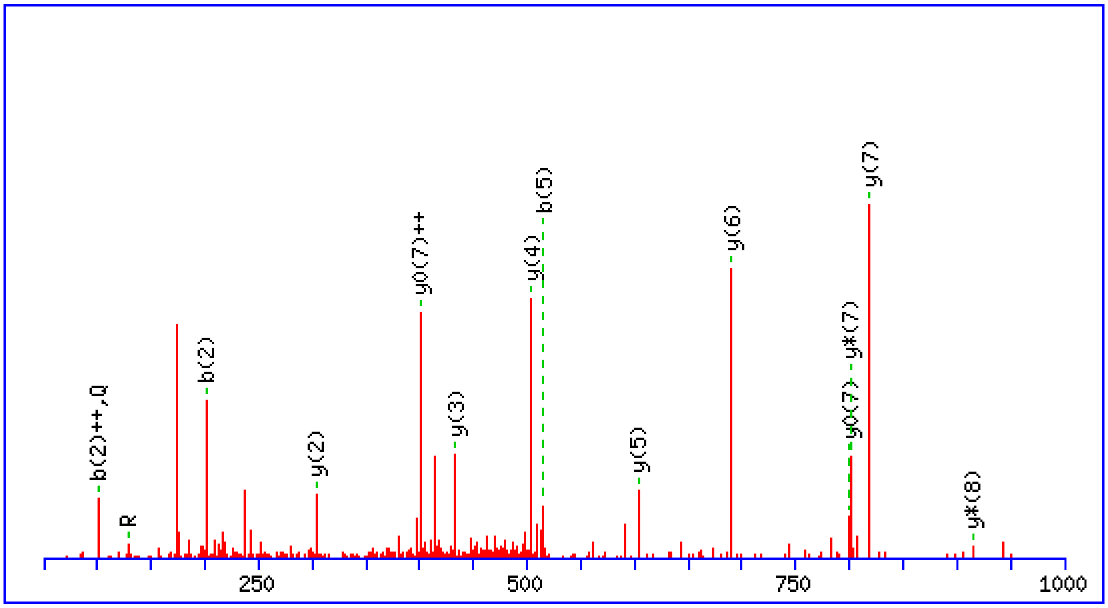


Monoisotopic mass of neutral peptide Mr(calc): 880.5382
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.0024
Matches (Bold Red): 14/73 fragment ions using 18 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			I							9
2	30.0338	171.1128	**86.0600**			G	**768.4614**	384.7343	751.4349	376.2211	750.4509	375.7291	8
3	70.0651	268.1656	134.5864			P	**711.4400**	**356.2236**	694.4134	347.7103	693.4294	347.2183	7
4	**86.0964**	381.2496	191.1285			L	**614.3872**	307.6972	597.3606	299.1840	596.3766	298.6919	6
5	30.0338	**438.2711**	219.6392			G	**501.3031**	251.1552	484.2766	242.6419	483.2926	**242.1499**	5
6	**86.0964**	**551.3552**	276.1812			L	**444.2817**	222.6445	427.2551	214.1312	426.2711	213.6392	4
7	60.0444	638.3872	319.6972	620.3766	310.6919	S	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
8	70.0651	735.4400	368.2236	717.4294	359.2183	P	**244.1656**	122.5864	227.1390	114.0731			2
9	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **SLQSVAEER**
Found in **P61313**, P61313|RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2

Match to Query 359: 1017.503392 from(509.758972,2+)

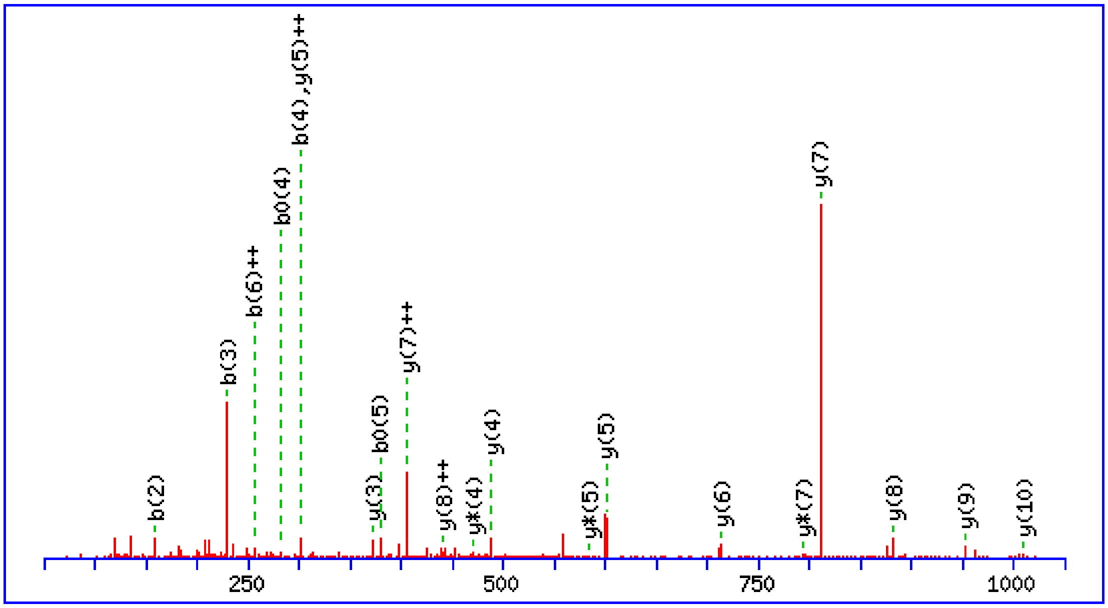


Monoisotopic mass of neutral peptide Mr(calc): 1017.5091
Fixed modifications: Carbamidomethyl (C)
Ions Score: 47 **Expect:** 0.0016
Matches (Bold Red): 15/99 fragment ions using 27 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	**S**							**9**
2	86.0964	**201.1234**	**101.0653**			183.1128	92.0600	**L**	931.4843	466.2458	**914.4578**	457.7325	913.4738	457.2405	**8**
3	**101.0709**	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	**Q**	**818.4003**	409.7038	**801.3737**	401.1905	**800.3897**	**400.6985**	**7**
4	60.0444	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	**S**	**690.3417**	345.6745	673.3151	337.1612	672.3311	336.6692	**6**
5	72.0808	**515.2824**	258.1448	498.2558	249.6316	497.2718	249.1395	**V**	**603.3097**	302.1585	586.2831	293.6452	585.2991	293.1532	**5**
6	44.0495	586.3195	293.6634	569.2930	285.1501	568.3089	284.6581	**A**	**504.2413**	252.6243	487.2147	244.1110	486.2307	243.6190	**4**
7	102.0550	715.3621	358.1847	698.3355	349.6714	697.3515	349.1794	**E**	**433.2041**	217.1057	416.1776	208.5924	415.1936	208.1004	**3**
8	102.0550	844.4047	422.7060	827.3781	414.1927	826.3941	413.7007	**E**	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	**2**
9	**129.1135**							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **TGAAPIIDVVR**
Found in **P46776**, P46776|RL27A_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2

Match to Query 416: 1110.638054 from(556.326303,2+)

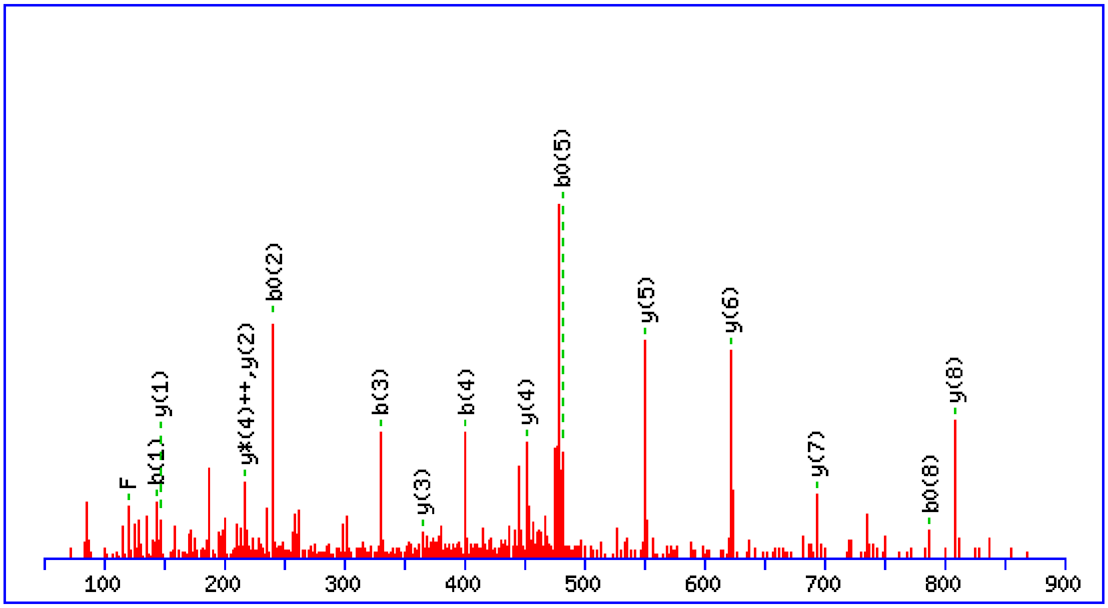


Monoisotopic mass of neutral peptide Mr(calc): 1110.6397
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 **Expect:** 0.00015
Matches (Bold Red): 20/105 fragment ions using 41 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							11
2	30.0338	**159.0764**	80.0418	141.0659	71.0366	G	**1010.5993**	505.8033	993.5728	497.2900	992.5887	496.7980	10
3	44.0495	**230.1135**	115.5604	212.1030	106.5551	A	**953.5778**	477.2926	936.5513	468.7793	935.5673	468.2873	9
4	44.0495	**301.1506**	151.0790	**283.1401**	142.0737	A	**882.5407**	**441.7740**	865.5142	433.2607	864.5302	432.7687	8
5	70.0651	398.2034	199.6053	**380.1928**	190.6001	P	**811.5036**	**406.2554**	**794.4771**	397.7422	793.4930	397.2502	7
6	86.0964	511.2875	**256.1474**	493.2769	247.1421	I	**714.4509**	357.7291	697.4243	349.2158	696.4403	348.7238	6
7	86.0964	624.3715	312.6894	606.3610	303.6841	I	**601.3668**	**301.1870**	**584.3402**	292.6738	583.3562	292.1817	5
8	88.0393	739.3985	370.2029	721.3879	361.1976	D	**488.2827**	244.6450	**471.2562**	236.1317	470.2722	235.6397	4
9	72.0808	838.4669	419.7371	820.4563	410.7318	V	**373.2558**	187.1315	356.2292	178.6183			3
10	72.0808	937.5353	469.2713	919.5247	460.2660	V	274.1874	137.5973	257.1608	129.0840			2
11	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TDAAVSFAK**
Found in **P05141**, P05141|ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=6

Match to Query 166: 950.537758 from(476.276155,2+)

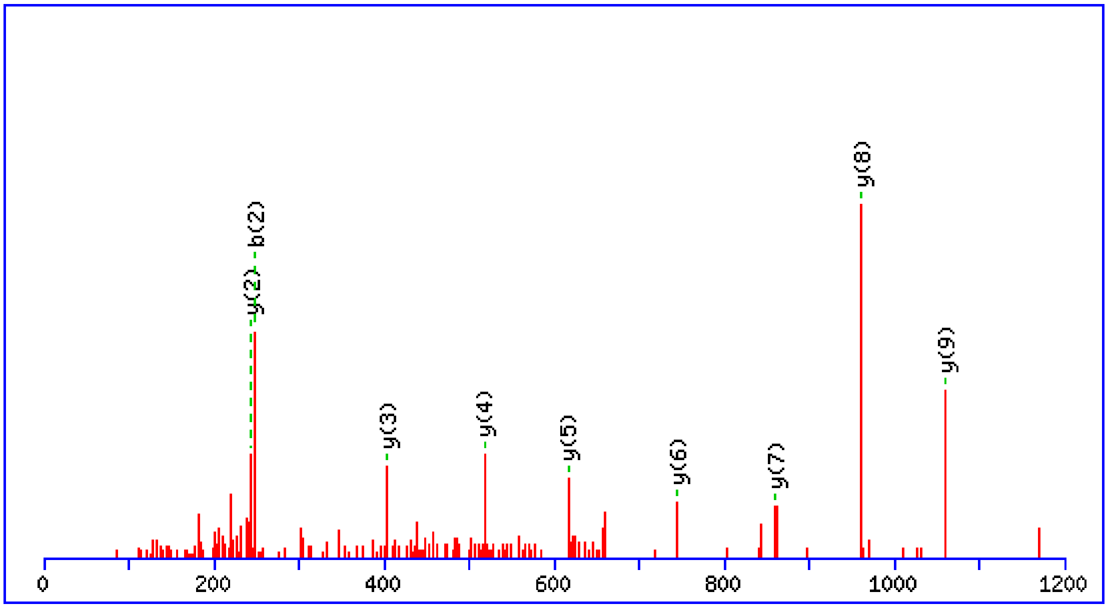


Monoisotopic mass of neutral peptide Mr(calc): 950.4709
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
N-term : Acetyl (Protein N-term)
Ions Score: 47 **Expect:** 0.0013
Matches (Bold Red): 16/83 fragment ions using 46 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	**144.0655**	72.5364	126.0549	63.5311	T							9
2	88.0393	259.0925	130.0499	**241.0819**	121.0446	D	**808.4199**	404.7136	791.3934	396.2003	790.4094	395.7083	8
3	44.0495	**330.1296**	165.5684	312.1190	156.5631	A	**693.3930**	347.2001	676.3665	338.6869	675.3824	338.1949	7
4	44.0495	**401.1667**	201.0870	383.1561	192.0817	A	**622.3559**	311.6816	605.3293	303.1683	604.3453	302.6763	6
5	72.0808	500.2351	250.6212	**482.2245**	241.6159	V	**551.3188**	276.1630	534.2922	267.6498	533.3082	267.1577	5
6	60.0444	587.2671	294.1372	569.2566	285.1319	S	**452.2504**	226.6288	435.2238	**218.1155**	434.2398	217.6235	4
7	**120.0808**	734.3355	367.6714	716.3250	358.6661	F	**365.2183**	183.1128	348.1918	174.5995			3
8	44.0495	805.3727	403.1900	**787.3621**	394.1847	A	**218.1499**	109.5786	201.1234	101.0653			2
9	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **MTVTDQVNCPK**
Found in **P05090**, P05090|APOD_HUMAN Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1

Match to Query 446: 1307.673980 from(654.844266,2+)

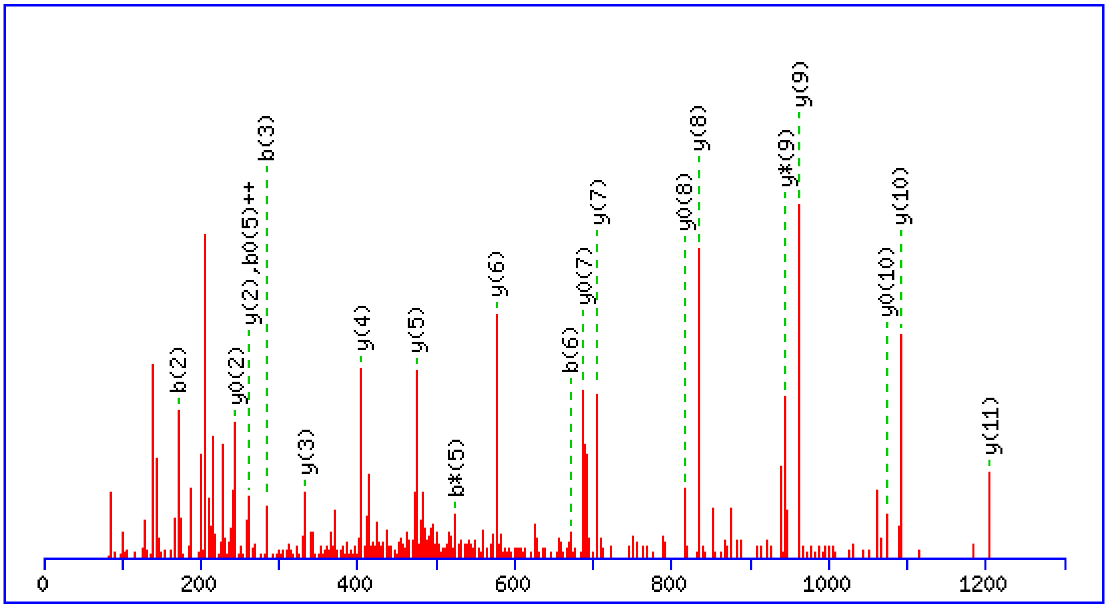


Monoisotopic mass of neutral peptide Mr(calc): 1307.5850
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 55 **Expect:** 0.00024
Matches (Bold Red): 9/156 fragment ions using 14 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	120.0478	148.0427	74.5250					M							11
2	74.0600	**249.0904**	125.0488			231.0798	116.0435	T	1161.5569	581.2821	1144.5303	572.7688	1143.5463	572.2768	10
3	72.0808	348.1588	174.5830			330.1482	165.5777	V	**1060.5092**	530.7582	1043.4826	522.2449	1042.4986	521.7529	9
4	74.0600	449.2065	225.1069			431.1959	216.1016	T	**961.4408**	481.2240	944.4142	472.7107	943.4302	472.2187	8
5	88.0393	564.2334	282.6203			546.2228	273.6151	D	**860.3931**	430.7002	843.3665	422.1869	842.3825	421.6949	7
6	101.0709	692.2920	346.6496	675.2654	338.1364	674.2814	337.6443	Q	**745.3661**	373.1867	728.3396	364.6734			6
7	72.0808	791.3604	396.1838	774.3338	387.6706	773.3498	387.1785	V	**617.3076**	309.1574	600.2810	300.6441			5
8	87.0553	905.4033	453.2053	888.3768	444.6920	887.3927	444.2000	N	**518.2391**	259.6232	501.2126	251.1099			4
9	133.0430	1065.4340	533.2206	1048.4074	524.7073	1047.4234	524.2153	C	**404.1962**	202.6017	387.1697	194.0885			3
10	70.0651	1162.4867	581.7470	1145.4602	573.2337	1144.4762	572.7417	P	**244.1656**	122.5864	227.1390	114.0731			2
11	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AVLEQEETAAASR**
Found in **Q9Y2J2**, Q9Y2J2|E41L3_HUMAN Band 4.1-like protein 3 OS=Homo sapiens GN=EPB41L3 PE=1 SV=2

Match to Query 396: 1373.657264 from(687.835908,2+)

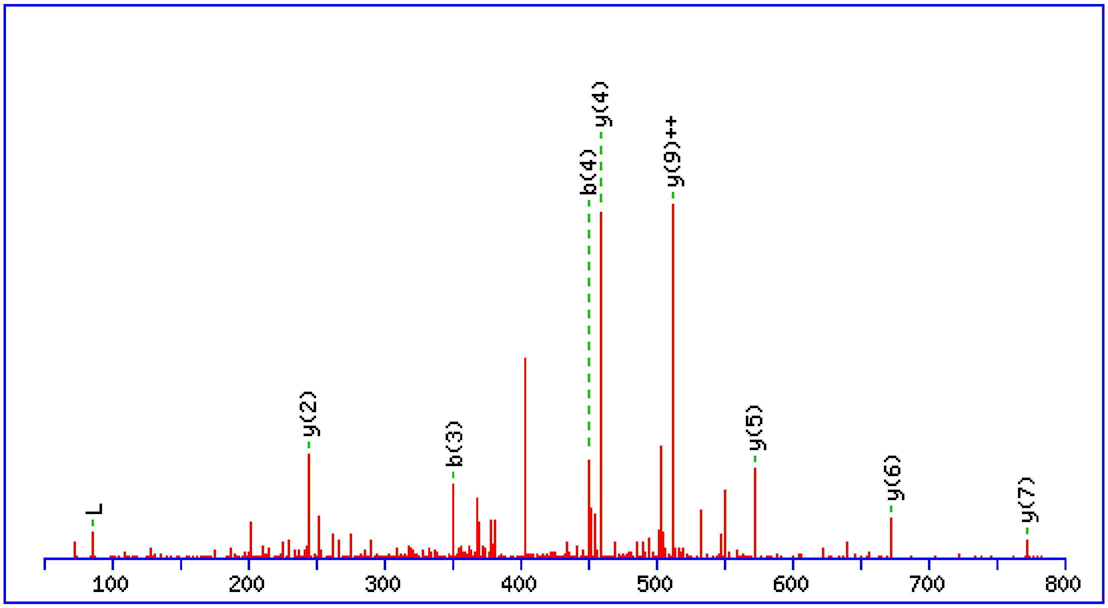


Monoisotopic mass of neutral peptide Mr(calc): 1373.6786
Fixed modifications: Carbamidomethyl (C)
Ions Score: 75 **Expect:** 2.1e-006
Matches (Bold Red): 20/141 fragment ions using 26 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					**A**							**13**
2	72.0808	**171.1128**	86.0600					**V**	1303.6488	652.3281	1286.6223	643.8148	1285.6383	643.3228	**12**
3	86.0964	**284.1969**	142.6021					**L**	**1204.5804**	602.7938	1187.5539	594.2806	1186.5699	593.7886	**11**
4	102.0550	413.2395	207.1234			395.2289	198.1181	**E**	**1091.4964**	546.2518	1074.4698	537.7385	**1073.4858**	537.2465	**10**
5	101.0709	541.2980	271.1527	**524.2715**	262.6394	523.2875	**262.1474**	**Q**	**962.4538**	481.7305	**945.4272**	473.2172	944.4432	472.7252	**9**
6	102.0550	**670.3406**	335.6740	653.3141	327.1607	652.3301	326.6687	**E**	**834.3952**	417.7012	817.3686	409.1880	**816.3846**	408.6959	**8**
7	102.0550	799.3832	400.1953	782.3567	391.6820	781.3727	391.1900	**E**	**705.3526**	353.1799	688.3260	344.6667	**687.3420**	344.1747	**7**
8	74.0600	900.4309	450.7191	883.4044	442.2058	882.4203	441.7138	**T**	**576.3100**	288.6586	559.2835	280.1454	558.2994	279.6534	**6**
9	44.0495	971.4680	486.2376	954.4415	477.7244	953.4575	477.2324	**A**	**475.2623**	238.1348	458.2358	229.6215	457.2518	229.1295	**5**
10	44.0495	1042.5051	521.7562	1025.4786	513.2429	1024.4946	512.7509	**A**	**404.2252**	202.6162	387.1987	194.1030	386.2146	193.6110	**4**
11	44.0495	1113.5422	557.2748	1096.5157	548.7615	1095.5317	548.2695	**A**	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	**3**
12	60.0444	1200.5743	600.7908	1183.5477	592.2775	1182.5637	591.7855	**S**	**262.1510**	131.5791	245.1244	123.0659	**244.1404**	122.5738	**2**
13	129.1135							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VNHVTLSQPK**
Found in **P61769**, P61769|B2MG_HUMAN Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1

Match to Query 292: 1121.530833 from(374.850887,3+)

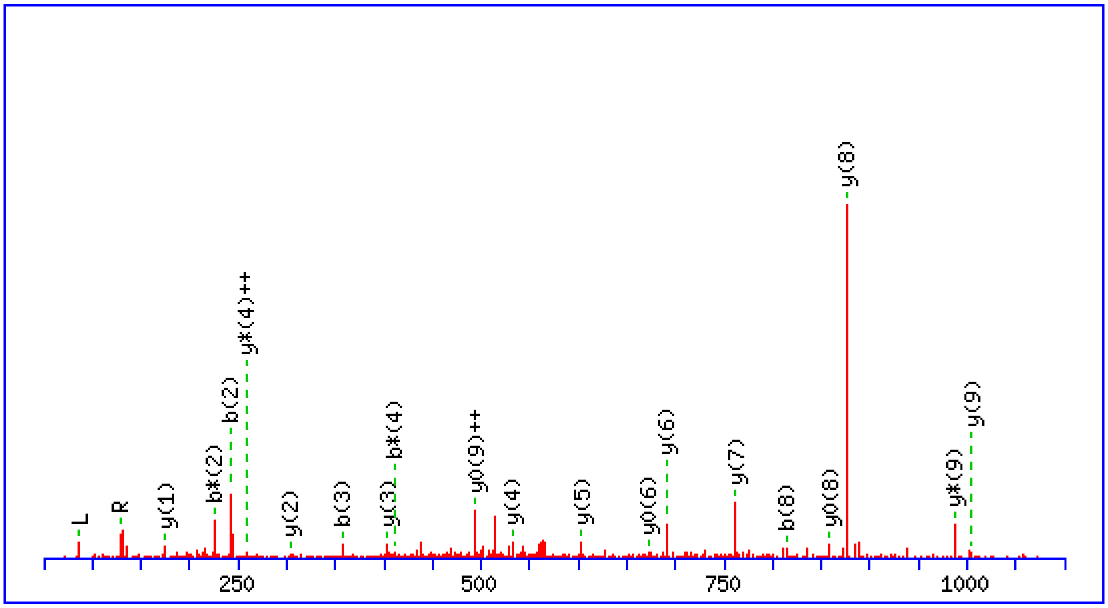


Monoisotopic mass of neutral peptide Mr(calc): 1121.6193
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.0086
Matches (Bold Red): 9/102 fragment ions using 11 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							10
2	87.0553	214.1186	107.5629	197.0921	99.0497			N	1023.5582	**512.2827**	1006.5316	503.7694	1005.5476	503.2774	9
3	110.0713	**351.1775**	176.0924	334.1510	167.5791			H	909.5152	455.2613	892.4887	446.7480	891.5047	446.2560	8
4	72.0808	**450.2459**	225.6266	433.2194	217.1133			V	**772.4563**	386.7318	755.4298	378.2185	754.4458	377.7265	7
5	74.0600	551.2936	276.1504	534.2671	267.6372	533.2831	267.1452	T	**673.3879**	337.1976	656.3614	328.6843	655.3774	328.1923	6
6	**86.0964**	664.3777	332.6925	647.3511	324.1792	646.3671	323.6872	L	**572.3402**	286.6738	555.3137	278.1605	554.3297	277.6685	5
7	60.0444	751.4097	376.2085	734.3832	367.6952	733.3991	367.2032	S	**459.2562**	230.1317	442.2296	221.6185	441.2456	221.1264	4
8	101.0709	879.4683	440.2378	862.4417	431.7245	861.4577	431.2325	Q	372.2241	186.6157	355.1976	178.1024			3
9	70.0651	976.5211	488.7642	959.4945	480.2509	958.5105	479.7589	P	**244.1656**	122.5864	227.1390	114.0731			2
10	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **LQDASAEVER**
Found in **Q10589**, Q10589|BST2_HUMAN Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1

Match to Query 395: 1116.507912 from(559.261232,2+)

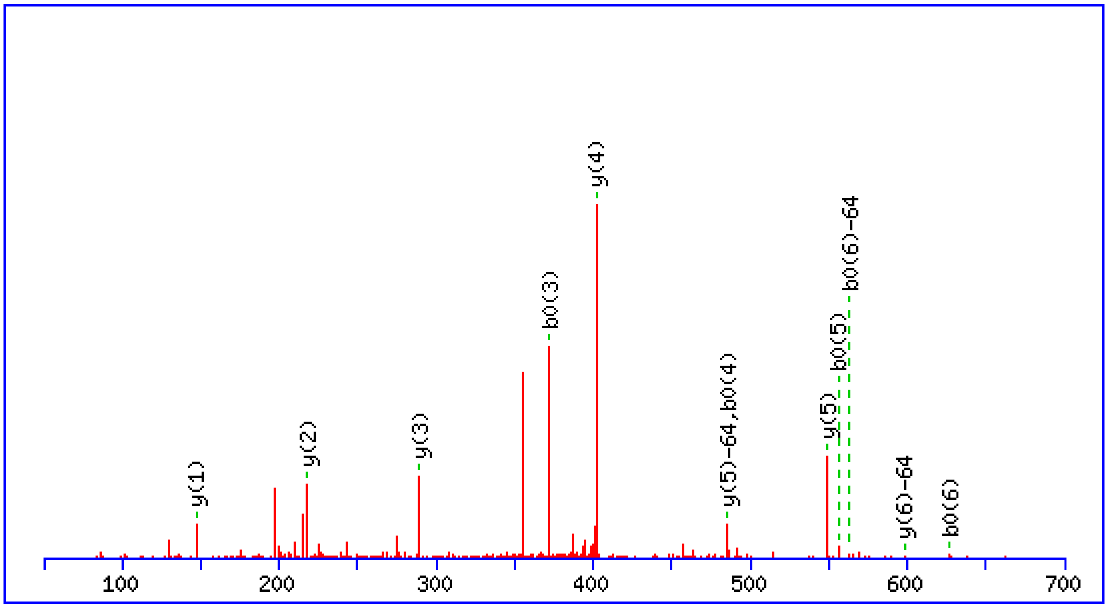


Monoisotopic mass of neutral peptide Mr(calc): 1116.5411
Fixed modifications: Carbamidomethyl (C)
Ions Score: 49 **Expect:** 0.0011
Matches (Bold Red): 22/110 fragment ions using 59 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							10
2	101.0709	**242.1499**	121.5786	**225.1234**	113.0653			Q	**1004.4643**	502.7358	**987.4378**	494.2225	986.4538	**493.7305**	9
3	88.0393	**357.1769**	179.0921	340.1503	170.5788	339.1663	170.0868	D	**876.4058**	438.7065	859.3792	430.1932	**858.3952**	429.7012	8
4	44.0495	428.2140	214.6106	**411.1874**	206.0974	410.2034	205.6053	A	**761.3788**	381.1930	744.3523	372.6798	743.3682	372.1878	7
5	60.0444	515.2460	**258.1266**	498.2195	249.6134	497.2354	249.1214	S	**690.3417**	345.6745	673.3151	337.1612	**672.3311**	336.6692	6
6	44.0495	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	A	**603.3097**	302.1585	586.2831	293.6452	585.2991	293.1532	5
7	102.0550	715.3257	358.1665	698.2992	349.6532	697.3151	349.1612	E	**532.2726**	266.6399	515.2460	**258.1266**	514.2620	257.6346	4
8	72.0808	**814.3941**	407.7007	797.3676	399.1874	796.3836	398.6954	V	**403.2300**	202.1186	386.2034	193.6053	385.2194	193.1133	3
9	102.0550	943.4367	472.2220	926.4102	463.7087	925.4262	463.2167	E	**304.1615**	152.5844	287.1350	144.0711	286.1510	143.5791	2
10	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **EIMLAAK**
Found in **P10606**, P10606|COX5B_HUMAN Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2

Match to Query 38: 790.330084 from(396.172318,2+)

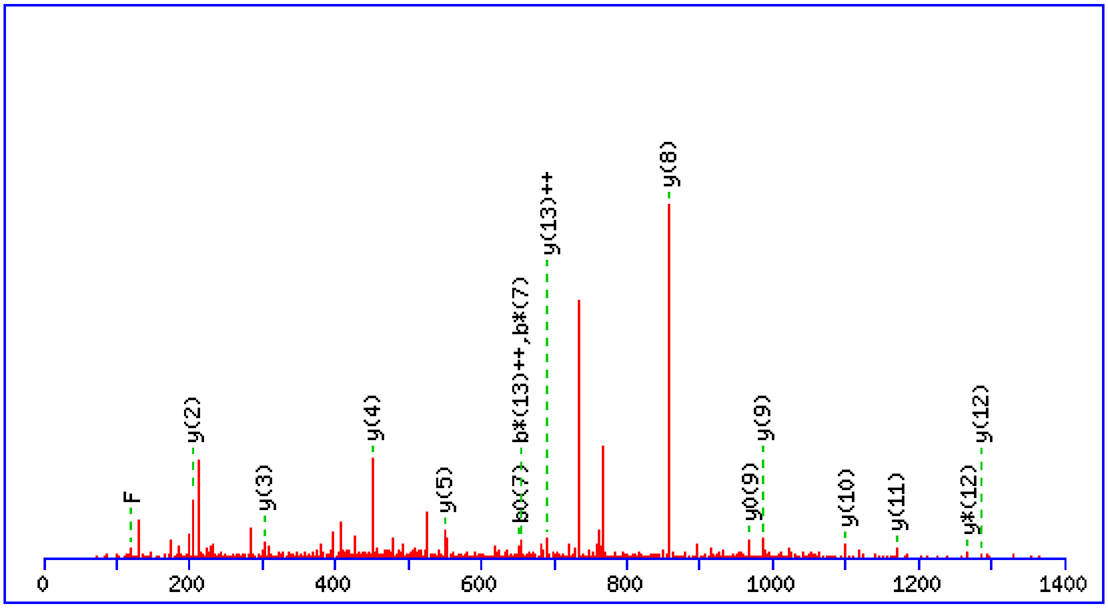


Monoisotopic mass of neutral peptide Mr(calc): 790.4258
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.0094
Matches (Bold Red): 12/80 fragment ions using 21 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	102.0550	130.0499	65.5286	112.0393	56.5233	E					7
2	86.0964	243.1339	122.0706	225.1234	113.0653	I	**598.3923**	299.6998	581.3657	291.1865	6
3	56.0495	326.1711	163.5892	308.1605	154.5839	M	**485.3082**	243.1577	468.2817	234.6445	5
4	86.0964	439.2551	220.1312	421.2446	211.1259	L	**402.2711**	201.6392	385.2445	193.1259	4
5	44.0495	510.2922	255.6498	492.2817	246.6445	A	**289.1870**	145.0972	272.1605	136.5839	3
6	44.0495	581.3293	291.1683	**563.3188**	282.1630	A	**218.1499**	109.5786	201.1234	101.0653	2
7	101.1073					K	**147.1128**	74.0600	130.0863	65.5468	1

MS/MS Fragmentation of **GSPNANEPPLVFVGK**
Found in **P28838**, P28838|AMPL_HUMAN Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3

Match to Query 420: 1524.755510 from(763.385031,2+)

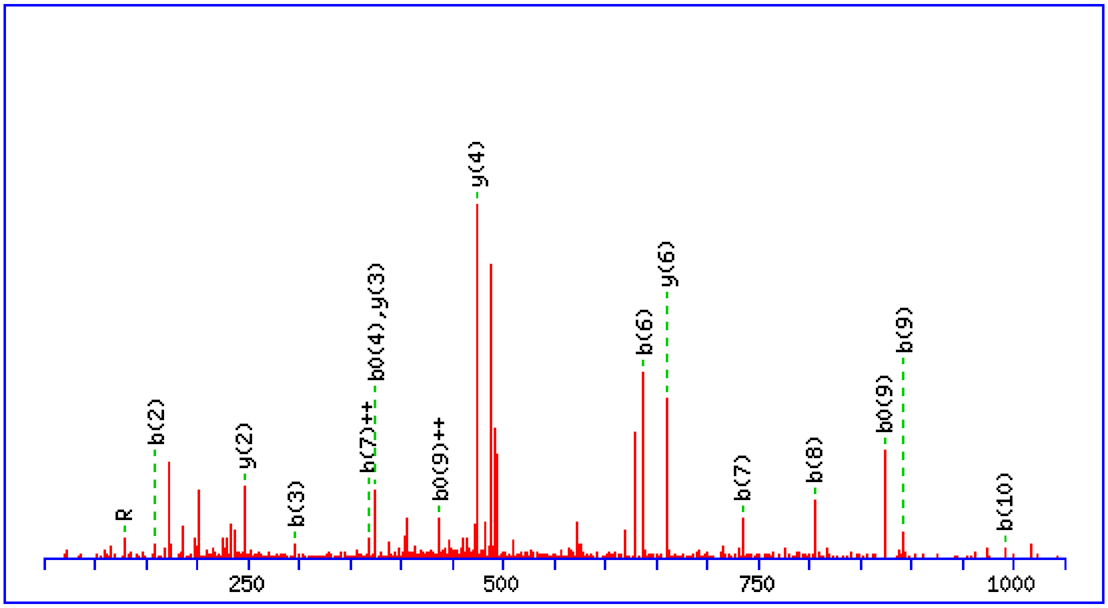


Monoisotopic mass of neutral peptide Mr(calc): 1524.7936
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00047
Matches (Bold Red): 16/159 fragment ions using 30 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180					G							15
2	60.0444	145.0608	73.0340			127.0502	64.0287	S	1468.7795	734.8934	1451.7529	726.3801	1450.7689	725.8881	14
3	70.0651	242.1135	121.5604			224.1030	112.5551	P	1381.7474	**691.3774**	1364.7209	682.8641	1363.7369	682.3721	13
4	87.0553	356.1565	178.5819	339.1299	170.0686	338.1459	169.5766	N	**1284.6947**	642.8510	**1267.6681**	634.3377	1266.6841	633.8457	12
5	44.0495	427.1936	214.1004	410.1670	205.5871	409.1830	205.0951	A	**1170.6517**	585.8295	1153.6252	577.3162	1152.6412	576.8242	11
6	87.0553	541.2365	271.1219	524.2100	262.6086	523.2259	262.1166	N	**1099.6146**	550.3109	1082.5881	541.7977	1081.6041	541.3057	10
7	102.0550	670.2791	335.6432	**653.2525**	327.1299	**652.2685**	326.6379	E	**985.5717**	493.2895	968.5451	484.7762	**967.5611**	484.2842	9
8	70.0651	767.3319	384.1696	750.3053	375.6563	749.3213	375.1643	P	**856.5291**	428.7682	839.5026	420.2549			8
9	70.0651	864.3846	432.6959	847.3581	424.1827	846.3741	423.6907	P	759.4763	380.2418	742.4498	371.7285			7
10	86.0964	977.4687	489.2380	960.4421	480.7247	959.4581	480.2327	L	662.4236	331.7154	645.3970	323.2022			6
11	72.0808	1076.5371	538.7722	1059.5106	530.2589	1058.5265	529.7669	V	**549.3395**	275.1734	532.3130	266.6601			5
12	**120.0808**	1223.6055	612.3064	1206.5790	603.7931	1205.5949	603.3011	F	**450.2711**	225.6392	433.2445	217.1259			4
13	72.0808	1322.6739	661.8406	1305.6474	**653.3273**	1304.6634	652.8353	V	**303.2027**	152.1050	286.1761	143.5917			3
14	30.0338	1379.6954	690.3513	1362.6688	681.8381	1361.6848	681.3461	G	**204.1343**	102.5708	187.1077	94.0575			2
15	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ASHPEDPASVVEAR**
Found in **Q9UHL4**, Q9UHL4|DPP2_HUMAN Dipeptidyl-peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=2

Match to Query 385: 1463.630766 from(488.884198,3+)

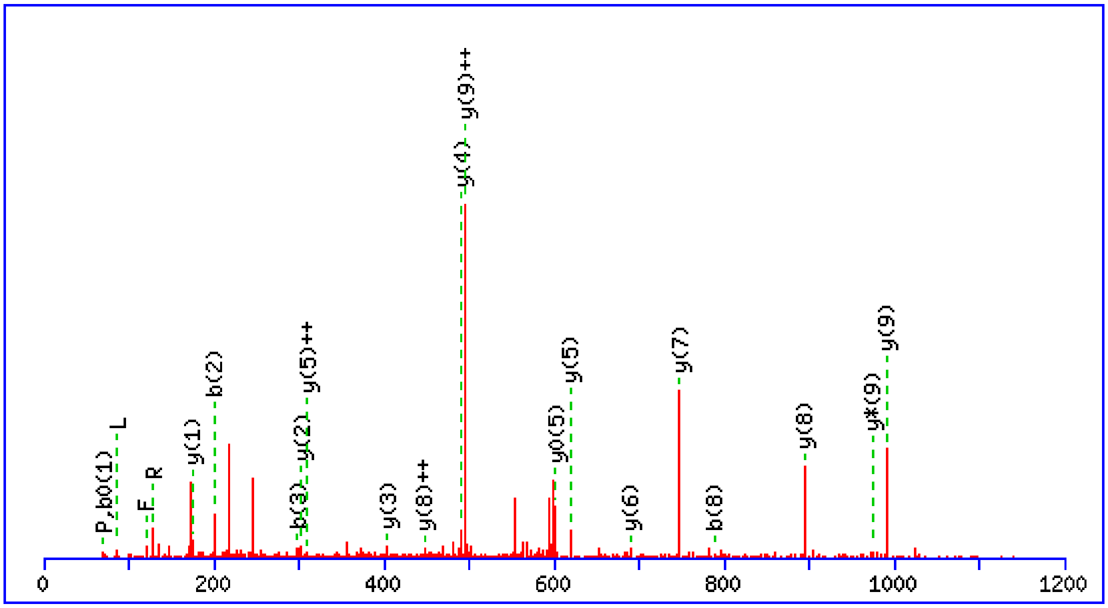


Monoisotopic mass of neutral peptide Mr(calc): 1463.7005
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00037
Matches (Bold Red): 16/138 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			**A**							**14**
2	60.0444	**159.0764**	80.0418	141.0659	71.0366	**S**	1393.6706	697.3390	1376.6441	688.8257	1375.6601	688.3337	**13**
3	110.0713	**296.1353**	148.5713	278.1248	139.5660	**H**	1306.6386	653.8229	1289.6121	645.3097	1288.6280	644.8177	**12**
4	70.0651	393.1881	197.0977	**375.1775**	188.0924	**P**	1169.5797	585.2935	1152.5531	576.7802	1151.5691	576.2882	**11**
5	102.0550	522.2307	261.6190	504.2201	252.6137	**E**	1072.5269	536.7671	1055.5004	528.2538	1054.5164	527.7618	**10**
6	88.0393	**637.2576**	319.1325	619.2471	310.1272	**D**	943.4843	472.2458	926.4578	463.7325	925.4738	463.2405	**9**
7	70.0651	**734.3104**	**367.6588**	716.2998	358.6536	**P**	828.4574	414.7323	811.4308	406.2191	810.4468	405.7271	**8**
8	44.0495	**805.3475**	403.1774	787.3369	394.1721	**A**	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	**7**
9	60.0444	**892.3795**	446.6934	**874.3690**	**437.6881**	**S**	**660.3675**	330.6874	643.3410	322.1741	642.3569	321.6821	**6**
10	72.0808	**991.4479**	496.2276	973.4374	487.2223	**V**	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	**5**
11	72.0808	1090.5164	545.7618	1072.5058	536.7565	**V**	**474.2671**	237.6372	457.2405	229.1239	456.2565	228.6319	**4**
12	102.0550	1219.5590	610.2831	1201.5484	601.2778	**E**	**375.1987**	188.1030	358.1721	179.5897	357.1881	179.0977	**3**
13	44.0495	1290.5961	645.8017	1272.5855	636.7964	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
14	**129.1135**					**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **SLPFGAQSTQR**
Found in **Q9UHL4**, Q9UHL4|DPP2_HUMAN Dipeptidyl-peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=2

Match to Query 353: 1190.672782 from(596.343667,2+)

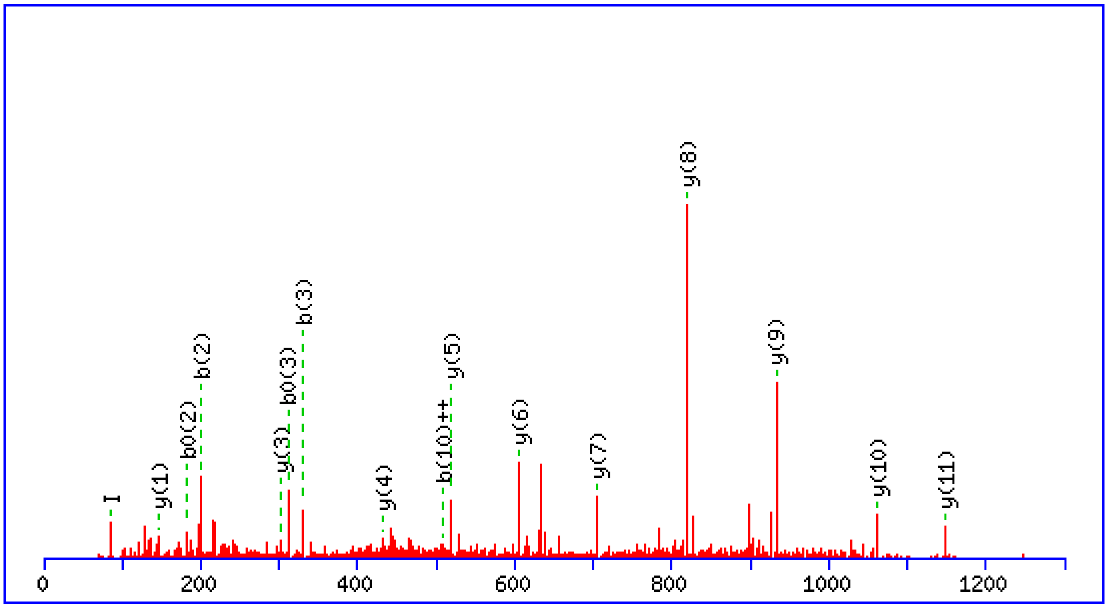


Monoisotopic mass of neutral peptide Mr(calc): 1190.6044
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 **Expect:** 0.018
Matches (Bold Red): 22/115 fragment ions using 84 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			**70.0287**	35.5180	**S**							**11**
2	**86.0964**	**201.1234**	101.0653			183.1128	92.0600	**L**	1104.5796	552.7935	1087.5531	544.2802	1086.5691	543.7882	**10**
3	**70.0651**	**298.1761**	149.5917			280.1656	140.5864	**P**	**991.4956**	**496.2514**	**974.4690**	487.7381	973.4850	487.2461	**9**
4	**120.0808**	445.2445	223.1259			427.2340	214.1206	**F**	**894.4428**	**447.7250**	877.4163	439.2118	876.4322	438.7198	**8**
5	30.0338	502.2660	251.6366			484.2554	242.6314	**G**	**747.3744**	374.1908	730.3478	365.6776	729.3638	365.1856	**7**
6	44.0495	573.3031	287.1552			555.2926	278.1499	**A**	**690.3529**	345.6801	673.3264	337.1668	672.3424	336.6748	**6**
7	101.0709	701.3617	351.1845	684.3352	342.6712	683.3511	342.1792	**Q**	**619.3158**	**310.1615**	602.2893	301.6483	**601.3053**	301.1563	**5**
8	60.0444	**788.3937**	394.7005	771.3672	386.1872	770.3832	385.6952	**S**	**491.2572**	246.1323	474.2307	237.6190	473.2467	237.1270	**4**
9	74.0600	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	**T**	**404.2252**	202.6162	387.1987	194.1030	386.2146	193.6110	**3**
10	101.0709	1017.5000	509.2536	1000.4734	500.7404	999.4894	500.2483	**Q**	**303.1775**	152.0924	286.1510	143.5791			**2**
11	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LSEIDVSSEGVK**
Found in **Q96C19**, Q96C19|EFHD2_HUMAN EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1

Match to Query 494: 1261.578392 from(631.796472,2+)

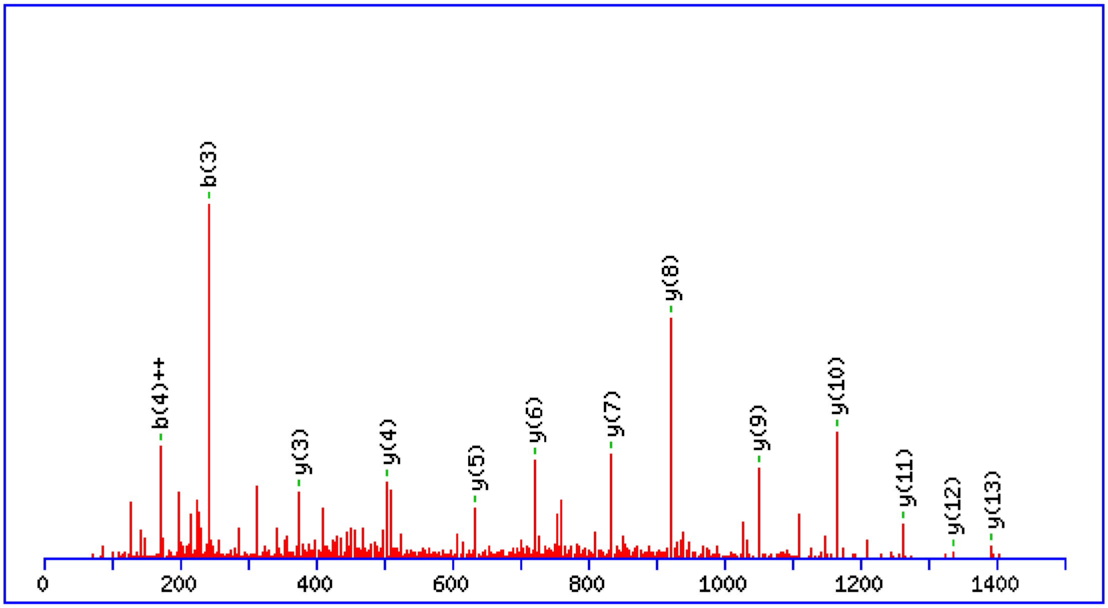


Monoisotopic mass of neutral peptide Mr(calc): 1261.6402
Fixed modifications: Carbamidomethyl (C)
Ions Score: 63 **Expect:** 3.6e-005
Matches (Bold Red): 17/114 fragment ions using 39 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			**L**							**12**
2	60.0444	**201.1234**	101.0653	**183.1128**	92.0600	**S**	**1149.5634**	575.2853	1132.5368	566.7721	1131.5528	566.2800	**11**
3	102.0550	**330.1660**	165.5866	**312.1554**	156.5813	**E**	**1062.5313**	531.7693	1045.5048	523.2560	1044.5208	522.7640	**10**
4	**86.0964**	443.2500	222.1287	425.2395	213.1234	**I**	**933.4888**	467.2480	916.4622	458.7347	915.4782	458.2427	**9**
5	88.0393	558.2770	279.6421	540.2664	270.6368	**D**	**820.4047**	410.7060	803.3781	402.1927	802.3941	401.7007	**8**
6	72.0808	657.3454	329.1763	639.3348	320.1710	**V**	**705.3777**	353.1925	688.3512	344.6792	687.3672	344.1872	**7**
7	60.0444	744.3774	372.6923	726.3668	363.6871	**S**	**606.3093**	303.6583	589.2828	295.1450	588.2988	294.6530	**6**
8	60.0444	831.4094	416.2084	813.3989	407.2031	**S**	**519.2773**	260.1423	502.2508	251.6290	501.2667	251.1370	**5**
9	102.0550	960.4520	480.7297	942.4415	471.7244	**E**	**432.2453**	216.6263	415.2187	208.1130	414.2347	207.6210	**4**
10	30.0338	1017.4735	**509.2404**	999.4629	500.2351	**G**	**303.2027**	152.1050	286.1761	143.5917			**3**
11	72.0808	1116.5419	558.7746	1098.5313	549.7693	**V**	246.1812	123.5942	229.1547	115.0810			**2**
12	101.1073					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **LGAVDESLSEETQK**
Found in **Q96HE7**, Q96HE7|ERO1A_HUMAN ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2

Match to Query 646: 1504.671992 from(753.343272,2+)

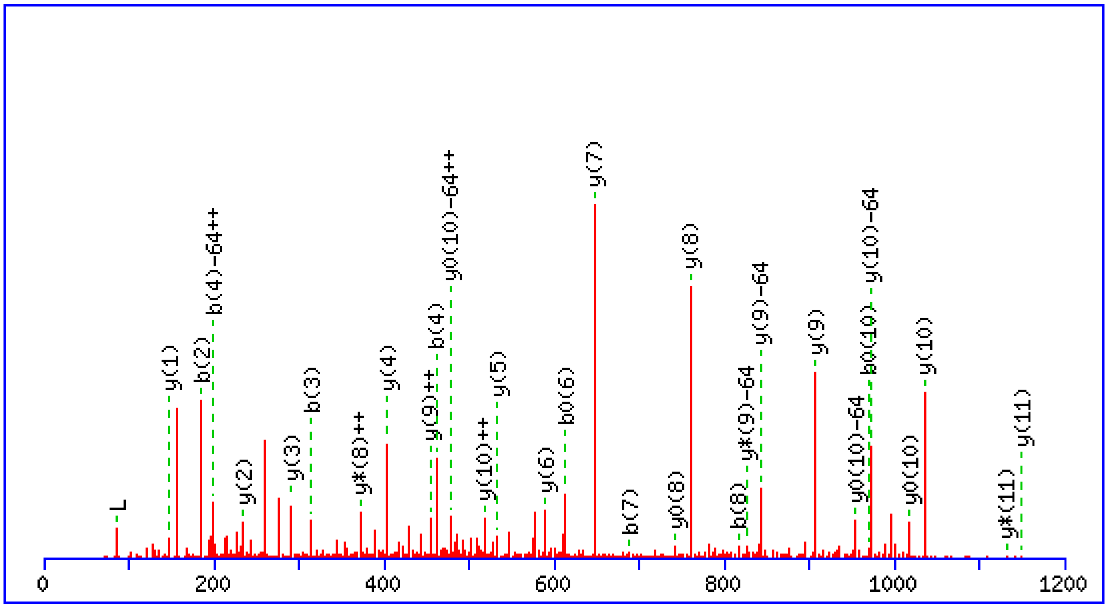


Monoisotopic mass of neutral peptide Mr(calc): 1504.7257
Fixed modifications: Carbamidomethyl (C)
Ions Score: 119 **Expect:** 7.9e-011
Matches (Bold Red): 14/134 fragment ions using 15 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	86.0964	114.0913	57.5493					L							14
2	30.0338	**171.1128**	86.0600					G	**1392.6489**	696.8281	1375.6223	688.3148	1374.6383	687.8228	13
3	44.0495	**242.1499**	121.5786					A	**1335.6274**	668.3174	1318.6009	659.8041	1317.6169	659.3121	12
4	72.0808	341.2183	**171.1128**					V	**1264.5903**	632.7988	1247.5638	624.2855	1246.5798	623.7935	11
5	88.0393	456.2453	228.6263			438.2347	219.6210	D	**1165.5219**	583.2646	1148.4954	574.7513	1147.5113	574.2593	10
6	102.0550	585.2879	293.1476			567.2773	284.1423	E	**1050.4950**	525.7511	1033.4684	517.2378	1032.4844	516.7458	9
7	60.0444	672.3199	336.6636			654.3093	327.6583	S	**921.4524**	461.2298	904.4258	452.7165	903.4418	452.2245	8
8	86.0964	785.4040	393.2056			767.3934	384.2003	L	**834.4203**	417.7138	817.3938	409.2005	816.4098	408.7085	7
9	60.0444	872.4360	436.7216			854.4254	427.7163	S	**721.3363**	361.1718	704.3097	352.6585	703.3257	352.1665	6
10	102.0550	1001.4786	501.2429			983.4680	492.2376	E	**634.3042**	317.6558	617.2777	309.1425	616.2937	308.6505	5
11	102.0550	1130.5212	565.7642			1112.5106	556.7589	E	**505.2617**	253.1345	488.2351	244.6212	487.2511	244.1292	4
12	74.0600	1231.5689	616.2881			1213.5583	607.2828	T	**376.2191**	188.6132	359.1925	180.0999	358.2085	179.6079	3
13	101.0709	1359.6274	680.3174	1342.6009	671.8041	1341.6169	671.3121	Q	275.1714	138.0893	258.1448	129.5761			2
14	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AIEMLGGELGSK**
Found in **P07954**, P07954|FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3

Match to Query 456: 1219.572344 from(610.793448,2+)

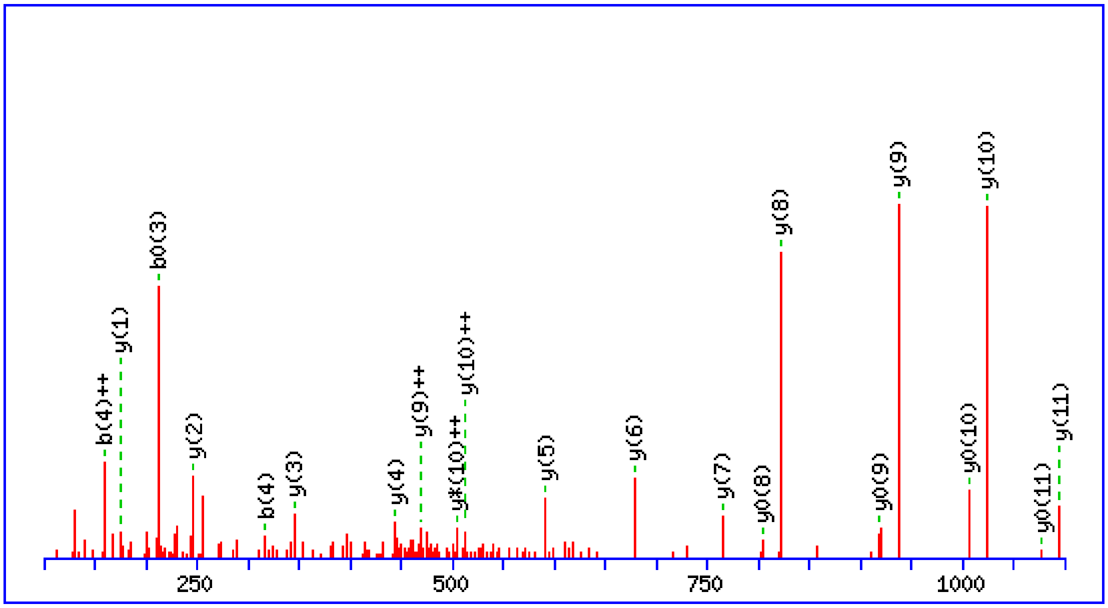


Monoisotopic mass of neutral peptide Mr(calc): 1219.6118
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 72 **Expect:** 5e-006
Matches (Bold Red): 33/167 fragment ions using 61 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							12
2	**86.0964**	**185.1285**	93.0679			I	**1149.5820**	575.2946	**1132.5555**	566.7814	1131.5714	566.2894	11
3	102.0550	**314.1710**	157.5892	296.1605	148.5839	E	**1036.4979**	**518.7526**	1019.4714	510.2393	**1018.4874**	509.7473	10
4	120.0478	**461.2065**	231.1069	443.1959	222.1016	M	**907.4553**	**454.2313**	890.4288	445.7180	889.4448	445.2260	9
5	**86.0964**	574.2905	287.6489	556.2799	278.6436	L	**760.4199**	380.7136	743.3934	**372.2003**	**742.4094**	371.7083	8
6	30.0338	631.3120	316.1596	**613.3014**	307.1543	G	**647.3359**	324.1716	630.3093	315.6583	629.3253	315.1663	7
7	30.0338	**688.3334**	344.6704	670.3229	335.6651	G	**590.3144**	295.6608	573.2879	287.1476	572.3039	286.6556	6
8	102.0550	**817.3760**	409.1917	799.3655	400.1864	E	**533.2930**	267.1501	516.2664	258.6368	515.2824	258.1448	5
9	**86.0964**	930.4601	465.7337	912.4495	456.7284	L	**404.2504**	202.6288	387.2238	194.1155	386.2398	193.6235	4
10	30.0338	987.4816	494.2444	**969.4710**	485.2391	G	**291.1663**	146.0868	274.1397	137.5735	273.1557	137.0815	3
11	60.0444	1074.5136	537.7604	1056.5030	528.7552	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
12	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ASASDGSSFVVAR**
Found in **Q9H4G4**, Q9H4G4|GAPR1_HUMAN Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3

Match to Query 315: 1252.592890 from(627.303721,2+)

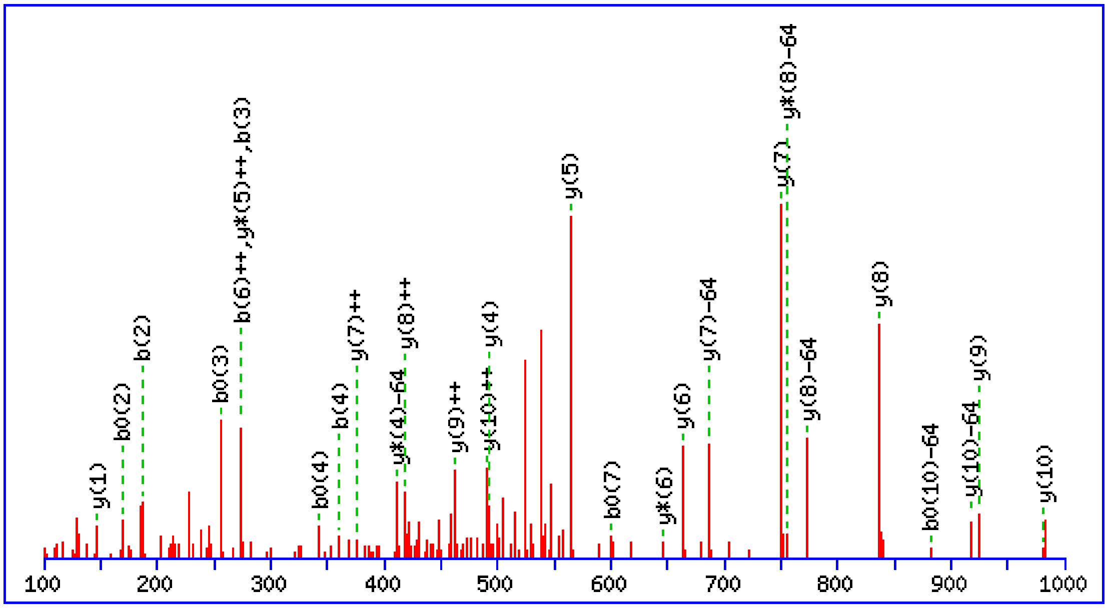


Monoisotopic mass of neutral peptide Mr(calc): 1252.6048
Fixed modifications: Carbamidomethyl (C)
Ions Score: 98 **Expect:** 1e-008
Matches (Bold Red): 22/121 fragment ions using 31 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							13
2	60.0444	**159.0764**	80.0418	141.0659	71.0366	S	1182.5749	591.7911	1165.5484	583.2778	1164.5644	582.7858	12
3	44.0495	230.1135	115.5604	**212.1030**	106.5551	A	**1095.5429**	548.2751	1078.5164	539.7618	**1077.5323**	539.2698	11
4	60.0444	**317.1456**	**159.0764**	299.1350	150.0711	S	**1024.5058**	**512.7565**	1007.4792	**504.2433**	**1006.4952**	503.7513	10
5	88.0393	432.1725	216.5899	414.1619	207.5846	D	**937.4738**	**469.2405**	920.4472	460.7272	**919.4632**	460.2352	9
6	30.0338	489.1940	245.1006	471.1834	236.0953	G	**822.4468**	411.7271	805.4203	403.2138	**804.4363**	402.7218	8
7	60.0444	576.2260	288.6166	558.2154	279.6114	S	**765.4254**	383.2163	748.3988	374.7030	747.4148	374.2110	7
8	60.0444	663.2580	332.1326	645.2475	323.1274	S	**678.3933**	339.7003	661.3668	331.1870	660.3828	330.6950	6
9	120.0808	810.3264	405.6669	792.3159	396.6616	F	**591.3613**	296.1843	574.3348	287.6710			5
10	72.0808	909.3949	455.2011	891.3843	446.1958	V	**444.2929**	222.6501	427.2663	214.1368			4
11	72.0808	1008.4633	504.7353	990.4527	495.7300	V	**345.2245**	173.1159	328.1979	164.6026			3
12	44.0495	1079.5004	540.2538	1061.4898	531.2485	A	**246.1561**	123.5817	229.1295	115.0684			2
13	129.1135					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SGSSSVAAMKK**
Found in **P63218**, P63218|GBG5_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GNG5 PE=1 SV=3

Match to Query 153: 1109.393288 from(555.703920,2+)

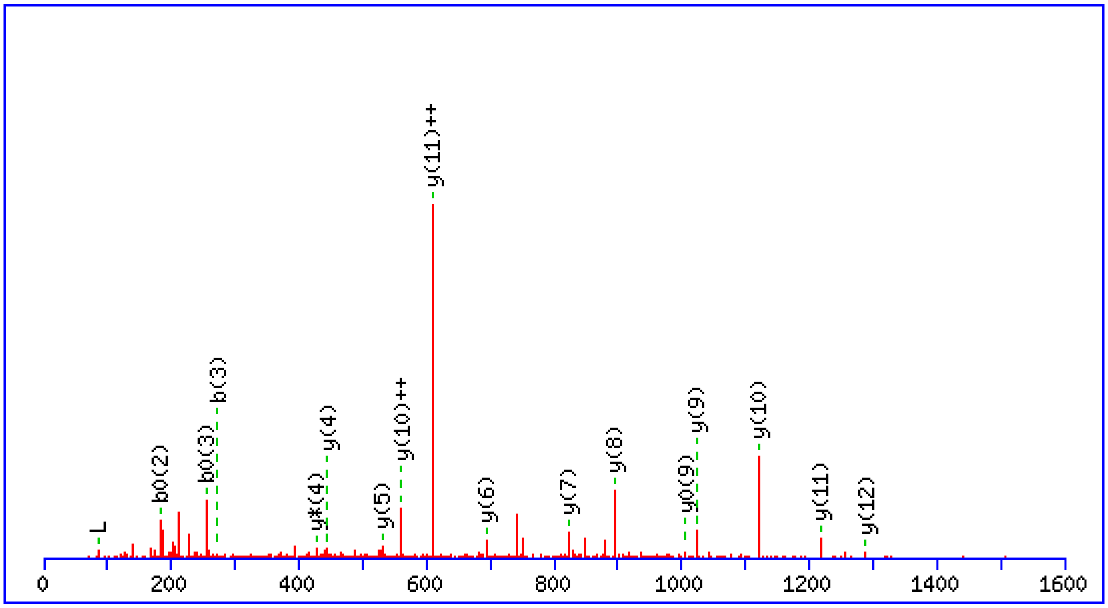


Monoisotopic mass of neutral peptide Mr(calc): 1109.5387
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
N-term : Acetyl (Protein N-term)
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 **Expect:** 0.00075
Matches (Bold Red): 28/152 fragment ions using 47 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	130.0499	65.5286			112.0393	56.5233	S							11
2	30.0338	**187.0713**	94.0393			**169.0608**	85.0340	G	**981.5034**	**491.2553**	964.4768	482.7420	963.4928	482.2500	10
3	60.0444	**274.1034**	137.5553			**256.0928**	128.5500	S	**924.4819**	**462.7446**	907.4553	454.2313	906.4713	453.7393	9
4	60.0444	**361.1354**	181.0713			**343.1248**	172.0660	S	**837.4499**	**419.2286**	820.4233	410.7153	819.4393	410.2233	8
5	60.0444	448.1674	224.5873			430.1568	215.5821	S	**750.4178**	**375.7126**	733.3913	367.1993	732.4073	366.7073	7
6	72.0808	547.2358	**274.1216**			529.2253	265.1163	V	**663.3858**	332.1965	**646.3593**	323.6833			6
7	44.0495	618.2729	309.6401			**600.2624**	300.6348	A	**564.3174**	282.6623	547.2908	**274.1491**			5
8	44.0495	689.3101	345.1587			671.2995	336.1534	A	**493.2803**	247.1438	476.2537	238.6305			4
9	120.0478	836.3455	418.6764			818.3349	409.6711	M	422.2432	211.6252	405.2166	203.1119			3
10	101.1073	964.4404	482.7238	947.4139	474.2106	946.4299	473.7186	K	275.2078	138.1075	258.1812	129.5942			2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VTAPPEAEYSGLVR**
Found in **P08648**, P08648|ITA5_HUMAN Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2

Match to Query 597: 1487.817770 from(744.916161,2+)

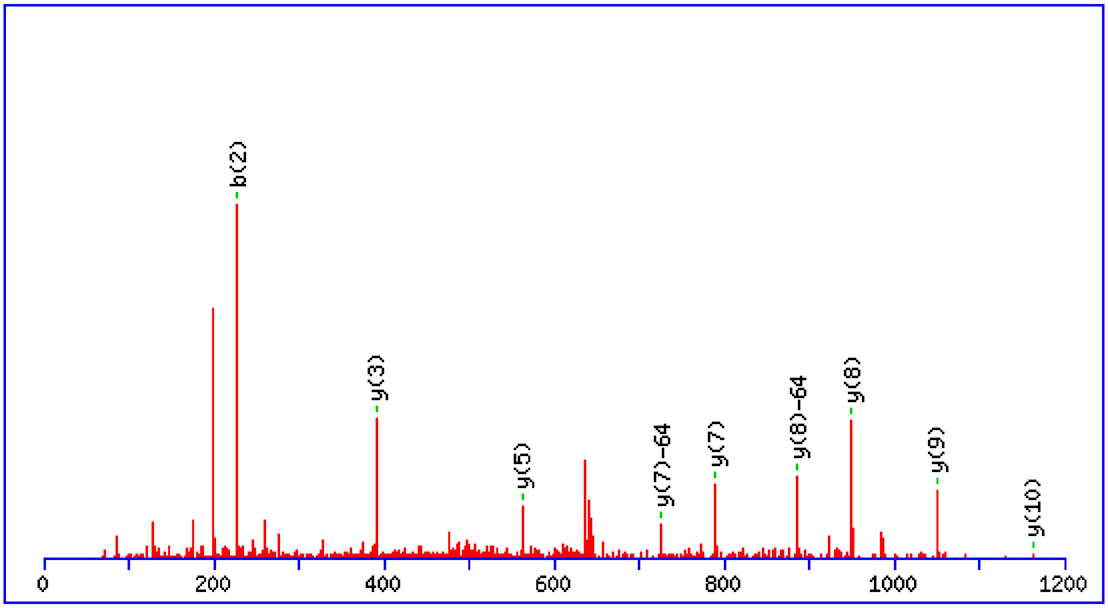


Monoisotopic mass of neutral peptide Mr(calc): 1487.7620
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 **Expect:** 0.0035
Matches (Bold Red): 17/134 fragment ions using 45 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			V							14
2	74.0600	201.1234	101.0653	**183.1128**	92.0600	T	1389.7009	695.3541	1372.6743	686.8408	1371.6903	686.3488	13
3	44.0495	**272.1605**	136.5839	**254.1499**	127.5786	A	**1288.6532**	644.8302	1271.6266	636.3170	1270.6426	635.8250	12
4	70.0651	369.2132	185.1103	351.2027	176.1050	P	**1217.6161**	**609.3117**	1200.5895	600.7984	1199.6055	600.3064	11
5	70.0651	466.2660	233.6366	448.2554	224.6314	P	**1120.5633**	**560.7853**	1103.5368	552.2720	1102.5528	551.7800	10
6	102.0550	595.3086	298.1579	577.2980	289.1527	E	**1023.5106**	512.2589	1006.4840	503.7456	**1005.5000**	503.2536	9
7	44.0495	666.3457	333.6765	648.3352	324.6712	A	**894.4680**	447.7376	877.4414	439.2243	876.4574	438.7323	8
8	102.0550	795.3883	398.1978	777.3777	389.1925	E	**823.4308**	412.2191	806.4043	403.7058	805.4203	403.2138	7
9	136.0757	958.4516	479.7295	940.4411	470.7242	Y	**694.3883**	347.6978	677.3617	339.1845	676.3777	338.6925	6
10	60.0444	1045.4837	523.2455	1027.4731	514.2402	S	**531.3249**	266.1661	514.2984	257.6528	513.3144	257.1608	5
11	30.0338	1102.5051	551.7562	1084.4946	542.7509	G	**444.2929**	222.6501	**427.2663**	214.1368			4
12	**86.0964**	1215.5892	608.2982	1197.5786	599.2930	L	387.2714	194.1394	370.2449	185.6261			3
13	72.0808	1314.6576	657.8324	1296.6470	648.8272	V	274.1874	137.5973	257.1608	129.0840			2
14	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LLVCDLGNPMK**
Found in **P08648**, P08648|ITA5_HUMAN Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2

Match to Query 373: 1274.841874 from(638.428213,2+)

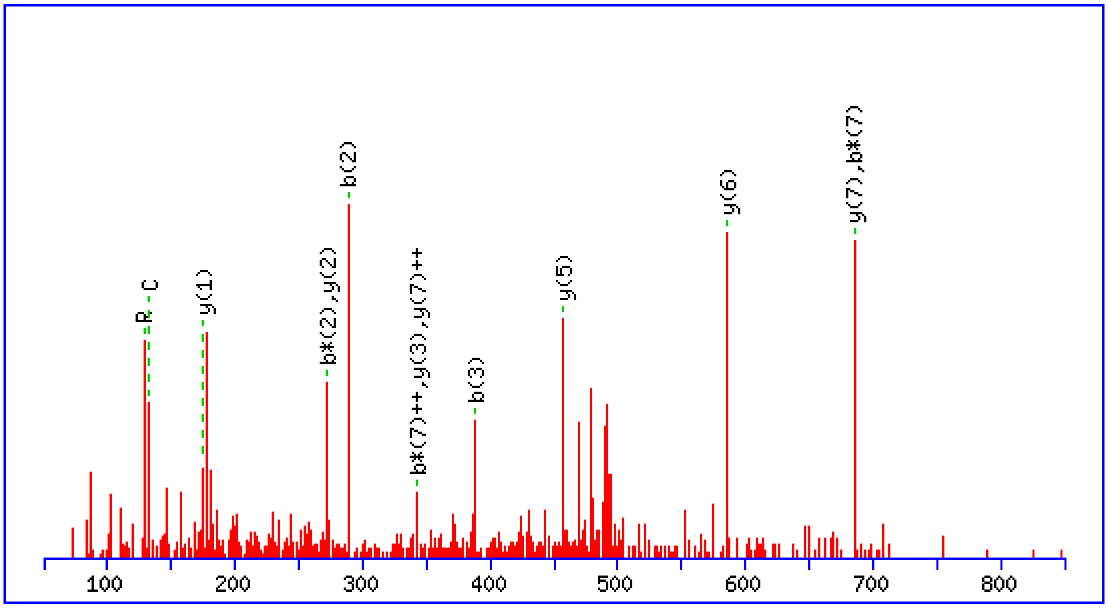


Monoisotopic mass of neutral peptide Mr(calc): 1274.6363
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 **Expect:** 0.0093
Matches (Bold Red): 9/148 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	86.0964	114.0913	57.5493					**L**							**11**
2	86.0964	**227.1754**	114.0913					**L**	**1162.5595**	581.7834	1145.5329	573.2701	1144.5489	572.7781	**10**
3	72.0808	326.2438	163.6255					**V**	**1049.4754**	525.2414	1032.4489	516.7281	1031.4649	516.2361	**9**
4	133.0430	486.2745	243.6409					**C**	**950.4070**	475.7071	933.3805	467.1939	932.3965	466.7019	**8**
5	88.0393	601.3014	301.1543			583.2908	292.1491	**D**	**790.3764**	395.6918	773.3498	387.1785	772.3658	386.6865	**7**
6	86.0964	714.3855	357.6964			696.3749	348.6911	**L**	675.3494	338.1784	658.3229	329.6651			**6**
7	30.0338	771.4069	386.2071			753.3964	377.2018	**G**	**562.2654**	281.6363	545.2388	273.1230			**5**
8	87.0553	885.4499	443.2286	868.4233	434.7153	867.4393	434.2233	**N**	505.2439	253.1256	488.2173	244.6123			**4**
9	70.0651	982.5026	491.7550	965.4761	483.2417	964.4921	482.7497	**P**	**391.2010**	196.1041	374.1744	187.5908			**3**
10	120.0478	1129.5380	565.2727	1112.5115	556.7594	1111.5275	556.2674	**M**	294.1482	147.5777	277.1217	139.0645			**2**
11	101.1073							**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **CQVEGGAPR**
Found in **P05362**, P05362|ICAM1_HUMAN Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=1 SV=2

Match to Query 175: 972.279418 from(487.146985,2+)

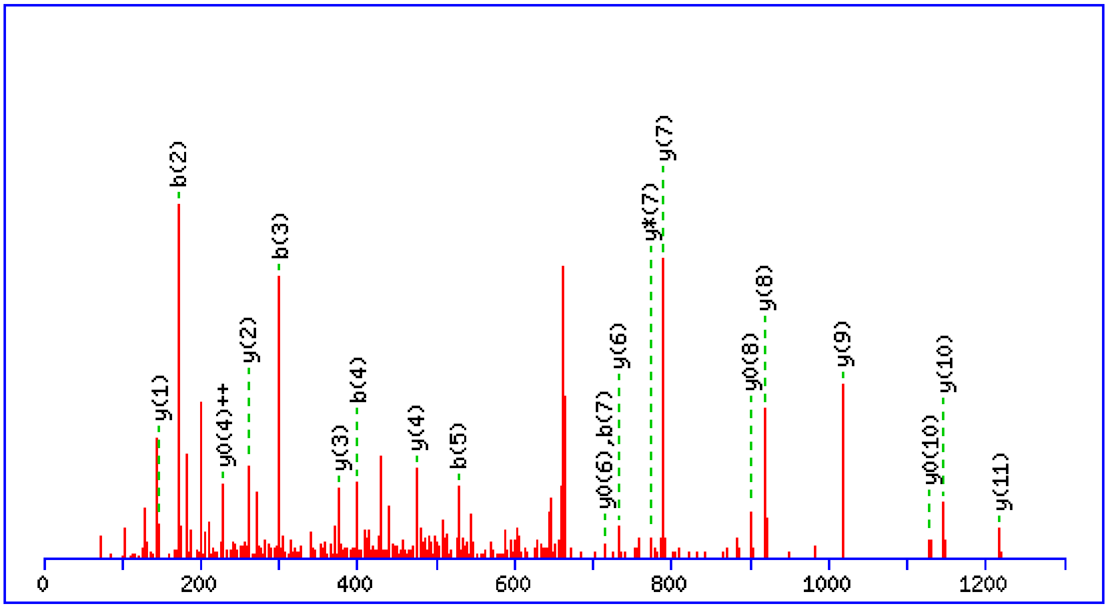


Monoisotopic mass of neutral peptide Mr(calc): 972.4447
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 **Expect:** 0.0062
Matches (Bold Red): 14/87 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	**133.0430**	161.0379	81.0226					C							9
2	101.0709	**289.0965**	145.0519	**272.0700**	136.5386			Q	813.4213	407.2143	796.3948	398.7010	795.4108	398.2090	8
3	72.0808	**388.1649**	194.5861	371.1384	186.0728			V	**685.3628**	**343.1850**	668.3362	334.6717	667.3522	334.1797	7
4	102.0550	517.2075	259.1074	500.1810	250.5941	499.1969	250.1021	E	**586.2944**	293.6508	569.2678	285.1375	568.2838	284.6455	6
5	30.0338	574.2290	287.6181	557.2024	279.1049	556.2184	278.6128	G	**457.2518**	229.1295	440.2252	220.6162			5
6	30.0338	631.2504	316.1289	614.2239	307.6156	613.2399	307.1236	G	400.2303	200.6188	383.2037	192.1055			4
7	44.0495	702.2876	351.6474	**685.2610**	**343.1341**	684.2770	342.6421	A	**343.2088**	172.1081	326.1823	163.5948			3
8	70.0651	799.3403	400.1738	782.3138	391.6605	781.3298	391.1685	P	**272.1717**	136.5895	255.1452	128.0762			2
9	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VAEVEGEQVDNK**
Found in **O95202**, O95202|LETM1_HUMAN LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1

Match to Query 396: 1315.684898 from(658.849725,2+)

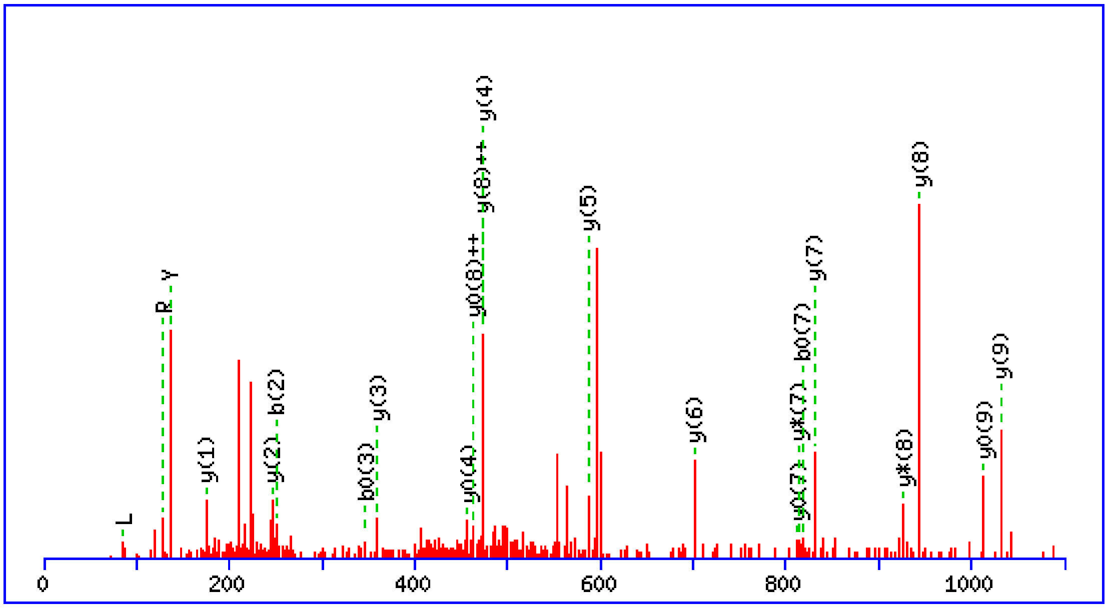


Monoisotopic mass of neutral peptide Mr(calc): 1315.6256
Fixed modifications: Carbamidomethyl (C)
Ions Score: 62 **Expect:** 5.6e-005
Matches (Bold Red): 20/122 fragment ions using 53 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							12
2	44.0495	**171.1128**	86.0600					A	**1217.5644**	609.2859	1200.5379	600.7726	1199.5539	600.2806	11
3	102.0550	**300.1554**	150.5813			282.1448	141.5761	E	**1146.5273**	573.7673	1129.5008	565.2540	**1128.5168**	564.7620	10
4	72.0808	**399.2238**	200.1155			381.2132	191.1103	V	**1017.4847**	509.2460	1000.4582	500.7327	999.4742	500.2407	9
5	102.0550	**528.2664**	264.6368			510.2558	255.6316	E	**918.4163**	459.7118	901.3898	451.1985	**900.4058**	450.7065	8
6	30.0338	585.2879	293.1476			567.2773	284.1423	G	**789.3737**	395.1905	**772.3472**	386.6772	771.3632	386.1852	7
7	102.0550	**714.3305**	357.6689			696.3199	348.6636	E	**732.3523**	366.6798	715.3257	358.1665	**714.3417**	357.6745	6
8	101.0709	842.3890	421.6982	825.3625	413.1849	824.3785	412.6929	Q	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	5
9	72.0808	941.4575	471.2324	924.4309	462.7191	923.4469	462.2271	V	**475.2511**	238.1292	458.2245	229.6159	457.2405	**229.1239**	4
10	88.0393	1056.4844	528.7458	1039.4578	520.2326	1038.4738	519.7406	D	**376.1827**	188.5950	359.1561	180.0817	358.1721	179.5897	3
11	87.0553	1170.5273	585.7673	1153.5008	577.2540	1152.5168	576.7620	N	**261.1557**	131.0815	244.1292	122.5682			2
12	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **YSNENLDLAR**
Found in **P36776**, P36776|LONM_HUMAN Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=2 SV=2

Match to Query 543: 1193.503028 from(597.758790,2+)

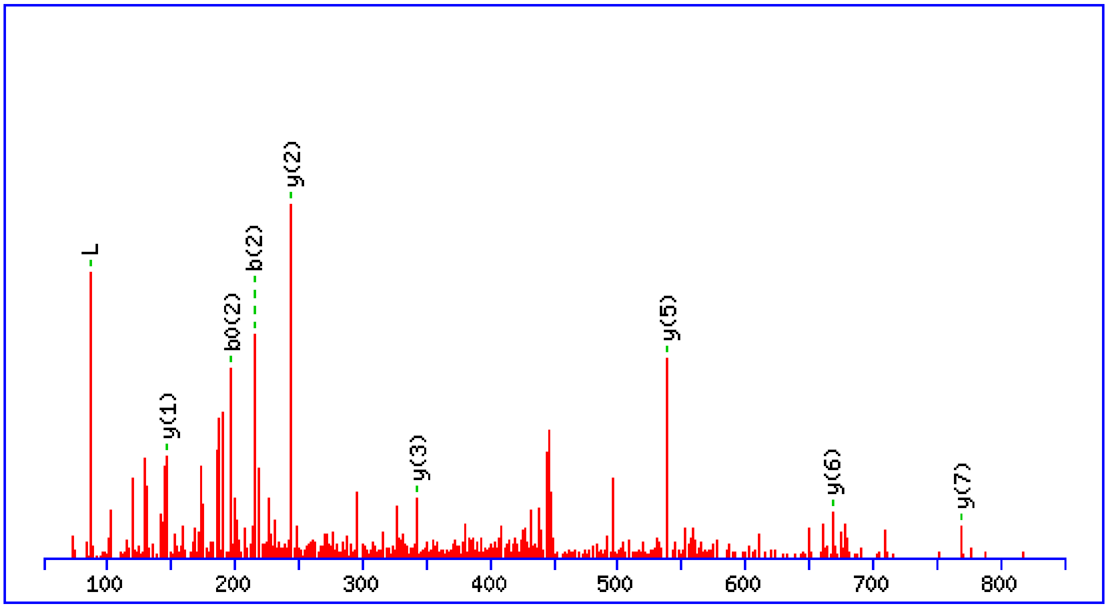


Monoisotopic mass of neutral peptide Mr(calc): 1193.5676
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.00076
Matches (Bold Red): 23/106 fragment ions using 49 most intense peaks

#	**Immon.**	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	**136.0757**	164.0706	82.5389					**Y**							**10**
2	60.0444	**251.1026**	126.0550			233.0921	117.0497	**S**	**1031.5116**	516.2594	1014.4851	507.7462	**1013.5010**	507.2542	**9**
3	87.0553	365.1456	183.0764	348.1190	174.5631	**347.1350**	174.0711	**N**	**944.4796**	**472.7434**	**927.4530**	464.2302	926.4690	**463.7381**	**8**
4	102.0550	494.1882	247.5977	477.1616	239.0844	476.1776	238.5924	**E**	**830.4367**	415.7220	**813.4101**	407.2087	**812.4261**	406.7167	**7**
5	87.0553	608.2311	304.6192	591.2045	296.1059	590.2205	295.6139	**N**	**701.3941**	351.2007	684.3675	342.6874	683.3835	342.1954	**6**
6	**86.0964**	721.3151	361.1612	704.2886	352.6479	703.3046	352.1559	**L**	**587.3511**	294.1792	570.3246	285.6659	569.3406	285.1739	**5**
7	88.0393	836.3421	418.6747	819.3155	410.1614	**818.3315**	409.6694	**D**	**474.2671**	237.6372	457.2405	229.1239	**456.2565**	228.6319	**4**
8	**86.0964**	949.4262	475.2167	932.3996	466.7034	931.4156	466.2114	**L**	**359.2401**	180.1237	342.2136	171.6104			**3**
9	44.0495	1020.4633	510.7353	1003.4367	502.2220	1002.4527	501.7300	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
10	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LTEPVVPK**
Found in **P11117**, P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3

Match to Query 116: 881.363092 from(441.688822,2+)

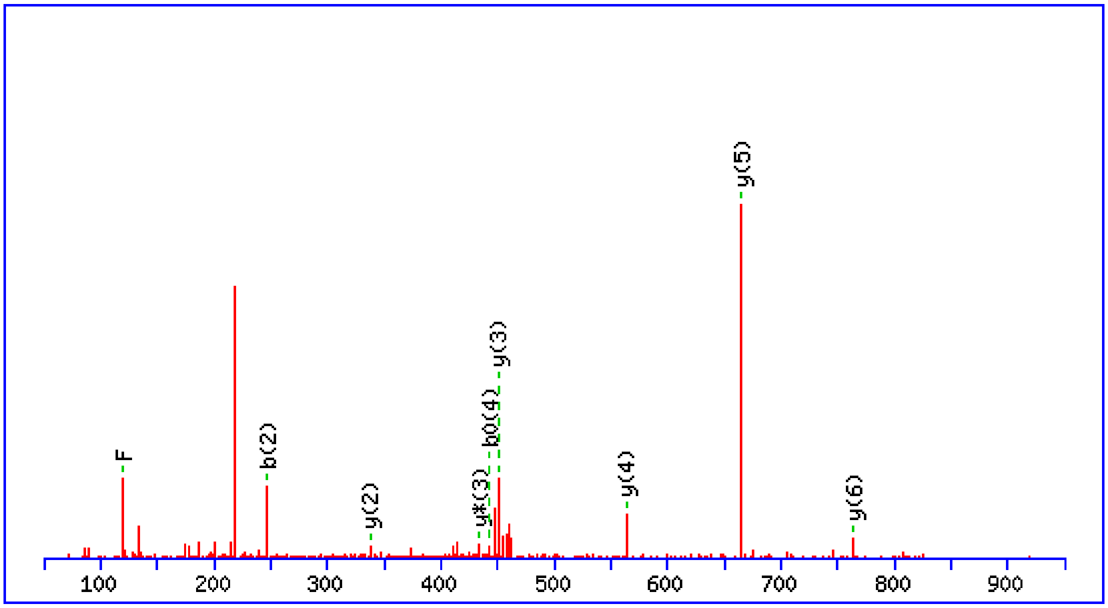


Monoisotopic mass of neutral peptide Mr(calc): 881.5222
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 **Expect:** 0.0095
Matches (Bold Red): 9/66 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			**L**							**8**
2	74.0600	**215.1390**	108.0731	**197.1285**	99.0679	**T**	**769.4454**	385.2264	752.4189	376.7131	751.4349	376.2211	**7**
3	102.0550	344.1816	172.5944	326.1710	163.5892	**E**	**668.3978**	334.7025	651.3712	326.1892	650.3872	325.6972	**6**
4	70.0651	441.2344	221.1208	423.2238	212.1155	**P**	**539.3552**	270.1812	522.3286	261.6679			**5**
5	72.0808	540.3028	270.6550	522.2922	261.6498	**V**	442.3024	221.6548	425.2758	213.1416			**4**
6	72.0808	639.3712	320.1892	621.3606	311.1840	**V**	**343.2340**	172.1206	326.2074	163.6074			**3**
7	70.0651	736.4240	368.7156	718.4134	359.7103	**P**	**244.1656**	122.5864	227.1390	114.0731			**2**
8	101.1073					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **FVTLLYR**
Found in **P11117**, P11117|PPAL_HUMAN Lysosomal acid phosphatase OS=Homo sapiens GN=ACP2 PE=1 SV=3

Match to Query 174: 910.472850 from(456.243701,2+)

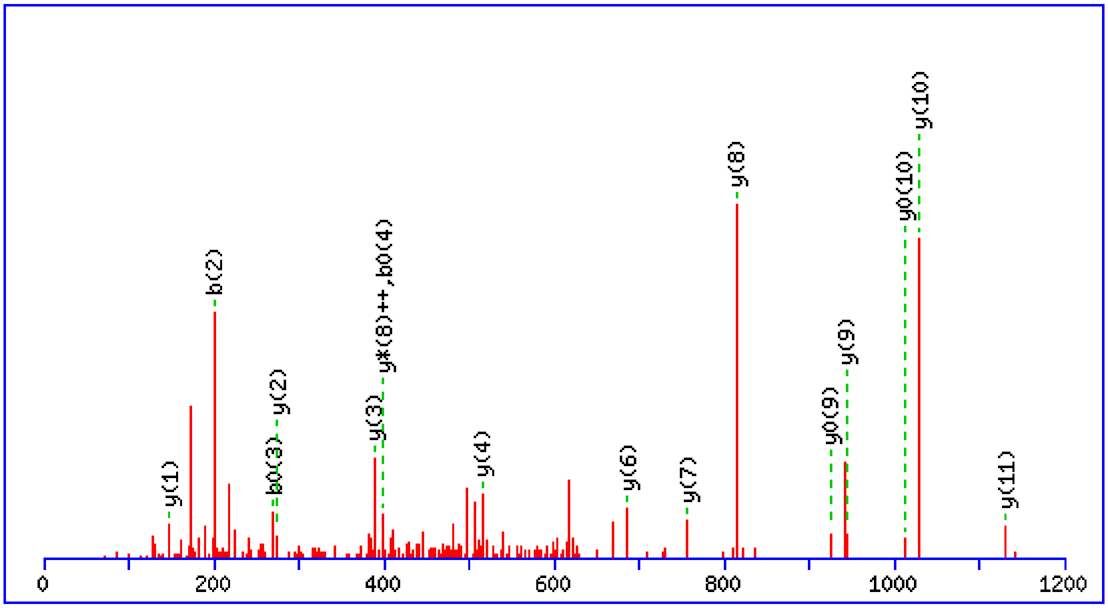


Monoisotopic mass of neutral peptide Mr(calc): 910.5276
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 **Expect:** 0.0042
Matches (Bold Red): 9/55 fragment ions using 14 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415			F							7
2	72.0808	**247.1441**	124.0757			V	**764.4665**	382.7369	747.4400	374.2236	746.4559	373.7316	6
3	74.0600	348.1918	174.5995	330.1812	165.5942	T	**665.3981**	333.2027	648.3715	324.6894	647.3875	324.1974	5
4	86.0964	461.2758	231.1416	**443.2653**	222.1363	L	**564.3504**	282.6788	547.3239	274.1656			4
5	86.0964	574.3599	287.6836	556.3493	278.6783	L	**451.2663**	226.1368	**434.2398**	217.6235			3
6	136.0757	737.4232	369.2153	719.4127	360.2100	Y	**338.1823**	169.5948	321.1557	161.0815			2
7	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VTSEGAGLQLQK**
Found in **P10253**, P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=2

Match to Query 295: 1229.596230 from(615.805391,2+)

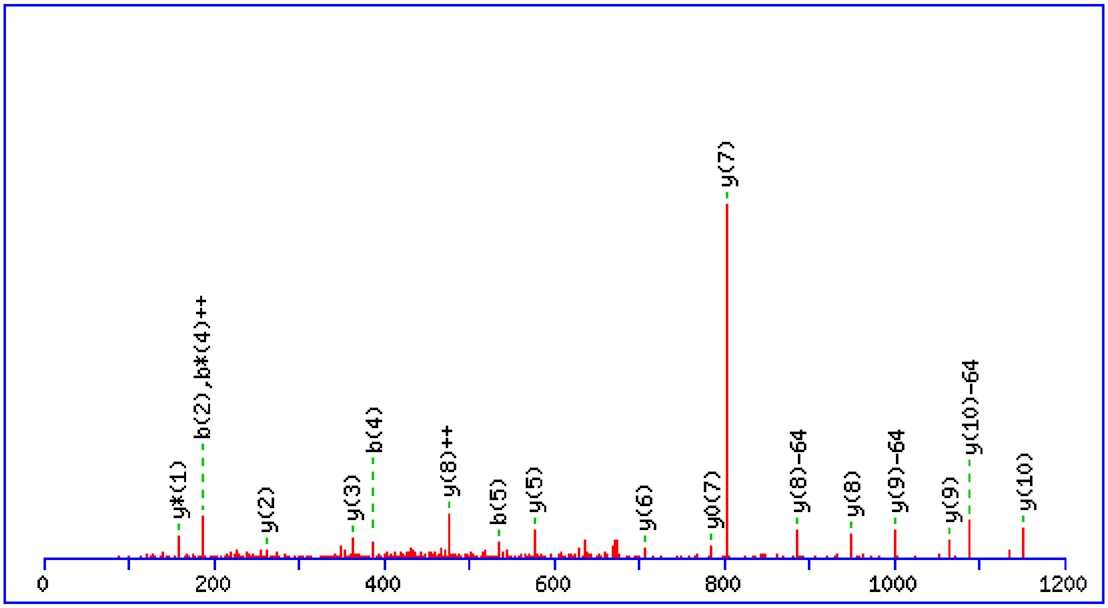


Monoisotopic mass of neutral peptide Mr(calc): 1229.6616
Fixed modifications: Carbamidomethyl (C)
Ions Score: 80 **Expect:** 8.1e-007
Matches (Bold Red): 16/110 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							12
2	74.0600	**201.1234**	101.0653			183.1128	92.0600	T	**1131.6004**	566.3039	1114.5739	557.7906	1113.5899	557.2986	11
3	60.0444	288.1554	144.5813			**270.1448**	135.5761	S	**1030.5528**	515.7800	1013.5262	507.2667	**1012.5422**	506.7747	10
4	102.0550	417.1980	209.1026			**399.1874**	200.0974	E	**943.5207**	472.2640	926.4942	463.7507	**925.5102**	463.2587	9
5	30.0338	474.2195	237.6134			456.2089	228.6081	G	**814.4781**	407.7427	797.4516	**399.2294**			8
6	44.0495	545.2566	273.1319			527.2460	264.1266	A	**757.4567**	379.2320	740.4301	370.7187			7
7	30.0338	602.2780	301.6427			584.2675	292.6374	G	**686.4196**	343.7134	669.3930	335.2001			6
8	86.0964	715.3621	358.1847			697.3515	349.1794	L	629.3981	315.2027	612.3715	306.6894			5
9	101.0709	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	Q	**516.3140**	258.6607	499.2875	250.1474			4
10	86.0964	956.5047	478.7560	939.4782	470.2427	938.4942	469.7507	L	**388.2554**	194.6314	371.2289	186.1181			3
11	101.0709	1084.5633	542.7853	1067.5368	534.2720	1066.5528	533.7800	Q	**275.1714**	138.0893	258.1448	129.5761			2
12	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **NASDMPETITSR**
Found in **Q8TCT9**, Q8TCT9|HM13_HUMAN Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1

Match to Query 647: 1336.559834 from(669.287193,2+)

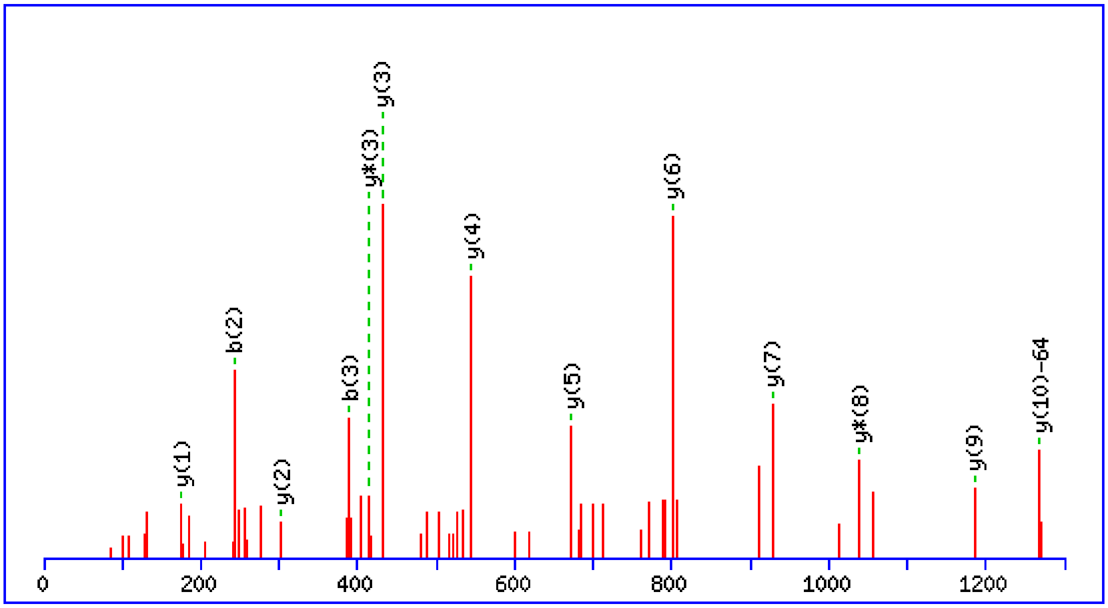


Monoisotopic mass of neutral peptide Mr(calc): 1336.5929
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 68 **Expect:** 1.1e-005
Matches (Bold Red): 18/205 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	87.0553	115.0502	58.0287	98.0237	49.5155			N							12
2	44.0495	**186.0873**	93.5473	169.0608	85.0340			A	1159.5590	580.2831	1142.5324	571.7698	1141.5484	571.2778	11
3	60.0444	273.1193	137.0633	256.0928	128.5500	255.1088	128.0580	S	**1088.5218**	544.7646	1071.4953	536.2513	1070.5113	535.7593	10
4	88.0393	**388.1463**	194.5768	371.1197	**186.0635**	370.1357	185.5715	D	**1001.4898**	501.2485	984.4633	492.7353	983.4793	492.2433	9
5	56.0495	471.1834	236.0953	454.1569	227.5821	453.1728	227.0901	M	**886.4629**	443.7351	869.4363	435.2218	868.4523	434.7298	8
6	70.0651	568.2362	284.6217	551.2096	276.1084	550.2256	275.6164	P	**803.4258**	402.2165	786.3992	393.7032	**785.4152**	393.2112	7
7	102.0550	697.2788	349.1430	680.2522	340.6297	679.2682	340.1377	E	**706.3730**	353.6901	689.3464	345.1769	688.3624	344.6849	6
8	74.0600	798.3264	399.6669	781.2999	391.1536	780.3159	390.6616	T	**577.3304**	289.1688	560.3039	280.6556	559.3198	280.1636	5
9	86.0964	911.4105	456.2089	894.3840	447.6956	893.3999	447.2036	I	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
10	74.0600	1012.4582	506.7327	995.4316	498.2195	994.4476	497.7274	T	**363.1987**	182.1030	346.1721	173.5897	345.1881	173.0977	3
11	60.0444	1099.4902	550.2487	1082.4637	541.7355	1081.4796	541.2435	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
12	129.1135							R	175.1190	88.0631	**158.0924**	79.5498			1

MS/MS Fragmentation of **LQMEQQQQLQQR**
Found in **Q9NS69**, Q9NS69|TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3

Match to Query 462: 1572.794704 from(787.404628,2+)

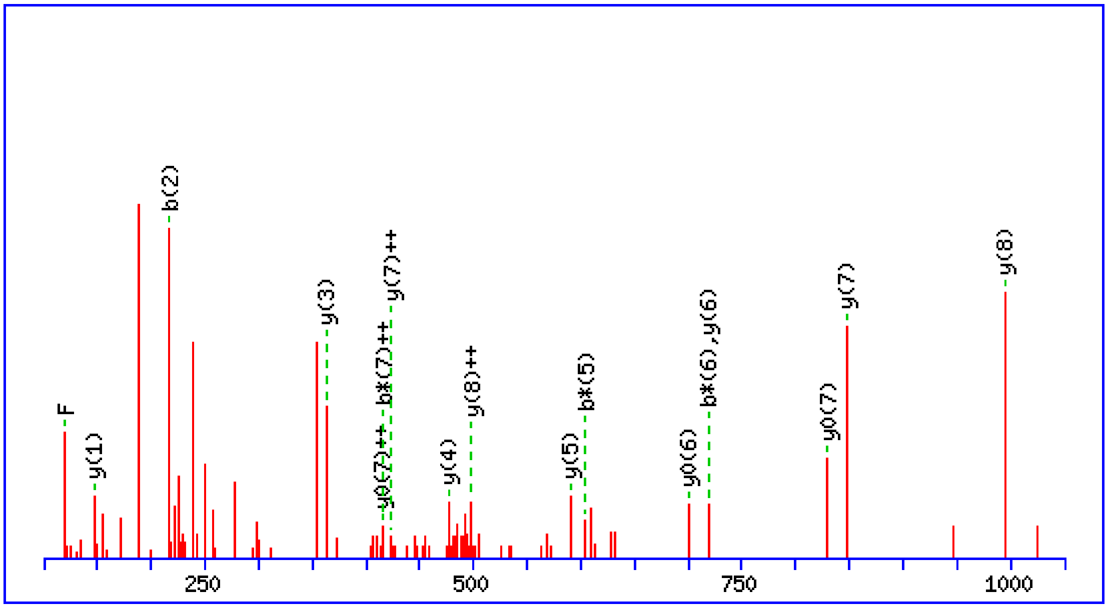


Monoisotopic mass of neutral peptide Mr(calc): 1572.7678
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 84 **Expect:** 2.8e-007
Matches (Bold Red): 13/185 fragment ions using 24 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	86.0964	114.0913	57.5493					L							12
2	101.0709	**242.1499**	121.5786	225.1234	113.0653			Q	1396.6928	698.8500	1379.6662	690.3368	1378.6822	689.8447	11
3	56.0495	325.1870	163.0972	308.1605	154.5839			M	**1268.6342**	634.8207	1251.6076	626.3075	1250.6236	625.8155	10
4	102.0550	454.2296	227.6185	437.2031	219.1052	436.2191	218.6132	E	**1185.5971**	593.3022	1168.5705	584.7889	1167.5865	584.2969	9
5	101.0709	582.2882	291.6477	565.2617	283.1345	564.2776	282.6425	Q	1056.5545	528.7809	**1039.5279**	520.2676			8
6	101.0709	710.3468	355.6770	693.3202	347.1638	692.3362	346.6717	Q	**928.4959**	464.7516	911.4694	456.2383			7
7	101.0709	838.4054	419.7063	821.3788	411.1930	820.3948	410.7010	Q	**800.4373**	400.7223	783.4108	392.2090			6
8	101.0709	966.4639	483.7356	949.4374	475.2223	948.4534	474.7303	Q	**672.3788**	336.6930	655.3522	328.1797			5
9	86.0964	1079.5480	540.2776	1062.5215	531.7644	1061.5374	531.2724	L	**544.3202**	272.6637	527.2936	264.1504			4
10	101.0709	1207.6066	604.3069	1190.5800	595.7937	1189.5960	595.3016	Q	**431.2361**	216.1217	**414.2096**	207.6084			3
11	101.0709	1335.6652	668.3362	1318.6386	659.8229	1317.6546	659.3309	Q	**303.1775**	152.0924	286.1510	143.5791			2
12	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SEFEQNLSEK**
Found in **Q16891**, Q16891|IMMT_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1

Match to Query 369: 1209.560048 from(605.787300,2+)

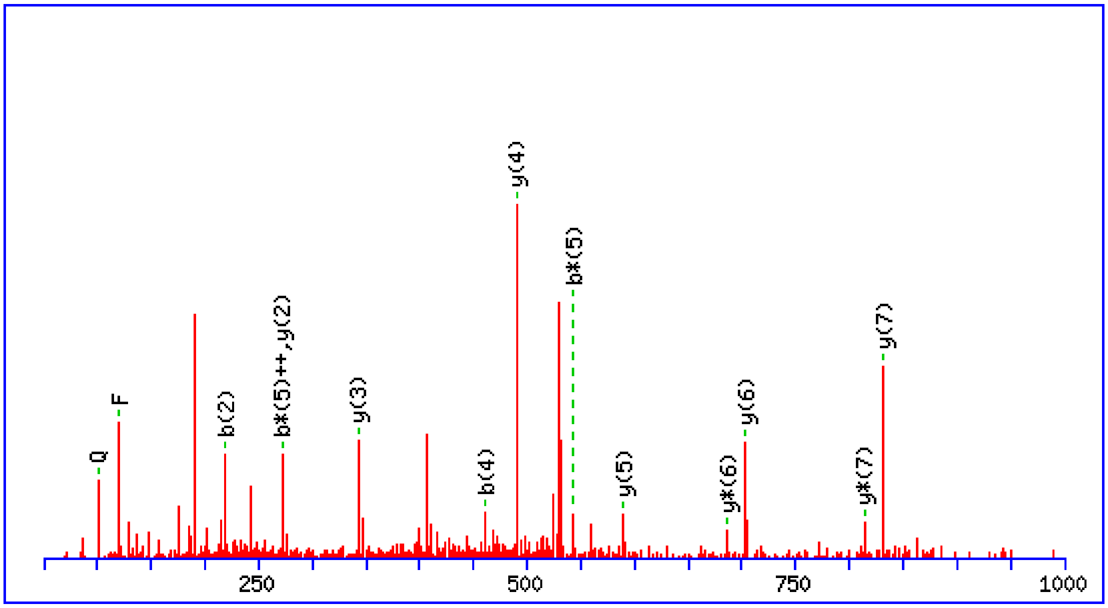


Monoisotopic mass of neutral peptide Mr(calc): 1209.5513
Fixed modifications: Carbamidomethyl (C)
Ions Score: 35 **Expect:** 0.024
Matches (Bold Red): 17/108 fragment ions using 32 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	**S**							**10**
2	102.0550	**217.0819**	109.0446			199.0713	100.0393	**E**	1123.5266	562.2669	1106.5000	553.7537	1105.5160	553.2617	**9**
3	**120.0808**	364.1503	182.5788			346.1397	173.5735	**F**	**994.4840**	**497.7456**	977.4575	489.2324	976.4734	488.7404	**8**
4	102.0550	493.1929	247.1001			475.1823	238.0948	**E**	**847.4156**	**424.2114**	830.3890	415.6982	**829.4050**	**415.2061**	**7**
5	101.0709	621.2515	311.1294	**604.2249**	302.6161	603.2409	302.1241	**Q**	**718.3730**	359.6901	701.3464	351.1769	**700.3624**	350.6849	**6**
6	87.0553	735.2944	368.1508	**718.2679**	359.6376	717.2838	359.1456	**N**	**590.3144**	295.6608	573.2879	287.1476	572.3039	286.6556	**5**
7	86.0964	848.3785	424.6929	831.3519	**416.1796**	830.3679	415.6876	**L**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
8	60.0444	935.4105	468.2089	918.3840	459.6956	917.3999	459.2036	**S**	**363.1874**	182.0974	346.1609	173.5841	345.1769	173.0921	**3**
9	102.0550	1064.4531	532.7302	1047.4265	524.2169	1046.4425	523.7249	**E**	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
10	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **AFQNVFAPR**
Found in **P15586**, P15586|GNS_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3

Match to Query 277: 1048.660214 from(525.337383,2+)

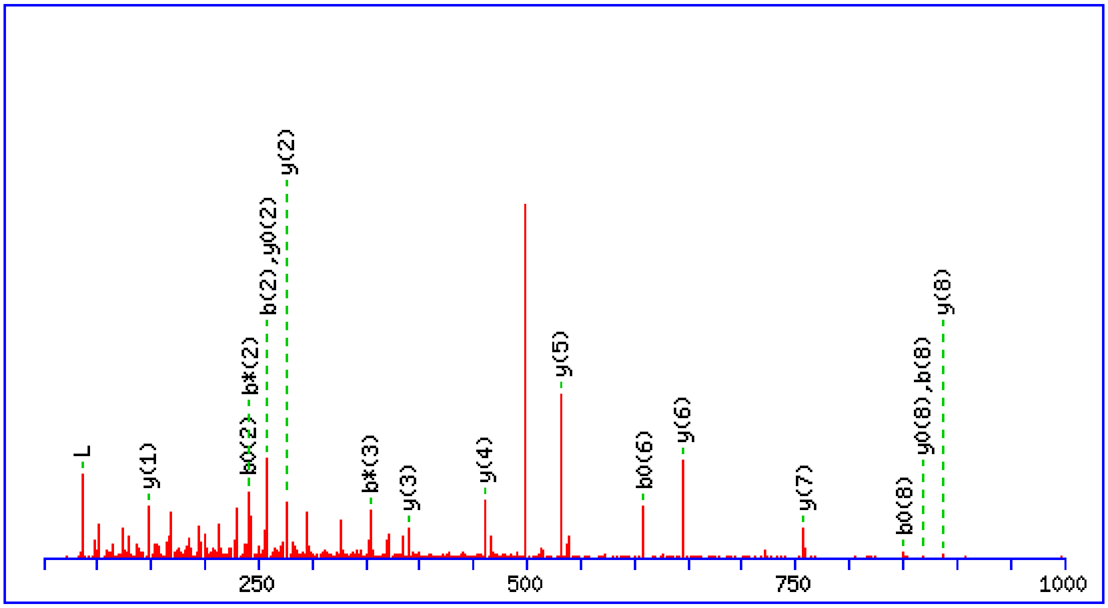


Monoisotopic mass of neutral peptide Mr(calc): 1048.5454
Fixed modifications: Carbamidomethyl (C)
Ions Score: 37 **Expect:** 0.014
Matches (Bold Red): 15/69 fragment ions using 27 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	Seq.	y	y^{++}	y*	y*$^{++}$	#
1	44.0495	72.0444	36.5258			A					9
2	**120.0808**	**219.1128**	110.0600			F	978.5156	489.7614	961.4890	481.2482	8
3	**101.0709**	347.1714	174.0893	330.1448	165.5761	Q	**831.4472**	416.2272	**814.4206**	407.7139	7
4	87.0553	**461.2143**	231.1108	444.1878	222.5975	N	**703.3886**	352.1979	**686.3620**	343.6847	6
5	72.0808	560.2827	280.6450	**543.2562**	**272.1317**	V	**589.3457**	295.1765	572.3191	286.6632	5
6	**120.0808**	707.3511	354.1792	690.3246	345.6659	F	**490.2772**	245.6423	473.2507	237.1290	4
7	44.0495	778.3883	389.6978	761.3617	381.1845	A	**343.2088**	172.1081	326.1823	163.5948	3
8	70.0651	875.4410	438.2241	858.4145	429.7109	P	**272.1717**	136.5895	255.1452	128.0762	2
9	129.1135					R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **QEILAALEK**
Found in **P07602**, P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2

Match to Query 145: 1013.413896 from(507.714224,2+)

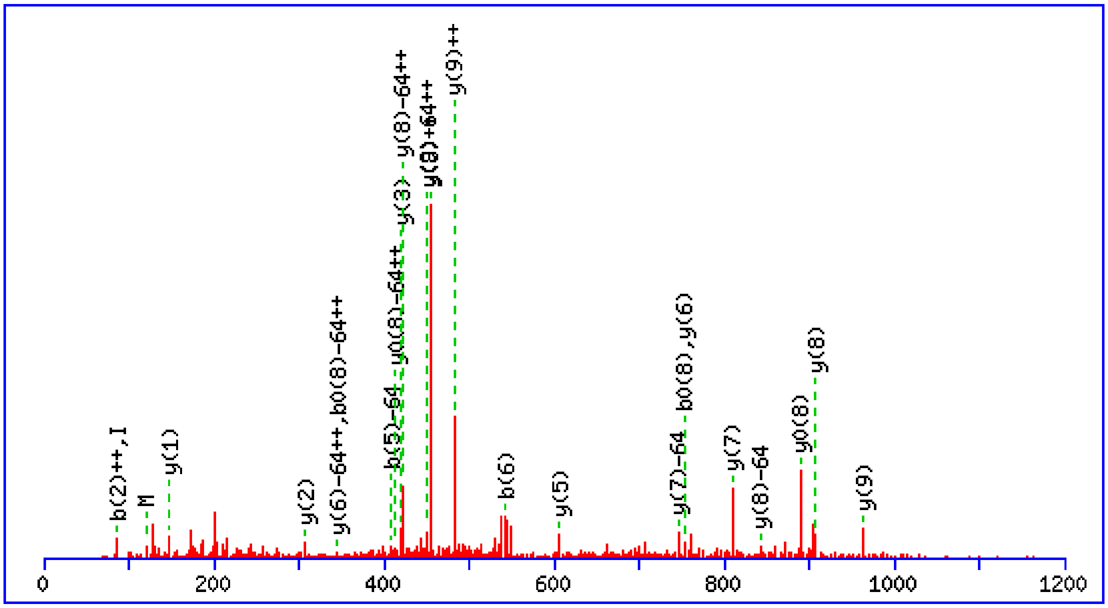


Monoisotopic mass of neutral peptide Mr(calc): 1013.5757
Fixed modifications: Carbamidomethyl (C)
Ions Score: 83 **Expect:** 3.8e-007
Matches (Bold Red): 20/101 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b*	$b*^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	$y*^{++}$	y^{0}	y^{0++}	#
1	101.0709	129.0659	65.0366	112.0393	56.5233			Q							9
2	102.0550	**258.1084**	129.5579	**241.0819**	121.0446	**240.0979**	120.5526	E	**886.5244**	443.7658	869.4979	435.2526	**868.5138**	434.7606	8
3	**86.0964**	371.1925	186.0999	**354.1660**	177.5866	353.1819	177.0946	I	**757.4818**	379.2445	740.4553	370.7313	739.4713	370.2393	7
4	**86.0964**	484.2766	242.6419	467.2500	234.1287	466.2660	233.6366	L	**644.3978**	322.7025	627.3712	314.1892	626.3872	313.6972	6
5	44.0495	555.3137	278.1605	538.2871	269.6472	537.3031	269.1552	A	**531.3137**	266.1605	514.2871	257.6472	513.3031	257.1552	5
6	44.0495	626.3508	313.6790	609.3243	305.1658	**608.3402**	304.6738	A	**460.2766**	230.6419	443.2500	222.1287	442.2660	221.6366	4
7	**86.0964**	739.4349	370.2211	722.4083	361.7078	721.4243	361.2158	L	**389.2395**	195.1234	372.2129	186.6101	371.2289	186.1181	3
8	102.0550	**868.4775**	434.7424	851.4509	426.2291	**850.4669**	425.7371	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
9	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **LGPGMADICK**
Found in **P07602**, P07602|SAP_HUMAN Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2

Match to Query 421: 1076.473922 from(539.244237,2+)

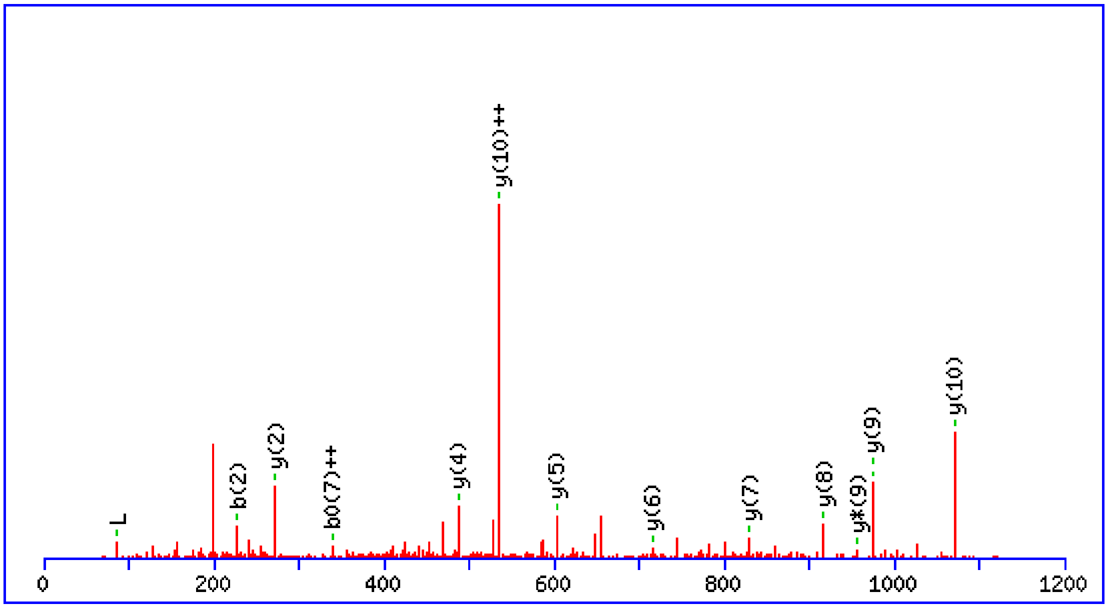


Monoisotopic mass of neutral peptide Mr(calc): 1076.4995
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 38 **Expect:** 0.013
Matches (Bold Red): 25/123 fragment ions using 57 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			L							10
2	30.0338	171.1128	**86.0600**			G	**964.4227**	**482.7150**	947.3961	474.2017	946.4121	473.7097	9
3	70.0651	268.1656	134.5864			P	**907.4012**	**454.2042**	890.3747	445.6910	**889.3906**	445.1990	8
4	30.0338	325.1870	163.0972			G	**810.3484**	405.6779	793.3219	397.1646	792.3379	396.6726	7
5	**120.0478**	472.2224	236.6149			M	**753.3270**	377.1671	736.3004	368.6539	735.3164	368.1618	6
6	44.0495	**543.2595**	272.1334			A	**606.2916**	303.6494	589.2650	295.1362	588.2810	294.6441	5
7	88.0393	658.2865	329.6469	640.2759	320.6416	D	535.2545	268.1309	518.2279	259.6176	517.2439	259.1256	4
8	**86.0964**	771.3706	386.1889	**753.3600**	377.1836	I	**420.2275**	210.6174	403.2010	202.1041			3
9	133.0430	931.4012	466.2042	913.3906	457.1990	C	**307.1435**	154.0754	290.1169	145.5621			2
10	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **LIPGSNLDSEPR**
Found in **Q6P4E1**, Q6P4E1|CASC4_HUMAN Protein CASC4 OS=Homo sapiens GN=CASC4 PE=2 SV=1

Match to Query 342: 1296.614988 from(649.314770,2+)

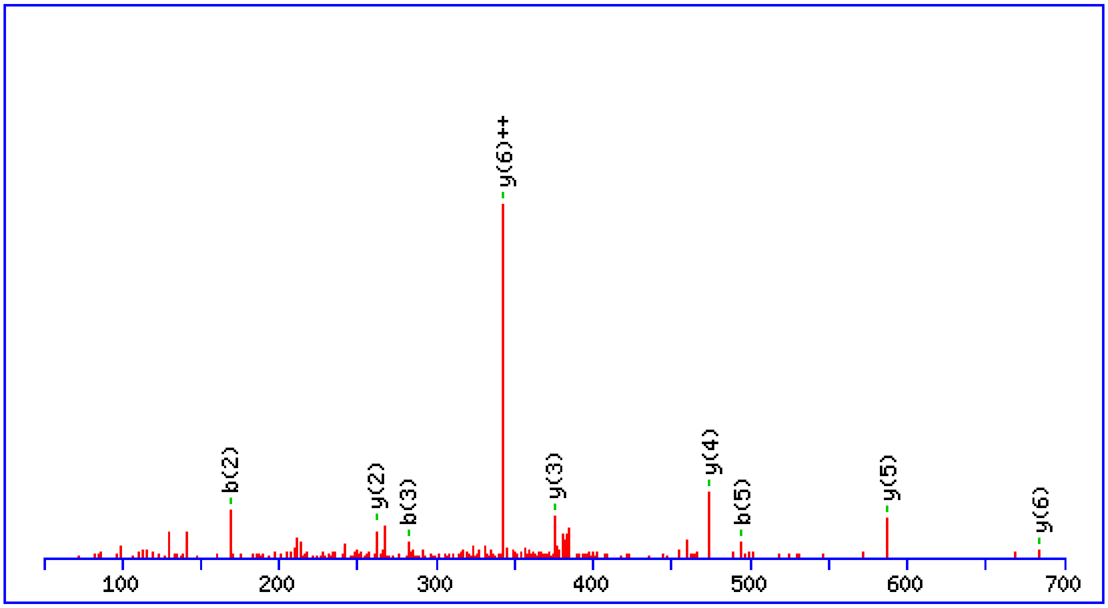


Monoisotopic mass of neutral peptide Mr(calc): 1296.6674
Fixed modifications: Carbamidomethyl (C)
Ions Score: 51 **Expect:** 0.00057
Matches (Bold Red): 15/122 fragment ions using 24 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							12
2	**86.0964**	**227.1754**	114.0913					I	1184.5906	592.7989	1167.5640	584.2857	1166.5800	583.7937	11
3	70.0651	324.2282	162.6177					P	**1071.5065**	**536.2569**	1054.4800	527.7436	1053.4960	527.2516	10
4	30.0338	381.2496	191.1285					G	**974.4538**	487.7305	**957.4272**	479.2172	956.4432	478.7252	9
5	60.0444	468.2817	234.6445			450.2711	225.6392	S	**917.4323**	459.2198	900.4058	450.7065	899.4217	450.2145	8
6	87.0553	582.3246	291.6659	565.2980	283.1527	564.3140	282.6606	N	**830.4003**	415.7038	813.3737	407.1905	812.3897	406.6985	7
7	**86.0964**	695.4087	348.2080	678.3821	339.6947	677.3981	**339.2027**	L	**716.3573**	358.6823	699.3308	350.1690	698.3468	349.6770	6
8	88.0393	810.4356	405.7214	793.4090	397.2082	792.4250	396.7162	D	**603.2733**	302.1403	586.2467	293.6270	585.2627	293.1350	5
9	60.0444	897.4676	449.2374	880.4411	440.7242	879.4571	440.2322	S	**488.2463**	244.6268	471.2198	236.1135	470.2358	235.6215	4
10	102.0550	1026.5102	513.7587	1009.4837	505.2455	1008.4997	504.7535	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
11	70.0651	1123.5630	562.2851	1106.5364	553.7719	1105.5524	553.2798	P	**272.1717**	136.5895	255.1452	128.0762			2
12	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **APLVLKD**
Found in **Q99497**, Q99497|PARK7_HUMAN Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2

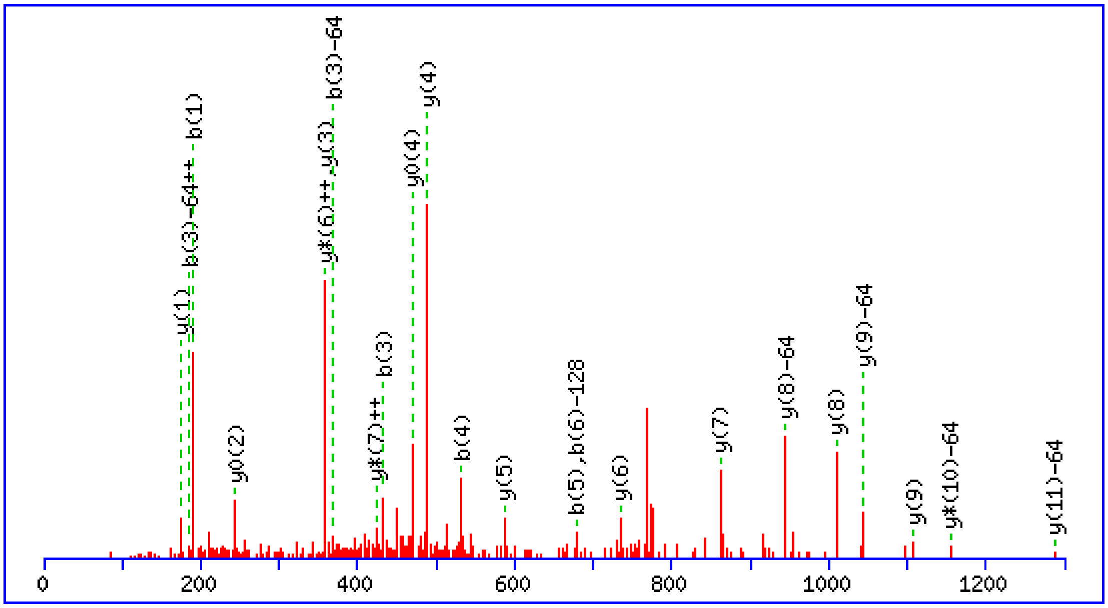
Match to Query 44: 754.435238 from(378.224895,2+)



#	Immon.	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							7
2	70.0651	**169.0972**	85.0522			P	**684.4291**	**342.7182**	667.4025	334.2049	666.4185	333.7129	6
3	86.0964	**282.1812**	141.5942			L	**587.3763**	294.1918	570.3497	285.6785	569.3657	285.1865	5
4	72.0808	381.2496	191.1285			V	**474.2922**	237.6498	457.2657	229.1365	456.2817	228.6445	4
5	86.0964	**494.3337**	247.6705			L	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
6	101.1073	622.4287	311.7180	605.4021	303.2047	K	**262.1397**	131.5735	245.1132	123.0602	244.1292	122.5682	2
7	88.0393					D	134.0448	67.5260			116.0342	58.5207	1

MS/MS Fragmentation of **MDQVMQFVEPSR**
Found in **P60059**, P60059|SC61G_HUMAN Protein transport protein Sec61 subunit gamma OS=Homo sapiens GN=SEC61G PE=2 SV=1

Match to Query 458: 1539.573820 from(770.794186,2+)

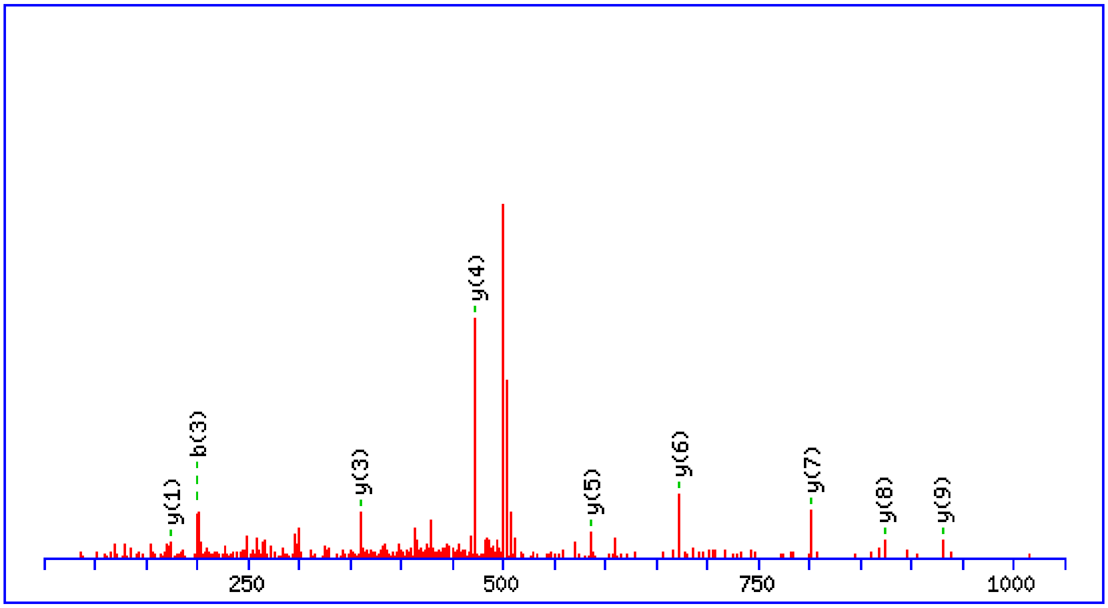


Monoisotopic mass of neutral peptide Mr(calc): 1539.6698
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
N-term : Acetyl (Protein N-term)
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
M5 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 63 **Expect:** 3.5e-005
Matches (Bold Red): 23/222 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	56.0495	126.0550	63.5311					M							12
2	88.0393	241.0819	121.0446			223.0713	112.0393	D	**1287.6328**	644.3200	1270.6062	635.8068	1269.6222	635.3148	11
3	101.0709	**369.1405**	**185.0739**	352.1139	176.5606	351.1299	176.0686	Q	1172.6059	586.8066	**1155.5793**	578.2933	1154.5953	577.8013	10
4	72.0808	468.2089	234.6081	451.1823	226.0948	450.1983	225.6028	V	**1044.5473**	522.7773	1027.5207	514.2640	1026.5367	513.7720	9
5	56.0495	551.2460	276.1266	534.2195	267.6134	533.2354	267.1214	M	**945.4789**	473.2431	928.4523	464.7298	927.4683	464.2378	8
6	101.0709	**679.3046**	340.1559	662.2780	331.6427	661.2940	331.1506	Q	**862.4417**	431.7245	845.4152	**423.2112**	844.4312	422.7192	7
7	120.0808	826.3730	413.6901	809.3465	405.1769	808.3624	404.6849	F	**734.3832**	367.6952	717.3566	**359.1819**	716.3726	358.6899	6
8	72.0808	925.4414	463.2243	908.4149	454.7111	907.4308	454.2191	V	**587.3148**	294.1610	570.2882	285.6477	569.3042	285.1557	5
9	102.0550	1054.4840	527.7456	1037.4575	519.2324	1036.4734	518.7404	E	**488.2463**	244.6268	471.2198	236.1135	**470.2358**	235.6215	4
10	70.0651	1151.5368	576.2720	1134.5102	567.7587	1133.5262	567.2667	P	**359.2037**	180.1055	342.1772	171.5922	341.1932	171.1002	3
11	60.0444	1238.5688	619.7880	1221.5423	611.2748	1220.5582	610.7828	S	262.1510	131.5791	245.1244	123.0659	**244.1404**	122.5738	2
12	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AGAESILANR**
Found in **P15498**, P15498|VAV_HUMAN Proto-oncogene vav OS=Homo sapiens GN=VAV1 PE=1 SV=4

Match to Query 251: 1000.494024 from(501.254288,2+)

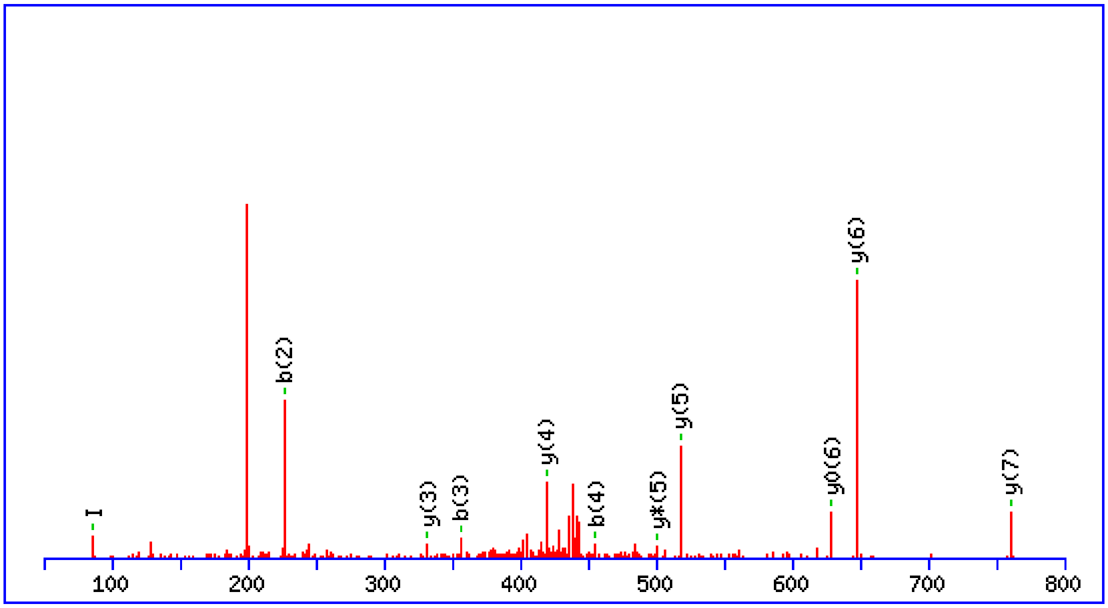


Monoisotopic mass of neutral peptide Mr(calc): 1000.5301
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00034
Matches (Bold Red): 9/86 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							10
2	30.0338	129.0659	65.0366					G	**930.5003**	465.7538	913.4738	457.2405	912.4898	456.7485	9
3	44.0495	**200.1030**	100.5551					A	**873.4789**	437.2431	856.4523	428.7298	855.4683	428.2378	8
4	102.0550	329.1456	165.0764			311.1350	156.0711	E	**802.4417**	401.7245	785.4152	393.2112	784.4312	392.7192	7
5	60.0444	416.1776	208.5924			398.1670	199.5871	S	**673.3991**	337.2032	656.3726	328.6899	655.3886	328.1979	6
6	86.0964	529.2617	265.1345			511.2511	256.1292	I	**586.3671**	293.6872	569.3406	285.1739			5
7	86.0964	642.3457	321.6765			624.3352	312.6712	L	**473.2831**	237.1452	456.2565	228.6319			4
8	44.0495	713.3828	357.1951			695.3723	348.1898	A	**360.1990**	180.6031	343.1724	172.0899			3
9	87.0553	827.4258	414.2165	810.3992	405.7032	809.4152	405.2112	N	289.1619	145.0846	272.1353	136.5713			2
10	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IIEVSGQK**
Found in **P61106**, P61106|RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4

Match to Query 192: 872.563578 from(437.289065,2+)

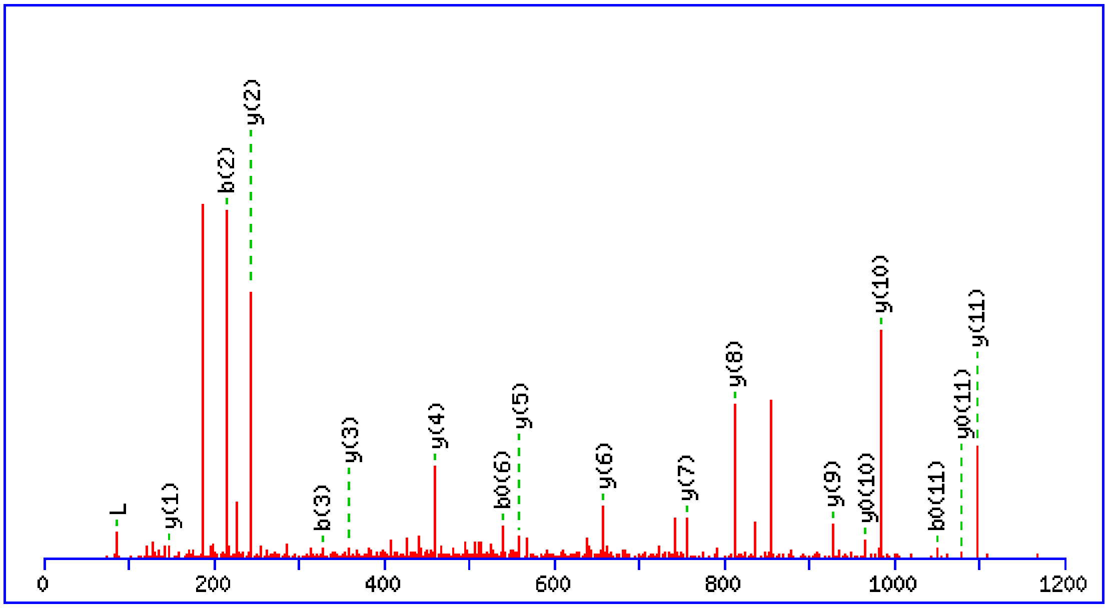


Monoisotopic mass of neutral peptide Mr(calc): 872.4967
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 **Expect:** 0.011
Matches (Bold Red): 12/70 fragment ions using 24 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							8
2	**86.0964**	**227.1754**	114.0913					I	**760.4199**	380.7136	743.3934	372.2003	742.4094	371.7083	7
3	102.0550	**356.2180**	178.6126			338.2074	169.6074	E	**647.3359**	324.1716	630.3093	315.6583	**629.3253**	315.1663	6
4	72.0808	**455.2864**	228.1468			437.2758	219.1416	V	**518.2933**	259.6503	**501.2667**	251.1370	500.2827	250.6450	5
5	60.0444	542.3184	271.6629			524.3079	262.6576	S	**419.2249**	210.1161	402.1983	201.6028	401.2143	201.1108	4
6	30.0338	599.3399	300.1736			581.3293	291.1683	G	**332.1928**	166.6001	315.1663	158.0868			3
7	101.0709	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	Q	275.1714	138.0893	258.1448	129.5761			2
8	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **TLLGDGPVVTDPK**
Found in **P52566**, P52566|GDIR2_HUMAN Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3

Match to Query 319: 1310.646764 from(656.330658,2+)

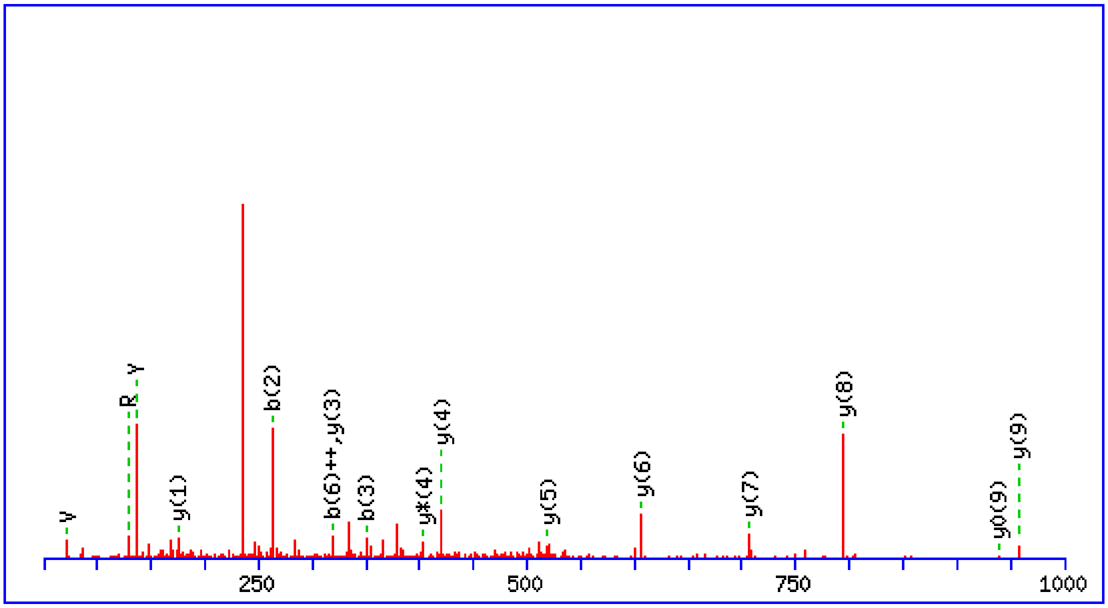


Monoisotopic mass of neutral peptide Mr(calc): 1310.7082
Fixed modifications: Carbamidomethyl (C)
Ions Score: 86 **Expect:** 1.7e-007
Matches (Bold Red): 19/129 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	**T**							**13**
2	**86.0964**	**215.1390**	108.0731	197.1285	99.0679	**L**	1210.6678	605.8375	1193.6412	597.3243	1192.6572	596.8322	**12**
3	**86.0964**	**328.2231**	164.6152	310.2125	155.6099	**L**	**1097.5837**	549.2955	1080.5572	540.7822	**1079.5732**	540.2902	**11**
4	30.0338	385.2445	193.1259	367.2340	184.1206	**G**	**984.4997**	492.7535	967.4731	484.2402	**966.4891**	483.7482	**10**
5	88.0393	500.2715	250.6394	482.2609	241.6341	**D**	**927.4782**	464.2427	910.4516	455.7295	909.4676	455.2375	**9**
6	30.0338	557.2930	279.1501	**539.2824**	270.1448	**G**	**812.4512**	406.7293	795.4247	398.2160	794.4407	397.7240	**8**
7	70.0651	654.3457	327.6765	636.3352	318.6712	**P**	**755.4298**	378.2185	738.4032	369.7053	737.4192	369.2132	**7**
8	72.0808	753.4141	377.2107	735.4036	368.2054	**V**	**658.3770**	329.6921	641.3505	321.1789	640.3665	320.6869	**6**
9	72.0808	852.4825	426.7449	834.4720	417.7396	**V**	**559.3086**	280.1579	542.2821	271.6447	541.2980	271.1527	**5**
10	74.0600	953.5302	477.2688	935.5197	468.2635	**T**	**460.2402**	230.6237	443.2136	222.1105	442.2296	221.6185	**4**
11	88.0393	1068.5572	534.7822	**1050.5466**	525.7769	**D**	**359.1925**	180.0999	342.1660	171.5866	341.1819	171.0946	**3**
12	70.0651	1165.6099	583.3086	1147.5994	574.3033	**P**	**244.1656**	122.5864	227.1390	114.0731			**2**
13	101.1073					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **VYSTSVTGSR**
Found in **Q9H299**, Q9H299|SH3L3_HUMAN SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1

Match to Query 168: 1055.344256 from(528.679404,2+)

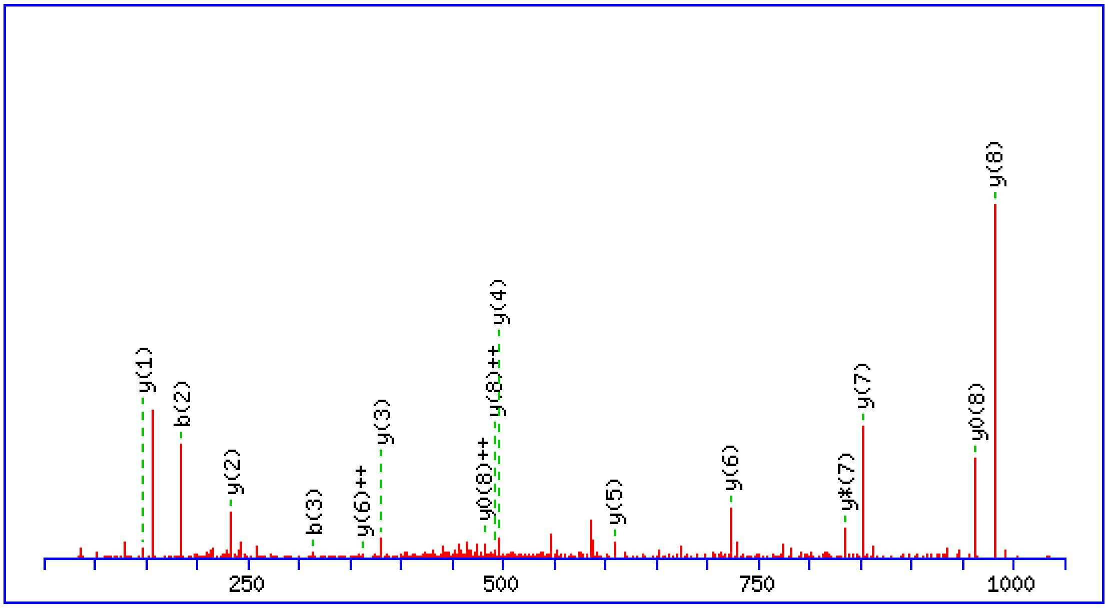


Monoisotopic mass of neutral peptide Mr(calc): 1055.5248
Fixed modifications: Carbamidomethyl (C)
Ions Score: 67 **Expect:** 1.3e-005
Matches (Bold Red): 17/94 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**72.0808**	100.0757	50.5415			V							10
2	**136.0757**	**263.1390**	132.0731			Y	**957.4636**	479.2354	940.4371	470.7222	**939.4530**	470.2302	9
3	60.0444	**350.1710**	175.5892	332.1605	166.5839	S	**794.4003**	397.7038	777.3737	389.1905	776.3897	388.6985	8
4	74.0600	451.2187	226.1130	433.2082	217.1077	T	**707.3682**	354.1878	690.3417	345.6745	689.3577	345.1825	7
5	60.0444	538.2508	269.6290	520.2402	260.6237	S	**606.3206**	303.6639	589.2940	295.1506	588.3100	294.6586	6
6	**72.0808**	637.3192	**319.1632**	619.3086	310.1579	V	**519.2885**	260.1479	502.2620	251.6346	501.2780	251.1426	5
7	74.0600	738.3668	369.6871	720.3563	360.6818	T	**420.2201**	210.6137	**403.1936**	202.1004	402.2096	201.6084	4
8	30.0338	795.3883	398.1978	777.3777	389.1925	G	**319.1724**	160.0899	302.1459	151.5766	301.1619	151.0846	3
9	60.0444	882.4203	441.7138	864.4098	432.7085	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10	**129.1135**					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AIEENNNFSK**
Found in **P16949**, P16949|STMN1_HUMAN Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3

Match to Query 451: 1164.526660 from(583.270606,2+)



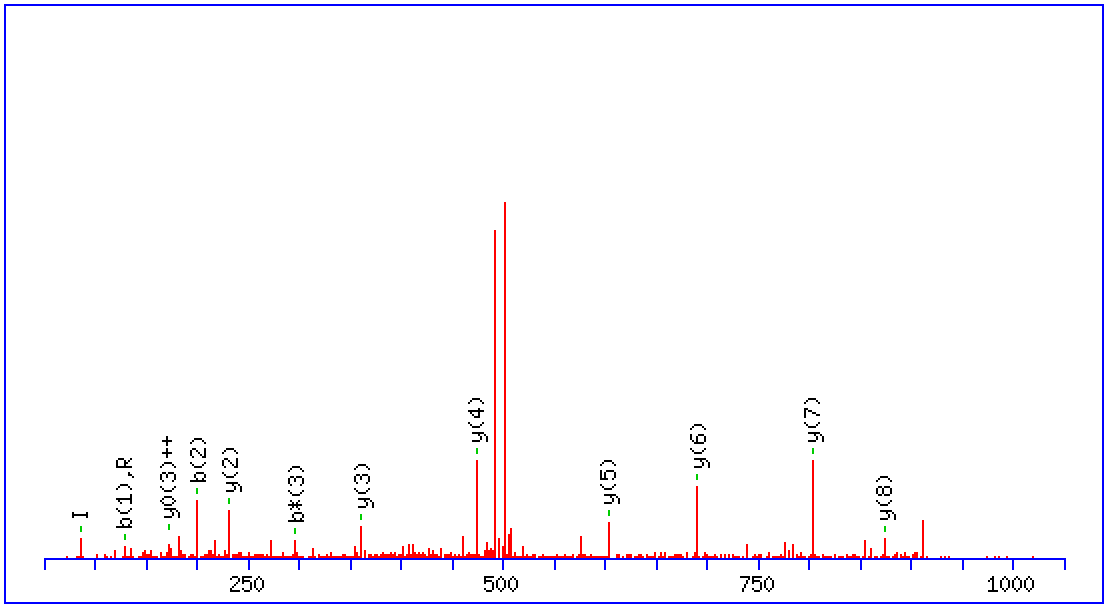
Monoisotopic mass of neutral peptide Mr(calc): 1164.5411
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.00069
Matches (Bold Red): 15/104 fragment ions using 32 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							10
2	86.0964	**185.1285**	93.0679					I	1094.5113	547.7593	1077.4847	539.2460	1076.5007	538.7540	9
3	102.0550	**314.1710**	157.5892			296.1605	148.5839	E	**981.4272**	**491.2172**	964.4007	482.7040	**963.4166**	**482.2120**	8
4	102.0550	443.2136	222.1105			425.2031	213.1052	E	**852.3846**	426.6959	**835.3581**	418.1827	834.3741	417.6907	7
5	87.0553	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	N	**723.3420**	**362.1747**	706.3155	353.6614	705.3315	353.1694	6
6	87.0553	671.2995	336.1534	654.2729	327.6401	653.2889	327.1481	N	**609.2991**	305.1532	592.2726	296.6399	591.2885	296.1479	5
7	87.0553	785.3424	393.1748	768.3159	384.6616	767.3319	384.1696	N	**495.2562**	248.1317	478.2296	239.6185	477.2456	239.1264	4
8	120.0808	932.4108	466.7091	915.3843	458.1958	914.4003	457.7038	F	**381.2132**	191.1103	364.1867	182.5970	363.2027	182.1050	3
9	60.0444	1019.4429	510.2251	1002.4163	501.7118	1001.4323	501.2198	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
10	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

Stathmin (P16949): single-peptide based protein identifications indicated as (+) could possibly also be assigned to STMN2_HUMAN Stathmin-2 (Q93045)

MS/MS Fragmentation of **QALSEIEGR**
Found in **Q13277**, Q13277|STX3_HUMAN Syntaxin-3 OS=Homo sapiens GN=STX3 PE=1 SV=3

Match to Query 330: 1001.464440 from(501.739496,2+)

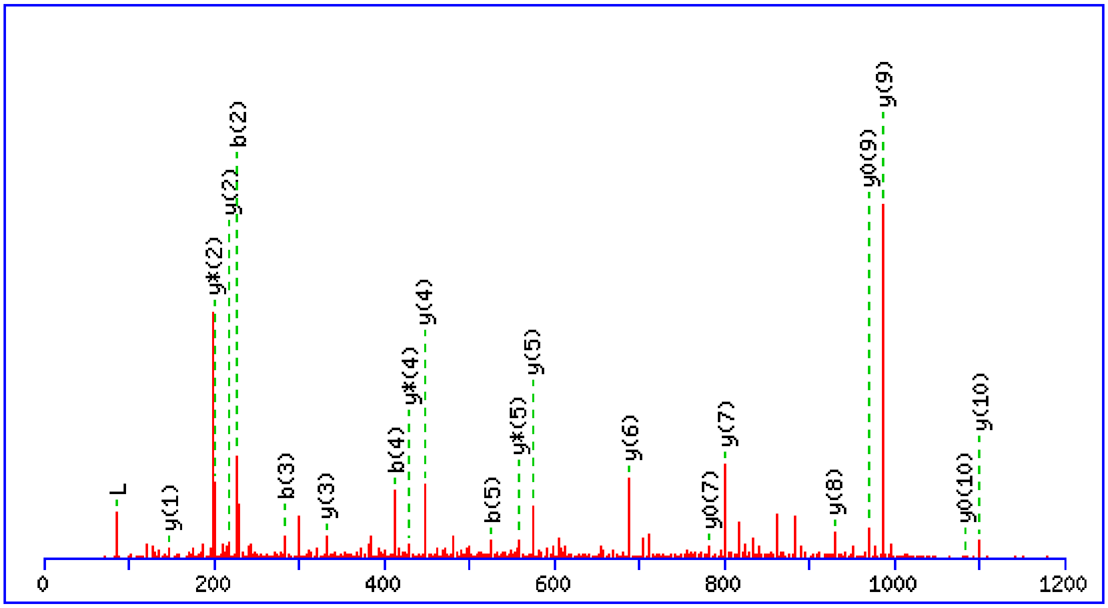


Monoisotopic mass of neutral peptide Mr(calc): 1001.5141
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 **Expect:** 0.016
Matches (Bold Red): 14/95 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0709	**129.0659**	65.0366	112.0393	56.5233			Q							9
2	44.0495	**200.1030**	100.5551	183.0764	92.0418			A	**874.4629**	437.7351	857.4363	429.2218	856.4523	428.7298	8
3	**86.0964**	313.1870	157.0972	**296.1605**	148.5839			L	**803.4258**	402.2165	786.3992	393.7032	785.4152	393.2112	7
4	60.0444	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	S	**690.3417**	345.6745	673.3151	337.1612	672.3311	336.6692	6
5	102.0550	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	E	**603.3097**	302.1585	586.2831	293.6452	585.2991	293.1532	5
6	**86.0964**	642.3457	321.6765	625.3192	313.1632	624.3352	312.6712	I	**474.2671**	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	102.0550	771.3883	386.1978	754.3618	377.6845	753.3777	377.1925	E	**361.1830**	181.0951	344.1565	172.5819	343.1724	**172.0899**	3
8	30.0338	828.4098	414.7085	811.3832	406.1953	810.3992	405.7032	G	**232.1404**	116.5738	215.1139	108.0606			2
9	**129.1135**							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LLGELLQDNAK**
Found in **P37837**, P37837|TALDO_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2

Match to Query 492: 1212.633868 from(607.324210,2+)

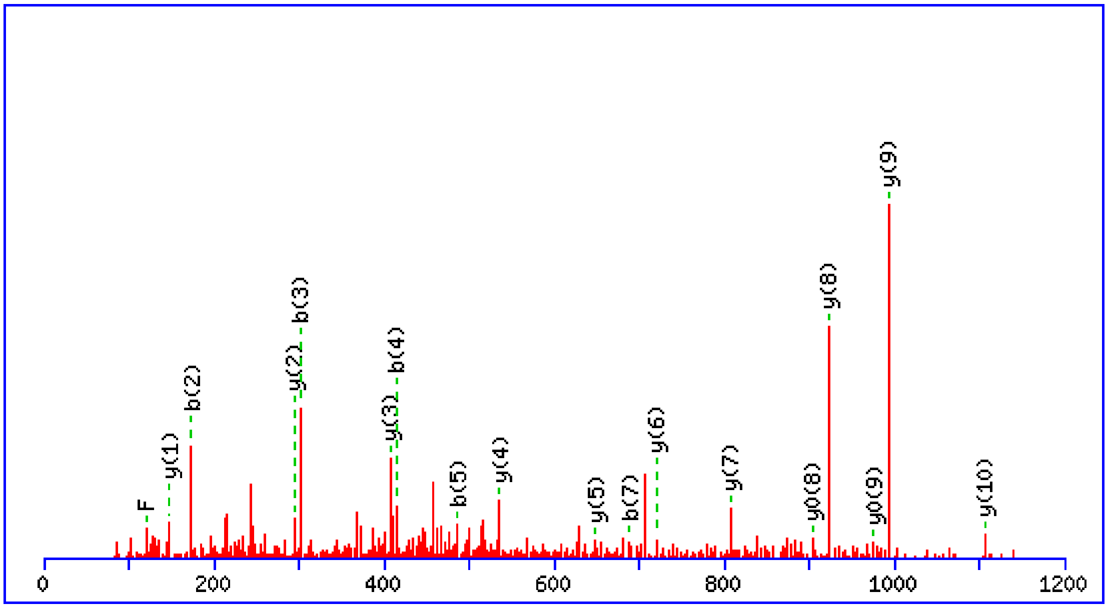


Monoisotopic mass of neutral peptide Mr(calc): 1212.6714
Fixed modifications: Carbamidomethyl (C)
Ions Score: 55 **Expect:** 0.00021
Matches (Bold Red): 24/107 fragment ions using 65 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**11**
2	**86.0964**	**227.1754**	114.0913					**L**	**1100.5946**	550.8009	1083.5681	542.2877	**1082.5841**	541.7957	**10**
3	30.0338	**284.1969**	142.6021					**G**	**987.5106**	494.2589	970.4840	485.7456	**969.5000**	485.2536	**9**
4	102.0550	**413.2395**	207.1234			395.2289	198.1181	**E**	**930.4891**	465.7482	913.4625	457.2349	912.4785	456.7429	**8**
5	**86.0964**	**526.3235**	263.6654			508.3130	254.6601	**L**	**801.4465**	401.2269	784.4199	392.7136	**783.4359**	392.2216	**7**
6	**86.0964**	639.4076	320.2074			621.3970	311.2022	**L**	**688.3624**	344.6849	671.3359	336.1716	670.3519	335.6796	**6**
7	101.0709	767.4662	384.2367	750.4396	375.7234	749.4556	375.2314	**Q**	**575.2784**	288.1428	**558.2518**	279.6295	557.2678	279.1375	**5**
8	88.0393	882.4931	441.7502	865.4666	433.2369	864.4825	432.7449	**D**	**447.2198**	224.1135	**430.1932**	215.6003	429.2092	215.1082	**4**
9	87.0553	996.5360	498.7717	979.5095	490.2584	978.5255	489.7664	**N**	**332.1928**	166.6001	315.1663	158.0868			**3**
10	44.0495	1067.5732	534.2902	1050.5466	525.7769	1049.5626	525.2849	**A**	**218.1499**	109.5786	**201.1234**	101.0653			**2**
11	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **GDELADSALEIFK**
Found in **Q15582**, Q15582|BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1

Match to Query 615: 1406.651150 from(704.332851,2+)

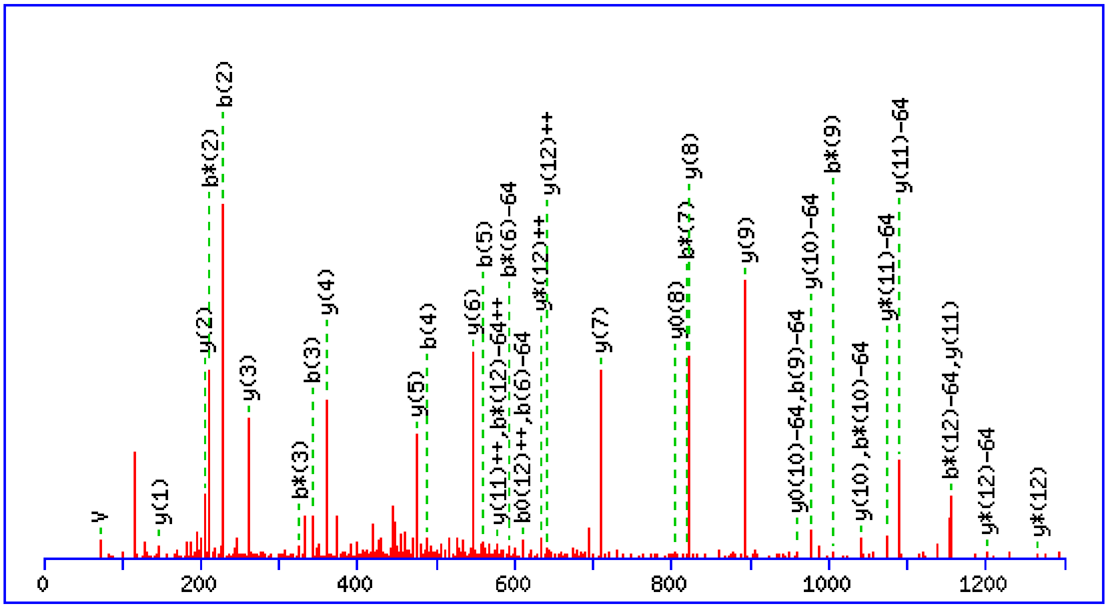


Monoisotopic mass of neutral peptide Mr(calc): 1406.6929
Fixed modifications: Carbamidomethyl (C)
Ions Score: 71 **Expect:** 6e-006
Matches (Bold Red): 18/125 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			G							13
2	88.0393	**173.0557**	87.0315	155.0451	78.0262	D	1350.6787	675.8430	1333.6522	667.3297	1332.6682	666.8377	12
3	102.0550	**302.0983**	151.5528	284.0877	142.5475	E	1235.6518	618.3295	1218.6252	609.8163	1217.6412	609.3243	11
4	86.0964	**415.1823**	208.0948	397.1718	199.0895	L	**1106.6092**	553.8082	1089.5827	545.2950	1088.5986	544.8030	10
5	44.0495	**486.2195**	243.6134	468.2089	234.6081	A	**993.5251**	497.2662	976.4986	488.7529	**975.5146**	488.2609	9
6	88.0393	601.2464	301.1268	583.2358	292.1216	D	**922.4880**	461.7477	905.4615	453.2344	**904.4775**	452.7424	8
7	60.0444	**688.2784**	344.6429	670.2679	335.6376	S	**807.4611**	404.2342	790.4345	395.7209	789.4505	395.2289	7
8	44.0495	759.3155	380.1614	741.3050	371.1561	A	**720.4291**	360.7182	703.4025	352.2049	702.4185	351.7129	6
9	86.0964	872.3996	436.7034	854.3890	427.6982	L	**649.3919**	325.1996	632.3654	316.6863	631.3814	316.1943	5
10	102.0550	1001.4422	501.2247	983.4316	492.2195	E	**536.3079**	268.6576	519.2813	260.1443	518.2973	259.6523	4
11	86.0964	1114.5263	557.7668	1096.5157	548.7615	I	**407.2653**	204.1363	390.2387	195.6230			3
12	**120.0808**	1261.5947	631.3010	1243.5841	622.2957	F	**294.1812**	147.5942	277.1547	139.0810			2
13	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VQNMALYADVGGK**
Found in **P51571**, P51571|SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1

Match to Query 415: 1380.725486 from(691.370019,2+)

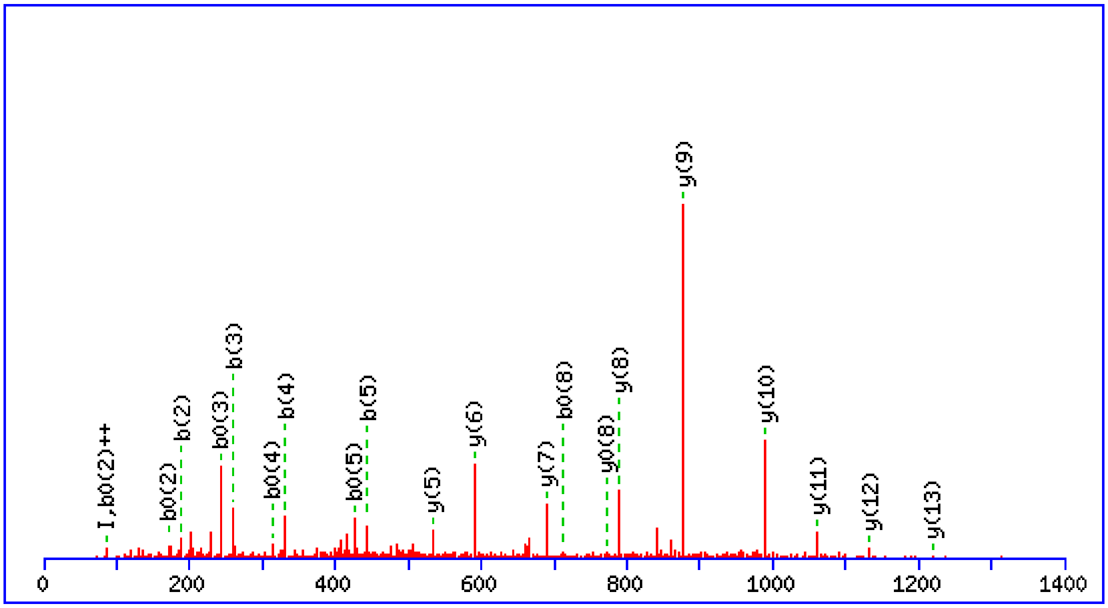


Monoisotopic mass of neutral peptide Mr(calc): 1380.6707
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M4 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 67 **Expect:** 1.3e-005
Matches (Bold Red): 38/194 fragment ions using 69 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**72.0808**	100.0757	50.5415					V							13
2	101.0709	**228.1343**	114.5708	**211.1077**	106.0575			Q	1218.6113	609.8093	**1201.5848**	601.2960	1200.6008	600.8040	12
3	87.0553	**342.1772**	171.5922	**325.1506**	163.0790			N	**1090.5528**	545.7800	**1073.5262**	537.2667	1072.5422	536.7747	11
4	56.0495	425.2143	213.1108	408.1878	204.5975			M	**976.5098**	488.7586	959.4833	480.2453	**958.4993**	479.7533	10
5	44.0495	496.2514	248.6294	479.2249	240.1161			A	**893.4727**	447.2400	876.4462	438.7267	875.4621	438.2347	9
6	86.0964	**609.3355**	305.1714	**592.3089**	296.6581			L	**822.4356**	411.7214	805.4090	403.2082	**804.4250**	402.7162	8
7	136.0757	772.3988	386.7030	755.3723	378.1898			Y	**709.3515**	355.1794	692.3250	346.6661	691.3410	346.1741	7
8	44.0495	843.4359	422.2216	826.4094	413.7083			A	**546.2882**	273.6477	529.2617	265.1345	528.2776	264.6425	6
9	88.0393	**958.4629**	479.7351	941.4363	471.2218	940.4523	470.7298	D	**475.2511**	238.1292	458.2245	229.6159	457.2405	229.1239	5
10	**72.0808**	1057.5313	529.2693	**1040.5047**	520.7560	1039.5207	520.2640	V	**360.2241**	180.6157	343.1976	172.1024			4
11	30.0338	1114.5528	557.7800	1097.5262	549.2667	1096.5422	548.7747	G	**261.1557**	131.0815	244.1292	122.5682			3
12	30.0338	1171.5742	586.2907	**1154.5477**	**577.7775**	1153.5637	577.2855	G	**204.1343**	102.5708	187.1077	94.0575			2
13	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **TSAALSTVGSAISR**
Found in **O43399**, O43399|TPD54_HUMAN Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2

Match to Query 554: 1319.691698 from(660.853125,2+)

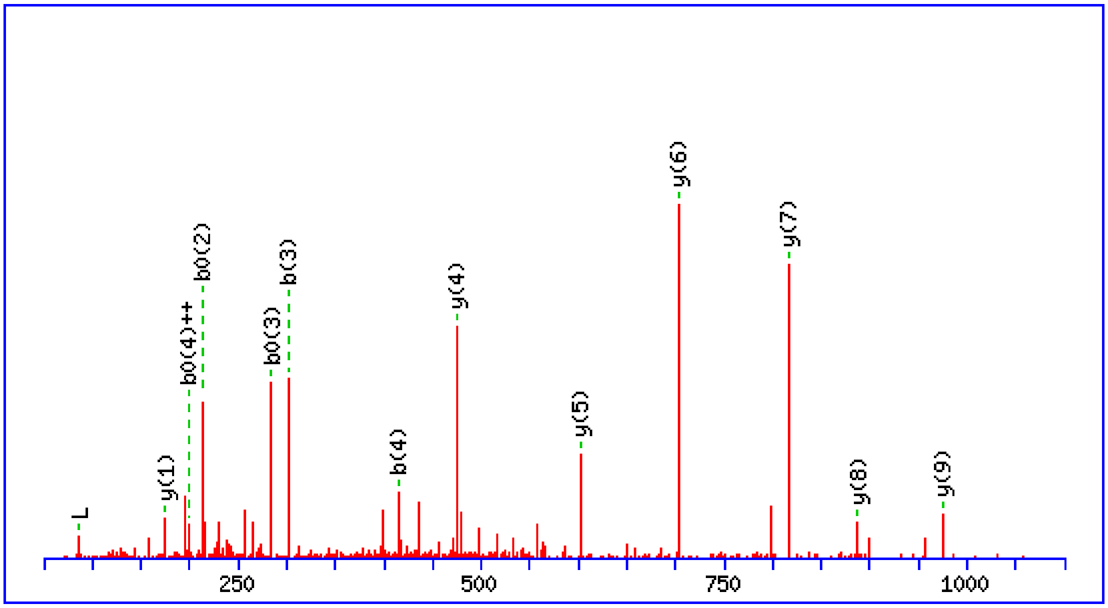


Monoisotopic mass of neutral peptide Mr(calc): 1319.7045
Fixed modifications: Carbamidomethyl (C)
Ions Score: 73 **Expect:** 3.7e-006
Matches (Bold Red): 22/142 fragment ions using 30 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							14
2	60.0444	**189.0870**	95.0471	**171.0764**	**86.0418**	S	**1219.6641**	610.3357	1202.6375	601.8224	1201.6535	601.3304	13
3	44.0495	**260.1241**	130.5657	**242.1135**	121.5604	A	**1132.6321**	566.8197	1115.6055	558.3064	1114.6215	557.8144	12
4	44.0495	**331.1612**	166.0842	**313.1506**	157.0790	A	**1061.5949**	531.3011	1044.5684	522.7878	1043.5844	522.2958	11
5	**86.0964**	**444.2453**	222.6263	**426.2347**	213.6210	L	**990.5578**	495.7826	973.5313	487.2693	972.5473	486.7773	10
6	60.0444	531.2773	266.1423	513.2667	257.1370	S	**877.4738**	439.2405	860.4472	430.7272	859.4632	430.2352	9
7	74.0600	632.3250	316.6661	614.3144	307.6608	T	**790.4417**	395.7245	773.4152	387.2112	**772.4312**	386.7192	8
8	72.0808	731.3934	366.2003	**713.3828**	357.1951	V	**689.3941**	345.2007	672.3675	336.6874	671.3835	336.1954	7
9	30.0338	788.4149	394.7111	770.4043	385.7058	G	**590.3257**	295.6665	573.2991	287.1532	572.3151	286.6612	6
10	60.0444	875.4469	438.2271	857.4363	429.2218	S	**533.3042**	267.1557	516.2776	258.6425	515.2936	258.1504	5
11	44.0495	946.4840	473.7456	928.4734	464.7404	A	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
12	**86.0964**	1059.5681	530.2877	1041.5575	521.2824	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	60.0444	1146.6001	573.8037	1128.5895	564.7984	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TSALTQGLER**
Found in **Q0VGL1**, Q0VGL1|CG059_HUMAN UPF0539 protein C7orf59 OS=Homo sapiens GN=C7orf59 PE=3 SV=1

Match to Query 287: 1116.509622 from(559.262087,2+)

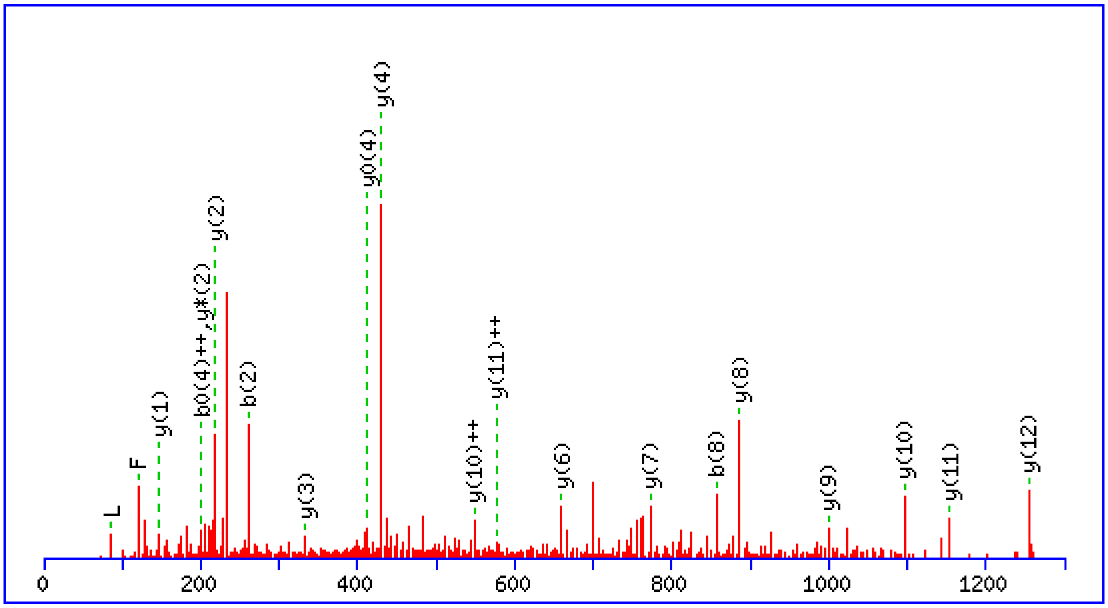


Monoisotopic mass of neutral peptide Mr(calc): 1116.5775
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
N-term : Acetyl (Protein N-term)
Ions Score: 62 **Expect:** 4.8e-005
Matches (Bold Red): 14/106 fragment ions using 14 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	144.0655	72.5364			126.0549	63.5311	T							10
2	60.0444	231.0975	116.0524			**213.0870**	107.0471	S	**974.5265**	487.7669	957.5000	479.2536	956.5160	478.7616	9
3	44.0495	**302.1347**	151.5710			**284.1241**	142.5657	A	**887.4945**	444.2509	870.4680	435.7376	869.4839	435.2456	8
4	**86.0964**	**415.2187**	208.1130			397.2082	**199.1077**	L	**816.4574**	408.7323	799.4308	400.2191	798.4468	399.7271	7
5	74.0600	516.2664	258.6368			498.2558	249.6316	T	**703.3733**	352.1903	686.3468	343.6770	685.3628	343.1850	6
6	101.0709	644.3250	322.6661	627.2984	314.1529	626.3144	313.6608	Q	**602.3257**	301.6665	585.2991	293.1532	584.3151	292.6612	5
7	30.0338	701.3464	351.1769	684.3199	342.6636	683.3359	342.1716	G	**474.2671**	237.6372	457.2405	229.1239	456.2565	228.6319	4
8	**86.0964**	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
9	102.0550	943.4731	472.2402	926.4465	463.7269	925.4625	463.2349	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FLTGPLNLNDPDAK**
Found in **O95766**, O95766|CG028_HUMAN UPF0550 protein C7orf28 OS=Homo sapiens GN=C7orf28A PE=1 SV=1

Match to Query 408: 1513.753854 from(757.884203,2+)

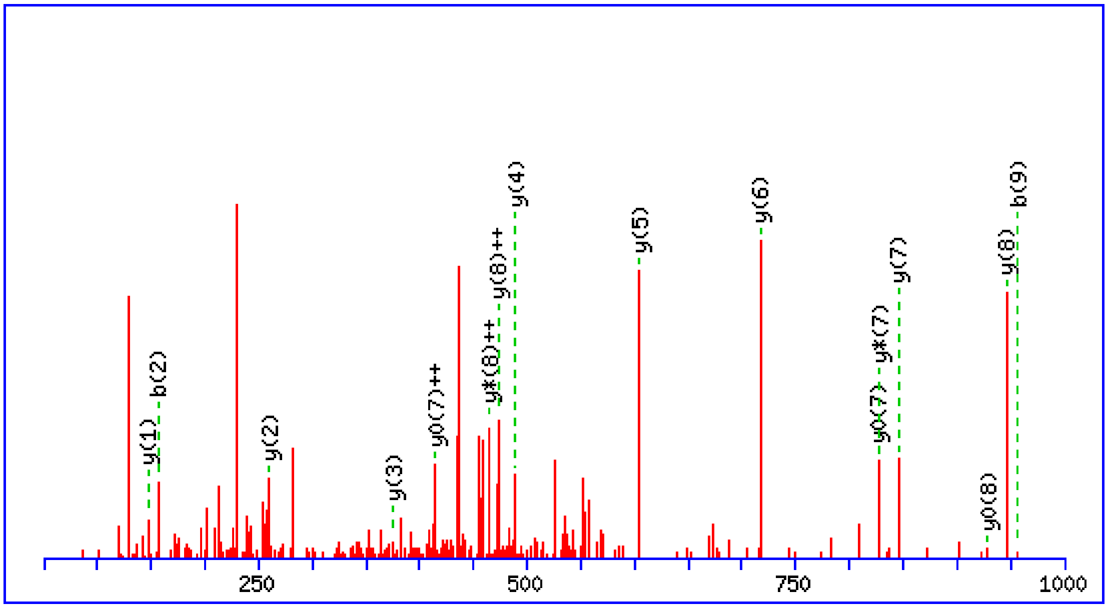


Monoisotopic mass of neutral peptide Mr(calc): 1513.7776
Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 **Expect:** 7.6e-005
Matches (Bold Red): 22/150 fragment ions using 57 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							14
2	**86.0964**	**261.1598**	131.0835					L	1367.7165	684.3619	1350.6900	675.8486	1349.7060	675.3566	13
3	74.0600	362.2074	181.6074			344.1969	172.6021	T	**1254.6325**	627.8199	1237.6059	619.3066	1236.6219	618.8146	12
4	30.0338	419.2289	210.1181			401.2183	**201.1128**	G	**1153.5848**	**577.2960**	1136.5582	568.7828	1135.5742	568.2907	11
5	70.0651	516.2817	258.6445			498.2711	249.6392	P	**1096.5633**	**548.7853**	1079.5368	540.2720	1078.5527	539.7800	10
6	**86.0964**	629.3657	315.1865			611.3552	306.1812	L	**999.5106**	500.2589	982.4840	491.7456	981.5000	491.2536	9
7	87.0553	743.4087	372.2080	726.3821	363.6947	725.3981	363.2027	N	**886.4265**	443.7169	869.3999	435.2036	868.4159	434.7116	8
8	**86.0964**	**856.4927**	428.7500	839.4662	420.2367	838.4822	419.7447	L	**772.3836**	386.6954	755.3570	378.1821	754.3730	377.6901	7
9	87.0553	970.5356	485.7715	953.5091	477.2582	952.5251	476.7662	N	**659.2995**	330.1534	642.2729	321.6401	641.2889	321.1481	6
10	88.0393	1085.5626	543.2849	1068.5360	534.7717	1067.5520	534.2796	D	545.2566	273.1319	528.2300	264.6186	527.2460	264.1266	5
11	70.0651	1182.6154	591.8113	1165.5888	583.2980	1164.6048	582.8060	P	**430.2296**	215.6185	413.2031	207.1052	**412.2191**	206.6132	4
12	88.0393	1297.6423	649.3248	1280.6157	640.8115	1279.6317	640.3195	D	**333.1769**	167.0921	316.1503	158.5788	315.1663	158.0868	3
13	44.0495	1368.6794	684.8433	1351.6529	676.3301	1350.6688	675.8381	A	**218.1499**	109.5786	**201.1234**	101.0653			2
14	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **GVTQIDNDLK**
Found in **P21283**, P21283|VATC1_HUMAN Vacuolar proton pump subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4

Match to Query 314: 1101.550052 from(551.782302,2+)

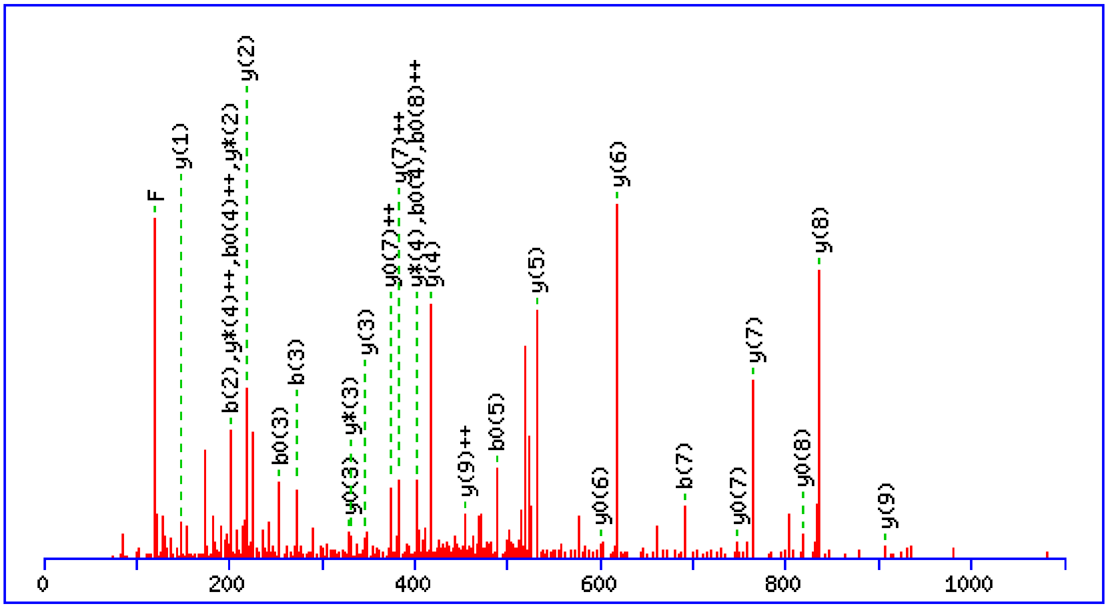


Monoisotopic mass of neutral peptide Mr(calc): 1101.5666
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.0034
Matches (Bold Red): 16/104 fragment ions using 40 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180					G							10
2	72.0808	**157.0972**	79.0522					V	1045.5524	523.2798	1028.5259	514.7666	1027.5419	514.2746	9
3	74.0600	258.1448	129.5761			240.1343	120.5708	T	**946.4840**	**473.7456**	929.4575	**465.2324**	**928.4734**	464.7404	8
4	101.0709	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	Q	**845.4363**	423.2218	**828.4098**	414.7085	**827.4258**	**414.2165**	7
5	86.0964	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	I	**717.3777**	359.1925	700.3512	350.6792	699.3672	350.1872	6
6	88.0393	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	D	**604.2937**	302.6505	587.2671	294.1372	586.2831	293.6452	5
7	87.0553	728.3573	364.6823	711.3308	356.1690	710.3468	355.6770	N	**489.2667**	245.1370	472.2402	236.6237	471.2562	236.1317	4
8	88.0393	843.3843	422.1958	826.3577	413.6825	825.3737	413.1905	D	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	3
9	86.0964	**956.4684**	478.7378	939.4418	470.2245	938.4578	469.7325	L	**260.1969**	130.6021	243.1703	122.0888			2
10	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **EAAFSLAEAK**
Found in **Q9Y5K8**, Q9Y5K8|VATD_HUMAN Vacuolar proton pump subunit D OS=Homo sapiens GN=ATP6V1D PE=1 SV=1

Match to Query 236: 1035.515420 from(518.764986,2+)

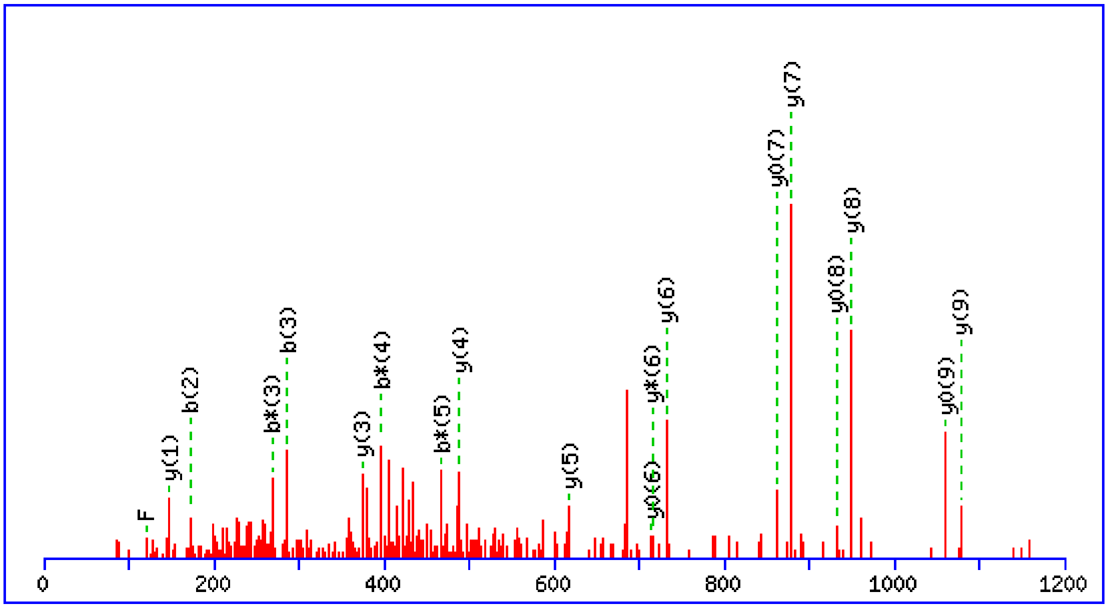


Monoisotopic mass of neutral peptide Mr(calc): 1035.5236
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00046
Matches (Bold Red): 29/96 fragment ions using 57 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286	112.0393	56.5233	E							10
2	44.0495	**201.0870**	101.0471	183.0764	92.0418	A	**907.4884**	**454.2478**	890.4618	445.7345	889.4778	445.2425	9
3	44.0495	**272.1241**	136.5657	**254.1135**	127.5604	A	**836.4512**	418.7293	819.4247	410.2160	**818.4407**	409.7240	8
4	**120.0808**	419.1925	210.0999	**401.1819**	**201.0946**	F	**765.4141**	**383.2107**	748.3876	374.6974	**747.4036**	**374.2054**	7
5	60.0444	506.2245	253.6159	**488.2140**	244.6106	S	**618.3457**	309.6765	601.3192	301.1632	**600.3352**	300.6712	6
6	86.0964	619.3086	310.1579	601.2980	301.1527	L	**531.3137**	266.1605	514.2871	257.6472	513.3031	257.1552	5
7	44.0495	**690.3457**	345.6765	672.3352	336.6712	A	**418.2296**	209.6185	**401.2031**	**201.1052**	400.2191	200.6132	4
8	102.0550	819.3883	410.1978	801.3777	**401.1925**	E	**347.1925**	174.0999	**330.1660**	165.5866	**329.1819**	165.0946	3
9	44.0495	890.4254	445.7164	872.4149	436.7111	A	**218.1499**	109.5786	**201.1234**	101.0653			2
10	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **NGNQAFNEDNLK**
Found in **Q9Y2Q5**, Q9Y2Q5|MAPIP_HUMAN Mitogen-activated protein-binding protein-interacting protein OS=Homo sapiens GN=MAPBPIP PE=2 SV=1

Match to Query 558: 1362.728758 from(682.371655,2+)

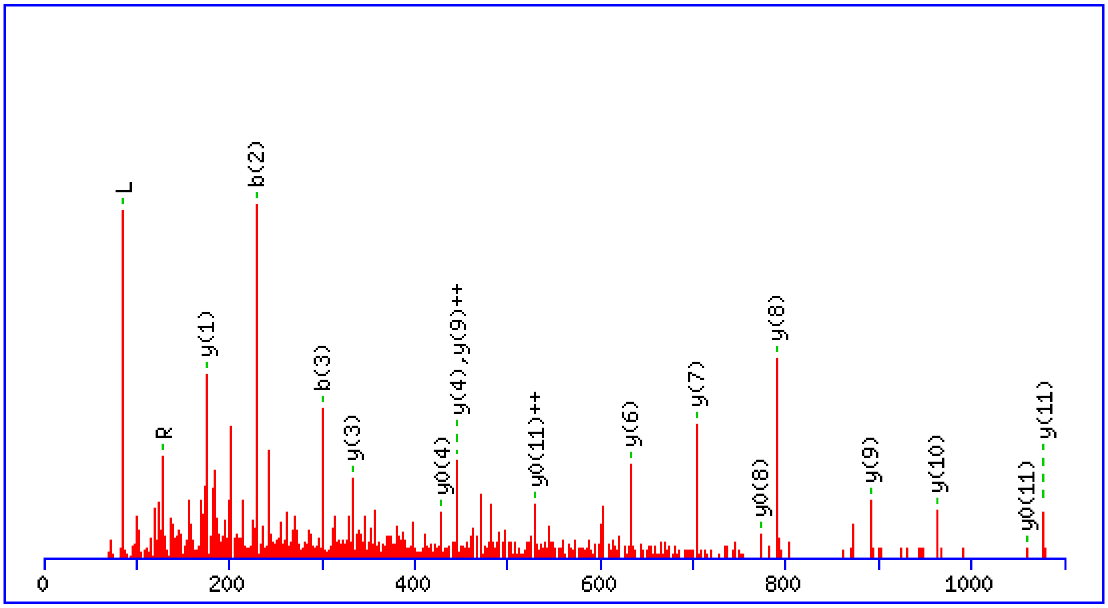


Monoisotopic mass of neutral peptide Mr(calc): 1362.6164
Fixed modifications: Carbamidomethyl (C)
Ions Score: 48 **Expect:** 0.001
Matches (Bold Red): 19/124 fragment ions using 34 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	87.0553	115.0502	58.0287	98.0237	49.5155			N							12
2	30.0338	**172.0717**	86.5395	155.0451	78.0262			G	1249.5808	625.2940	1232.5542	616.7807	1231.5702	616.2887	11
3	87.0553	**286.1146**	143.5609	**269.0880**	135.0477			N	1192.5593	596.7833	1175.5327	588.2700	1174.5487	587.7780	10
4	101.0709	414.1732	207.5902	**397.1466**	199.0769			Q	**1078.5164**	539.7618	1061.4898	531.2485	**1060.5058**	530.7565	9
5	44.0495	485.2103	243.1088	**468.1837**	234.5955			A	**950.4578**	475.7325	933.4312	467.2193	**932.4472**	466.7272	8
6	**120.0808**	632.2787	316.6430	615.2522	308.1297			F	**879.4207**	440.2140	862.3941	431.7007	**861.4101**	431.2087	7
7	87.0553	746.3216	373.6645	729.2951	365.1512			N	**732.3523**	366.6798	**715.3257**	358.1665	**714.3417**	357.6745	6
8	102.0550	875.3642	438.1857	858.3377	429.6725	857.3537	429.1805	E	**618.3093**	309.6583	601.2828	301.1450	600.2988	300.6530	5
9	88.0393	990.3912	495.6992	973.3646	487.1859	972.3806	486.6939	D	**489.2667**	245.1370	472.2402	236.6237	471.2562	236.1317	4
10	87.0553	1104.4341	552.7207	1087.4075	544.2074	1086.4235	543.7154	N	**374.2398**	187.6235	357.2132	179.1103			3
11	86.0964	1217.5182	609.2627	1200.4916	600.7494	1199.5076	600.2574	L	260.1969	130.6021	243.1703	122.0888			2
12	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IDATSASVLASR**
Found in **P13667**, P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2

Match to Query 196: 1189.476794 from(595.745673,2+)

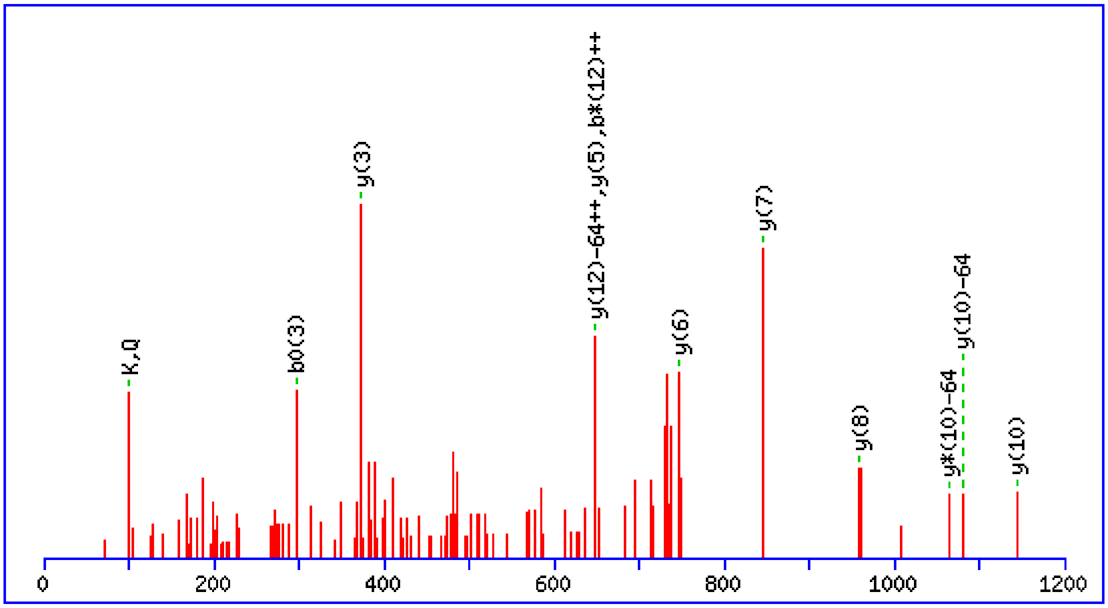


Monoisotopic mass of neutral peptide Mr(calc): 1189.6302
Fixed modifications: Carbamidomethyl (C)
Ions Score: 81 **Expect:** 6e-007
Matches (Bold Red): 19/118 fragment ions using 24 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**86.0964**	114.0913	57.5493			**I**							**12**
2	88.0393	**229.1183**	115.0628	211.1077	106.0575	**D**	**1077.5535**	539.2804	1060.5269	530.7671	**1059.5429**	**530.2751**	**11**
3	44.0495	**300.1554**	150.5813	282.1448	141.5761	**A**	**962.5265**	481.7669	945.5000	473.2536	944.5160	472.7616	**10**
4	74.0600	401.2031	201.1052	383.1925	192.0999	**T**	**891.4894**	**446.2483**	874.4629	437.7351	873.4789	437.2431	**9**
5	60.0444	488.2351	244.6212	470.2245	235.6159	**S**	**790.4417**	395.7245	773.4152	387.2112	**772.4312**	386.7192	**8**
6	44.0495	559.2722	280.1397	541.2617	271.1345	**A**	**703.4097**	352.2085	686.3832	343.6952	685.3991	343.2032	**7**
7	60.0444	646.3042	323.6558	628.2937	314.6505	**S**	**632.3726**	316.6899	615.3461	308.1767	614.3620	307.6847	**6**
8	72.0808	745.3727	373.1900	727.3621	364.1847	**V**	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	**5**
9	**86.0964**	858.4567	429.7320	840.4462	420.7267	**L**	**446.2722**	223.6397	429.2456	215.1264	**428.2616**	214.6344	**4**
10	44.0495	929.4938	465.2506	911.4833	456.2453	**A**	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	**3**
11	60.0444	1016.5259	508.7666	998.5153	499.7613	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
12	**129.1135**					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VSQGQLVVMQPEK**
Found in **P13667**, P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2

Match to Query 338: 1457.869582 from(729.942067,2+)

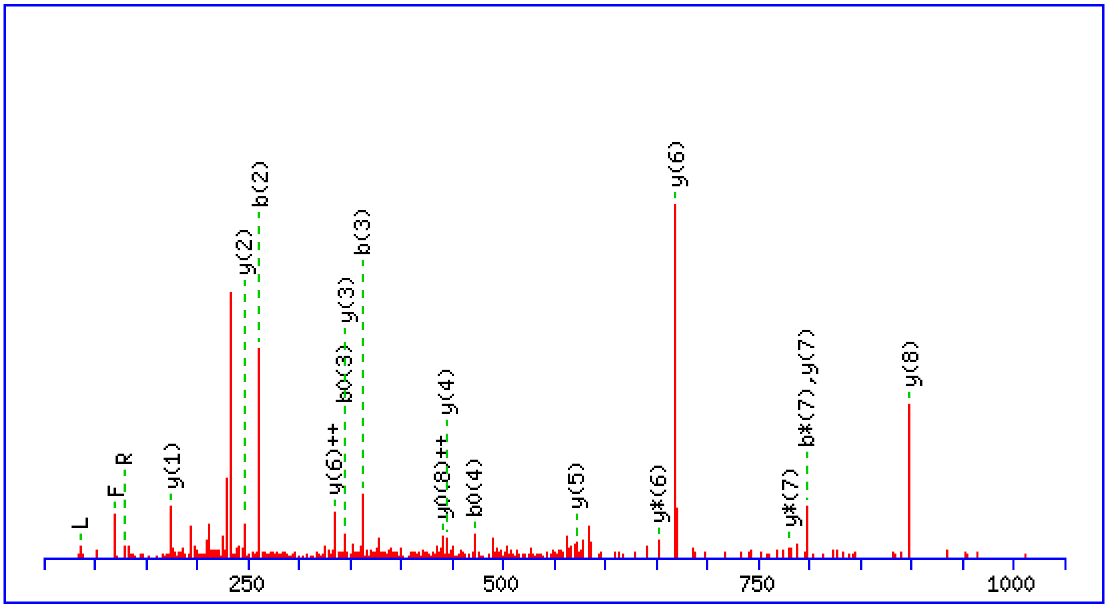


Monoisotopic mass of neutral peptide Mr(calc): 1457.7548
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 **Expect:** 0.0081
Matches (Bold Red): 15/222 fragment ions using 14 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							13
2	60.0444	187.1077	94.0575			169.0972	85.0522	S	1359.6937	680.3505	1342.6671	671.8372	1341.6831	671.3452	12
3	**101.0709**	315.1663	158.0868	298.1397	149.5735	**297.1557**	149.0815	Q	1272.6617	636.8345	1255.6351	628.3212	1254.6511	627.8292	11
4	30.0338	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	G	**1144.6031**	572.8052	1127.5765	564.2919	1126.5925	563.7999	10
5	**101.0709**	500.2463	250.6268	483.2198	242.1135	482.2358	241.6215	Q	1087.5816	544.2944	1070.5551	535.7812	1069.5710	535.2892	9
6	86.0964	613.3304	307.1688	596.3039	298.6556	595.3198	298.1636	L	**959.5230**	480.2652	942.4965	471.7519	941.5125	471.2599	8
7	72.0808	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	V	**846.4390**	423.7231	829.4124	415.2098	828.4284	414.7178	7
8	72.0808	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	V	**747.3706**	374.1889	730.3440	365.6756	729.3600	365.1836	6
9	120.0478	958.5026	479.7550	941.4761	471.2417	940.4921	470.7497	M	**648.3021**	324.6547	631.2756	316.1414	630.2916	315.6494	5
10	**101.0709**	1086.5612	543.7842	1069.5347	535.2710	1068.5506	534.7790	Q	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	4
11	70.0651	1183.6140	592.3106	1166.5874	583.7974	1165.6034	583.3053	P	**373.2082**	187.1077	356.1816	178.5944	355.1976	178.1024	3
12	102.0550	1312.6566	656.8319	1295.6300	**648.3186**	1294.6460	647.8266	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13	**101.1073**							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **FLTQPQVVAR**
Found in **O43760**, O43760|SNG2_HUMAN Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1

Match to Query 117: 1157.545278 from(579.779915,2+)

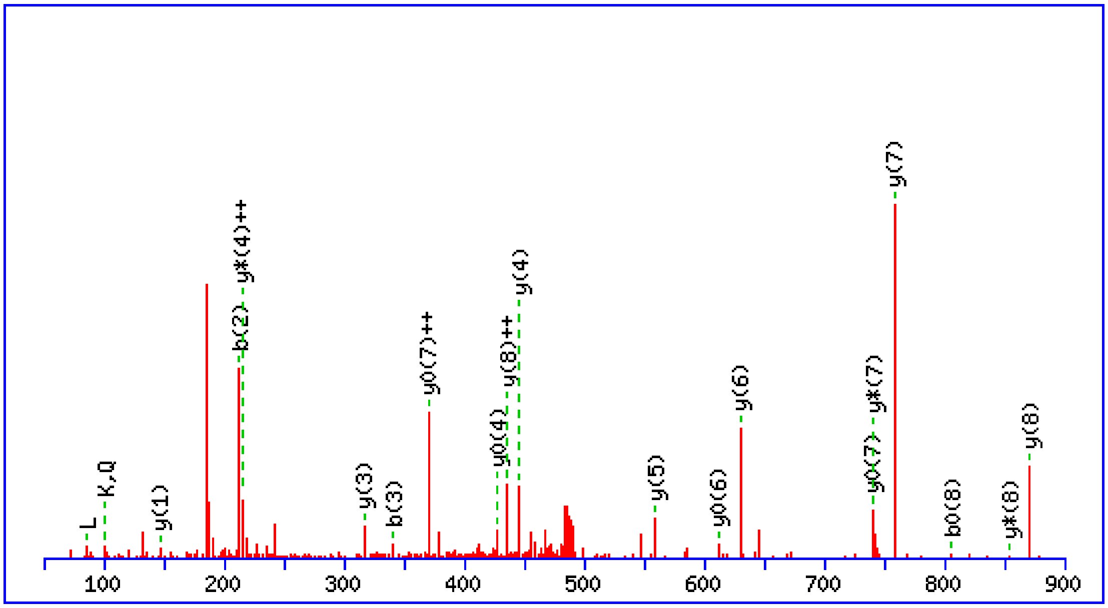


Monoisotopic mass of neutral peptide Mr(calc): 1157.6557
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.0032
Matches (Bold Red): 20/94 fragment ions using 46 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					**F**							**10**
2	**86.0964**	**261.1598**	131.0835					**L**	1011.5946	506.3009	994.5680	497.7876	993.5840	497.2956	**9**
3	74.0600	**362.2074**	181.6074			**344.1969**	172.6021	**T**	**898.5105**	449.7589	881.4839	441.2456	880.4999	**440.7536**	**8**
4	101.0709	490.2660	245.6366	473.2395	237.1234	**472.2554**	236.6314	**Q**	**797.4628**	399.2350	**780.4363**	390.7218			**7**
5	70.0651	587.3188	294.1630	570.2922	285.6498	569.3082	285.1577	**P**	**669.4042**	**335.2058**	**652.3777**	326.6925			**6**
6	101.0709	715.3774	358.1923	698.3508	349.6790	697.3668	349.1870	**Q**	**572.3515**	286.6794	555.3249	278.1661			**5**
7	72.0808	814.4458	407.7265	**797.4192**	399.2132	796.4352	398.7212	**V**	**444.2929**	222.6501	427.2663	214.1368			**4**
8	72.0808	913.5142	457.2607	896.4876	448.7475	895.5036	448.2554	**V**	**345.2245**	173.1159	328.1979	164.6026			**3**
9	44.0495	984.5513	492.7793	967.5247	484.2660	966.5407	483.7740	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
10	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VLQALEGLK**
Found in **P39019**, P39019|RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2

Match to Query 230: 969.524674 from(485.769613,2+)

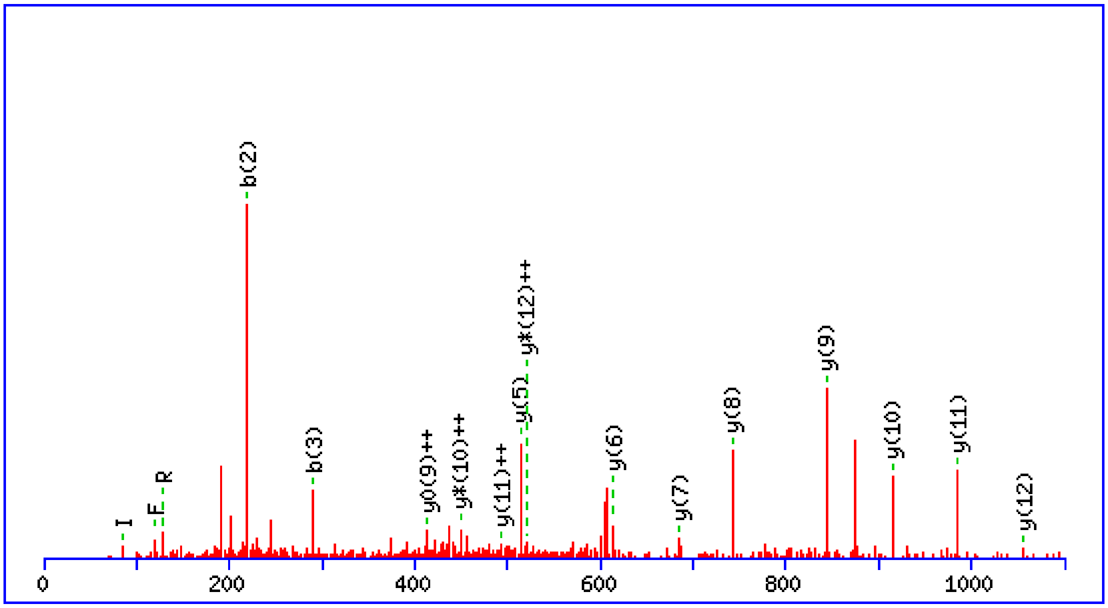


Monoisotopic mass of neutral peptide Mr(calc): 969.5859
Fixed modifications: Carbamidomethyl (C)
Ions Score: 49 **Expect:** 0.00093
Matches (Bold Red): 23/85 fragment ions using 37 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							9
2	**86.0964**	**213.1598**	107.0835					L	**871.5247**	**436.2660**	**854.4982**	427.7527	853.5142	427.2607	8
3	**101.0709**	**341.2183**	171.1128	324.1918	162.5995			Q	**758.4407**	379.7240	**741.4141**	371.2107	**740.4301**	**370.7187**	7
4	44.0495	412.2554	206.6314	395.2289	198.1181			A	**630.3821**	315.6947	613.3556	307.1814	**612.3715**	306.6894	6
5	**86.0964**	525.3395	263.1734	508.3130	254.6601			L	**559.3450**	280.1761	542.3184	271.6629	541.3344	271.1709	5
6	102.0550	654.3821	327.6947	637.3556	319.1814	636.3715	318.6894	E	**446.2609**	223.6341	429.2344	**215.1208**	**428.2504**	214.6288	4
7	30.0338	711.4036	356.2054	694.3770	347.6921	693.3930	347.2001	G	**317.2183**	159.1128	300.1918	150.5995			3
8	**86.0964**	824.4876	412.7475	807.4611	404.2342	**806.4771**	403.7422	L	260.1969	130.6021	243.1703	122.0888			2
9	**101.1073**							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **FAAATGATPIAGR**
Found in **P08865**, P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4

Match to Query 380: 1202.703798 from(602.359175,2+)

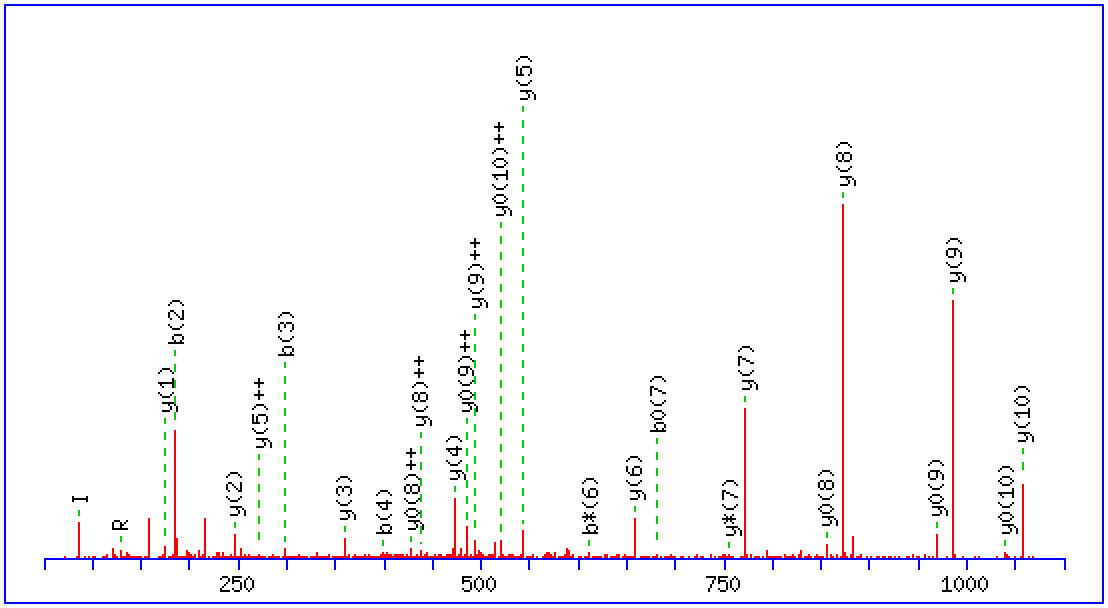


Monoisotopic mass of neutral peptide Mr(calc): 1202.6408
Fixed modifications: Carbamidomethyl (C)
Ions Score: 46 **Expect:** 0.0022
Matches (Bold Red): 17/115 fragment ions using 38 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415			F							13
2	44.0495	**219.1128**	110.0600			A	**1056.5796**	528.7935	1039.5531	**520.2802**	1038.5691	519.7882	12
3	44.0495	**290.1499**	145.5786			A	**985.5425**	**493.2749**	968.5160	484.7616	967.5320	484.2696	11
4	44.0495	361.1870	181.0972			A	**914.5054**	457.7563	897.4789	**449.2431**	896.4948	448.7511	10
5	74.0600	462.2347	231.6210	444.2241	222.6157	T	**843.4683**	422.2378	826.4417	413.7245	825.4577	**413.2325**	9
6	30.0338	519.2562	260.1317	501.2456	251.1264	G	**742.4206**	371.7139	725.3941	363.2007	724.4100	362.7087	8
7	44.0495	590.2933	295.6503	572.2827	286.6450	A	**685.3992**	343.2032	668.3726	334.6899	667.3886	334.1979	7
8	74.0600	691.3410	346.1741	673.3304	337.1688	T	**614.3620**	307.6847	597.3355	299.1714	596.3515	298.6794	6
9	70.0651	788.3937	394.7005	770.3832	385.6952	P	**513.3144**	257.1608	496.2878	248.6475			5
10	**86.0964**	901.4778	451.2425	883.4672	442.2373	I	416.2616	208.6344	399.2350	200.1212			4
11	44.0495	972.5149	486.7611	954.5043	477.7558	A	303.1775	152.0924	286.1510	143.5791			3
12	30.0338	1029.5364	515.2718	1011.5258	506.2665	G	232.1404	116.5738	215.1139	108.0606			2
13	**129.1135**					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IALTDNALIAR**
Found in **P18124**, P18124|RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1

Match to Query 472: 1169.643584 from(585.829068,2+)

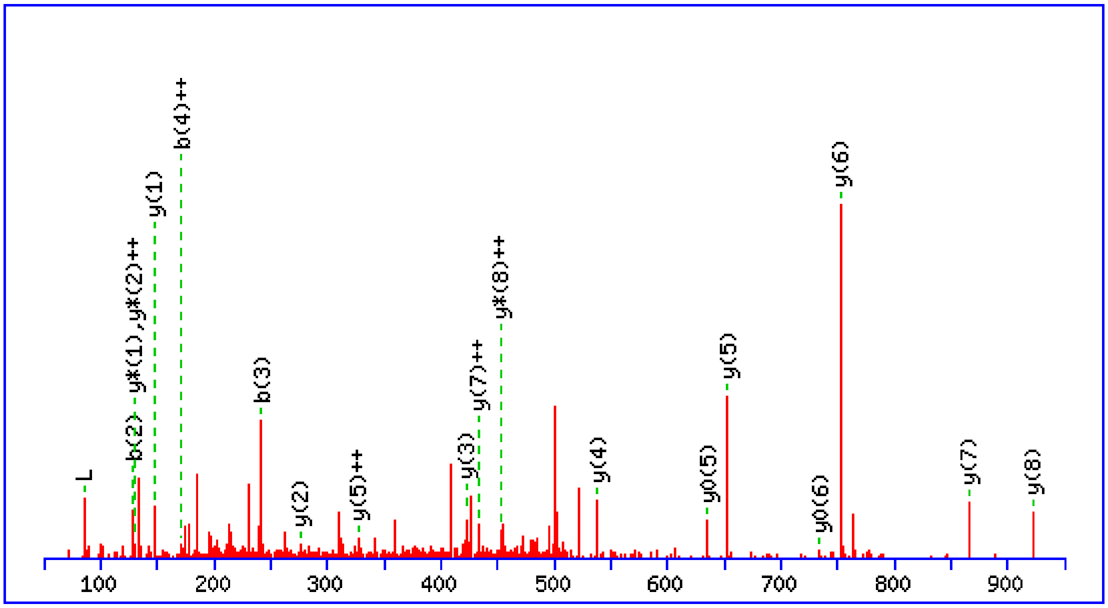


Monoisotopic mass of neutral peptide Mr(calc): 1169.6768
Fixed modifications: Carbamidomethyl (C)
Ions Score: 76 **Expect:** 1.8e-006
Matches (Bold Red): 30/103 fragment ions using 51 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							11
2	44.0495	**185.1285**	93.0679					A	**1057.6000**	529.3037	1040.5735	520.7904	**1039.5895**	**520.2984**	10
3	**86.0964**	**298.2125**	149.6099					L	**986.5629**	**493.7851**	969.5364	485.2718	**968.5524**	**484.7798**	9
4	74.0600	**399.2602**	200.1337			381.2496	191.1285	T	**873.4789**	**437.2431**	856.4523	428.7298	**855.4683**	**428.2378**	8
5	88.0393	514.2871	257.6472			496.2766	248.6419	D	**772.4312**	386.7192	**755.4046**	378.2060	754.4206	377.7139	7
6	87.0553	628.3301	314.6687	**611.3035**	306.1554	610.3195	305.6634	N	**657.4042**	329.2058	640.3777	320.6925			6
7	44.0495	699.3672	350.1872	682.3406	341.6740	**681.3566**	341.1819	A	**543.3613**	**272.1843**	526.3348	263.6710			5
8	**86.0964**	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	L	**472.3242**	236.6657	455.2976	228.1525			4
9	**86.0964**	925.5353	463.2713	908.5088	454.7580	907.5247	454.2660	I	**359.2401**	180.1237	342.2136	171.6104			3
10	44.0495	996.5724	498.7898	979.5459	490.2766	978.5619	489.7846	A	**246.1561**	123.5817	229.1295	115.0684			2
11	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **AGLVDDFEK**
Found in **O75947**, O75947|ATP5H_HUMAN ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3

Match to Query 139: 992.441310 from(497.227931,2+)

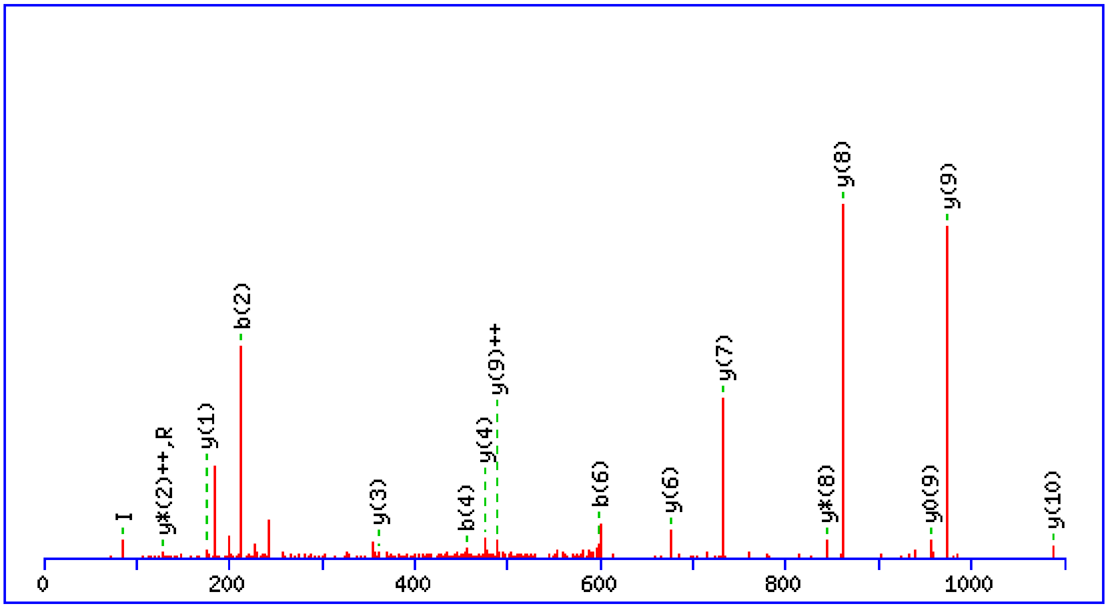


Monoisotopic mass of neutral peptide Mr(calc): 992.4815
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 **Expect:** 0.0073
Matches (Bold Red): 19/79 fragment ions using 59 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							9
2	30.0338	**129.0659**	65.0366			G	**922.4516**	461.7295	905.4251	**453.2162**	904.4411	452.7242	8
3	**86.0964**	**242.1499**	121.5786			L	**865.4302**	**433.2187**	848.4036	424.7055	847.4196	424.2134	7
4	72.0808	341.2183	**171.1128**			V	**752.3461**	376.6767	735.3196	368.1634	**734.3355**	367.6714	6
5	88.0393	456.2453	228.6263	438.2347	219.6210	D	**653.2777**	**327.1425**	636.2511	318.6292	**635.2671**	318.1372	5
6	88.0393	571.2722	286.1397	553.2617	277.1345	D	**538.2508**	269.6290	521.2242	261.1157	520.2402	260.6237	4
7	120.0808	718.3406	359.6740	700.3301	350.6687	F	**423.2238**	212.1155	406.1973	203.6023	405.2132	203.1103	3
8	102.0550	847.3832	424.1953	829.3727	415.1900	E	**276.1554**	138.5813	259.1288	**130.0681**	258.1448	129.5761	2
9	101.1073					K	**147.1128**	74.0600	**130.0863**	65.5468			1

MS/MS Fragmentation of **VLIEGSINSVR**
Found in **P59998**, P59998|ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3

Match to Query 401: 1185.624560 from(593.819556,2+)

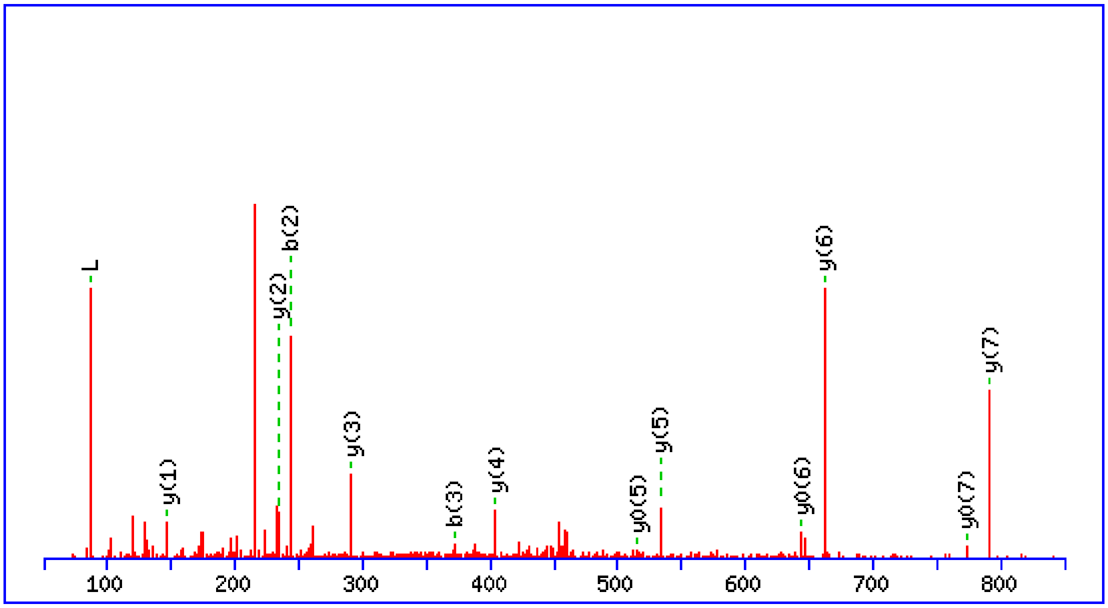


Monoisotopic mass of neutral peptide Mr(calc): 1185.6717
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00029
Matches (Bold Red): 19/107 fragment ions using 23 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							11
2	**86.0964**	**213.1598**	107.0835					L	**1087.6106**	544.3089	1070.5840	535.7957	1069.6000	535.3037	10
3	**86.0964**	326.2438	163.6255					I	**974.5265**	**487.7669**	957.5000	479.2536	**956.5160**	478.7616	9
4	102.0550	**455.2864**	228.1468			437.2758	219.1416	E	**861.4425**	431.2249	**844.4159**	422.7116	843.4319	422.2196	8
5	30.0338	512.3079	256.6576			494.2973	247.6523	G	**732.3999**	366.7036	715.3733	358.1903	714.3893	357.6983	7
6	60.0444	**599.3399**	300.1736			581.3293	291.1683	S	**675.3784**	338.1928	658.3519	329.6796	657.3678	329.1876	6
7	**86.0964**	712.4240	356.7156			694.4134	347.7103	I	588.3464	294.6768	571.3198	286.1636	570.3358	285.6715	5
8	87.0553	826.4669	413.7371	809.4403	405.2238	808.4563	404.7318	N	**475.2623**	238.1348	458.2358	229.6215	457.2518	229.1295	4
9	60.0444	913.4989	457.2531	896.4724	448.7398	895.4884	448.2478	S	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	72.0808	1012.5673	506.7873	995.5408	498.2740	994.5568	497.7820	V	274.1874	137.5973	257.1608	**129.0840**			2
11	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IEEELGSK**
Found in **P06733**, P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2

Match to Query 35: 903.304444 from(452.659498,2+)

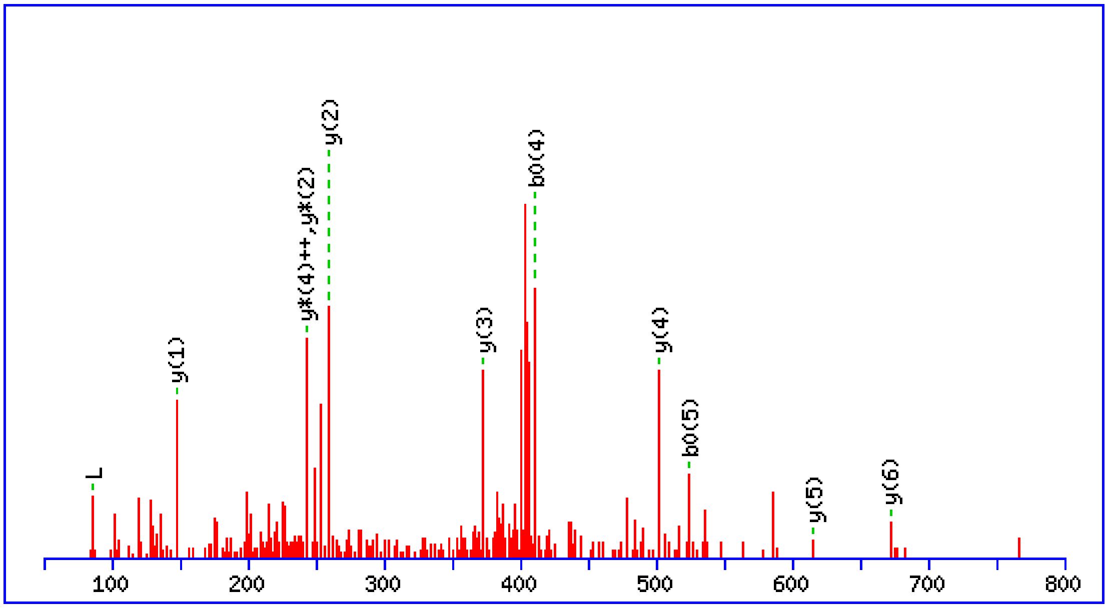


Monoisotopic mass of neutral peptide Mr(calc): 903.4549
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 **Expect:** 0.005
Matches (Bold Red): 14/74 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			I							8
2	102.0550	**243.1339**	122.0706	225.1234	113.0653	E	**791.3781**	396.1927	774.3516	387.6794	**773.3676**	387.1874	7
3	102.0550	**372.1765**	186.5919	354.1660	177.5866	E	**662.3355**	331.6714	645.3090	323.1581	**644.3250**	322.6661	6
4	102.0550	501.2191	251.1132	483.2086	242.1079	E	**533.2930**	267.1501	516.2664	258.6368	**515.2824**	258.1448	5
5	**86.0964**	614.3032	307.6552	596.2926	298.6499	L	**404.2504**	202.6288	387.2238	194.1155	386.2398	193.6235	4
6	30.0338	671.3246	336.1660	653.3141	327.1607	G	**291.1663**	146.0868	274.1397	137.5735	273.1557	137.0815	3
7	60.0444	758.3567	379.6820	740.3461	370.6767	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
8	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **EGLELLK**
Found in **P06733**, P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2

Match to Query 58: 800.442244 from(401.228398,2+)

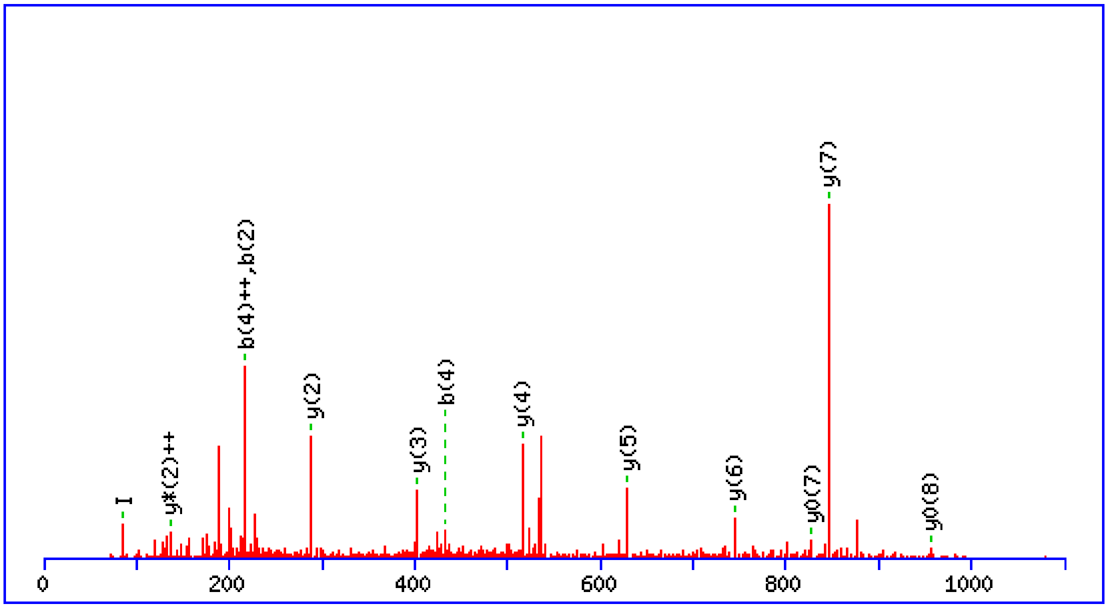


Monoisotopic mass of neutral peptide Mr(calc): 800.4643
Fixed modifications: Carbamidomethyl (C)
Ions Score: 35 **Expect:** 0.035
Matches (Bold Red): 13/61 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286	112.0393	56.5233	E							7
2	30.0338	187.0713	94.0393	169.0608	85.0340	G	**672.4291**	336.7182	655.4025	328.2049	654.4185	327.7129	6
3	**86.0964**	300.1554	150.5813	282.1448	141.5761	L	**615.4076**	308.2074	598.3810	299.6942	597.3970	299.2022	5
4	102.0550	429.1980	215.1026	**411.1874**	206.0974	E	**502.3235**	251.6654	485.2970	**243.1521**	484.3130	242.6601	4
5	**86.0964**	542.2821	271.6447	**524.2715**	262.6394	L	**373.2809**	187.1441	356.2544	178.6308			3
6	**86.0964**	655.3661	328.1867	637.3556	319.1814	L	**260.1969**	130.6021	**243.1703**	122.0888			2
7	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **SETDLLDIR**
Found in **P50995**, P50995|ANX11_HUMAN Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1

Match to Query 414: 1060.505664 from(531.260108,2+)

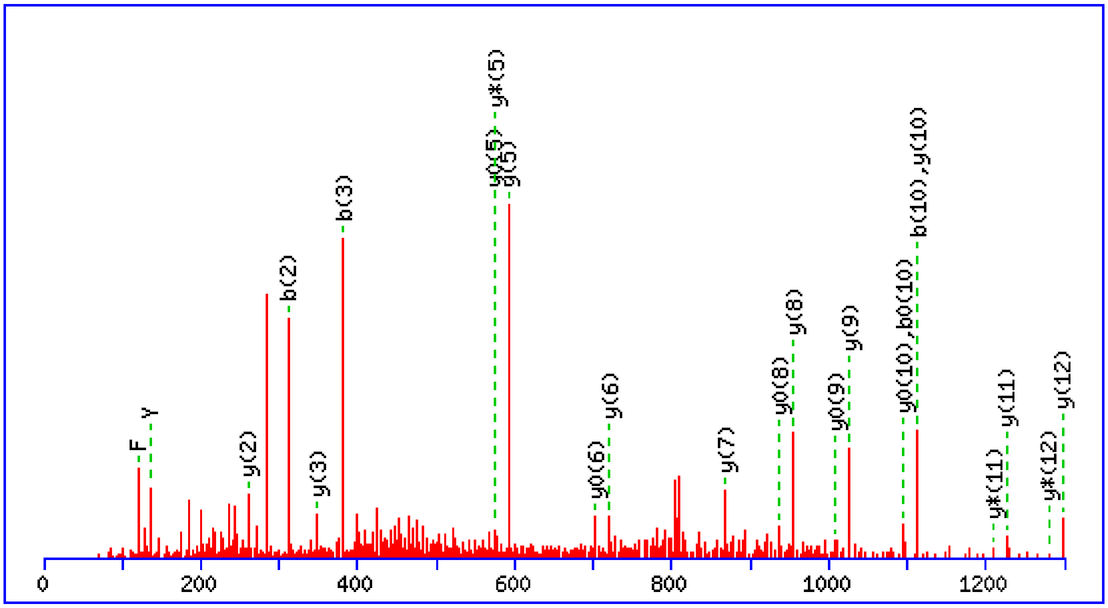


Monoisotopic mass of neutral peptide Mr(calc): 1060.5400
Fixed modifications: Carbamidomethyl (C)
Ions Score: 41 **Expect:** 0.0072
Matches (Bold Red): 15/85 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233	70.0287	35.5180	S							9
2	102.0550	**217.0819**	109.0446	199.0713	100.0393	E	974.5153	487.7613	957.4888	479.2480	**956.5047**	478.7560	8
3	74.0600	318.1296	159.5684	300.1190	150.5631	T	**845.4727**	423.2400	828.4462	414.7267	**827.4621**	414.2347	7
4	88.0393	**433.1565**	**217.0819**	415.1460	208.0766	D	**744.4250**	372.7162	727.3985	364.2029	726.4145	363.7109	6
5	**86.0964**	546.2406	273.6239	528.2300	264.6186	L	**629.3981**	315.2027	612.3715	306.6894	611.3875	306.1974	5
6	**86.0964**	659.3246	330.1660	641.3141	321.1607	L	**516.3140**	258.6606	499.2875	250.1474	498.3035	249.6554	4
7	88.0393	774.3516	387.6794	756.3410	378.6742	D	**403.2300**	202.1186	386.2034	193.6053	385.2194	193.1133	3
8	**86.0964**	887.4357	444.2215	869.4251	435.2162	I	**288.2030**	144.6051	271.1765	**136.0919**			2
9	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FYALSASFEPFSNK**
Found in **P27797**, P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1

Match to Query 710: 1606.751640 from(804.383096,2+)

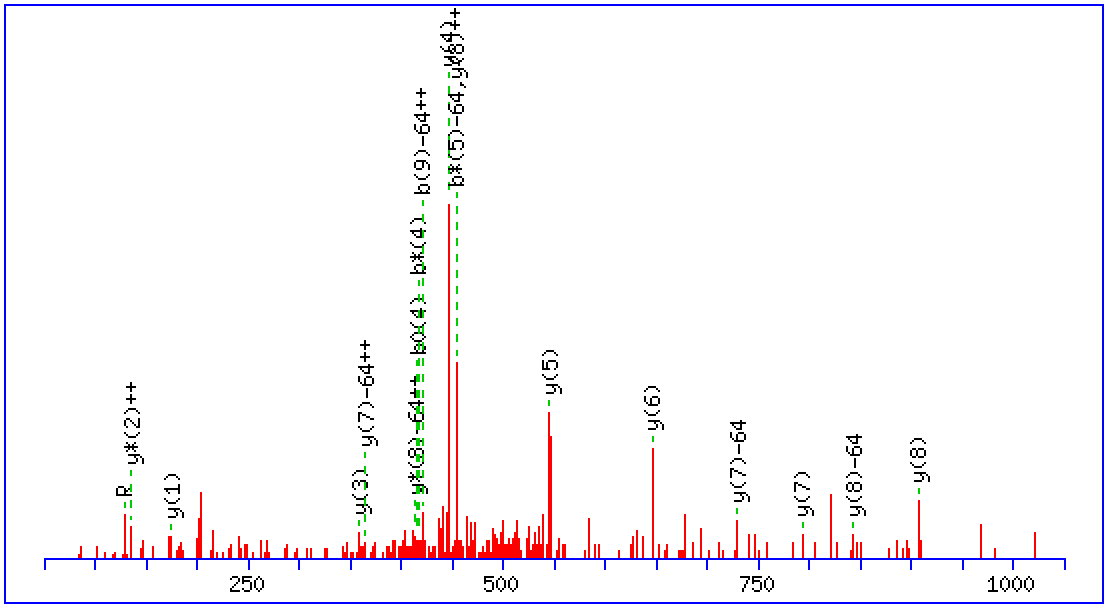


Monoisotopic mass of neutral peptide Mr(calc): 1606.7667
Fixed modifications: Carbamidomethyl (C)
Ions Score: 66 **Expect:** 1.6e-005
Matches (Bold Red): 26/134 fragment ions using 49 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							14
2	**136.0757**	**311.1390**	156.0731					Y	1460.7056	730.8564	1443.6791	722.3432	1442.6951	721.8512	13
3	44.0495	**382.1761**	191.5917					A	**1297.6423**	649.3248	**1280.6157**	640.8115	1279.6317	640.3195	12
4	86.0964	495.2602	248.1337					L	**1226.6052**	613.8062	**1209.5786**	605.2930	1208.5946	604.8009	11
5	60.0444	582.2922	291.6498			564.2817	282.6445	S	**1113.5211**	557.2642	1096.4946	548.7509	**1095.5105**	548.2589	10
6	44.0495	653.3293	327.1683			635.3188	318.1630	A	**1026.4891**	513.7482	1009.4625	505.2349	**1008.4785**	504.7429	9
7	60.0444	740.3614	370.6843			722.3508	361.6790	S	**955.4520**	478.2296	938.4254	469.7163	**937.4414**	469.2243	8
8	**120.0808**	887.4298	444.2185			869.4192	435.2132	F	**868.4199**	434.7136	851.3934	426.2003	850.4094	425.7083	7
9	102.0550	1016.4724	508.7398			998.4618	499.7345	E	**721.3515**	361.1794	704.3250	352.6661	**703.3410**	352.1741	6
10	70.0651	**1113.5251**	557.2662			**1095.5146**	548.2609	P	**592.3089**	296.6581	**575.2824**	288.1448	**574.2984**	287.6528	5
11	**120.0808**	1260.5936	630.8004			1242.5830	621.7951	F	495.2562	248.1317	478.2296	239.6185	477.2456	239.1264	4
12	60.0444	1347.6256	674.3164			1329.6150	665.3111	S	**348.1878**	174.5975	331.1612	166.0842	330.1772	165.5922	3
13	87.0553	1461.6685	731.3379	1444.6420	722.8246	1443.6579	722.3326	N	**261.1557**	131.0815	244.1292	122.5682			2
14	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ATNMTVSAIR**
Found in **P23786**, P23786|CPT2_HUMAN Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2

Match to Query 299: 1078.558952 from(540.286752,2+)

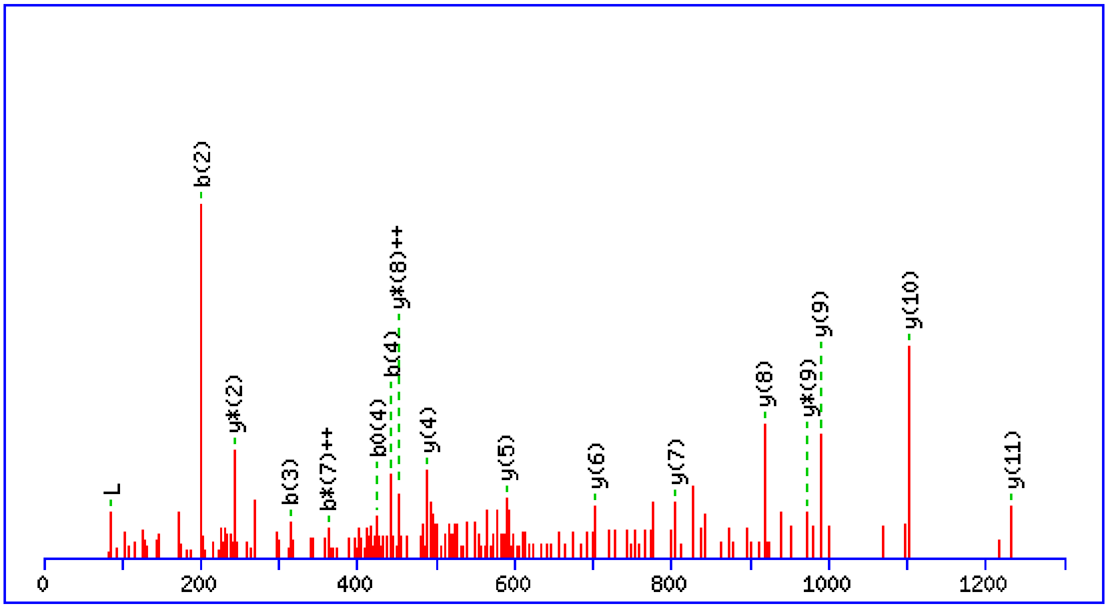


Monoisotopic mass of neutral peptide Mr(calc): 1078.5441
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M4 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.0096
Matches (Bold Red): 18/161 fragment ions using 45 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							10
2	74.0600	173.0921	87.0497			155.0815	78.0444	T	944.5160	472.7616	927.4894	464.2484	926.5054	463.7563	9
3	87.0553	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	N	**843.4683**	422.2378	826.4417	**413.7245**	825.4577	413.2325	8
4	56.0495	370.1721	185.5897	353.1456	177.0764	352.1615	176.5844	M	**729.4254**	**365.2163**	712.3988	356.7030	711.4148	356.2110	7
5	74.0600	471.2198	236.1135	**454.1932**	227.6003	453.2092	227.1083	T	**646.3883**	323.6978	629.3617	315.1845	628.3777	314.6925	6
6	72.0808	570.2882	285.6477	553.2617	277.1345	552.2776	276.6425	V	**545.3406**	273.1739	528.3140	264.6606	527.3300	264.1686	5
7	60.0444	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	S	**446.2722**	223.6397	429.2456	215.1264	428.2616	214.6344	4
8	44.0495	728.3573	364.6823	711.3308	356.1690	710.3468	355.6770	A	**359.2401**	180.1237	342.2136	171.6104			3
9	86.0964	841.4414	**421.2243**	824.4149	412.7111	823.4308	412.2191	I	288.2030	144.6051	271.1765	**136.0919**			2
10	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **EALENANTNTEVLK**
Found in **Q9H444**, Q9H444|CHM4B_HUMAN Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1

Match to Query 687: 1544.690262 from(773.352407,2+)

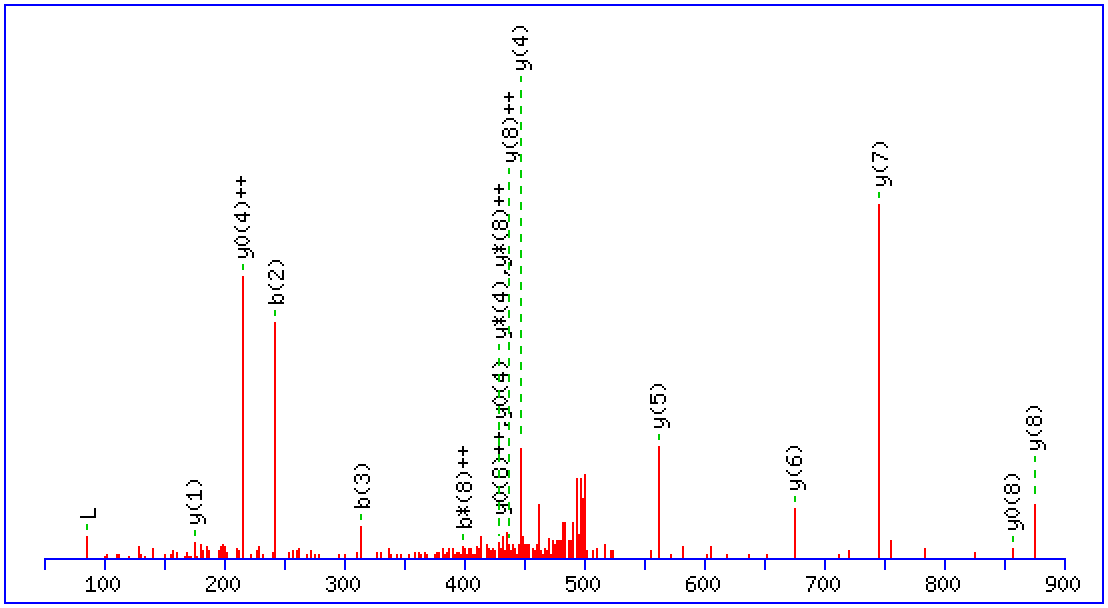


Monoisotopic mass of neutral peptide Mr(calc): 1544.7682
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 **Expect:** 0.00014
Matches (Bold Red): 18/156 fragment ions using 31 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286			112.0393	56.5233	E							14
2	44.0495	**201.0870**	101.0471			183.0764	92.0418	A	1416.7329	708.8701	1399.7063	700.3568	1398.7223	699.8648	13
3	**86.0964**	**314.1710**	157.5892			296.1605	148.5839	L	1345.6958	673.3515	1328.6692	664.8383	1327.6852	664.3462	12
4	102.0550	**443.2136**	222.1105			**425.2031**	213.1052	E	**1232.6117**	616.8095	1215.5852	608.2962	1214.6012	607.8042	11
5	87.0553	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	N	**1103.5691**	552.2882	1086.5426	543.7749	1085.5586	543.2829	10
6	44.0495	628.2937	314.6505	611.2671	306.1372	610.2831	305.6452	A	**989.5262**	495.2667	**972.4997**	486.7535	971.5156	486.2615	9
7	87.0553	742.3366	371.6719	725.3101	**363.1587**	724.3260	362.6667	N	**918.4891**	459.7482	901.4625	**451.2349**	900.4785	450.7429	8
8	74.0600	843.3843	422.1958	826.3577	413.6825	825.3737	413.1905	T	**804.4462**	402.7267	787.4196	394.2134	786.4356	393.7214	7
9	87.0553	957.4272	479.2172	940.4007	470.7040	939.4166	470.2120	N	**703.3985**	352.2029	686.3719	343.6896	685.3879	343.1976	6
10	74.0600	1058.4749	529.7411	1041.4483	521.2278	1040.4643	520.7358	T	**589.3556**	295.1814	572.3290	286.6681	571.3450	286.1761	5
11	102.0550	1187.5175	594.2624	1170.4909	585.7491	1169.5069	585.2571	E	**488.3079**	244.6576	471.2813	236.1443	470.2973	235.6523	4
12	72.0808	1286.5859	643.7966	1269.5594	635.2833	1268.5753	634.7913	V	359.2653	180.1363	342.2387	171.6230			3
13	**86.0964**	1399.6700	700.3386	1382.6434	691.8253	1381.6594	691.3333	L	260.1969	130.6021	**243.1703**	122.0888			2
14	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **LEALDANSR**
Found in **P09496**, P09496|CLCA_HUMAN Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1

Match to Query 275: 987.431450 from(494.723001,2+)

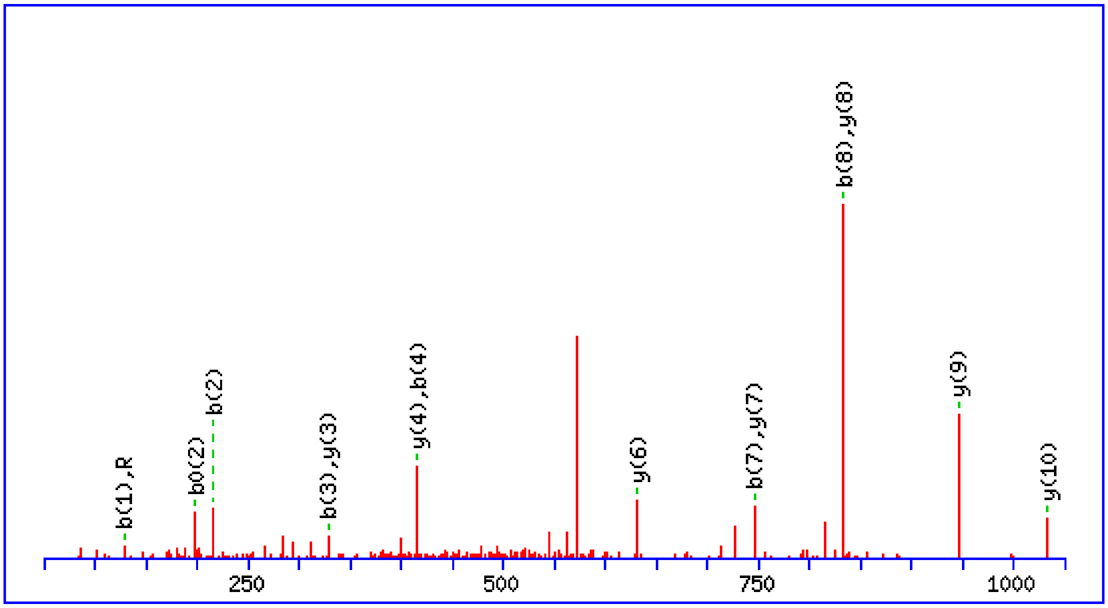


Monoisotopic mass of neutral peptide Mr(calc): 987.4985
Fixed modifications: Carbamidomethyl (C)
Ions Score: 49 **Expect:** 0.0013
Matches (Bold Red): 18/89 fragment ions using 47 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**9**
2	102.0550	**243.1339**	122.0706			225.1234	113.0653	**E**	**875.4217**	**438.2145**	858.3952	**429.7012**	**857.4112**	**429.2092**	**8**
3	44.0495	**314.1710**	157.5892			296.1605	148.5839	**A**	**746.3791**	373.6932	729.3526	365.1799	728.3686	364.6879	**7**
4	**86.0964**	427.2551	214.1312			409.2445	205.1259	**L**	**675.3420**	338.1747	658.3155	329.6614	657.3315	329.1694	**6**
5	88.0393	542.2821	271.6447			524.2715	262.6394	**D**	**562.2580**	281.6326	545.2314	273.1193	544.2474	272.6273	**5**
6	44.0495	613.3192	307.1632			595.3086	298.1579	**A**	**447.2310**	224.1191	**430.2045**	215.6059	**429.2205**	**215.1139**	**4**
7	87.0553	727.3621	364.1847	710.3355	355.6714	709.3515	355.1794	**N**	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	**3**
8	60.0444	814.3941	407.7007	797.3676	**399.1874**	796.3836	398.6954	**S**	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	**2**
9	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **QSISNSESGPR**
Found in **P04839**, P04839|CY24B_HUMAN Cytochrome b-245 heavy chain OS=Homo sapiens GN=CYBB PE=1 SV=2

Match to Query 552: 1160.520506 from(581.267529,2+)

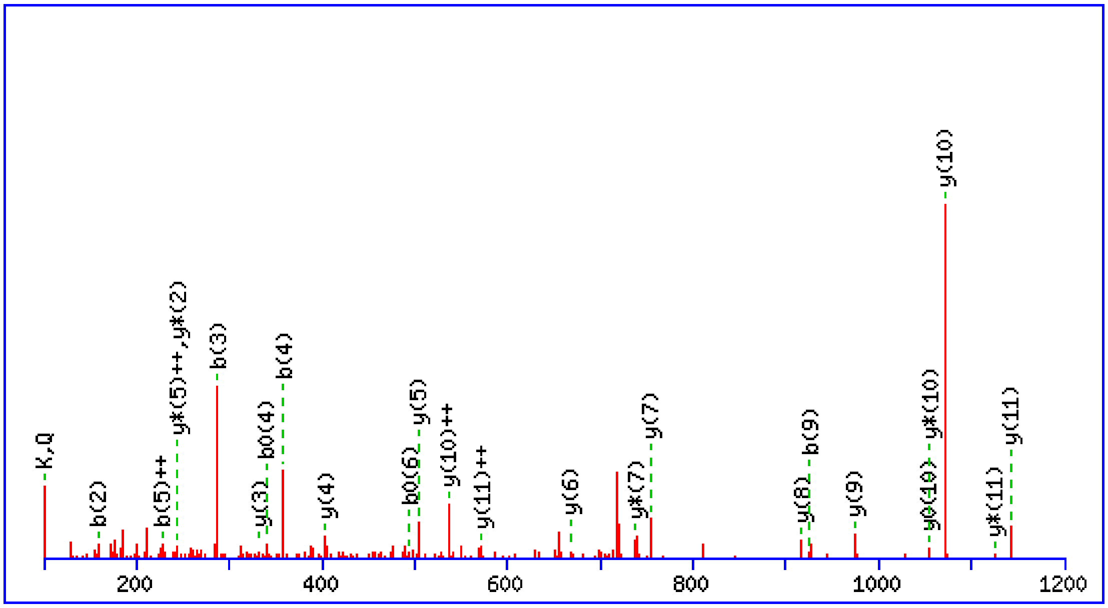


Monoisotopic mass of neutral peptide Mr(calc): 1160.5422
Fixed modifications: Carbamidomethyl (C)
Ions Score: 77 **Expect:** 1.7e-006
Matches (Bold Red): 15/123 fragment ions using 11 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0709	**129.0659**	65.0366	112.0393	56.5233			Q							11
2	60.0444	**216.0979**	108.5526	199.0713	100.0393	**198.0873**	99.5473	S	**1033.4909**	517.2491	1016.4643	508.7358	1015.4803	508.2438	10
3	86.0964	**329.1819**	165.0946	312.1554	156.5813	311.1714	156.0893	I	**946.4588**	473.7331	929.4323	465.2198	928.4483	464.7278	9
4	60.0444	**416.2140**	208.6106	399.1874	200.0974	398.2034	199.6053	S	**833.3748**	417.1910	816.3482	408.6778	815.3642	408.1857	8
5	87.0553	530.2569	265.6321	513.2304	257.1188	512.2463	256.6268	N	**746.3428**	373.6750	729.3162	365.1617	728.3322	364.6697	7
6	60.0444	617.2889	309.1481	600.2624	300.6348	599.2784	300.1428	S	**632.2998**	316.6536	615.2733	308.1403	614.2893	307.6483	6
7	102.0550	**746.3315**	373.6694	729.3050	365.1561	728.3210	364.6641	E	545.2678	273.1375	528.2413	264.6243	527.2572	264.1323	5
8	60.0444	**833.3635**	417.1854	816.3370	408.6721	815.3530	408.1801	S	**416.2252**	208.6162	399.1987	200.1030	398.2146	199.6110	4
9	30.0338	890.3850	445.6961	873.3585	437.1829	872.3744	436.6909	G	**329.1932**	165.1002	312.1666	156.5870			3
10	70.0651	987.4378	494.2225	970.4112	485.7093	969.4272	485.2172	P	272.1717	136.5895	255.1452	128.0762			2
11	**129.1135**							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TGQAPGYSYTAANK**
Found in **P99999**, P99999|CYC_HUMAN Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2

Match to Query 212: 1427.491608 from(714.753080,2+)

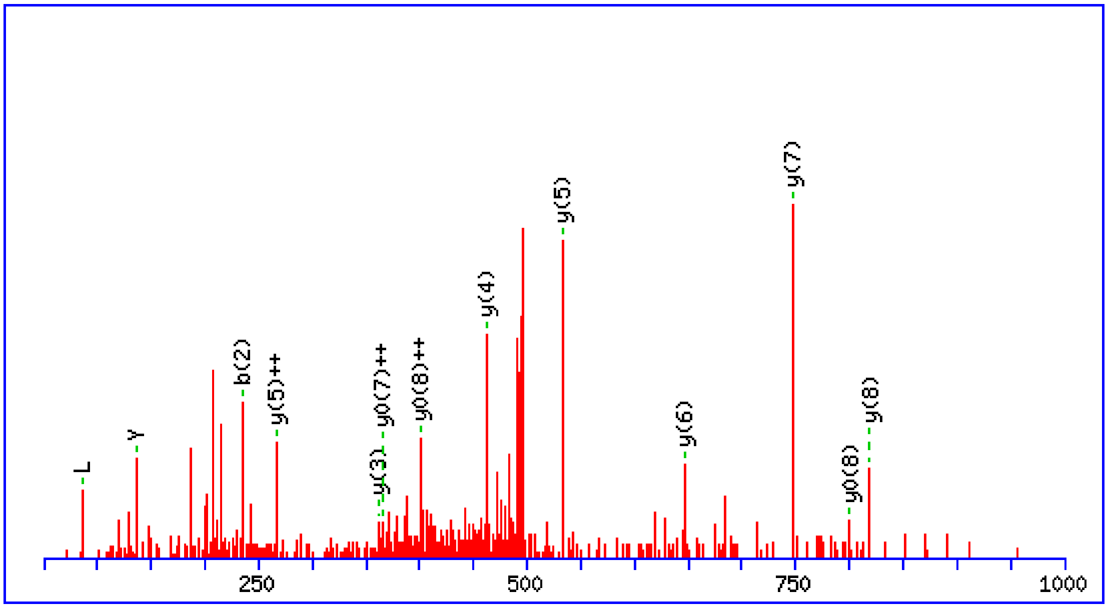


Monoisotopic mass of neutral peptide Mr(calc): 1427.6681
Fixed modifications: Carbamidomethyl (C)
Ions Score: 37 **Expect:** 0.015
Matches (Bold Red): 26/158 fragment ions using 70 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	T							14
2	30.0338	**159.0764**	80.0418			141.0659	71.0366	G	1327.6277	664.3175	1310.6012	655.8042	1309.6171	655.3122	13
3	**101.0709**	**287.1350**	144.0711	270.1084	135.5579	269.1244	135.0659	Q	1270.6062	635.8068	1253.5797	627.2935	1252.5957	626.8015	12
4	44.0495	**358.1721**	179.5897	341.1456	171.0764	**340.1615**	170.5844	A	**1142.5477**	**571.7775**	**1125.5211**	563.2642	1124.5371	562.7722	11
5	70.0651	455.2249	**228.1161**	438.1983	219.6028	437.2143	219.1108	P	**1071.5106**	**536.2589**	**1054.4840**	527.7456	**1053.5000**	527.2536	10
6	30.0338	512.2463	256.6268	495.2198	248.1135	**494.2358**	247.6215	G	**974.4578**	487.7325	957.4312	479.2193	956.4472	478.7272	9
7	136.0757	675.3097	338.1585	658.2831	329.6452	657.2991	329.1532	Y	**917.4363**	459.2218	900.4098	450.7085	899.4258	450.2165	8
8	60.0444	762.3417	381.6745	745.3151	373.1612	744.3311	372.6692	S	**754.3730**	377.6901	**737.3464**	369.1769	736.3624	368.6849	7
9	136.0757	**925.4050**	463.2062	908.3785	454.6929	907.3945	454.2009	Y	**667.3410**	334.1741	650.3144	325.6608	649.3304	325.1688	6
10	74.0600	1026.4527	513.7300	1009.4262	505.2167	1008.4421	504.7247	T	**504.2776**	252.6425	487.2511	**244.1292**	486.2671	243.6372	5
11	44.0495	1097.4898	549.2485	1080.4633	540.7353	1079.4793	540.2433	A	**403.2300**	202.1186	386.2034	193.6053			4
12	44.0495	1168.5269	584.7671	1151.5004	576.2538	1150.5164	575.7618	A	**332.1928**	166.6001	315.1663	158.0868			3
13	87.0553	1282.5699	641.7886	1265.5433	633.2753	1264.5593	632.7833	N	261.1557	131.0815	**244.1292**	122.5682			2
14	**101.1073**							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **YATLATVSR**
Found in **Q14204**, Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5

Match to Query 314: 980.492660 from(491.253606,2+)

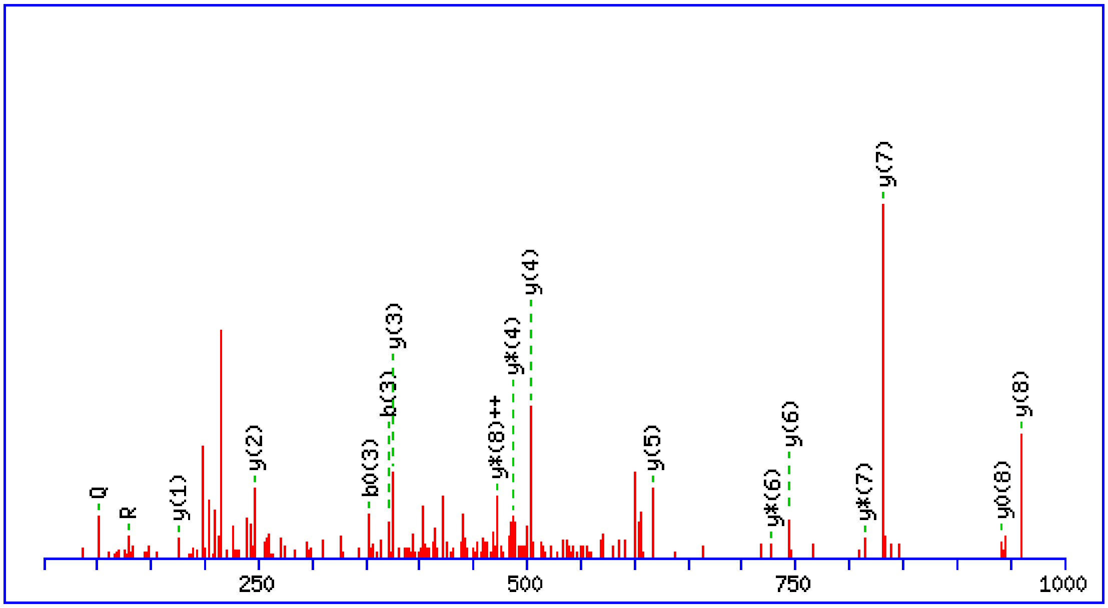


Monoisotopic mass of neutral peptide Mr(calc): 980.5291
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 **Expect:** 0.0041
Matches (Bold Red): 13/83 fragment ions using 27 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**136.0757**	164.0706	82.5389			Y							9
2	44.0495	**235.1077**	118.0575			A	**818.4730**	409.7402	801.4465	401.2269	**800.4625**	**400.7349**	8
3	74.0600	336.1554	168.5813	318.1448	159.5761	T	**747.4359**	374.2216	730.4094	365.7083	729.4254	**365.2163**	7
4	**86.0964**	449.2395	225.1234	431.2289	216.1181	L	**646.3883**	323.6978	629.3617	315.1845	628.3777	314.6925	6
5	44.0495	520.2766	260.6419	502.2660	251.6366	A	**533.3042**	**267.1557**	516.2776	258.6425	515.2936	258.1504	5
6	74.0600	621.3243	311.1658	603.3137	302.1605	T	**462.2671**	231.6372	445.2405	223.1239	444.2565	222.6319	4
7	72.0808	720.3927	360.7000	702.3821	351.6947	V	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	3
8	60.0444	807.4247	404.2160	789.4141	395.2107	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ELQSQIQEAR**
Found in **Q9P2X0**, Q9P2X0|DPM3_HUMAN Dolichol-phosphate mannosyltransferase subunit 3 OS=Homo sapiens GN=DPM3 PE=1 SV=2

Match to Query 454: 1200.640268 from(601.327410,2+)

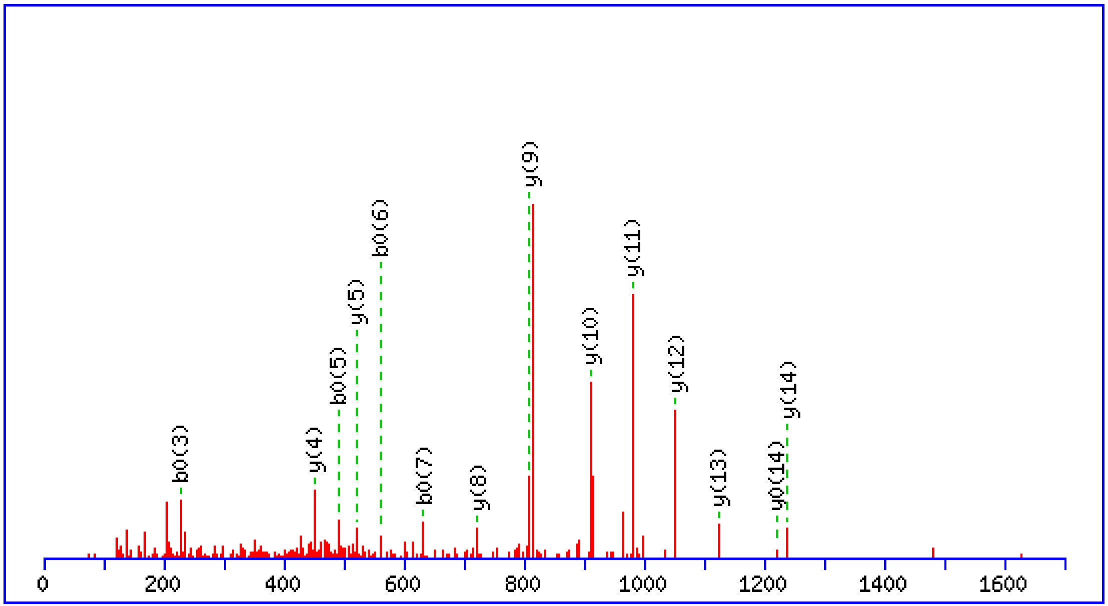


Monoisotopic mass of neutral peptide Mr(calc): 1200.6098
Fixed modifications: Carbamidomethyl (C)
Ions Score: 55 **Expect:** 0.00024
Matches (Bold Red): 19/110 fragment ions using 27 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286			112.0393	56.5233	**E**							**10**
2	86.0964	243.1339	122.0706			225.1234	113.0653	**L**	1072.5745	536.7909	1055.5480	528.2776	1054.5640	527.7856	**9**
3	**101.0709**	**371.1925**	186.0999	354.1660	177.5866	**353.1819**	177.0946	**Q**	**959.4905**	480.2489	942.4639	**471.7356**	**941.4799**	471.2436	**8**
4	60.0444	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	**S**	**831.4319**	416.2196	**814.4054**	407.7063	813.4213	407.2143	**7**
5	**101.0709**	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	**Q**	**744.3999**	372.7036	**727.3733**	364.1903	726.3893	363.6983	**6**
6	86.0964	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	**I**	**616.3413**	308.6743	599.3148	300.1610	598.3307	299.6690	**5**
7	**101.0709**	827.4258	414.2165	810.3992	405.7032	809.4152	405.2112	**Q**	**503.2572**	252.1323	**486.2307**	243.6190	485.2467	243.1270	**4**
8	102.0550	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	**E**	**375.1987**	188.1030	358.1721	179.5897	357.1881	179.0977	**3**
9	44.0495	1027.5055	514.2564	1010.4789	505.7431	1009.4949	505.2511	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
10	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **GTSFDAAATSGGSASSEK**
Found in **P13804**, P13804|ETFA_HUMAN Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1

Match to Query 602: 1629.719884 from(815.867218,2+)

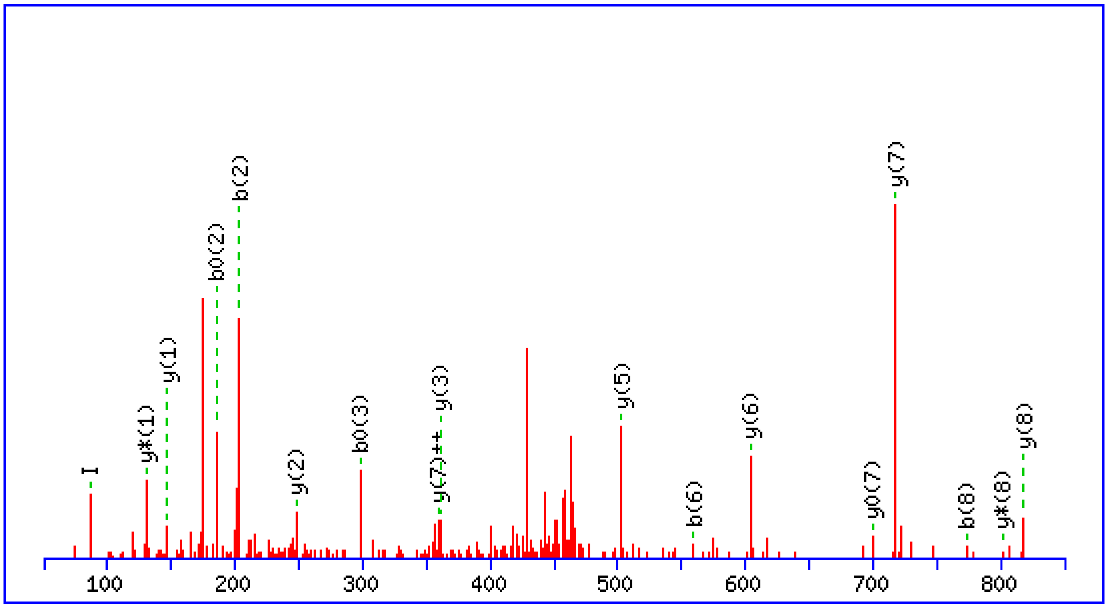


Monoisotopic mass of neutral peptide Mr(calc): 1629.7118
Fixed modifications: Carbamidomethyl (C)
Ions Score: 46 **Expect:** 0.0016
Matches (Bold Red): 14/184 fragment ions using 29 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			G							18
2	74.0600	159.0764	80.0418	141.0659	71.0366	T	1573.6976	787.3525	1556.6711	778.8392	1555.6871	778.3472	17
3	60.0444	246.1084	123.5579	**228.0979**	114.5526	S	1472.6500	736.8286	1455.6234	728.3153	1454.6394	727.8233	16
4	120.0808	393.1769	197.0921	375.1663	188.0868	F	1385.6179	693.3126	1368.5914	684.7993	1367.6074	684.3073	15
5	88.0393	508.2038	254.6055	**490.1932**	245.6003	D	**1238.5495**	619.7784	1221.5230	611.2651	**1220.5390**	610.7731	14
6	44.0495	579.2409	290.1241	**561.2304**	281.1188	A	**1123.5226**	562.2649	1106.4960	553.7516	1105.5120	553.2596	13
7	44.0495	650.2780	325.6427	**632.2675**	316.6374	A	**1052.4855**	526.7464	1035.4589	518.2331	1034.4749	517.7411	12
8	44.0495	721.3151	361.1612	703.3046	352.1559	A	**981.4483**	491.2278	964.4218	482.7145	963.4378	482.2225	11
9	74.0600	822.3628	411.6851	804.3523	402.6798	T	**910.4112**	455.7093	893.3847	447.1960	892.4007	446.7040	10
10	60.0444	909.3949	455.2011	891.3843	446.1958	S	**809.3636**	405.1854	792.3370	396.6721	791.3530	396.1801	9
11	30.0338	966.4163	483.7118	948.4058	474.7065	G	**722.3315**	361.6694	705.3050	353.1561	704.3210	352.6641	8
12	30.0338	1023.4378	512.2225	1005.4272	503.2172	G	665.3101	333.1587	648.2835	324.6454	647.2995	324.1534	7
13	60.0444	1110.4698	555.7385	1092.4592	546.7333	S	608.2886	304.6479	591.2620	296.1347	590.2780	295.6427	6
14	44.0495	1181.5069	591.2571	1163.4964	582.2518	A	**521.2566**	261.1319	504.2300	252.6186	503.2460	252.1266	5
15	60.0444	1268.5390	634.7731	1250.5284	625.7678	S	**450.2195**	225.6134	433.1929	217.1001	432.2089	216.6081	4
16	60.0444	1355.5710	678.2891	1337.5604	669.2838	S	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
17	102.0550	1484.6136	742.8104	1466.6030	733.8051	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
18	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **TTLTAAITK**
Found in **P49411**, P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2

Match to Query 139: 918.603748 from(460.309150,2+)

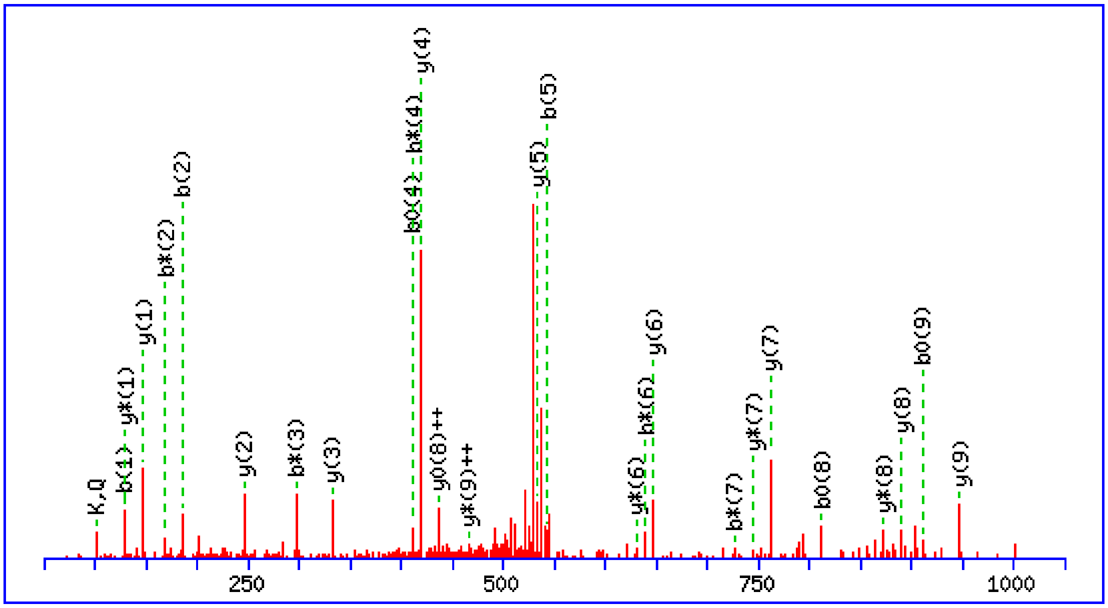


Monoisotopic mass of neutral peptide Mr(calc): 918.5386
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 **Expect:** 0.012
Matches (Bold Red): 18/87 fragment ions using 49 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							9
2	74.0600	**203.1026**	102.0550	**185.0921**	93.0497	T	**818.4982**	409.7527	**801.4716**	401.2395	800.4876	400.7475	8
3	**86.0964**	316.1867	158.5970	**298.1761**	149.5917	L	**717.4505**	**359.2289**	700.4240	350.7156	**699.4400**	350.2236	7
4	74.0600	417.2344	209.1208	399.2238	200.1155	T	**604.3665**	302.6869	587.3399	294.1736	586.3559	293.6816	6
5	44.0495	488.2715	244.6394	470.2609	235.6341	A	**503.3188**	252.1630	486.2922	243.6498	485.3082	243.1577	5
6	44.0495	**559.3086**	280.1579	541.2980	271.1527	A	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
7	**86.0964**	672.3927	336.7000	654.3821	327.6947	I	**361.2445**	181.1259	344.2180	172.6126	343.2340	172.1206	3
8	74.0600	**773.4403**	387.2238	755.4298	378.2185	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	2
9	101.1073					K	**147.1128**	74.0600	**130.0863**	65.5468			1

MS/MS Fragmentation of **QGQDNLSSVK**
Found in **P30040**, P30040|ERP29_HUMAN Endoplasmic reticulum protein ERp29 OS=Homo sapiens GN=ERP29 PE=1 SV=4

Match to Query 357: 1074.570634 from(538.292593,2+)

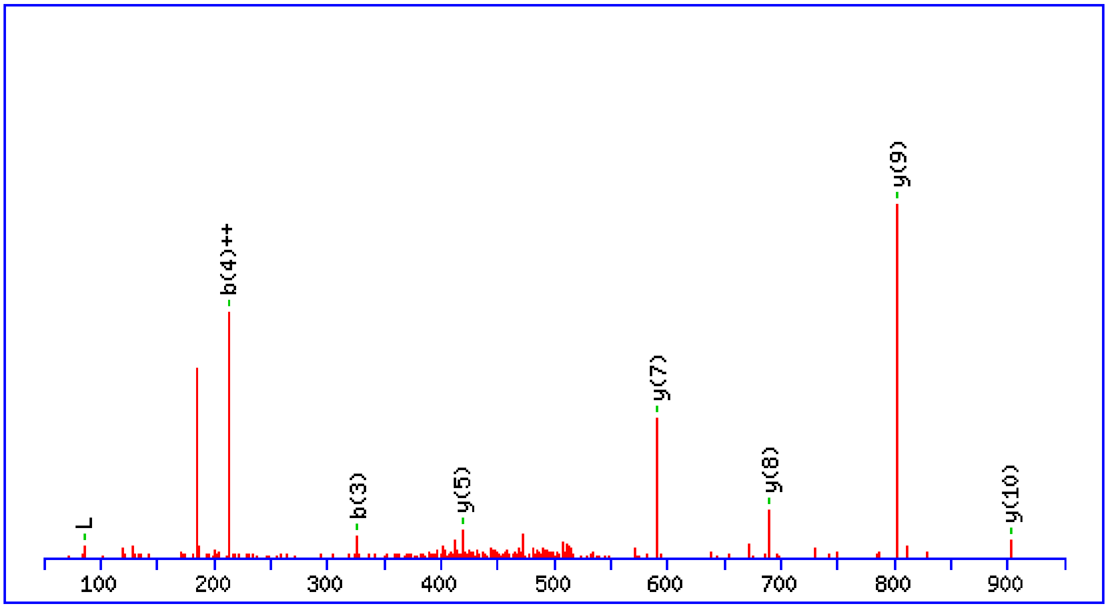


Monoisotopic mass of neutral peptide Mr(calc): 1074.5305
Fixed modifications: Carbamidomethyl (C)
Ions Score: 69 **Expect:** 9.3e-006
Matches (Bold Red): 29/108 fragment ions using 62 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**101.0709**	**129.0659**	65.0366	112.0393	56.5233			Q							10
2	30.0338	**186.0873**	93.5473	**169.0608**	85.0340			G	**947.4793**	474.2433	930.4527	**465.7300**	929.4687	465.2380	9
3	**101.0709**	314.1459	157.5766	**297.1193**	149.0633			Q	**890.4578**	445.7325	**873.4312**	437.2193	872.4472	**436.7272**	8
4	88.0393	429.1728	215.0901	**412.1463**	206.5768	**411.1623**	206.0848	D	**762.3992**	381.7032	**745.3727**	373.1900	744.3886	372.6980	7
5	87.0553	**543.2158**	272.1115	526.1892	263.5982	525.2052	263.1062	N	**647.3723**	324.1898	**630.3457**	315.6765	629.3617	315.1845	6
6	86.0964	656.2998	328.6536	**639.2733**	320.1403	638.2893	319.6483	L	**533.3293**	267.1683	516.3028	258.6550	515.3188	258.1630	5
7	60.0444	743.3319	372.1696	**726.3053**	363.6563	725.3213	363.1643	S	**420.2453**	210.6263	403.2187	202.1130	402.2347	201.6210	4
8	60.0444	830.3639	415.6856	813.3373	407.1723	**812.3533**	406.6803	S	**333.2132**	167.1103	316.1867	158.5970	315.2027	158.1050	3
9	72.0808	929.4323	465.2198	912.4058	456.7065	**911.4217**	456.2145	V	**246.1812**	123.5942	229.1547	115.0810			2
10	**101.1073**							K	**147.1128**	74.0600	**130.0863**	65.5468			1

MS/MS Fragmentation of **LVLVGDGGTGK**
Found in **P62826**, P62826|RAN_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3

Match to Query 198: 1014.516356 from(508.265454,2+)

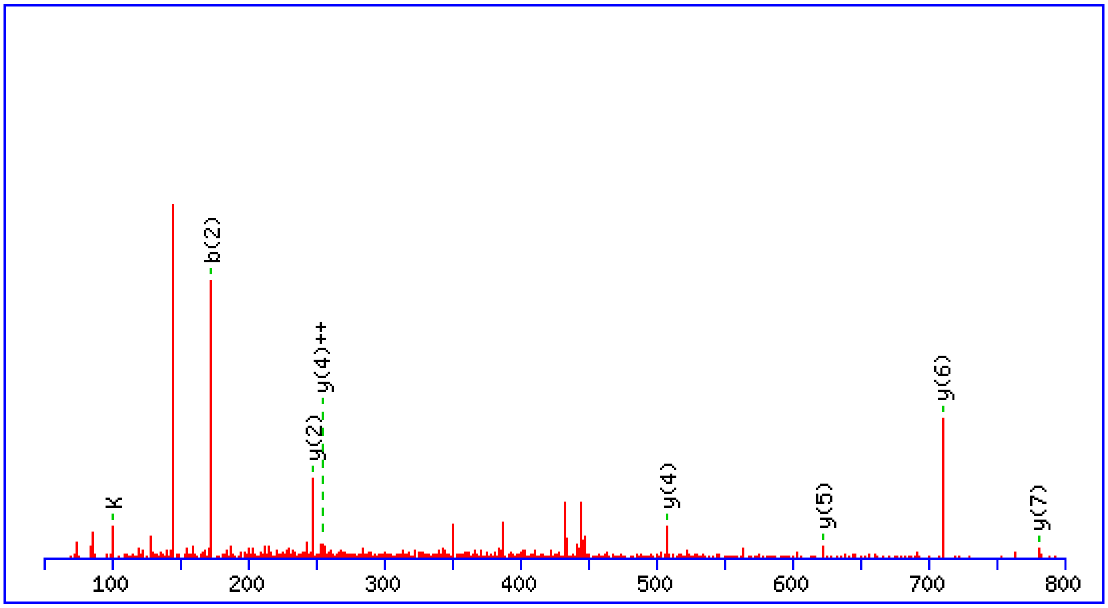


Monoisotopic mass of neutral peptide Mr(calc): 1014.5710
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 **Expect:** 0.0028
Matches (Bold Red): 10/97 fragment ions using 10 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			**L**							**11**
2	72.0808	**213.1598**	107.0835			**V**	**902.4942**	451.7507	885.4676	443.2375	884.4836	442.7454	**10**
3	**86.0964**	**326.2438**	163.6255			**L**	**803.4258**	402.2165	786.3992	393.7032	785.4152	393.2112	**9**
4	72.0808	425.3122	**213.1598**			**V**	**690.3417**	345.6745	673.3151	337.1612	672.3311	336.6692	**8**
5	30.0338	482.3337	241.6705			**G**	**591.2733**	296.1403	574.2467	287.6270	573.2627	287.1350	**7**
6	88.0393	597.3606	299.1840	579.3501	290.1787	**D**	534.2518	267.6295	517.2253	259.1163	516.2413	258.6243	**6**
7	30.0338	654.3821	327.6947	636.3715	318.6894	**G**	**419.2249**	210.1161	402.1983	201.6028	401.2143	201.1108	**5**
8	30.0338	711.4036	356.2054	693.3930	347.2001	**G**	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	**4**
9	74.0600	812.4512	406.7293	794.4407	397.7240	**T**	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	**3**
10	30.0338	869.4727	435.2400	851.4621	426.2347	**G**	204.1343	102.5708	187.1077	94.0575			**2**
11	101.1073					**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **TASDFITK**
Found in **P06396**, P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Match to Query 108: 881.311730 from(441.663141,2+)

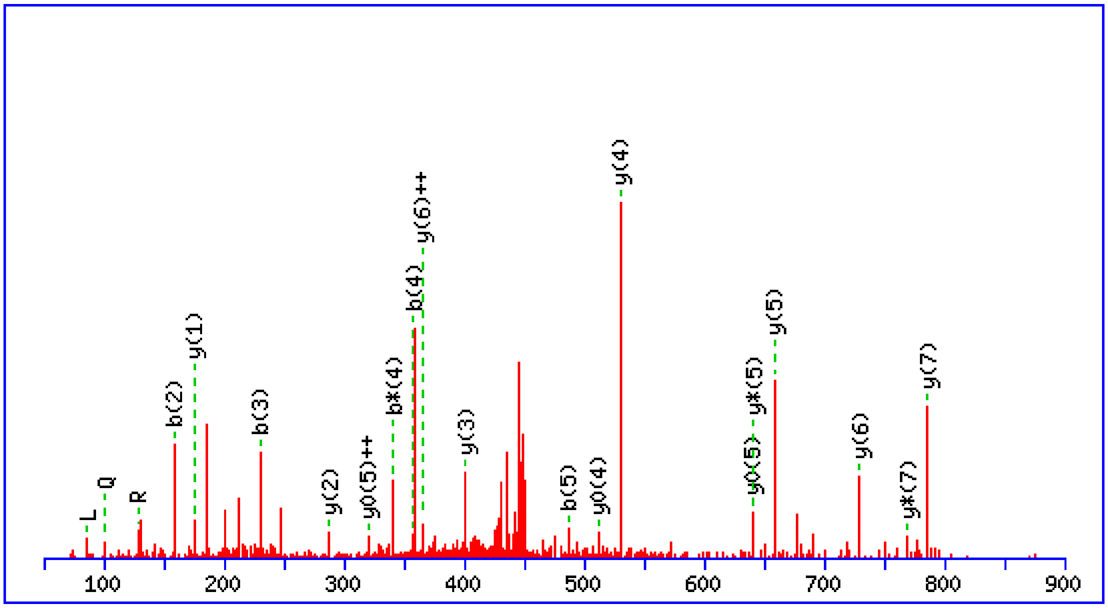


Monoisotopic mass of neutral peptide Mr(calc): 881.4494
Fixed modifications: Carbamidomethyl (C)
Ions Score: 31 **Expect:** 0.044
Matches (Bold Red): 8/76 fragment ions using 21 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							8
2	44.0495	**173.0921**	87.0497	155.0815	78.0444	A	**781.4090**	391.2082	764.3825	382.6949	763.3985	382.2029	7
3	60.0444	260.1241	130.5657	242.1135	121.5604	S	**710.3719**	355.6896	693.3454	347.1763	692.3614	346.6843	6
4	88.0393	375.1510	188.0792	357.1405	179.0739	D	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	5
5	120.0808	522.2195	261.6134	504.2089	252.6081	F	**508.3130**	**254.6601**	491.2864	246.1468	490.3024	245.6548	4
6	86.0964	635.3035	318.1554	617.2930	309.1501	I	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
7	74.0600	736.3512	368.6792	718.3406	359.6740	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	2
8	**101.1073**					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **TGAQELLR**
Found in **P06396**, P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

Match to Query 189: 886.494460 from(444.254506,2+)

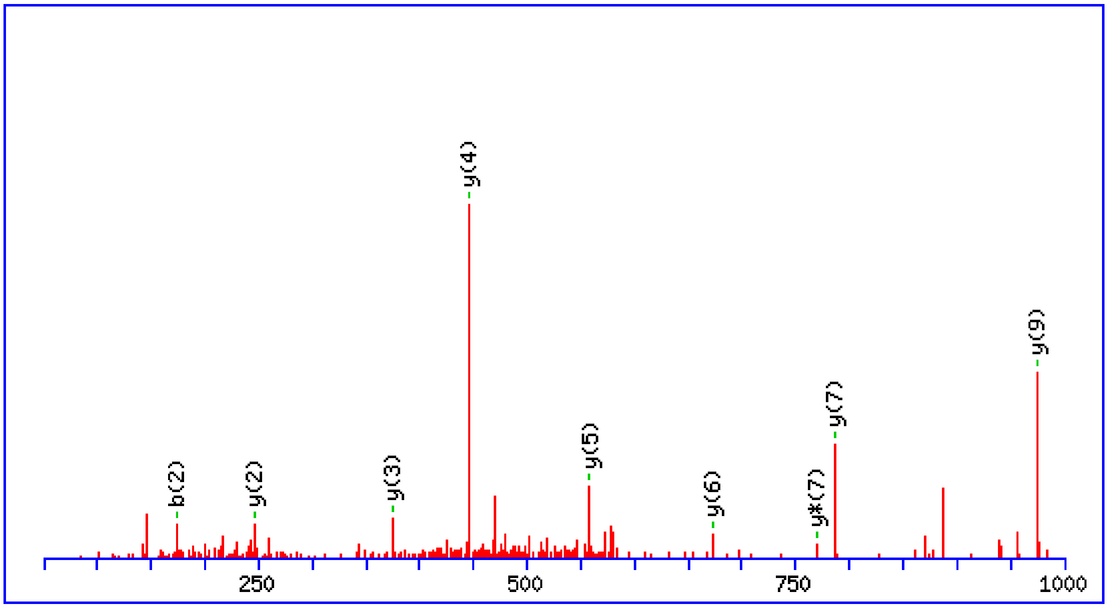


Monoisotopic mass of neutral peptide Mr(calc): 886.4872
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.012
Matches (Bold Red): 22/80 fragment ions using 51 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	T							8
2	30.0338	**159.0764**	80.0418			141.0659	71.0366	G	**786.4468**	393.7271	**769.4203**	385.2138	768.4363	384.7218	7
3	44.0495	**230.1135**	115.5604			212.1030	106.5551	A	**729.4254**	**365.2163**	712.3988	356.7030	711.4148	356.2110	6
4	**101.0709**	**358.1721**	179.5897	**341.1456**	171.0764	340.1615	170.5844	Q	**658.3883**	329.6978	**641.3617**	321.1845	**640.3777**	**320.6925**	5
5	102.0550	**487.2147**	244.1110	470.1882	235.5977	469.2041	235.1057	E	**530.3297**	265.6685	513.3031	257.1552	**512.3191**	256.6632	4
6	**86.0964**	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	L	**401.2871**	201.1472	384.2605	192.6339			3
7	**86.0964**	713.3828	357.1951	696.3563	348.6818	695.3723	348.1898	L	**288.2030**	144.6051	271.1765	136.0919			2
8	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TASTNNIAQAR**
Found in **Q9UBI6**, Q9UBI6|GBG12_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3

Match to Query 434: 1145.631020 from(573.822786,2+)

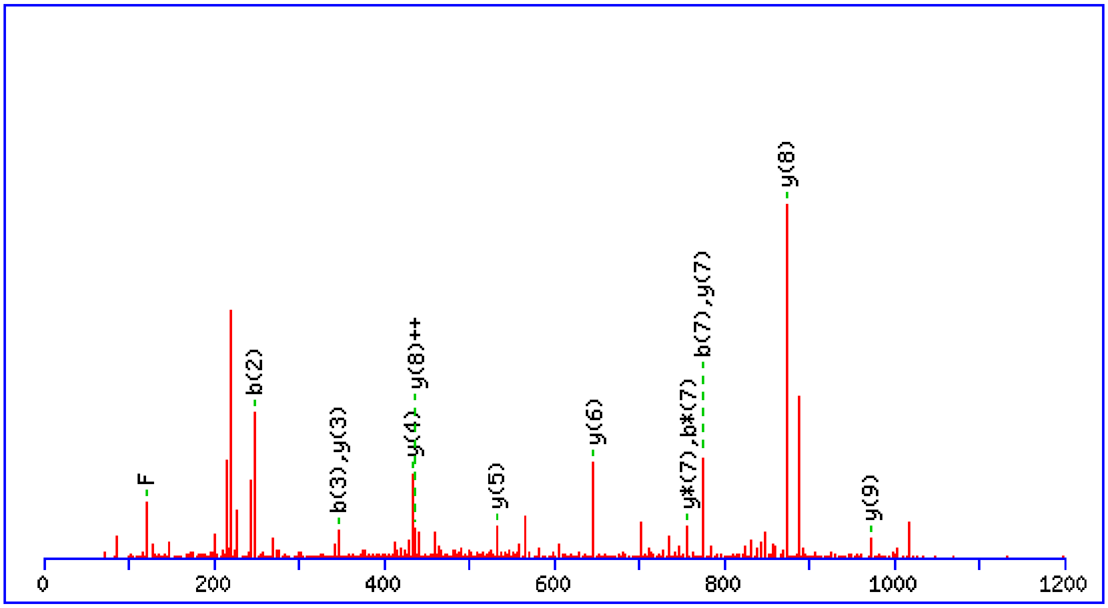


Monoisotopic mass of neutral peptide Mr(calc): 1145.5789
Fixed modifications: Carbamidomethyl (C)
Ions Score: 69 **Expect:** 9.5e-006
Matches (Bold Red): 9/109 fragment ions using 13 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	T							11
2	44.0495	**173.0921**	87.0497			155.0815	78.0444	A	1045.5385	523.2729	1028.5119	514.7596	1027.5279	514.2676	10
3	60.0444	260.1241	130.5657			242.1135	121.5604	S	**974.5014**	487.7543	957.4748	479.2411	956.4908	478.7490	9
4	74.0600	361.1718	181.0895			343.1612	172.0842	T	887.4694	444.2383	870.4428	435.7250	869.4588	435.2330	8
5	87.0553	475.2147	238.1110	458.1882	229.5977	457.2041	229.1057	N	**786.4217**	393.7145	**769.3951**	385.2012			7
6	87.0553	589.2576	295.1325	572.2311	286.6192	571.2471	286.1272	N	**672.3787**	336.6930	655.3522	328.1797			6
7	86.0964	702.3417	351.6745	685.3151	343.1612	684.3311	342.6692	I	**558.3358**	279.6715	541.3093	271.1583			5
8	44.0495	773.3788	387.1930	756.3523	378.6798	755.3682	378.1878	A	**445.2518**	223.1295	428.2252	214.6162			4
9	101.0709	901.4374	451.2223	884.4108	442.7091	883.4268	442.2170	Q	**374.2146**	187.6110	357.1881	179.0977			3
10	44.0495	972.4745	486.7409	955.4480	478.2276	954.4639	477.7356	A	**246.1561**	123.5817	229.1295	115.0684			2
11	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FVVQNVSAQK**
Found in **Q92598**, Q92598|HS105_HUMAN Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1

Match to Query 409: 1118.595160 from(560.304856,2+)

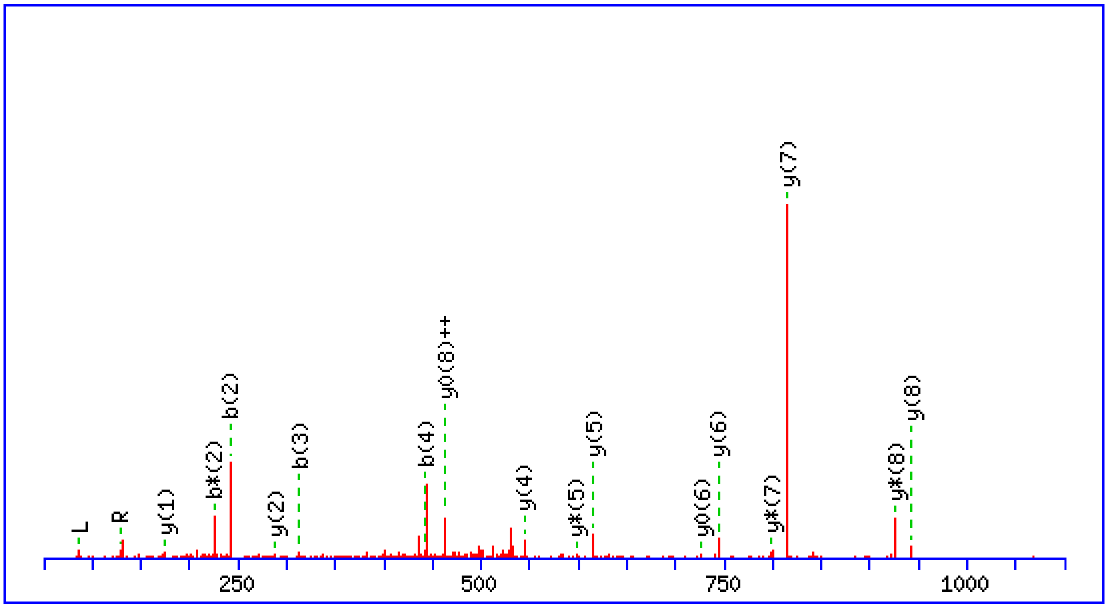


Monoisotopic mass of neutral peptide Mr(calc): 1118.6084
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.003
Matches (Bold Red): 14/94 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							10
2	72.0808	**247.1441**	124.0757					V	**972.5473**	486.7773	955.5207	478.2640	954.5367	477.7720	9
3	72.0808	**346.2125**	173.6099					V	**873.4789**	**437.2431**	856.4523	428.7298	855.4683	428.2378	8
4	101.0709	474.2711	237.6392	457.2445	229.1259			Q	**774.4104**	387.7089	**757.3839**	379.1956	756.3999	378.7036	7
5	87.0553	588.3140	294.6606	571.2875	286.1474			N	**646.3519**	323.6796	629.3253	315.1663	628.3413	314.6743	6
6	72.0808	687.3824	344.1949	670.3559	335.6816			V	**532.3089**	266.6581	515.2824	258.1448	514.2984	257.6528	5
7	60.0444	**774.4145**	387.7109	**757.3879**	379.1976	756.4039	378.7056	S	**433.2405**	217.1239	416.2140	208.6106	415.2300	208.1186	4
8	44.0495	845.4516	423.2294	828.4250	414.7162	827.4410	414.2241	A	**346.2085**	173.6079	329.1819	165.0946			3
9	101.0709	973.5102	487.2587	956.4836	478.7454	955.4996	478.2534	Q	275.1714	138.0893	258.1448	129.5761			2
10	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **LQAEAQQLR**
Found in **Q16543**, Q16543|CDC37_HUMAN Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1

Match to Query 370: 1055.564670 from (528.789611,2+)

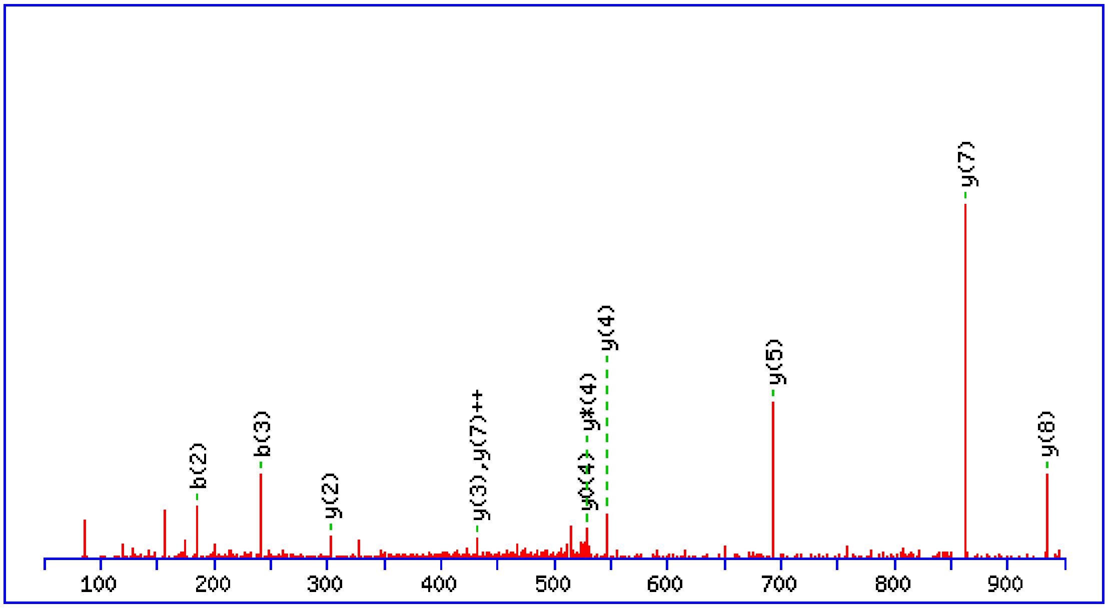


Monoisotopic mass of neutral peptide Mr(calc): 1055.5723
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 **Expect:** 0.0047
Matches (Bold Red): 19/87 fragment ions using 39 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**9**
2	101.0709	**242.1499**	121.5786	**225.1234**	113.0653			**Q**	**943.4956**	472.2514	**926.4690**	463.7381	925.4850	**463.2461**	**8**
3	44.0495	**313.1870**	157.0972	296.1605	148.5839			**A**	**815.4370**	408.2221	**798.4104**	399.7089	797.4264	399.2169	**7**
4	102.0550	**442.2296**	221.6185	425.2031	213.1052	424.2191	212.6132	**E**	**744.3999**	372.7036	727.3733	364.1903	**726.3893**	363.6983	**6**
5	44.0495	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	**A**	**615.3573**	308.1823	**598.3307**	299.6690			**5**
6	101.0709	641.3253	321.1663	624.2988	312.6530	623.3148	312.1610	**Q**	**544.3202**	272.6637	527.2936	264.1504			**4**
7	101.0709	769.3839	385.1956	752.3573	376.6823	751.3733	376.1903	**Q**	416.2616	208.6344	399.2350	200.1212			**3**
8	**86.0964**	882.4680	441.7376	865.4414	433.2243	864.4574	432.7323	**L**	**288.2030**	144.6051	271.1765	136.0919			**2**
9	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LAGLFNEQR**
Found in **Q9Y4L1**, Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1

Match to Query 289: 1046.520362 from(524.267457,2+)

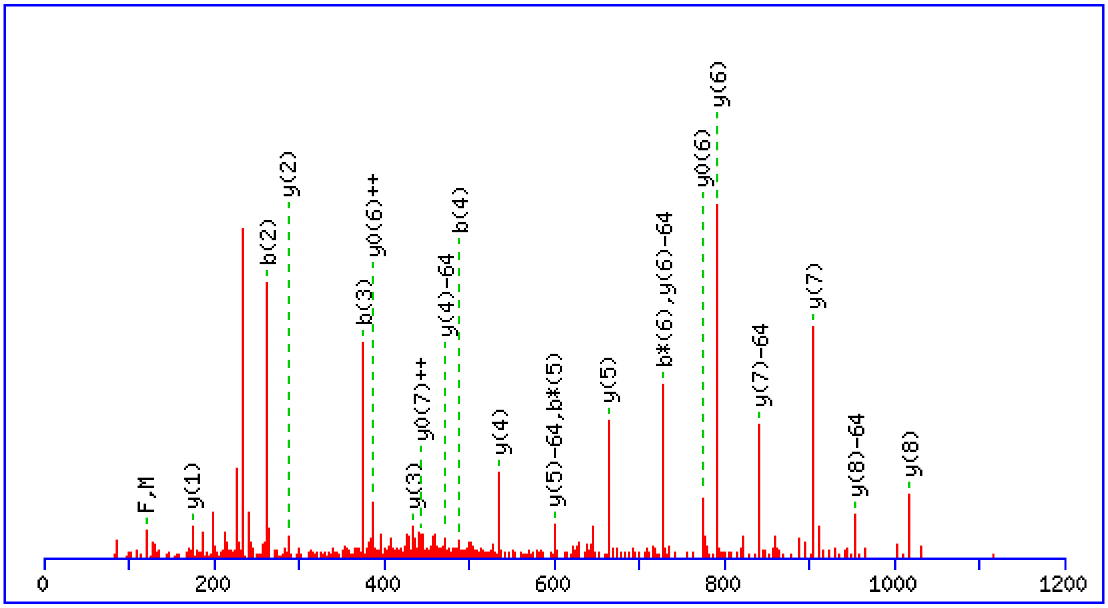


Monoisotopic mass of neutral peptide Mr(calc): 1046.5509
Fixed modifications: Carbamidomethyl (C)
Ions Score: 49 **Expect:** 0.00092
Matches (Bold Red): 11/79 fragment ions using 13 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	86.0964	114.0913	57.5493					L							9
2	44.0495	**185.1285**	93.0679					A	**934.4741**	467.7407	917.4476	459.2274	916.4635	458.7354	8
3	30.0338	**242.1499**	121.5786					G	**863.4370**	**432.2221**	846.4104	423.7089	845.4264	423.2169	7
4	86.0964	355.2340	178.1206					L	806.4155	403.7114	789.3890	395.1981	788.4050	394.7061	6
5	120.0808	502.3024	251.6548					F	**693.3315**	347.1694	676.3049	338.6561	675.3209	338.1641	5
6	87.0553	616.3453	308.6763	599.3188	300.1630			N	**546.2631**	273.6352	**529.2365**	265.1219	**528.2525**	264.6299	4
7	102.0550	745.3879	373.1976	728.3614	364.6843	727.3774	364.1923	E	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	3
8	101.0709	873.4465	437.2269	856.4199	428.7136	855.4359	428.2216	Q	**303.1775**	152.0924	286.1510	143.5791			2
9	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **DFLLQQTMLR**
Found in **Q04760**, Q04760|LGUL_HUMAN Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4

Match to Query 515: 1279.702918 from(640.858735,2+)

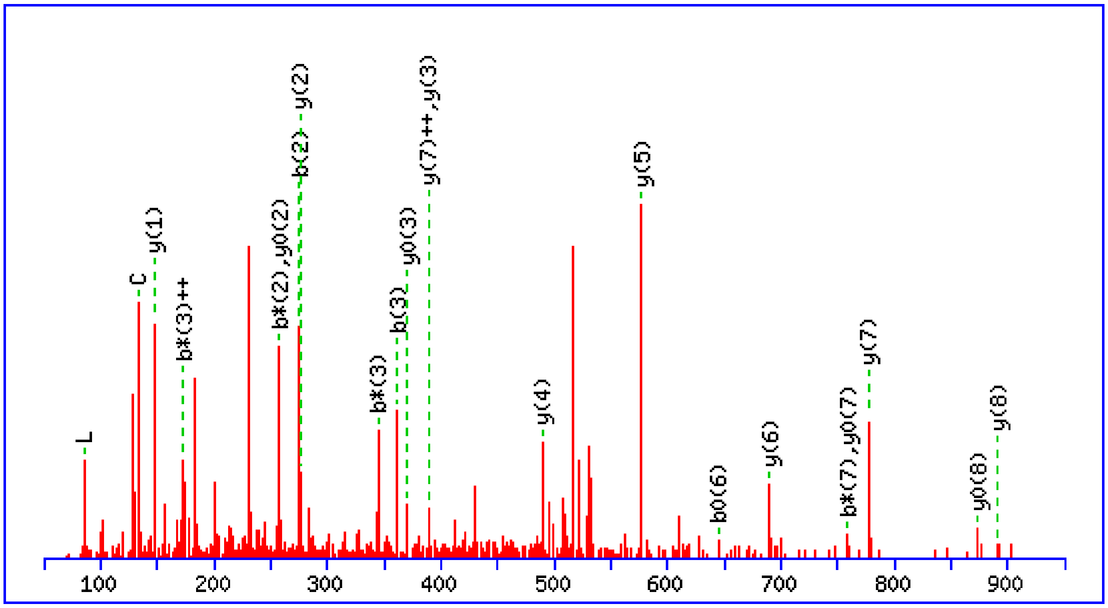


Monoisotopic mass of neutral peptide Mr(calc): 1279.6595
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 68 **Expect:** 1e-005
Matches (Bold Red): 23/157 fragment ions using 32 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	116.0342	58.5207			98.0237	49.5155	D							10
2	**120.0808**	**263.1026**	132.0550			245.0921	123.0497	F	1165.6398	583.3235	1148.6132	574.8103	1147.6292	574.3183	9
3	86.0964	**376.1867**	188.5970			358.1761	179.5917	L	**1018.5714**	509.7893	1001.5448	501.2761	1000.5608	500.7840	8
4	86.0964	**489.2708**	245.1390			471.2602	236.1337	L	**905.4873**	453.2473	888.4608	444.7340	887.4768	**444.2420**	7
5	101.0709	617.3293	309.1683	**600.3028**	300.6550	599.3188	300.1630	Q	**792.4033**	396.7053	775.3767	388.1920	**774.3927**	**387.7000**	6
6	101.0709	745.3879	373.1976	**728.3614**	364.6843	727.3774	364.1923	Q	**664.3447**	332.6760	647.3181	324.1627	646.3341	323.6707	5
7	74.0600	846.4356	423.7214	829.4090	415.2082	828.4250	414.7162	T	**536.2861**	268.6467	519.2595	260.1334	518.2755	259.6414	4
8	**120.0478**	993.4710	497.2391	976.4445	488.7259	975.4604	488.2339	M	**435.2384**	218.1228	418.2119	209.6096			3
9	86.0964	1106.5551	553.7812	1089.5285	545.2679	1088.5445	544.7759	L	**288.2030**	144.6051	271.1765	136.0919			2
10	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **CNSLSTLEK**
Found in **P13473**, P13473|LAMP2_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2

Match to Query 201: 1050.318548 from(526.166550,2+)

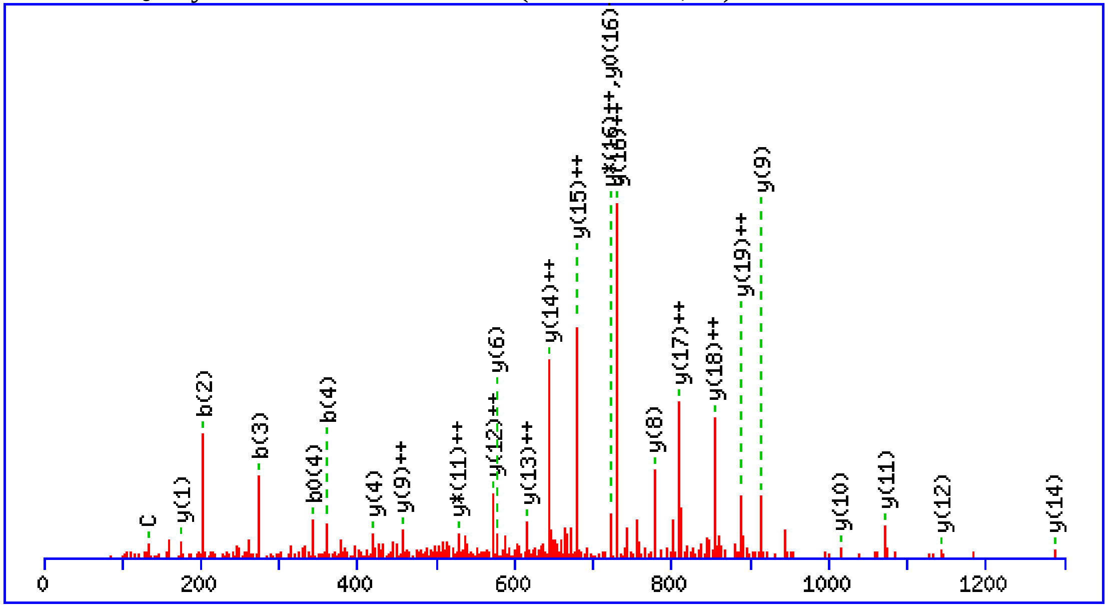


Monoisotopic mass of neutral peptide Mr(calc): 1050.5015
Fixed modifications: Carbamidomethyl (C)
Ions Score: 58 **Expect:** 7.4e-005
Matches (Bold Red): 23/97 fragment ions using 36 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**133.0430**	161.0379	81.0226					C							9
2	87.0553	**275.0809**	138.0441	**258.0543**	129.5308			N	**891.4782**	446.2427	874.4516	437.7295	**873.4676**	437.2374	8
3	60.0444	**362.1129**	181.5601	**345.0863**	**173.0468**	344.1023	172.5548	S	**777.4353**	**389.2213**	760.4087	380.7080	**759.4247**	380.2160	7
4	**86.0964**	475.1969	238.1021	458.1704	229.5888	457.1864	229.0968	L	**690.4032**	345.7053	673.3767	337.1920	672.3927	336.7000	6
5	60.0444	562.2290	281.6181	545.2024	273.1048	544.2184	272.6128	S	**577.3192**	289.1632	560.2926	280.6499	559.3086	280.1579	5
6	74.0600	663.2767	332.1420	646.2501	323.6287	**645.2661**	323.1367	T	**490.2871**	245.6472	473.2606	237.1339	472.2766	236.6419	4
7	**86.0964**	776.3607	388.6840	**759.3342**	380.1707	758.3501	379.6787	L	**389.2395**	195.1234	372.2129	186.6101	**371.2289**	186.1181	3
8	102.0550	905.4033	453.2053	888.3768	444.6920	887.3927	444.2000	E	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	2
9	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **SDASCTAGSAGTHSNGVSTGR**
Found in **Q99571**, Q99571|P2RX4_HUMAN P2X purinoceptor 4 OS=Homo sapiens GN=P2RX4 PE=2 SV=2

Match to Query 515: 1978.983351 from(660.668393,3+)

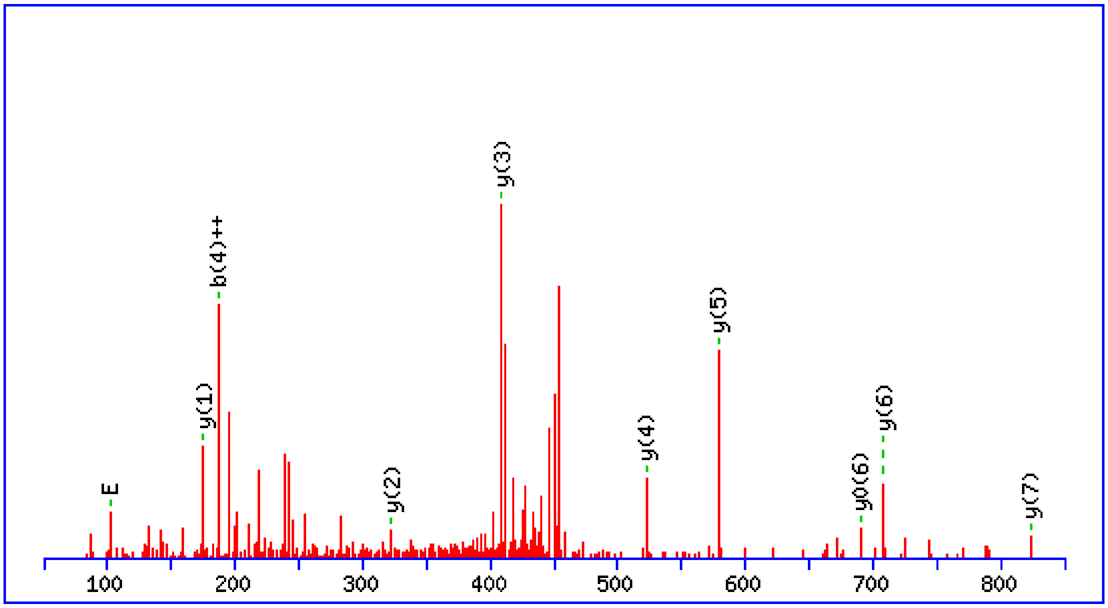


Monoisotopic mass of neutral peptide Mr(calc): 1978.8399
Fixed modifications: Carbamidomethyl (C)
Ions Score: 89 **Expect:** 7.3e-008
Matches (Bold Red): 26/229 fragment ions using 37 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							21
2	88.0393	**203.0662**	102.0368			185.0557	93.0315	D	1892.8151	946.9112	1875.7886	938.3979	1874.8046	937.9059	20
3	44.0495	**274.1034**	137.5553			256.0928	128.5500	A	1777.7882	**889.3977**	1760.7617	880.8845	1759.7776	880.3925	19
4	60.0444	**361.1354**	181.0713			**343.1248**	172.0660	S	1706.7511	**853.8792**	1689.7245	845.3659	1688.7405	844.8739	18
5	**133.0430**	521.1660	261.0867			503.1555	252.0814	C	1619.7191	**810.3632**	1602.6925	801.8499	1601.7085	801.3579	17
6	74.0600	622.2137	311.6105			604.2032	302.6052	T	1459.6884	**730.3478**	1442.6619	**721.8346**	1441.6778	**721.3426**	16
7	44.0495	693.2508	347.1291			675.2403	338.1238	A	1358.6407	**679.8240**	1341.6142	671.3107	1340.6302	670.8187	15
8	30.0338	750.2723	375.6398			732.2617	366.6345	G	**1287.6036**	**644.3054**	1270.5771	635.7922	1269.5931	635.3002	14
9	60.0444	837.3043	419.1558			819.2938	410.1505	S	1230.5822	**615.7947**	1213.5556	607.2814	1212.5716	606.7894	13
10	44.0495	908.3414	454.6744			890.3309	445.6691	A	**1143.5501**	**572.2787**	1126.5236	563.7654	1125.5396	563.2734	12
11	30.0338	965.3629	483.1851			947.3523	474.1798	G	**1072.5130**	536.7601	1055.4865	**528.2469**	1054.5024	527.7549	11
12	74.0600	1066.4106	533.7089			1048.4000	524.7036	T	**1015.4915**	508.2494	998.4650	499.7361	997.4810	499.2441	10
13	110.0713	1203.4695	602.2384			1185.4589	593.2331	H	**914.4439**	**457.7256**	897.4173	449.2123	896.4333	448.7203	9
14	60.0444	1290.5015	645.7544			1272.4910	636.7491	S	**777.3850**	389.1961	760.3584	380.6828	759.3744	380.1908	8
15	87.0553	1404.5444	702.7759	1387.5179	694.2626	1386.5339	693.7706	N	690.3529	345.6801	673.3264	337.1668	672.3424	336.6748	7
16	30.0338	1461.5659	731.2866	1444.5394	722.7733	1443.5553	722.2813	G	**576.3100**	288.6586	559.2835	280.1454	558.2994	279.6534	6
17	72.0808	1560.6343	780.8208	1543.6078	772.3075	1542.6238	771.8155	V	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
18	60.0444	1647.6664	824.3368	1630.6398	815.8235	1629.6558	815.3315	S	**420.2201**	210.6137	403.1936	202.1004	402.2096	201.6084	4
19	74.0600	1748.7140	874.8607	1731.6875	866.3474	1730.7035	865.8554	T	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
20	30.0338	1805.7355	903.3714	1788.7089	894.8581	1787.7249	894.3661	G	232.1404	116.5738	215.1139	108.0606			2
21	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ADEGISFR**
Found in **Q06830**, Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1

Match to Query 80: 893.367418 from(447.690985,2+)

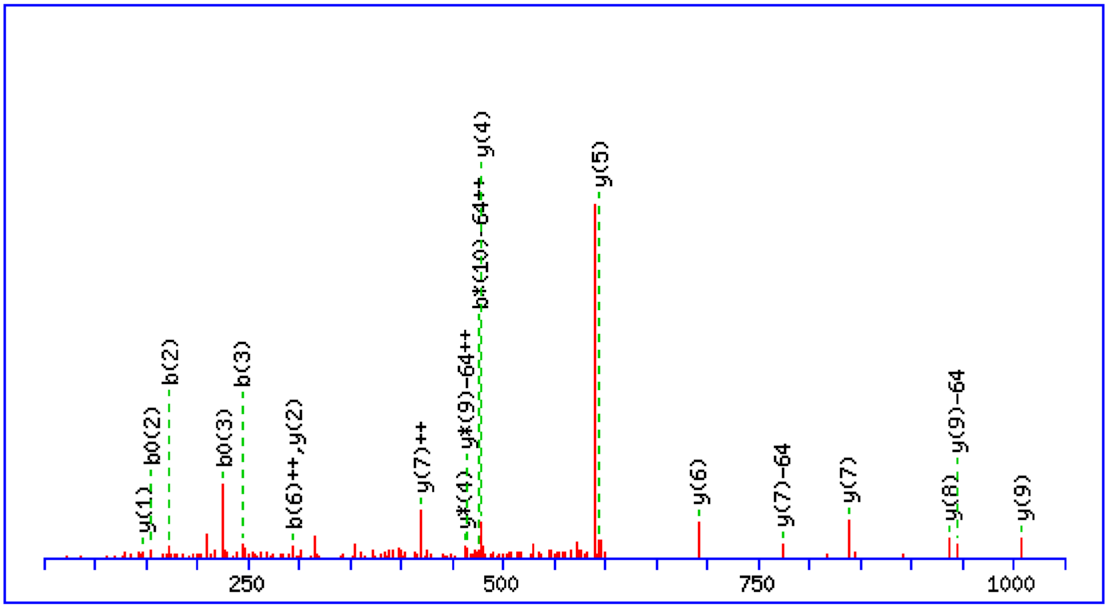


Monoisotopic mass of neutral peptide Mr(calc): 893.4243
Fixed modifications: Carbamidomethyl (C)
Ions Score: 53 **Expect:** 0.00033
Matches (Bold Red): 11/72 fragment ions using 32 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							8
2	88.0393	**187.0713**	94.0393	169.0608	85.0340	D	**823.3945**	412.2009	806.3679	403.6876	805.3839	403.1956	7
3	**102.0550**	316.1139	158.5606	298.1034	149.5553	E	**708.3675**	354.6874	691.3410	346.1741	**690.3569**	345.6821	6
4	30.0338	373.1354	**187.0713**	355.1248	178.0661	G	**579.3249**	290.1661	562.2984	281.6528	561.3144	281.1608	5
5	86.0964	486.2195	243.6134	468.2089	234.6081	I	**522.3035**	261.6554	505.2769	253.1421	504.2929	252.6501	4
6	60.0444	573.2515	287.1294	555.2409	278.1241	S	**409.2194**	205.1133	392.1928	196.6001	391.2088	196.1081	3
7	120.0808	720.3199	360.6636	702.3093	351.6583	F	**322.1874**	161.5973	305.1608	153.0840			2
8	129.1135					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ATAVMPDGQFK**
Found in **Q06830**, Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1

Match to Query 395: 1179.585206 from(590.799879,2+)

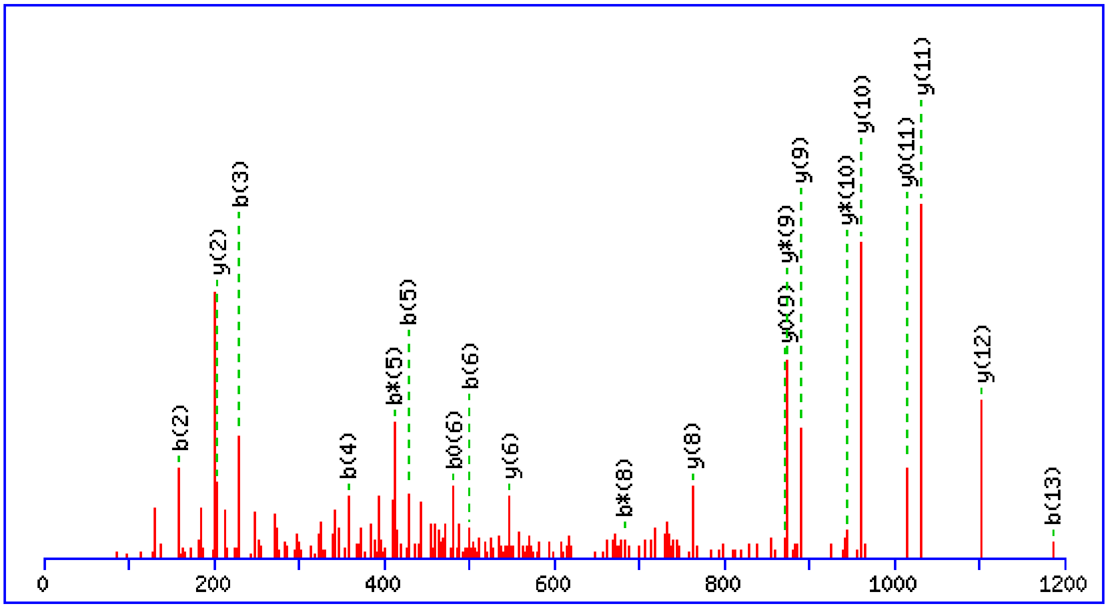


Monoisotopic mass of neutral peptide Mr(calc): 1179.5594
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 **Expect:** 0.0017
Matches (Bold Red): 19/158 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							11
2	74.0600	**173.0921**	87.0497			**155.0815**	78.0444	T	1109.5296	555.2684	1092.5030	546.7552	1091.5190	546.2631	10
3	44.0495	**244.1292**	122.5682			**226.1186**	113.5629	A	**1008.4819**	504.7446	991.4554	496.2313	990.4713	495.7393	9
4	72.0808	343.1976	172.1024			325.1870	163.0972	V	**937.4448**	469.2260	920.4182	460.7128	919.4342	460.2207	8
5	120.0478	490.2330	245.6201			472.2224	236.6149	M	**838.3764**	**419.6918**	821.3498	411.1785	820.3658	410.6865	7
6	70.0651	587.2858	**294.1465**			569.2752	285.1412	P	**691.3410**	346.1741	674.3144	337.6608	673.3304	337.1688	6
7	88.0393	702.3127	351.6600			684.3021	342.6547	D	**594.2882**	297.6477	577.2617	289.1345	576.2776	288.6425	5
8	30.0338	759.3342	380.1707			741.3236	371.1654	G	**479.2613**	240.1343	**462.2347**	231.6210			4
9	101.0709	887.3927	444.2000	870.3662	435.6867	869.3822	435.1947	Q	422.2398	211.6235	405.2132	203.1103			3
10	120.0808	1034.4612	517.7342	1017.4346	509.2209	1016.4506	508.7289	F	**294.1812**	147.5942	277.1547	139.0810			2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **SAAQAAAQTNSNAAGK**
Found in **Q8NC51**, Q8NC51|PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2

Match to Query 383: 1459.692142 from(730.853347,2+)

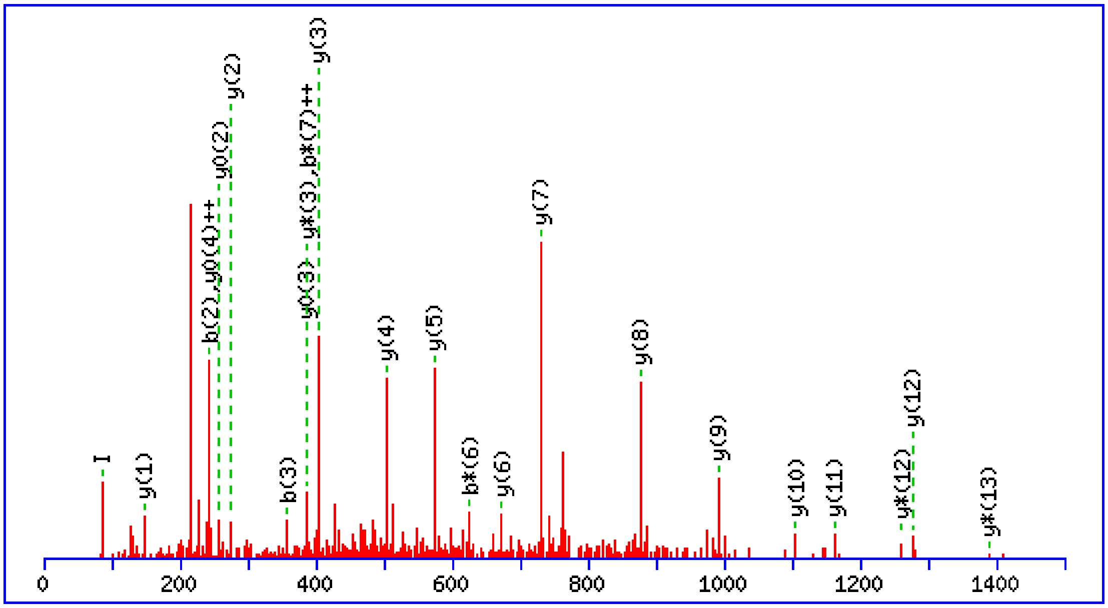


Monoisotopic mass of neutral peptide Mr(calc): 1459.7015
Fixed modifications: Carbamidomethyl (C)
Ions Score: 51 **Expect:** 0.00061
Matches (Bold Red): 20/180 fragment ions using 39 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							16
2	44.0495	**159.0764**	80.0418			141.0659	71.0366	A	1373.6768	687.3420	1356.6502	678.8288	1355.6662	678.3367	15
3	44.0495	**230.1135**	115.5604			212.1030	106.5551	A	1302.6397	651.8235	1285.6131	643.3102	1284.6291	642.8182	14
4	101.0709	**358.1721**	179.5897	341.1456	171.0764	340.1615	170.5844	Q	1231.6026	616.3049	1214.5760	607.7916	1213.5920	607.2996	13
5	44.0495	**429.2092**	215.1083	**412.1827**	206.5950	411.1987	206.1030	A	**1103.5440**	552.2756	1086.5174	543.7624	1085.5334	543.2703	12
6	44.0495	**500.2463**	250.6268	483.2198	242.1135	**482.2358**	241.6215	A	**1032.5069**	516.7571	1015.4803	508.2438	**1014.4963**	507.7518	11
7	44.0495	571.2835	286.1454	554.2569	277.6321	553.2729	277.1401	A	**961.4697**	481.2385	**944.4432**	472.7252	943.4592	472.2332	10
8	101.0709	699.3420	350.1747	**682.3155**	341.6614	681.3315	341.1694	Q	**890.4326**	445.7200	**873.4061**	437.2067	**872.4221**	436.7147	9
9	74.0600	800.3897	400.6985	783.3632	392.1852	782.3791	391.6932	T	**762.3741**	381.6907	745.3475	373.1774	744.3635	372.6854	8
10	87.0553	914.4326	457.7200	897.4061	449.2067	896.4221	448.7147	N	661.3264	331.1668	644.2998	322.6536	643.3158	322.1615	7
11	60.0444	1001.4647	501.2360	984.4381	492.7227	983.4541	492.2307	S	**547.2835**	274.1454	530.2569	265.6321	529.2729	265.1401	6
12	87.0553	1115.5076	558.2574	1098.4810	549.7442	1097.4970	549.2522	N	460.2514	230.6293	443.2249	222.1161			5
13	44.0495	**1186.5447**	593.7760	1169.5182	585.2627	1168.5341	584.7707	A	346.2085	173.6079	329.1819	165.0946			4
14	44.0495	1257.5818	629.2945	1240.5553	620.7813	1239.5713	620.2893	A	275.1714	138.0893	258.1448	129.5761			3
15	30.0338	1314.6033	657.8053	1297.5767	649.2920	1296.5927	648.8000	G	**204.1343**	102.5708	187.1077	94.0575			2
16	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IEDGNNFGVAVQEK**
Found in **Q06323**, Q06323|PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1

Match to Query 397: 1518.687830 from(760.351191,2+)

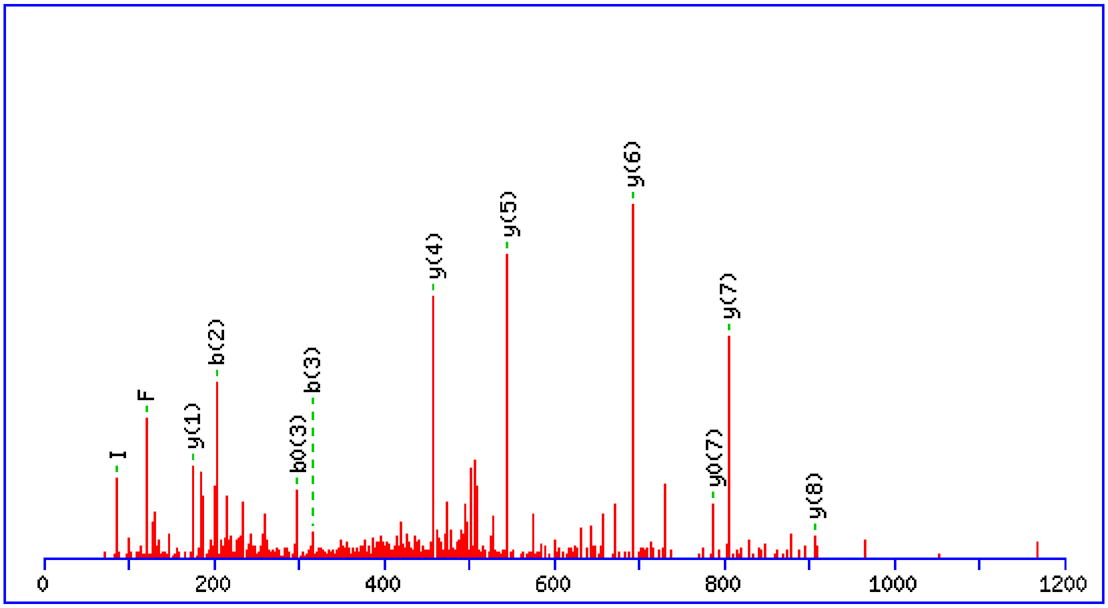


Monoisotopic mass of neutral peptide Mr(calc): 1518.7314
Fixed modifications: Carbamidomethyl (C)
Ions Score: 95 **Expect:** 2.4e-008
Matches (Bold Red): 23/158 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**I**							**14**
2	102.0550	**243.1339**	122.0706			225.1234	113.0653	**E**	1406.6546	703.8310	**1389.6281**	695.3177	1388.6441	694.8257	**13**
3	88.0393	**358.1609**	179.5841			340.1503	170.5788	**D**	**1277.6121**	639.3097	**1260.5855**	630.7964	1259.6015	630.3044	**12**
4	30.0338	415.1823	208.0948			397.1718	199.0895	**G**	**1162.5851**	581.7962	1145.5586	573.2829	1144.5745	572.7909	**11**
5	87.0553	529.2253	265.1163	512.1987	256.6030	511.2147	256.1110	**N**	**1105.5636**	553.2855	1088.5371	544.7722	1087.5531	544.2802	**10**
6	87.0553	643.2682	322.1377	**626.2416**	313.6245	625.2576	313.1325	**N**	**991.5207**	496.2640	974.4942	487.7507	973.5102	487.2587	**9**
7	120.0808	790.3366	395.6719	773.3101	**387.1587**	772.3260	386.6667	**F**	**877.4778**	439.2425	860.4512	430.7293	859.4672	430.2373	**8**
8	30.0338	847.3581	424.1827	830.3315	415.6694	829.3475	415.1774	**G**	**730.4094**	365.7083	713.3828	357.1951	712.3988	356.7030	**7**
9	72.0808	946.4265	473.7169	929.3999	465.2036	928.4159	464.7116	**V**	**673.3879**	337.1976	656.3614	328.6843	655.3774	328.1923	**6**
10	44.0495	1017.4636	509.2354	1000.4371	500.7222	999.4530	500.2302	**A**	**574.3195**	287.6634	557.2930	279.1501	556.3089	278.6581	**5**
11	72.0808	1116.5320	558.7696	1099.5055	550.2564	1098.5214	549.7644	**V**	**503.2824**	252.1448	486.2558	243.6316	485.2718	**243.1395**	**4**
12	101.0709	1244.5906	622.7989	1227.5640	614.2857	1226.5800	613.7937	**Q**	**404.2140**	202.6106	**387.1874**	194.0974	**386.2034**	193.6053	**3**
13	102.0550	1373.6332	687.3202	1356.6066	678.8070	1355.6226	678.3149	**E**	**276.1554**	138.5813	259.1288	130.0681	**258.1448**	129.5761	**2**
14	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **TTIFSPEGR**
Found in **P25789**, P25789|PSA4_HUMAN Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1

Match to Query 282: 1006.460818 from(504.237685,2+)

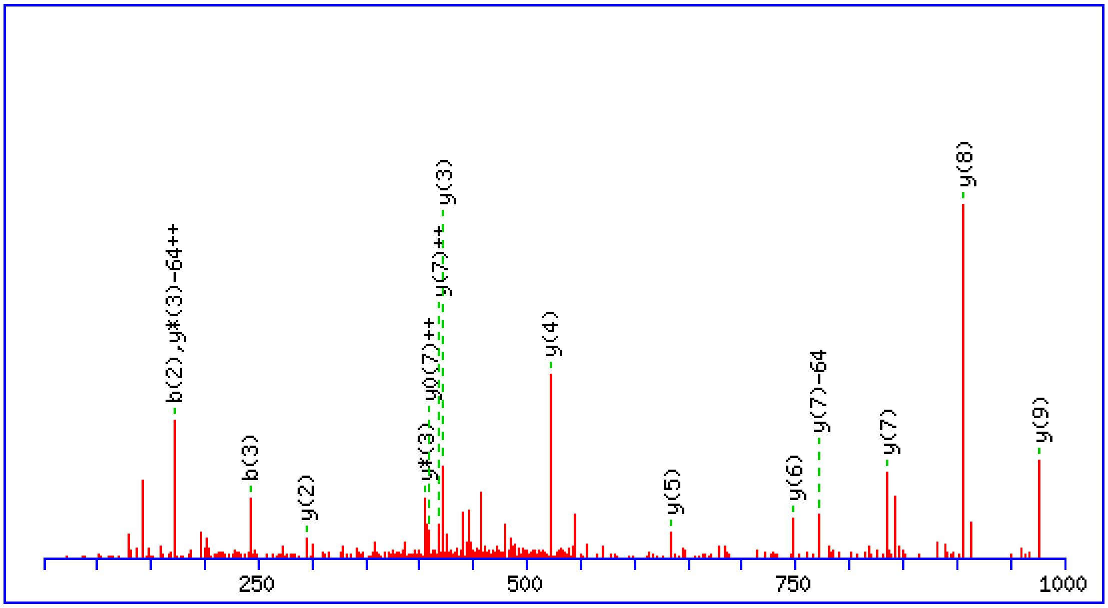


Monoisotopic mass of neutral peptide Mr(calc): 1006.5084
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.0029
Matches (Bold Red): 12/85 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	**T**							**9**
2	74.0600	**203.1026**	102.0550	185.0921	93.0497	**T**	**906.4680**	453.7376	889.4414	445.2243	888.4574	444.7323	**8**
3	**86.0964**	**316.1867**	158.5970	**298.1761**	149.5917	**I**	**805.4203**	403.2138	788.3937	394.7005	**787.4097**	394.2085	**7**
4	**120.0808**	463.2551	232.1312	445.2445	223.1259	**F**	**692.3362**	346.6717	675.3097	338.1585	674.3257	337.6665	**6**
5	60.0444	550.2871	275.6472	532.2766	266.6419	**S**	**545.2678**	273.1375	528.2413	264.6243	527.2572	264.1323	**5**
6	70.0651	647.3399	324.1736	629.3293	315.1683	**P**	**458.2358**	229.6215	441.2092	221.1083	440.2252	220.6162	**4**
7	102.0550	776.3825	388.6949	758.3719	379.6896	**E**	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	**3**
8	30.0338	833.4040	417.2056	815.3934	408.2003	**G**	232.1404	116.5738	215.1139	108.0606			**2**
9	129.1135					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VAASNIVQMK**
Found in **P49721**, P49721|PSB2_HUMAN Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1

Match to Query 381: 1075.597250 from(538.805901,2+)

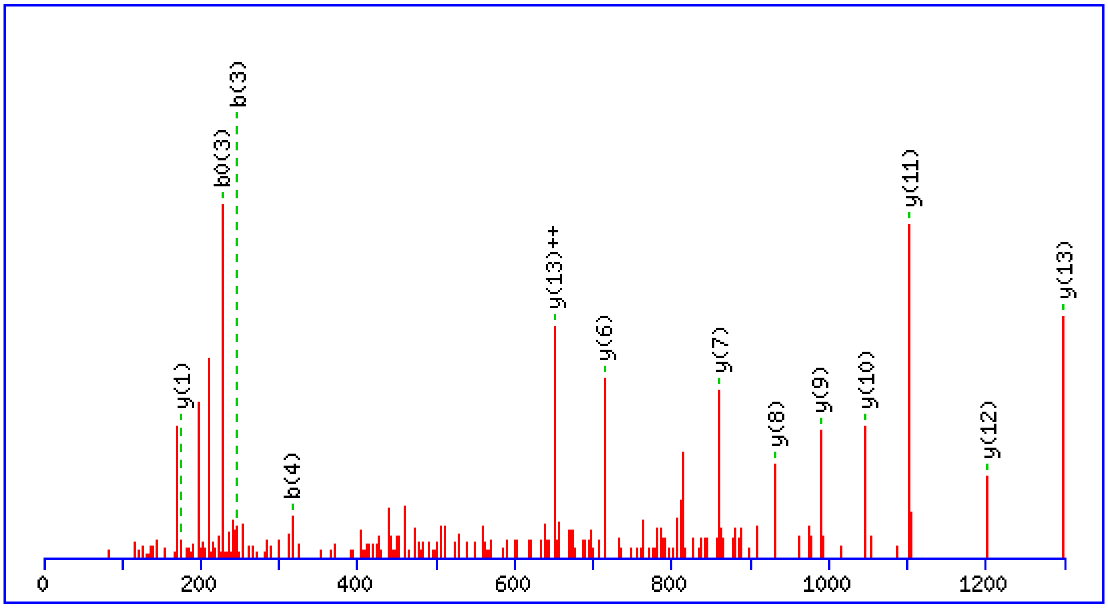


Monoisotopic mass of neutral peptide Mr(calc): 1075.5696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 71 **Expect:** 5.6e-006
Matches (Bold Red): 15/137 fragment ions using 18 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					**V**							**10**
2	44.0495	**171.1128**	86.0600					**A**	**977.5084**	489.2579	960.4819	480.7446	959.4979	480.2526	**9**
3	44.0495	**242.1499**	121.5786					**A**	**906.4713**	453.7393	889.4448	445.2260	888.4608	444.7340	**8**
4	60.0444	329.1819	165.0946			311.1714	156.0893	**S**	**835.4342**	**418.2207**	818.4077	409.7075	817.4237	**409.2155**	**7**
5	87.0553	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	**N**	**748.4022**	374.7047	731.3756	366.1915			**6**
6	86.0964	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	**I**	**634.3593**	317.6833	617.3327	309.1700			**5**
7	72.0808	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	**V**	**521.2752**	261.1412	504.2487	252.6280			**4**
8	101.0709	783.4359	392.2216	766.4094	383.7083	765.4254	383.2163	**Q**	**422.2068**	211.6070	**405.1802**	203.0938			**3**
9	120.0478	930.4713	465.7393	913.4448	457.2260	912.4608	456.7340	**M**	**294.1482**	147.5777	277.1217	139.0645			**2**
10	101.1073							**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **GSTAPVGGGAFPTIVER**
Found in **Q15084**, Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1

Match to Query 391: 1614.808706 from(808.411629,2+)

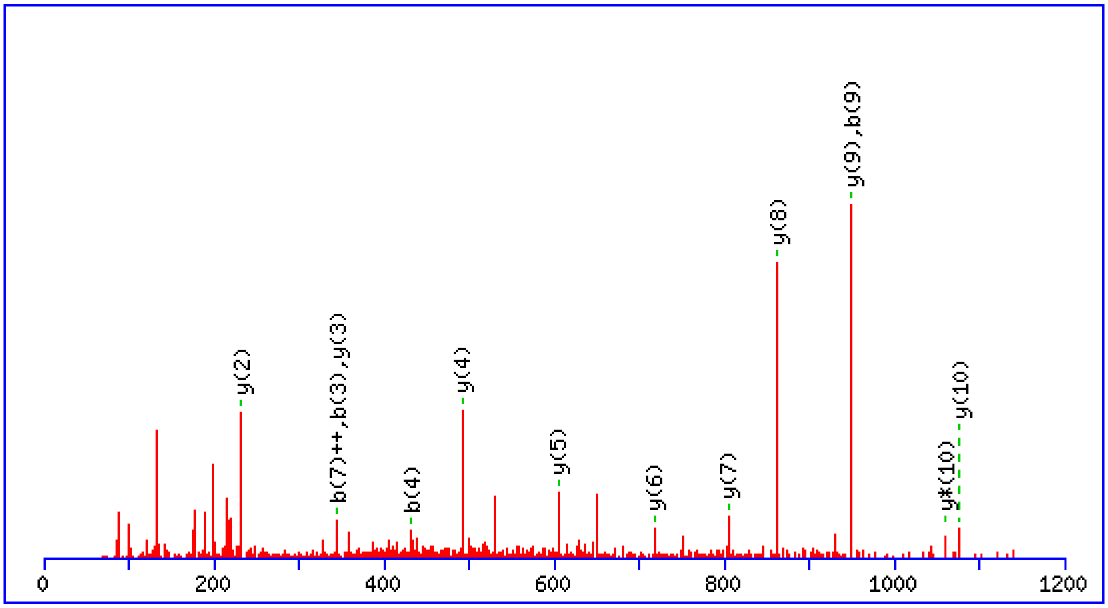


Monoisotopic mass of neutral peptide Mr(calc): 1614.8366
Fixed modifications: Carbamidomethyl (C)
Ions Score: 48 **Expect:** 0.00095
Matches (Bold Red): 13/173 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			G							17
2	60.0444	145.0608	73.0340	127.0502	64.0287	S	1558.8224	779.9148	1541.7958	771.4016	1540.8118	770.9095	16
3	74.0600	**246.1084**	123.5579	**228.0979**	114.5526	T	1471.7904	736.3988	1454.7638	727.8855	1453.7798	727.3935	15
4	44.0495	**317.1456**	159.0764	299.1350	150.0711	A	1370.7427	685.8750	1353.7161	677.3617	1352.7321	676.8697	14
5	70.0651	414.1983	207.6028	396.1878	198.5975	P	**1299.7056**	**650.3564**	1282.6790	641.8431	1281.6950	641.3511	13
6	72.0808	513.2667	257.1370	495.2562	248.1317	V	**1202.6528**	601.8300	1185.6263	593.3168	1184.6422	592.8248	12
7	30.0338	570.2882	285.6477	552.2776	276.6425	G	**1103.5844**	552.2958	1086.5578	543.7826	1085.5738	543.2905	11
8	30.0338	627.3097	314.1585	609.2991	305.1532	G	**1046.5629**	523.7851	1029.5364	515.2718	1028.5524	514.7798	10
9	30.0338	684.3311	342.6692	666.3206	333.6639	G	**989.5415**	495.2744	972.5149	486.7611	971.5309	486.2691	9
10	44.0495	755.3682	378.1878	737.3577	369.1825	A	**932.5200**	466.7636	915.4934	458.2504	914.5094	457.7584	8
11	120.0808	902.4367	451.7220	884.4261	442.7167	F	**861.4829**	431.2451	844.4563	422.7318	843.4723	422.2398	7
12	70.0651	999.4894	500.2483	981.4789	491.2431	P	**714.4145**	357.7109	697.3879	349.1976	696.4039	348.7056	6
13	74.0600	1100.5371	550.7722	1082.5265	541.7669	T	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
14	86.0964	1213.6212	607.3142	1195.6106	598.3089	I	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
15	72.0808	1312.6896	656.8484	1294.6790	647.8431	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	102.0550	1441.7322	721.3697	1423.7216	712.3644	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
17	129.1135					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **DTQSGSLLFIGR**
Found in **P50454**, P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2

Match to Query 508: 1292.619186 from(647.316869,2+)

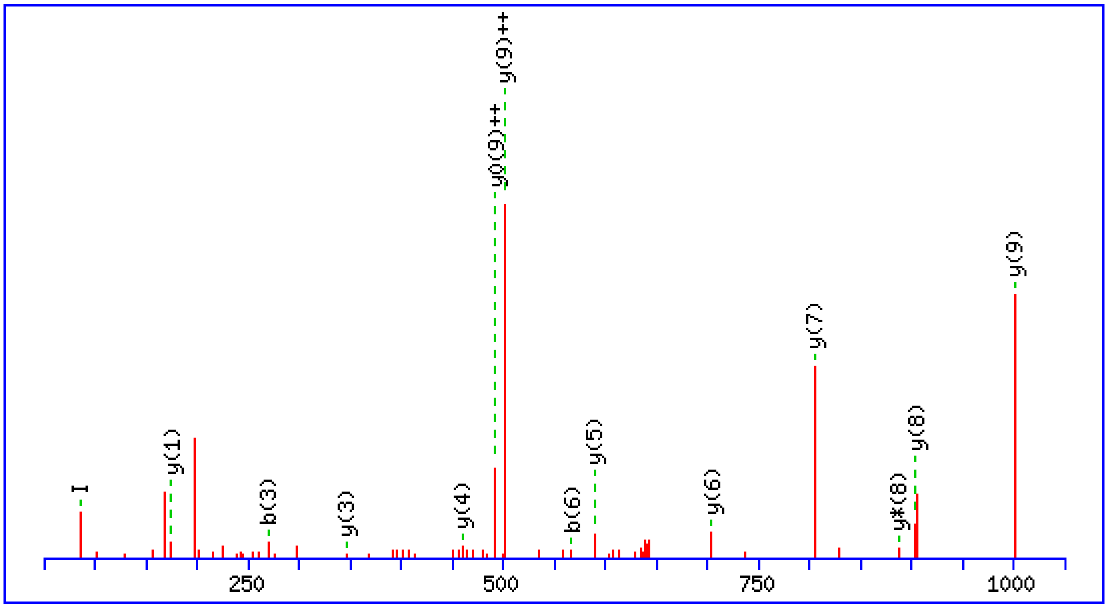


Monoisotopic mass of neutral peptide Mr(calc): 1292.6725
Fixed modifications: Carbamidomethyl (C)
Ions Score: 81 **Expect:** 6e-007
Matches (Bold Red): 14/128 fragment ions using 13 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.0393	116.0342	58.5207			98.0237	49.5155	D							12
2	74.0600	217.0819	109.0446			199.0713	100.0393	T	1178.6528	589.8300	1161.6262	581.3168	1160.6422	580.8248	11
3	101.0709	**345.1405**	173.0739	328.1139	164.5606	327.1299	164.0686	Q	**1077.6051**	539.3062	**1060.5786**	530.7929	1059.5946	530.3009	10
4	60.0444	**432.1725**	216.5899	415.1460	208.0766	414.1619	207.5846	S	**949.5465**	475.2769	932.5200	466.7636	931.5360	466.2716	9
5	30.0338	489.1940	245.1006	472.1674	236.5873	471.1834	236.0953	G	**862.5145**	431.7609	845.4880	423.2476	844.5039	422.7556	8
6	60.0444	576.2260	288.6166	559.1994	280.1034	558.2154	279.6114	S	**805.4930**	403.2502	788.4665	394.7369	787.4825	394.2449	7
7	86.0964	689.3101	**345.1587**	672.2835	336.6454	671.2995	336.1534	L	**718.4610**	359.7341	701.4345	351.2209			6
8	86.0964	802.3941	401.7007	785.3676	393.1874	784.3836	392.6954	L	**605.3770**	303.1921	588.3504	294.6788			5
9	120.0808	**949.4625**	475.2349	932.4360	466.7216	931.4520	466.2296	F	**492.2929**	246.6501	475.2663	238.1368			4
10	86.0964	1062.5466	531.7769	1045.5201	523.2637	1044.5360	522.7717	I	**345.2245**	173.1159	328.1979	164.6026			3
11	30.0338	1119.5681	560.2877	1102.5415	551.7744	1101.5575	551.2824	G	**232.1404**	116.5738	215.1139	108.0606			2
12	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VGIPVTDENGNR**
Found in **Q9H9B4**, Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4

Match to Query 236: 1269.893458 from(635.954005,2+)

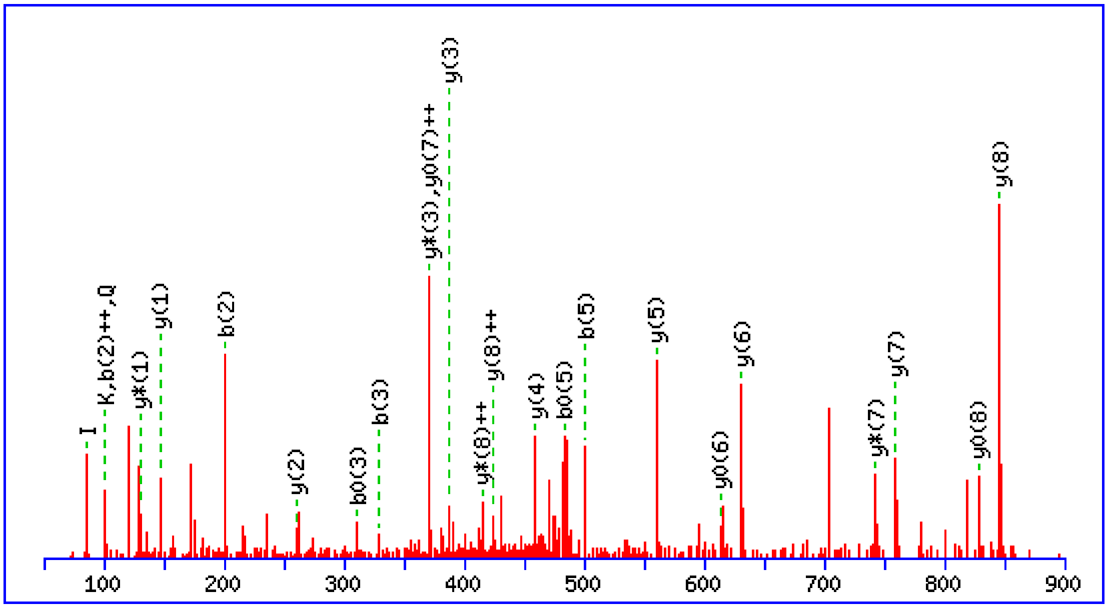


Monoisotopic mass of neutral peptide Mr(calc): 1269.6313
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.0006
Matches (Bold Red): 14/110 fragment ions using 37 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							12
2	30.0338	157.0972	79.0522					G	1171.5702	586.2887	1154.5436	577.7755	1153.5596	577.2835	11
3	**86.0964**	**270.1812**	135.5942					I	1114.5487	557.7780	1097.5222	549.2647	1096.5382	548.7727	10
4	70.0651	367.2340	184.1206					P	**1001.4647**	**501.2360**	984.4381	492.7227	983.4541	**492.2307**	9
5	72.0808	466.3024	233.6548					V	**904.4119**	452.7096	**887.3854**	444.1963	886.4013	443.7043	8
6	74.0600	**567.3501**	284.1787			549.3395	275.1734	T	**805.3435**	403.1754	788.3169	394.6621	787.3329	394.1701	7
7	88.0393	682.3770	341.6921			664.3665	332.6869	D	**704.2958**	352.6515	687.2693	344.1383	686.2852	343.6463	6
8	102.0550	811.4196	406.2134			793.4090	397.2082	E	**589.2689**	295.1381	572.2423	286.6248	571.2583	286.1328	5
9	87.0553	925.4625	463.2349	908.4360	454.7216	907.4520	454.2296	N	**460.2263**	230.6168	443.1997	222.1035			4
10	30.0338	982.4840	491.7456	965.4575	483.2324	964.4734	482.7404	G	**346.1833**	173.5953	329.1568	165.0820			3
11	87.0553	1096.5269	548.7671	1079.5004	540.2538	1078.5164	539.7618	N	289.1619	145.0846	272.1353	136.5713			2
12	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ISQATAQIK**
Found in **Q86Y82**, Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1

Match to Query 168: 958.652580 from(480.333566,2+)

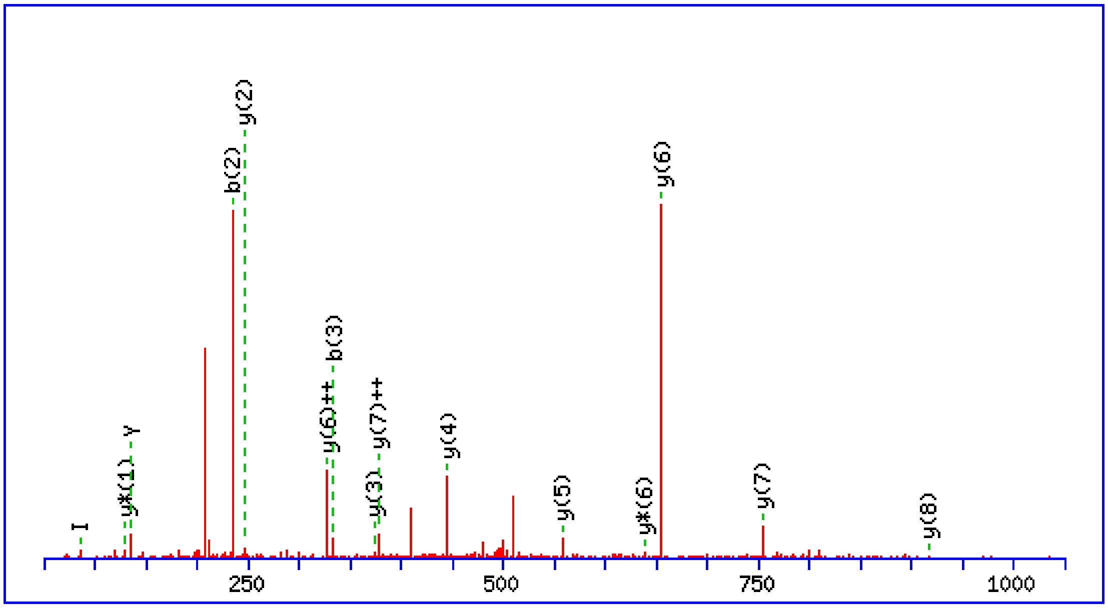


Monoisotopic mass of neutral peptide Mr(calc): 958.5447
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.0033
Matches (Bold Red): 27/91 fragment ions using 61 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							9
2	60.0444	**201.1234**	**101.0653**			183.1128	92.0600	S	**846.4680**	**423.7376**	829.4414	**415.2243**	**828.4574**	414.7323	8
3	**101.0709**	**329.1819**	165.0946	312.1554	156.5813	**311.1714**	156.0893	Q	**759.4359**	380.2216	**742.4094**	371.7083	741.4254	**371.2163**	7
4	44.0495	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	A	**631.3774**	316.1923	614.3508	307.6790	**613.3668**	307.1870	6
5	74.0600	**501.2667**	251.1370	484.2402	242.6237	**483.2562**	242.1317	T	**560.3402**	280.6738	543.3137	272.1605	542.3297	271.6685	5
6	44.0495	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	A	**459.2926**	230.1499	442.2660	221.6366			4
7	**101.0709**	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	Q	**388.2554**	194.6314	**371.2289**	186.1181			3
8	**86.0964**	813.4465	407.2269	796.4199	398.7136	795.4359	398.2216	I	**260.1969**	130.6021	243.1703	122.0888			2
9	**101.1073**							K	**147.1128**	74.0600	**130.0863**	65.5468			1

MS/MS Fragmentation of **AYVPIAQVK**
Found in **Q14956**, Q14956|GPNMB_HUMAN Transmembrane glycoprotein NMB OS=Homo sapiens GN=GPNMB PE=1 SV=2

Match to Query 352: 987.591344 from(494.802948,2+)

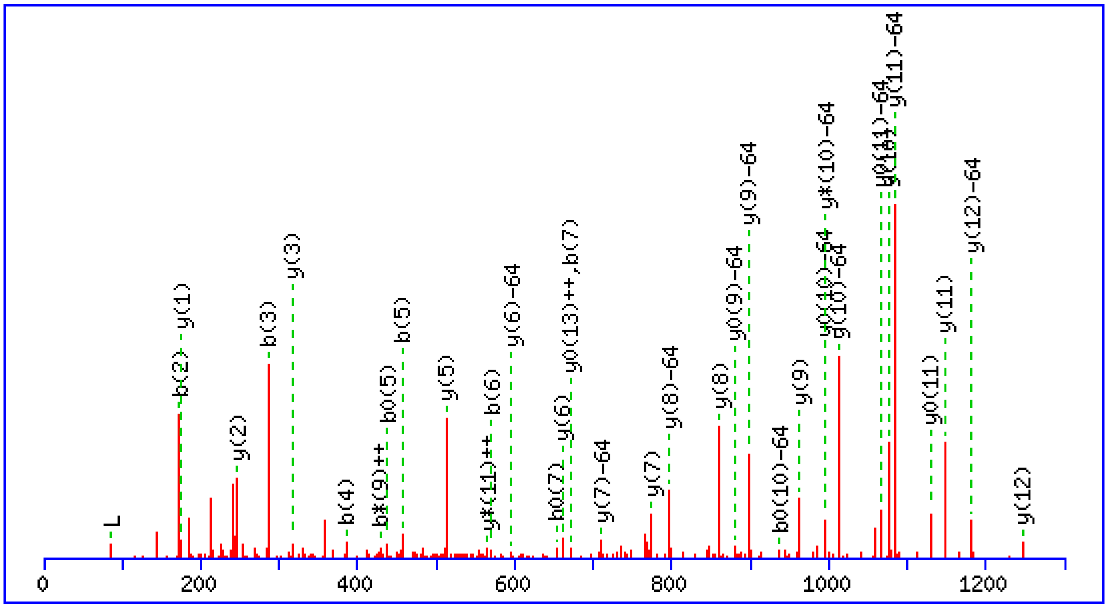


Monoisotopic mass of neutral peptide Mr(calc): 987.5753
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 **Expect:** 0.0094
Matches (Bold Red): 15/61 fragment ions using 39 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	44.0495	72.0444	36.5258			**A**					**9**
2	**136.0757**	**235.1077**	118.0575			**Y**	**917.5455**	459.2764	900.5189	450.7631	**8**
3	72.0808	**334.1761**	167.5917			**V**	**754.4822**	**377.7447**	737.4556	369.2314	**7**
4	70.0651	431.2289	216.1181			**P**	**655.4137**	**328.2105**	**638.3872**	319.6972	**6**
5	**86.0964**	544.3130	272.6601			**I**	**558.3610**	279.6841	541.3344	271.1709	**5**
6	44.0495	615.3501	308.1787			**A**	**445.2769**	223.1421	428.2504	214.6288	**4**
7	101.0709	743.4087	372.2080	726.3821	363.6947	**Q**	**374.2398**	187.6235	357.2132	179.1103	**3**
8	72.0808	842.4771	421.7422	825.4505	413.2289	**V**	**246.1812**	123.5942	229.1547	115.0810	**2**
9	101.1073					**K**	147.1128	74.0600	**130.0863**	65.5468	**1**

MS/MS Fragmentation of **TALVANTSNMPVAAR**
Found in **P38606**, P38606|VATA_HUMAN Vacuolar ATP synthase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2

Match to Query 656: 1530.747990 from(766.381271,2+)

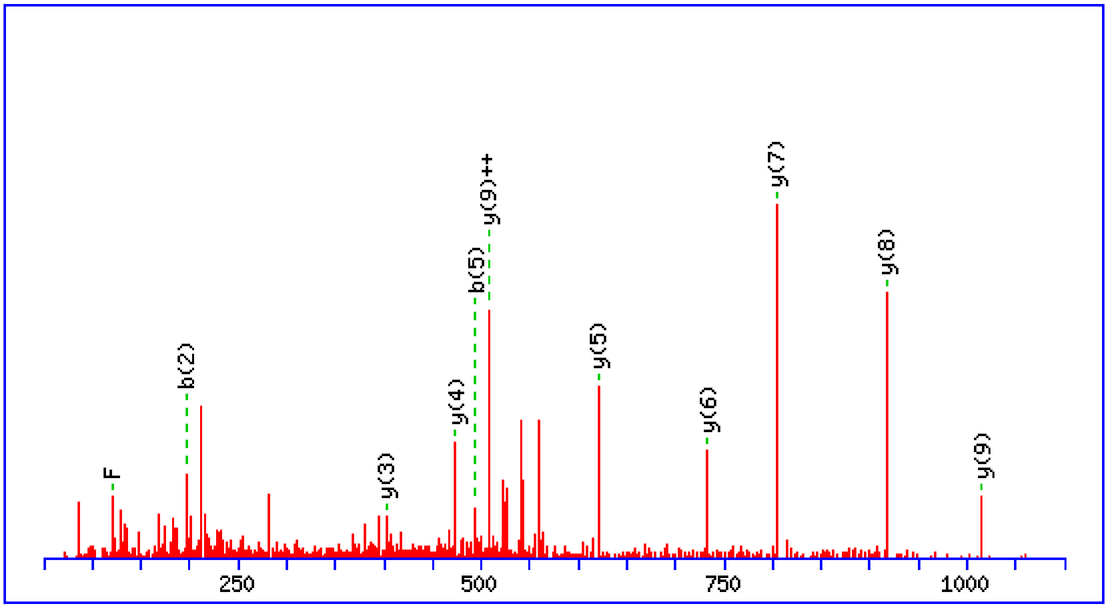


Monoisotopic mass of neutral peptide Mr(calc): 1530.7824
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M10   : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 86 **Expect:** 1.7e-007
Matches (Bold Red): 36/240 fragment ions using 48 most intense peaks

#	**Immon.**	**b**	**b^{++}**	**b***	**b^{*++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	74.0600	102.0550	51.5311			84.0444	42.5258	**T**							**15**
2	44.0495	**173.0921**	87.0497			155.0815	78.0444	**A**	1366.7437	683.8755	1349.7172	675.3622	1348.7332	674.8702	**14**
3	**86.0964**	**286.1761**	143.5917			268.1656	134.5864	**L**	1295.7066	648.3570	1278.6801	639.8437	1277.6961	639.3517	**13**
4	72.0808	**385.2445**	193.1259			367.2340	184.1206	**V**	**1182.6226**	591.8149	1165.5960	583.3016	1164.6120	582.8096	**12**
5	44.0495	**456.2817**	228.6445			**438.2711**	219.6392	**A**	**1083.5542**	542.2807	1066.5276	533.7674	**1065.5436**	533.2754	**11**
6	87.0553	**570.3246**	285.6659	553.2980	277.1527	552.3140	276.6606	**N**	**1012.5170**	506.7622	**995.4905**	498.2489	**994.5065**	497.7569	**10**
7	74.0600	**671.3723**	336.1898	654.3457	327.6765	**653.3617**	327.1845	**T**	**898.4741**	449.7407	881.4476	441.2274	**880.4635**	440.7354	**9**
8	60.0444	758.4043	379.7058	741.3777	371.1925	740.3937	370.7005	**S**	**797.4264**	399.2169	780.3999	390.7036	779.4159	390.2116	**8**
9	87.0553	872.4472	436.7272	855.4207	**428.2140**	854.4367	427.7220	**N**	**710.3944**	355.7008	693.3679	347.1876			**7**
10	56.0495	955.4843	478.2458	938.4578	469.7325	**937.4738**	469.2405	**M**	**596.3515**	298.6794	579.3249	290.1661			**6**
11	70.0651	1052.5371	526.7722	1035.5106	518.2589	1034.5265	517.7669	**P**	**513.3144**	257.1608	496.2878	248.6475			**5**
12	72.0808	1151.6055	576.3064	1134.5790	567.7931	1133.5950	567.3011	**V**	416.2616	208.6344	399.2350	200.1212			**4**
13	44.0495	1222.6426	611.8250	1205.6161	603.3117	1204.6321	602.8197	**A**	**317.1932**	159.1002	300.1666	150.5870			**3**
14	44.0495	1293.6797	647.3435	1276.6532	638.8302	1275.6692	638.3382	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
15	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VPLALFALNR**
Found in **P12955**, P12955|PEPD_HUMAN Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3

Match to Query 376: 1112.655128 from(557.334840,2+)

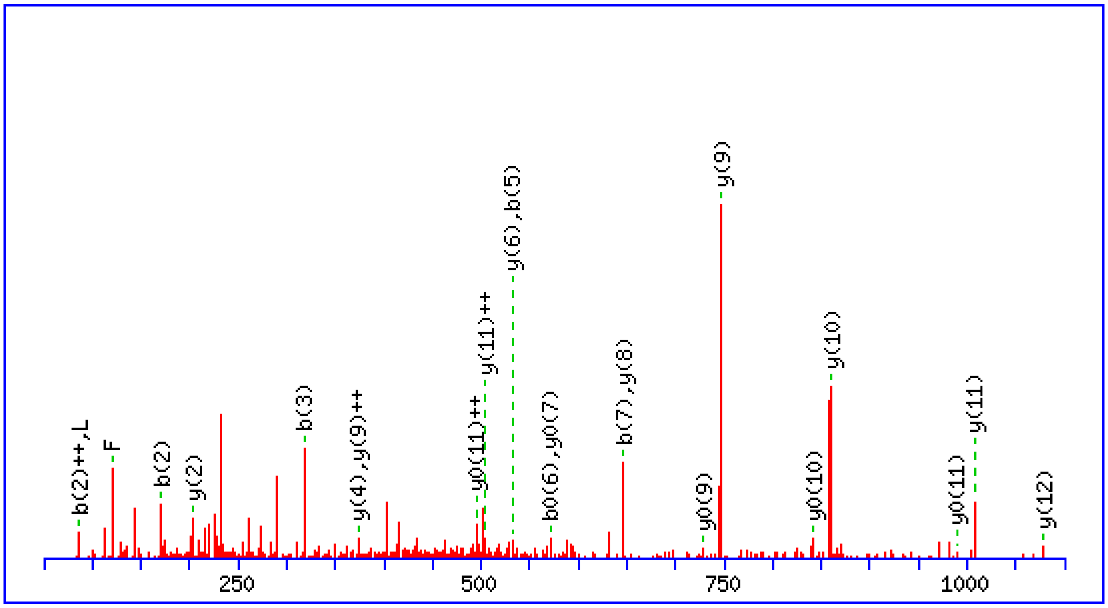


Monoisotopic mass of neutral peptide Mr(calc): 1112.6706
Fixed modifications: Carbamidomethyl (C)
Ions Score: 47 **Expect:** 0.0015
Matches (Bold Red): 11/66 fragment ions using 13 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	72.0808	100.0757	50.5415			V					10
2	70.0651	**197.1285**	99.0679			P	**1014.6095**	**507.8084**	997.5829	499.2951	9
3	86.0964	310.2125	155.6099			L	**917.5567**	459.2820	900.5302	450.7687	8
4	44.0495	381.2496	191.1285			A	**804.4726**	402.7400	787.4461	394.2267	7
5	86.0964	**494.3337**	247.6705			L	**733.4355**	367.2214	716.4090	358.7081	6
6	**120.0808**	641.4021	321.2047			F	**620.3515**	310.6794	603.3249	302.1661	5
7	44.0495	712.4392	356.7233			A	**473.2831**	237.1452	456.2565	228.6319	4
8	86.0964	825.5233	413.2653			L	**402.2459**	201.6266	385.2194	193.1133	3
9	87.0553	939.5662	470.2867	922.5397	461.7735	N	289.1619	145.0846	272.1353	136.5713	2
10	129.1135					R	175.1190	88.0631	158.0924	79.5498	1

MS/MS Fragmentation of **VAFITGGGTGLGK**
Found in **Q16698**, Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1

Match to Query 278: 1176.669858 from(589.342205,2+)

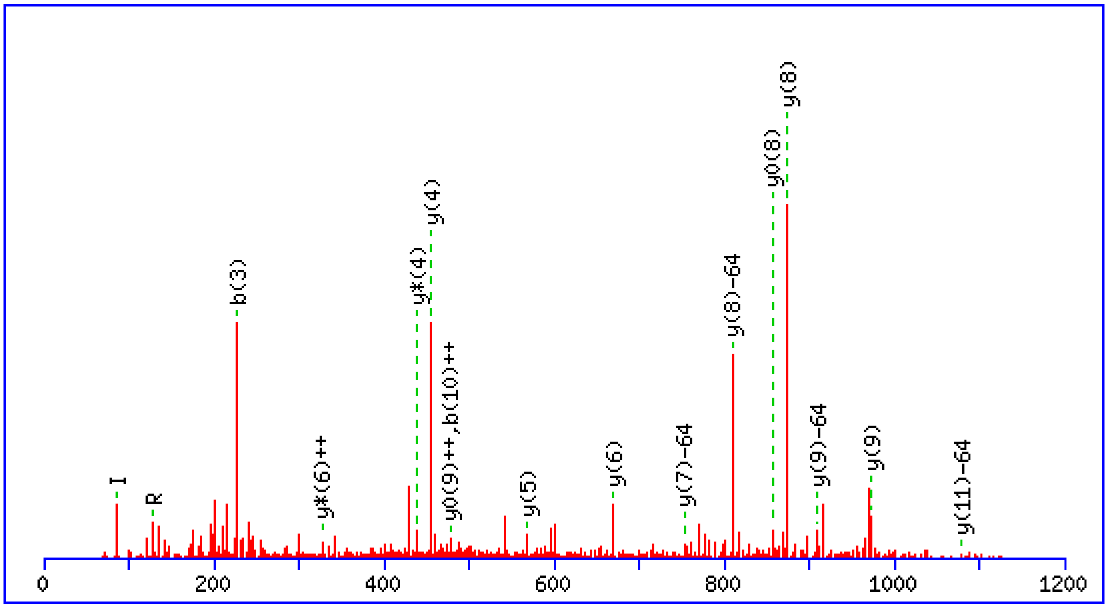


Monoisotopic mass of neutral peptide Mr(calc): 1176.6503
Fixed modifications: Carbamidomethyl (C)
Ions Score: 33 **Expect:** 0.042
Matches (Bold Red): 24/117 fragment ions using 52 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			V							13
2	44.0495	**171.1128**	**86.0600**			A	**1078.5891**	539.7982	1061.5626	531.2849	1060.5786	530.7929	12
3	**120.0808**	**318.1812**	159.5942			F	**1007.5520**	**504.2797**	990.5255	495.7664	**989.5415**	**495.2744**	11
4	**86.0964**	431.2653	216.1363			I	**860.4836**	430.7454	843.4571	422.2322	**842.4730**	421.7402	10
5	74.0600	**532.3130**	266.6601	514.3024	257.6548	T	**747.3995**	**374.2034**	730.3730	365.6901	**729.3890**	365.1981	9
6	30.0338	589.3344	295.1709	**571.3239**	286.1656	G	**646.3519**	323.6796	629.3253	315.1663	628.3413	314.6743	8
7	30.0338	**646.3559**	323.6816	628.3453	314.6763	G	589.3304	295.1688	572.3039	286.6556	**571.3198**	286.1636	7
8	30.0338	703.3774	352.1923	685.3668	343.1870	G	**532.3089**	266.6581	515.2824	258.1448	514.2984	257.6528	6
9	74.0600	804.4250	402.7162	786.4145	393.7109	T	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	5
10	30.0338	861.4465	431.2269	843.4359	422.2216	G	**374.2398**	187.6235	357.2132	179.1103			4
11	**86.0964**	974.5306	487.7689	956.5200	478.7636	L	317.2183	159.1128	300.1918	150.5995			3
12	30.0338	1031.5520	516.2797	1013.5415	507.2744	G	**204.1343**	102.5708	187.1077	94.0575			2
13	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **GGIVGMTLPIAR**
Found in **Q99714**, Q99714|HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3

Match to Query 474: 1199.667192 from(600.840872,2+)

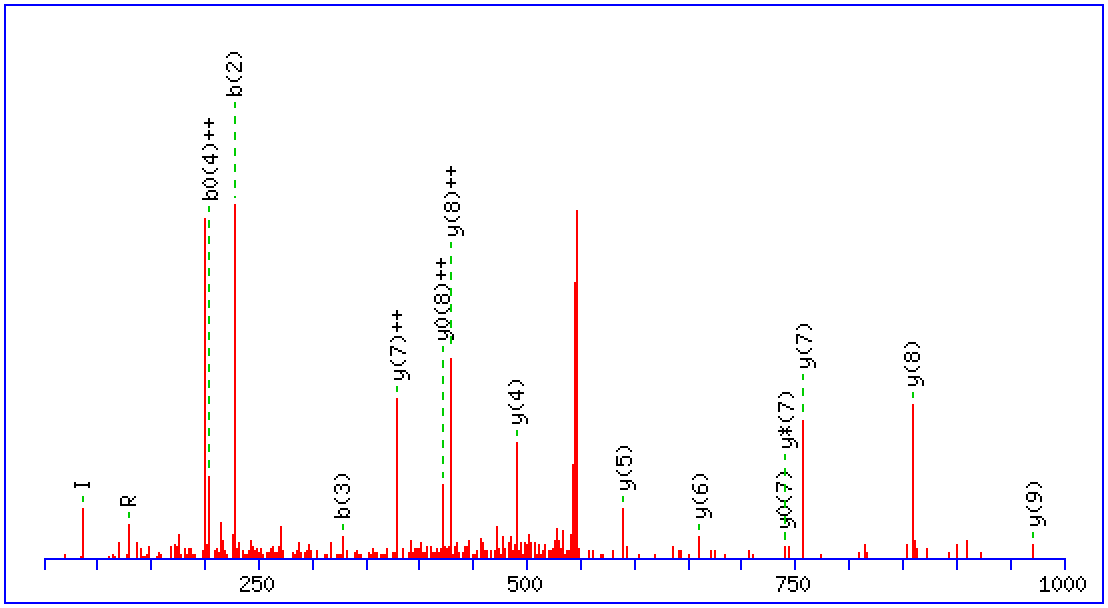


Monoisotopic mass of neutral peptide Mr(calc): 1199.6696
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.014
Matches (Bold Red): 20/153 fragment ions using 47 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			**G**							**12**
2	30.0338	115.0502	58.0287			**G**	**1079.6572**	540.3322	1062.6306	531.8189	1061.6466	531.3269	**11**
3	**86.0964**	**228.1343**	114.5708			**I**	1022.6357	511.8215	1005.6091	503.3082	1004.6251	502.8162	**10**
4	72.0808	**327.2027**	164.1050			**V**	**909.5516**	455.2795	892.5251	446.7662	891.5411	446.2742	**9**
5	30.0338	384.2241	192.6157			**G**	**810.4832**	405.7452	793.4567	397.2320	792.4727	396.7400	**8**
6	56.0495	467.2613	234.1343			**M**	**753.4618**	377.2345	736.4352	368.7212	735.4512	368.2292	**7**
7	74.0600	568.3089	284.6581	550.2984	275.6528	**T**	**670.4246**	335.7160	653.3981	**327.2027**	652.4141	326.7107	**6**
8	**86.0964**	681.3930	341.2001	663.3824	332.1949	**L**	**569.3770**	285.1921	552.3504	276.6788			**5**
9	70.0651	778.4458	389.7265	760.4352	380.7212	**P**	**456.2929**	228.6501	**439.2663**	220.1368			**4**
10	**86.0964**	891.5298	446.2686	873.5193	437.2633	**I**	359.2401	180.1237	342.2136	171.6104			**3**
11	44.0495	962.5669	481.7871	944.5564	472.7818	**A**	246.1561	123.5817	229.1295	115.0684			**2**
12	**129.1135**					**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LITPAVVSER**
Found in **P62851**, P62851|RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1

Match to Query 332: 1083.652664 from(542.833608,2+)

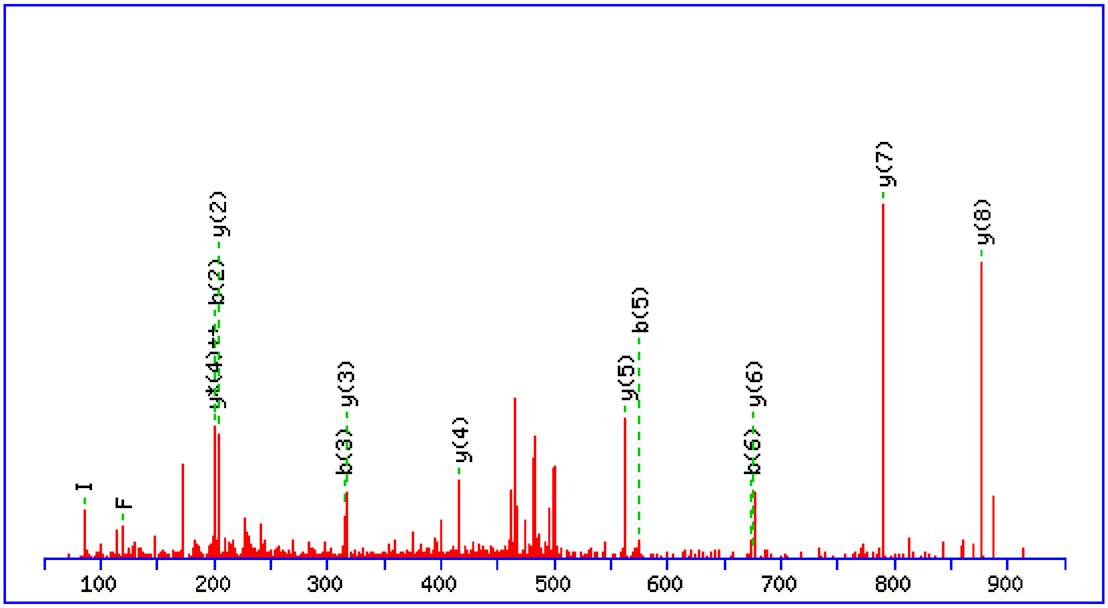


Monoisotopic mass of neutral peptide Mr(calc): 1083.6288
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 **Expect:** 0.018
Matches (Bold Red): 17/94 fragment ions using 29 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			L							10
2	**86.0964**	**227.1754**	114.0913			I	**971.5520**	486.2796	954.5255	477.7664	953.5415	477.2744	9
3	74.0600	**328.2231**	164.6152	310.2125	155.6099	T	**858.4680**	**429.7376**	841.4414	421.2243	840.4574	**420.7323**	8
4	70.0651	425.2758	213.1416	407.2653	**204.1363**	P	**757.4203**	**379.2138**	**740.3937**	370.7005	**739.4097**	370.2085	7
5	44.0495	496.3130	248.6601	478.3024	239.6548	A	**660.3675**	330.6874	643.3410	322.1741	642.3569	321.6821	6
6	72.0808	595.3814	298.1943	577.3708	289.1890	V	**589.3304**	295.1688	572.3039	286.6556	571.3198	286.1636	5
7	72.0808	694.4498	347.7285	676.4392	338.7232	V	**490.2620**	245.6346	473.2354	237.1214	472.2514	236.6293	4
8	60.0444	781.4818	391.2445	763.4713	382.2393	S	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
9	102.0550	910.5244	455.7658	892.5138	446.7606	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10	**129.1135**					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LSNIFVIGK**
Found in **P62701**, P62701|RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2

Match to Query 328: 989.563282 from(495.788917,2+)

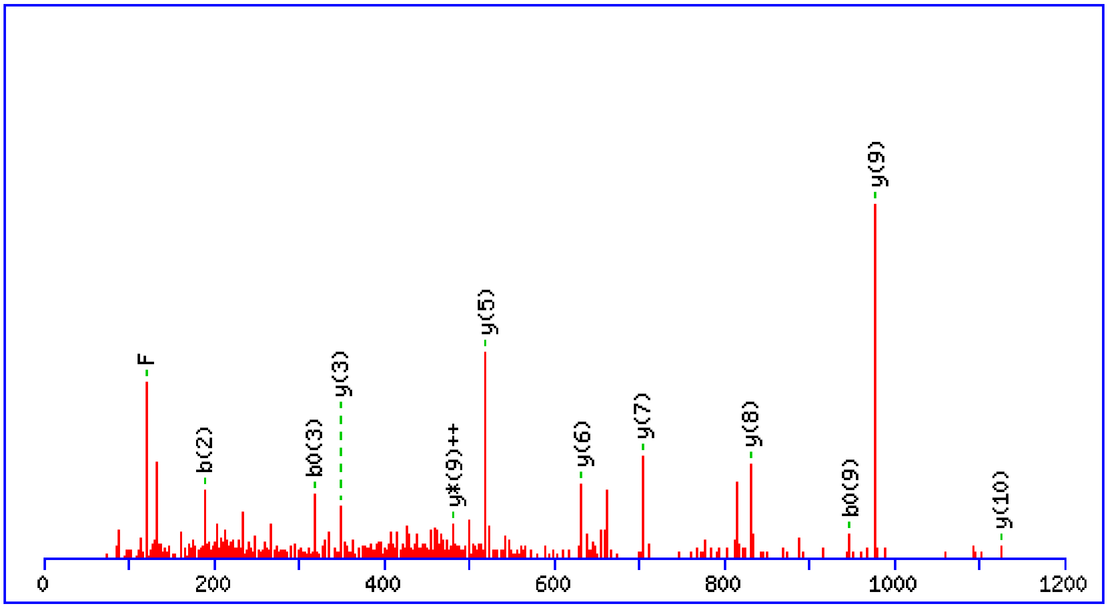


Monoisotopic mass of neutral peptide Mr(calc): 989.5910
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 **Expect:** 7.4e-005
Matches (Bold Red): 16/85 fragment ions using 21 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**9**
2	60.0444	**201.1234**	101.0653			183.1128	92.0600	**S**	**877.5142**	439.2607	860.4876	430.7475	859.5036	430.2554	**8**
3	87.0553	**315.1663**	158.0868	298.1397	149.5735	297.1557	149.0815	**N**	**790.4822**	395.7447	773.4556	387.2314			**7**
4	**86.0964**	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	**I**	**676.4392**	338.7233	659.4127	330.2100			**6**
5	**120.0808**	**575.3188**	288.1630	558.2922	279.6498	557.3082	279.1577	**F**	**563.3552**	282.1812	546.3286	273.6679			**5**
6	72.0808	**674.3872**	337.6972	657.3606	329.1840	656.3766	328.6919	**V**	**416.2867**	208.6470	399.2602	**200.1337**			**4**
7	**86.0964**	787.4713	394.2393	770.4447	385.7260	769.4607	385.2340	**I**	**317.2183**	159.1128	300.1918	150.5995			**3**
8	30.0338	844.4927	422.7500	827.4662	414.2367	826.4822	413.7447	**G**	**204.1343**	102.5708	187.1077	94.0575			**2**
9	101.1073							**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **TSFFQALGITTK**
Found in **P05388**, P05388|RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1

Match to Query 529: 1312.704818 from(657.359685,2+)

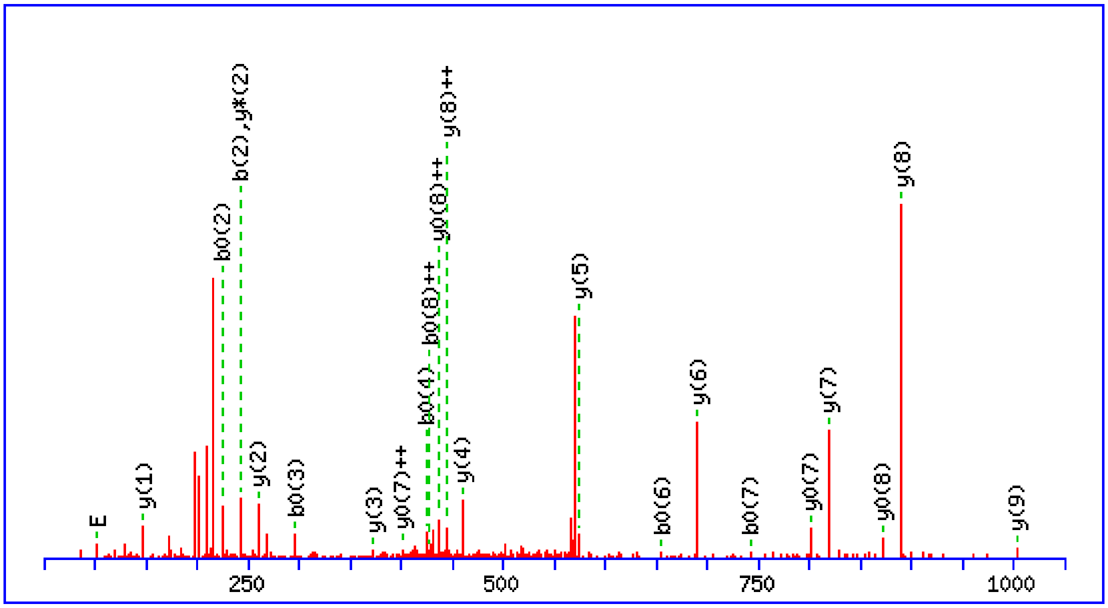


Monoisotopic mass of neutral peptide Mr(calc): 1312.7027
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 **Expect:** 0.0035
Matches (Bold Red): 13/134 fragment ions using 15 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	**T**							**12**
2	60.0444	**189.0870**	95.0471			171.0764	86.0418	**S**	1212.6623	606.8348	1195.6358	598.3215	1194.6517	597.8295	**11**
3	**120.0808**	336.1554	168.5813			**318.1448**	159.5761	**F**	**1125.6303**	563.3188	1108.6037	554.8055	1107.6197	554.3135	**10**
4	**120.0808**	483.2238	242.1155			465.2132	233.1103	**F**	**978.5619**	489.7846	961.5353	**481.2713**	960.5513	480.7793	**9**
5	101.0709	611.2824	306.1448	594.2558	297.6316	593.2718	297.1395	**Q**	**831.4934**	416.2504	814.4669	407.7371	813.4829	407.2451	**8**
6	44.0495	682.3195	341.6634	665.2930	333.1501	664.3089	332.6581	**A**	**703.4349**	352.2211	686.4083	343.7078	685.4243	343.2158	**7**
7	86.0964	795.4036	398.2054	778.3770	389.6921	777.3930	389.2001	**L**	**632.3978**	316.7025	615.3712	308.1892	614.3872	307.6972	**6**
8	30.0338	852.4250	426.7162	835.3985	418.2029	834.4145	417.7109	**G**	**519.3137**	260.1605	502.2871	251.6472	501.3031	251.1552	**5**
9	86.0964	965.5091	483.2582	948.4825	474.7449	**947.4985**	474.2529	**I**	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	**4**
10	74.0600	1066.5568	533.7820	1049.5302	525.2688	1048.5462	524.7767	**T**	**349.2082**	175.1077	332.1816	166.5944	331.1976	166.1024	**3**
11	74.0600	1167.6045	584.3059	1150.5779	575.7926	1149.5939	575.3006	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
12	101.1073							**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **ELAEDDSILK**
Found in **P56385**, P56385|ATP5I_HUMAN ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=2 SV=2

Match to Query 267: 1131.487464 from(566.751008,2+)

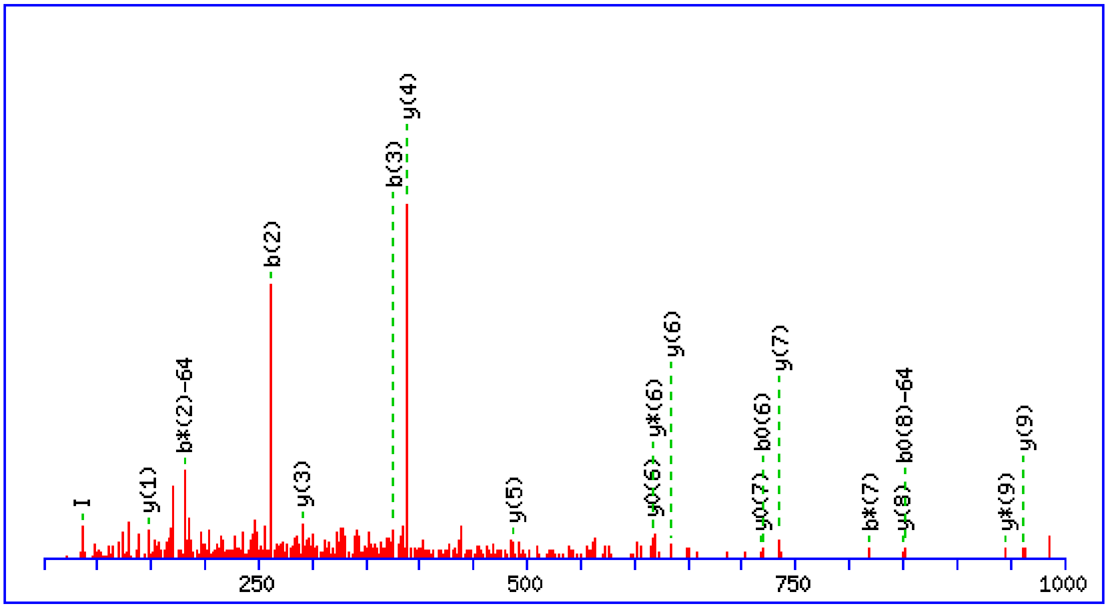


Monoisotopic mass of neutral peptide Mr(calc): 1131.5659
Fixed modifications: Carbamidomethyl (C)
Ions Score: 47 **Expect:** 0.0015
Matches (Bold Red): 24/94 fragment ions using 41 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**102.0550**	130.0499	65.5286	112.0393	56.5233	E							10
2	86.0964	**243.1339**	122.0706	**225.1234**	113.0653	L	**1003.5306**	502.2689	986.5041	493.7557	985.5201	493.2637	9
3	44.0495	314.1710	157.5892	**296.1605**	148.5839	A	**890.4466**	**445.7269**	873.4200	437.2136	**872.4360**	**436.7216**	8
4	**102.0550**	443.2136	222.1105	**425.2031**	213.1052	E	**819.4094**	410.2084	802.3829	401.6951	**801.3989**	**401.2031**	7
5	88.0393	558.2406	279.6239	540.2300	270.6186	D	**690.3668**	345.6871	673.3403	337.1738	672.3563	336.6818	6
6	88.0393	673.2675	337.1374	**655.2570**	328.1321	D	**575.3399**	288.1736	558.3134	279.6603	557.3293	279.1683	5
7	60.0444	760.2996	380.6534	**742.2890**	371.6481	S	**460.3130**	230.6601	443.2864	222.1468	442.3024	221.6548	4
8	86.0964	873.3836	437.1954	855.3731	**428.1902**	I	**373.2809**	187.1441	356.2544	178.6308			3
9	86.0964	986.4677	493.7375	968.4571	484.7322	L	**260.1969**	130.6021	**243.1703**	122.0888			2
10	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **NMINTFVPSGK**
Found in **Q13510**, Q13510|ASAH1_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=1 SV=4

Match to Query 208: 1222.385308 from(612.199930,2+)

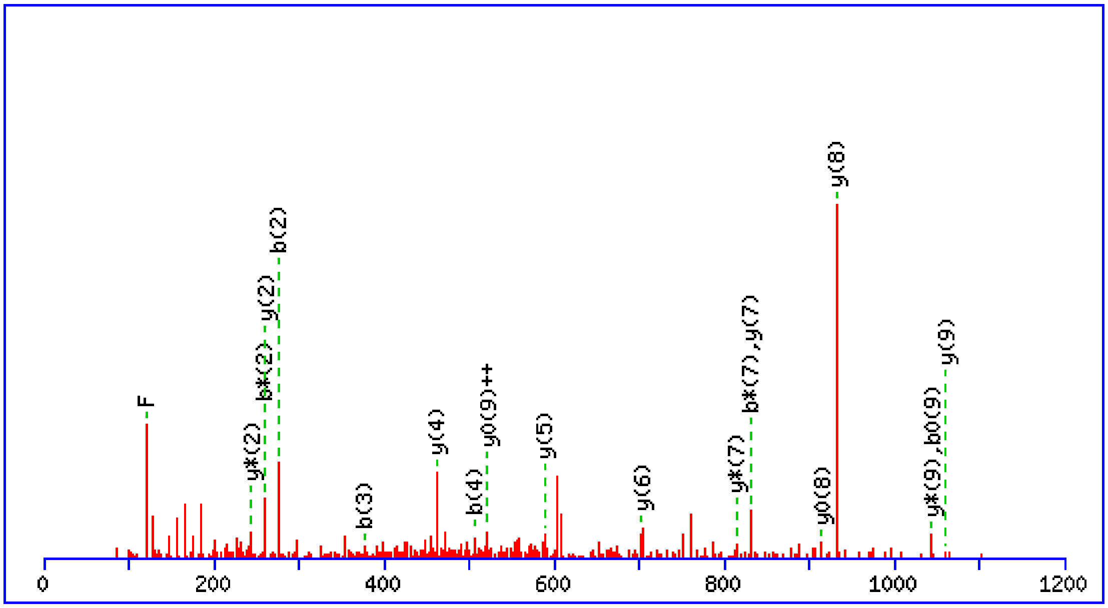


Monoisotopic mass of neutral peptide Mr(calc): 1222.6016
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 40 **Expect:** 0.0064
Matches (Bold Red): 19/174 fragment ions using 46 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	87.0553	115.0502	58.0287	98.0237	49.5155			N							11
2	120.0478	**262.0856**	131.5464	245.0591	123.0332			M	1109.5660	555.2866	1092.5394	546.7733	1091.5554	546.2813	10
3	**86.0964**	**375.1697**	188.0885	358.1431	179.5752			I	**962.5306**	481.7689	**945.5040**	473.2556	944.5200	472.7636	9
4	87.0553	489.2126	245.1099	472.1860	236.5967			N	**849.4465**	425.2269	832.4199	416.7136	831.4359	416.2216	8
5	74.0600	590.2603	295.6338	573.2337	287.1205	572.2497	286.6285	T	**735.4036**	368.2054	718.3770	359.6921	**717.3930**	359.2001	7
6	120.0808	737.3287	369.1680	720.3021	360.6547	**719.3181**	360.1627	F	**634.3559**	317.6816	**617.3293**	309.1683	**616.3453**	308.6763	6
7	72.0808	836.3971	418.7022	**819.3706**	410.1889	818.3865	409.6969	V	**487.2875**	244.1474	470.2609	235.6341	469.2769	235.1421	5
8	70.0651	933.4499	467.2286	916.4233	458.7153	915.4393	458.2233	P	**388.2191**	194.6132	371.1925	186.0999	370.2085	185.6079	4
9	60.0444	1020.4819	510.7446	1003.4553	502.2313	1002.4713	501.7393	S	**291.1663**	146.0868	274.1397	137.5735	273.1557	137.0815	3
10	30.0338	1077.5034	539.2553	1060.4768	530.7420	1059.4928	530.2500	G	204.1343	102.5708	187.1077	94.0575			2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **FQTEIQTVNK**
Found in **P14868**, P14868|SYDC_HUMAN Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2

Match to Query 308: 1206.600008 from(604.307280,2+)

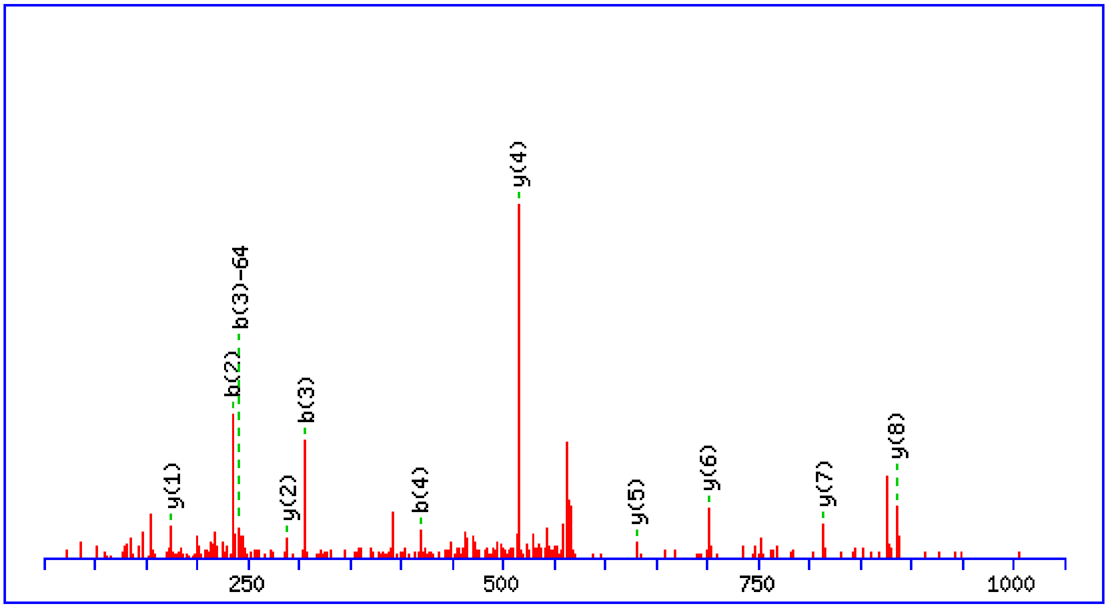


Monoisotopic mass of neutral peptide Mr(calc): 1206.6245
Fixed modifications: Carbamidomethyl (C)
Ions Score: 33 **Expect:** 0.035
Matches (Bold Red): 19/106 fragment ions using 47 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							10
2	101.0709	**276.1343**	138.5708	**259.1077**	130.0575			Q	**1060.5633**	530.7853	**1043.5368**	522.2720	1042.5528	**521.7800**	9
3	74.0600	**377.1819**	189.0946	360.1554	180.5813	359.1714	180.0893	T	**932.5047**	466.7560	915.4782	458.2427	**914.4942**	457.7507	8
4	102.0550	**506.2245**	253.6159	489.1980	245.1026	488.2140	244.6106	E	**831.4571**	416.2322	**814.4305**	407.7189	813.4465	407.2269	7
5	86.0964	619.3086	310.1579	602.2821	301.6447	601.2980	301.1527	I	**702.4145**	351.7109	685.3879	343.1976	684.4039	342.7056	6
6	101.0709	747.3672	374.1872	730.3406	365.6740	729.3566	365.1819	Q	**589.3304**	295.1688	572.3039	286.6556	571.3198	286.1636	5
7	74.0600	848.4149	424.7111	**831.3883**	416.1978	830.4043	415.7058	T	**461.2718**	231.1395	444.2453	222.6263	443.2613	222.1343	4
8	72.0808	947.4833	474.2453	930.4567	465.7320	929.4727	465.2400	V	360.2241	180.6157	343.1976	172.1024			3
9	87.0553	1061.5262	531.2667	1044.4997	522.7535	**1043.5156**	522.2615	N	**261.1557**	131.0815	**244.1292**	122.5682			2
10	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **SMALADPENR**
Found in **Q13884**, Q13884|SNTB1_HUMAN Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3

Match to Query 278: 1118.601752 from(560.308152,2+)

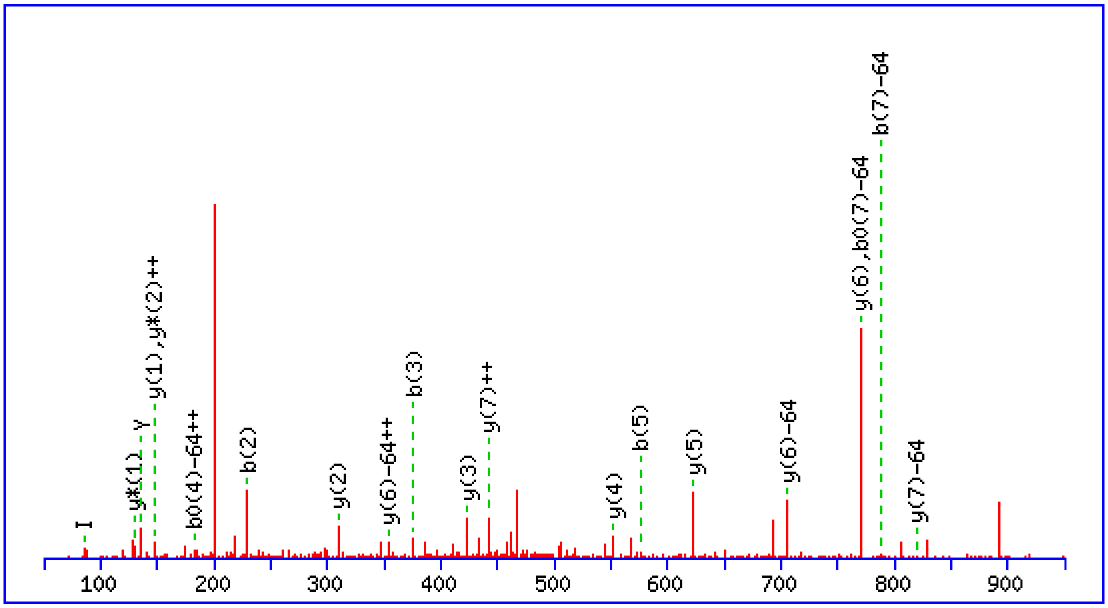


Monoisotopic mass of neutral peptide Mr(calc): 1118.5026
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 46 **Expect:** 0.0022
Matches (Bold Red): 11/139 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	**S**							**10**
2	120.0478	**235.0747**	118.0410			217.0641	109.0357	**M**	1032.4779	516.7426	1015.4513	508.2293	1014.4673	507.7373	**9**
3	44.0495	**306.1118**	153.5595			288.1013	144.5543	**A**	**885.4425**	443.2249	868.4159	434.7116	867.4319	434.2196	**8**
4	86.0964	**419.1959**	210.1016			401.1853	201.0963	**L**	**814.4054**	407.7063	797.3788	399.1930	796.3948	398.7010	**7**
5	44.0495	490.2330	245.6201			472.2224	236.6149	**A**	**701.3213**	351.1643	684.2947	342.6510	683.3107	342.1590	**6**
6	88.0393	605.2599	303.1336			587.2494	294.1283	**D**	**630.2842**	315.6457	613.2576	307.1325	612.2736	306.6404	**5**
7	70.0651	702.3127	351.6600			684.3021	342.6547	**P**	**515.2572**	258.1323	498.2307	249.6190	497.2467	249.1270	**4**
8	102.0550	831.3553	416.1813			813.3447	407.1760	**E**	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	**3**
9	87.0553	945.3982	473.2028	928.3717	464.6895	927.3877	464.1975	**N**	**289.1619**	145.0846	272.1353	136.5713			**2**
10	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **DIMAEIYK**
Found in **P07858**, P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3

Match to Query 354: 997.441480 from(499.728016,2+)

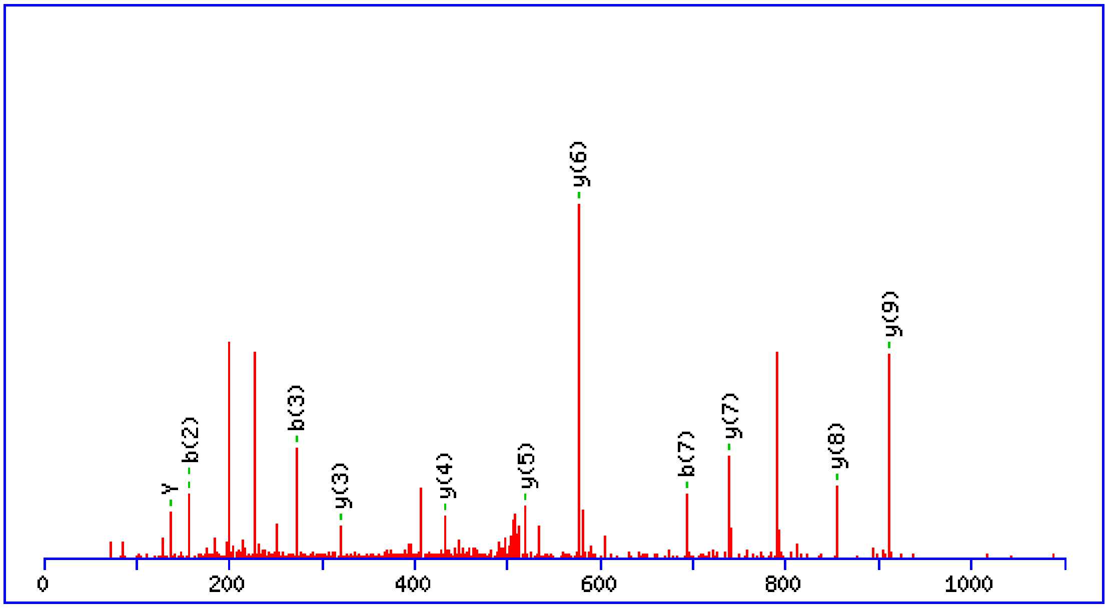


Monoisotopic mass of neutral peptide Mr(calc): 997.4790
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.02
Matches (Bold Red): 21/105 fragment ions using 45 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	116.0342	58.5207	98.0237	49.5155	D							8
2	**86.0964**	**229.1183**	115.0628	211.1077	106.0575	I	**819.4611**	410.2342	802.4345	401.7209	801.4505	401.2289	7
3	56.0495	312.1554	156.5813	294.1448	147.5761	M	**706.3770**	**353.6921**	689.3505	345.1789	688.3665	344.6869	6
4	44.0495	383.1925	192.0999	365.1820	**183.0946**	A	**623.3399**	312.1736	606.3134	303.6603	605.3293	303.1683	5
5	102.0550	512.2351	256.6212	494.2245	247.6159	E	**552.3028**	276.6550	535.2762	268.1418	534.2922	267.6498	4
6	**86.0964**	625.3192	313.1632	607.3086	304.1579	I	**423.2602**	212.1337	406.2336	203.6205			3
7	**136.0757**	**788.3825**	394.6949	**770.3719**	385.6896	Y	**310.1761**	155.5917	293.1496	**147.0784**			2
8	101.1073					K	**147.1128**	74.0600	**130.0863**	65.5468			1

MS/MS Fragmentation of **VGDYGSLSGR**
Found in **Q9UBR2**, Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1

Match to Query 179: 1009.564070 from(505.789311,2+)

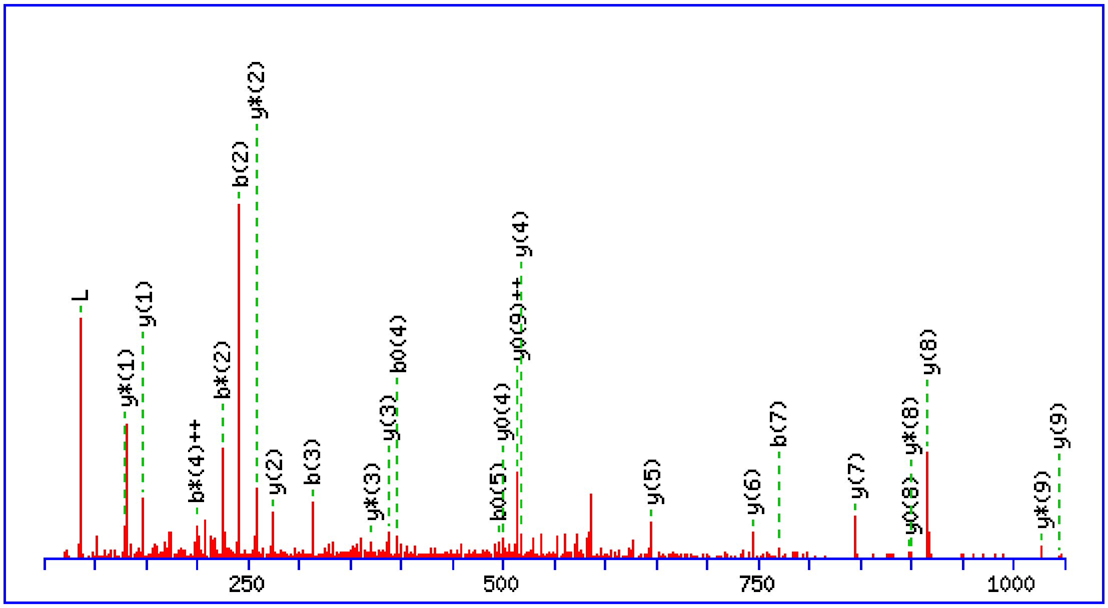


Monoisotopic mass of neutral peptide Mr(calc): 1009.4829
Fixed modifications: Carbamidomethyl (C)
Ions Score: 55 **Expect:** 0.00018
Matches (Bold Red): 11/92 fragment ions using 18 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415			V							10
2	30.0338	**157.0972**	79.0522			G	**911.4217**	456.2145	894.3952	447.7012	893.4112	447.2092	9
3	88.0393	**272.1241**	136.5657	254.1135	127.5604	D	**854.4003**	427.7038	837.3737	419.1905	836.3897	418.6985	8
4	**136.0757**	435.1874	218.0974	417.1769	209.0921	Y	**739.3733**	370.1903	722.3468	361.6770	721.3628	361.1850	7
5	30.0338	492.2089	246.6081	474.1983	237.6028	G	**576.3100**	288.6586	559.2835	280.1454	558.2994	279.6534	6
6	60.0444	579.2409	290.1241	561.2304	281.1188	S	**519.2885**	260.1479	502.2620	251.6346	501.2780	251.1426	5
7	86.0964	**692.3250**	346.6661	674.3144	337.6608	L	**432.2565**	216.6319	415.2300	208.1186	414.2459	207.6266	4
8	60.0444	779.3570	390.1821	761.3464	381.1769	S	**319.1724**	160.0899	302.1459	151.5766	301.1619	151.0846	3
9	30.0338	836.3785	418.6929	818.3679	409.6876	G	232.1404	116.5738	215.1139	108.0606			2
10	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LQATVQELQK**
Found in **P31146**, P31146|COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4

Match to Query 260: 1156.434300 from(579.224426,2+)

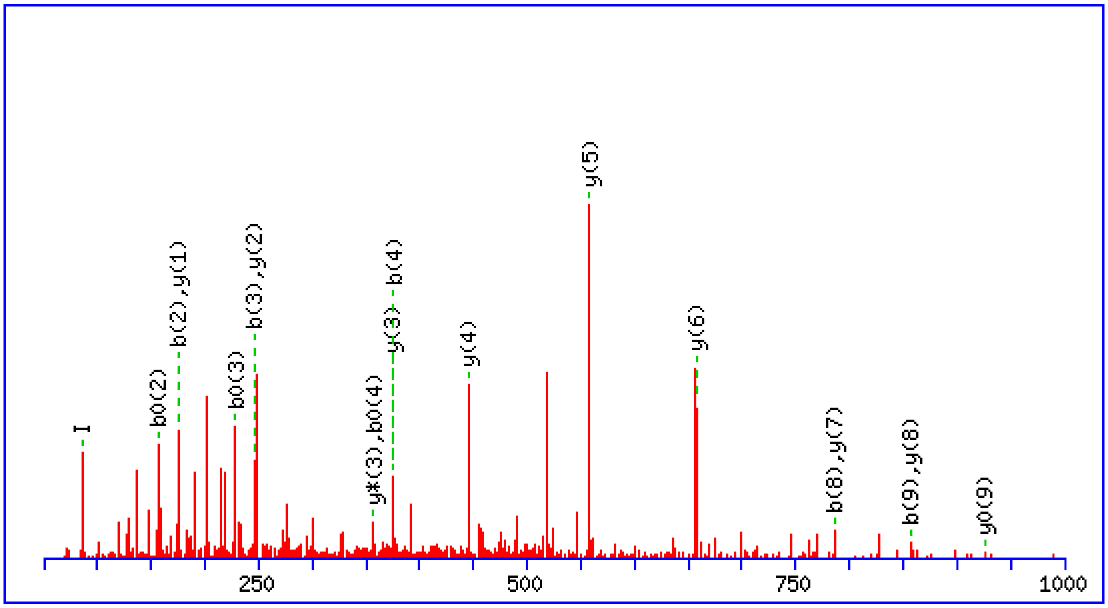


Monoisotopic mass of neutral peptide Mr(calc): 1156.6452
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 **Expect:** 0.00016
Matches (Bold Red): 26/104 fragment ions using 53 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							10
2	101.0709	**242.1499**	121.5786	**225.1234**	113.0653			Q	**1044.5684**	522.7878	**1027.5419**	514.2746	1026.5578	**513.7826**	9
3	44.0495	**313.1870**	157.0972	296.1605	148.5839			A	**916.5098**	458.7586	**899.4833**	450.2453	**898.4993**	449.7533	8
4	74.0600	414.2347	207.6210	397.2082	**199.1077**	**396.2241**	198.6157	T	**845.4727**	423.2400	828.4462	414.7267	827.4621	414.2347	7
5	72.0808	513.3031	257.1552	496.2766	248.6419	**495.2926**	248.1499	V	**744.4250**	372.7162	727.3985	364.2029	726.4145	363.7109	6
6	101.0709	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	Q	**645.3566**	323.1819	628.3301	314.6687	627.3461	314.1767	5
7	102.0550	**770.4043**	385.7058	753.3777	377.1925	752.3937	376.7005	E	**517.2980**	259.1527	500.2715	250.6394	**499.2875**	250.1474	4
8	**86.0964**	883.4884	442.2478	866.4618	433.7345	865.4778	433.2425	L	**388.2554**	194.6314	**371.2289**	186.1181			3
9	101.0709	1011.5469	506.2771	994.5204	497.7638	993.5364	497.2718	Q	**275.1714**	138.0893	**258.1448**	129.5761			2
10	101.1073							K	**147.1128**	74.0600	**130.0863**	65.5468			1

MS/MS Fragmentation of **SSAEVIAQAR**
Found in **Q16555**, Q16555|DPYL2_HUMAN Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1

Match to Query 160: 1030.390996 from(516.202774,2+)

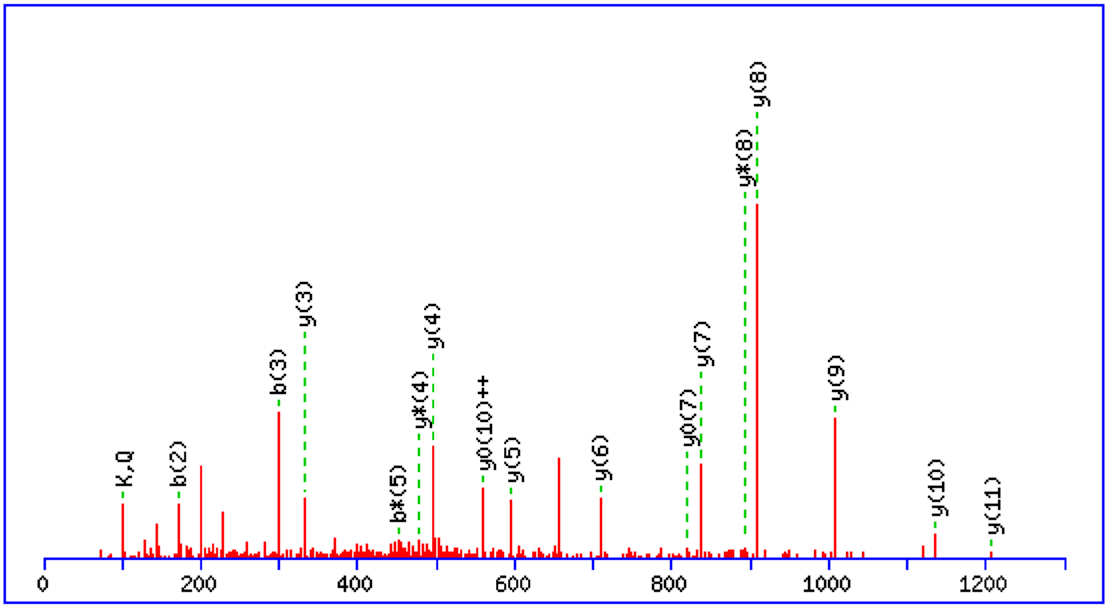


Monoisotopic mass of neutral peptide Mr(calc): 1030.5407
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 **Expect:** 0.023
Matches (Bold Red): 19/92 fragment ions using 47 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							10
2	60.0444	**175.0713**	88.0393			**157.0608**	79.0340	S	944.5160	472.7616	927.4894	464.2483	**926.5054**	463.7563	9
3	44.0495	**246.1084**	123.5579			**228.0979**	114.5526	A	**857.4839**	429.2456	840.4574	420.7323	839.4734	420.2403	8
4	102.0550	**375.1510**	188.0792			**357.1405**	179.0739	E	**786.4468**	393.7271	769.4203	385.2138	768.4363	384.7218	7
5	72.0808	474.2195	237.6134			456.2089	228.6081	V	**657.4042**	329.2058	640.3777	320.6925			6
6	**86.0964**	587.3035	294.1554			569.2930	285.1501	I	**558.3358**	279.6715	541.3093	271.1583			5
7	44.0495	658.3406	329.6740			640.3301	320.6687	A	**445.2518**	223.1295	428.2252	214.6162			4
8	101.0709	**786.3992**	393.7032	769.3727	385.1900	768.3886	384.6980	Q	**374.2146**	187.6110	**357.1881**	179.0977			3
9	44.0495	**857.4363**	429.2218	840.4098	420.7085	839.4258	420.2165	A	**246.1561**	123.5817	229.1295	115.0684			2
10	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VAQVAEITYGQK**
Found in **O94905**, O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1

Match to Query 515: 1305.658748 from(653.836650,2+)

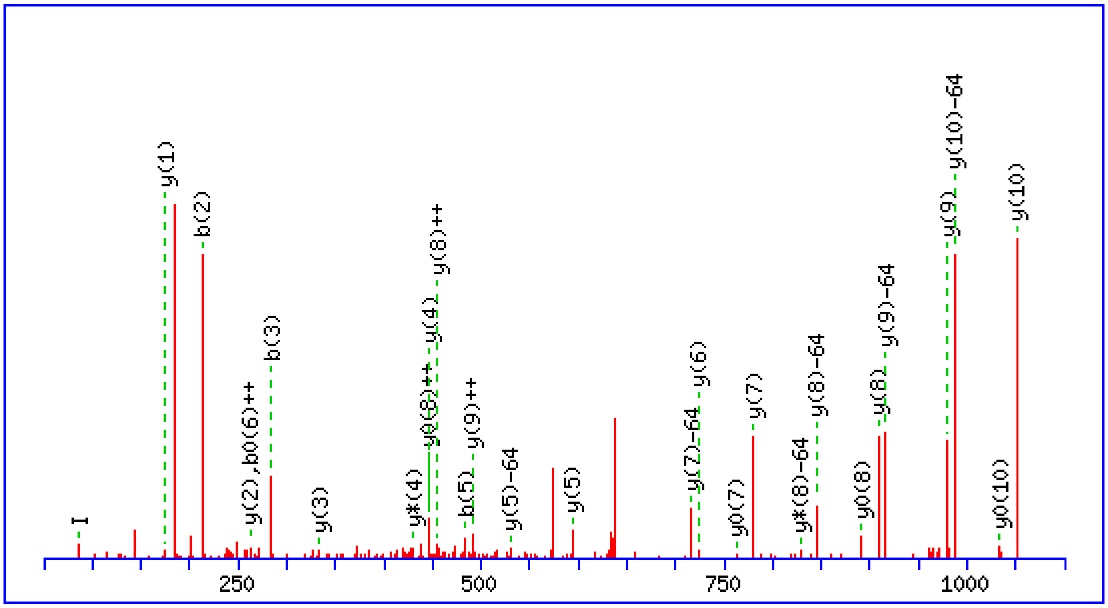


Monoisotopic mass of neutral peptide Mr(calc): 1305.6929
Fixed modifications: Carbamidomethyl (C)
Ions Score: 76 **Expect:** 1.6e-006
Matches (Bold Red): 19/122 fragment ions using 26 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					**V**							**12**
2	44.0495	**171.1128**	86.0600					**A**	**1207.6317**	604.3195	1190.6052	595.8062	1189.6212	595.3142	**11**
3	**101.0709**	**299.1714**	150.0893	282.1448	141.5761			**Q**	**1136.5946**	568.8009	1119.5681	560.2877	1118.5841	**559.7957**	**10**
4	72.0808	398.2398	199.6235	381.2132	191.1103			**V**	**1008.5360**	504.7717	991.5095	496.2584	990.5255	495.7664	**9**
5	44.0495	469.2769	235.1421	**452.2504**	226.6288			**A**	**909.4676**	455.2375	**892.4411**	446.7242	891.4571	446.2322	**8**
6	102.0550	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	**E**	**838.4305**	419.7189	821.4040	411.2056	**820.4199**	410.7136	**7**
7	86.0964	711.4036	356.2054	694.3770	347.6921	693.3930	347.2001	**I**	**709.3879**	355.1976	692.3614	346.6843	691.3774	346.1923	**6**
8	74.0600	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	**T**	**596.3039**	298.6556	579.2773	290.1423	578.2933	289.6503	**5**
9	136.0757	975.5146	488.2609	958.4880	479.7477	957.5040	479.2556	**Y**	**495.2562**	248.1317	**478.2296**	239.6185			**4**
10	30.0338	1032.5360	516.7717	1015.5095	508.2584	1014.5255	507.7664	**G**	**332.1928**	166.6001	315.1663	158.0868			**3**
11	**101.0709**	1160.5946	580.8009	1143.5681	572.2877	1142.5841	571.7957	**Q**	275.1714	138.0893	258.1448	129.5761			**2**
12	**101.1073**							**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **VIAAEGEMNASR**
Found in **P27105**, P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3

Match to Query 449: 1262.593980 from(632.304266,2+)

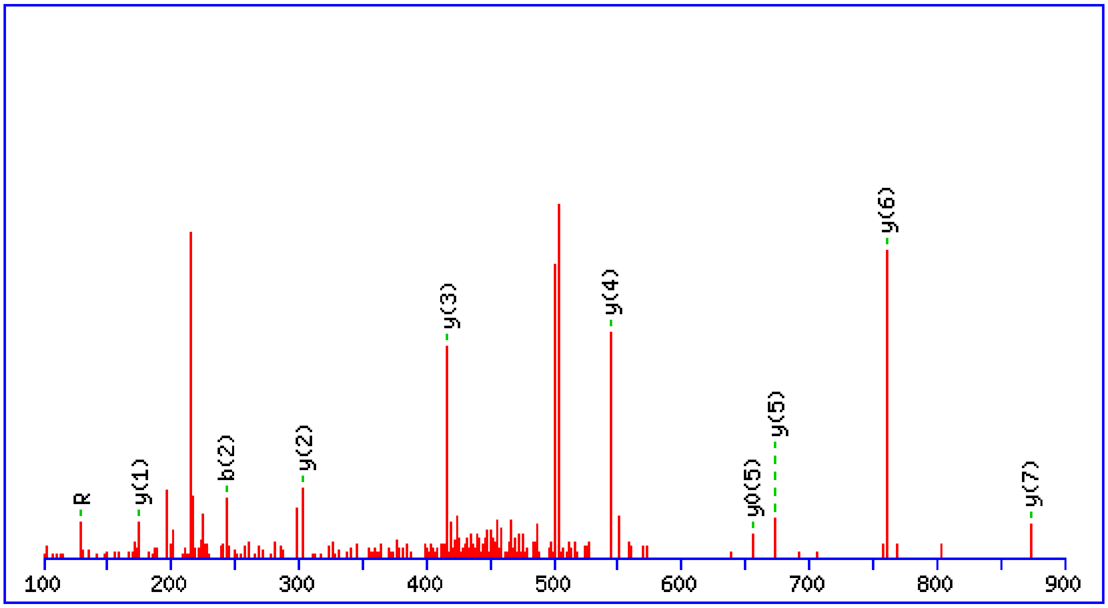


Monoisotopic mass of neutral peptide Mr(calc): 1262.5925
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 60 **Expect:** 8.1e-005
Matches (Bold Red): 28/183 fragment ions using 53 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							12
2	**86.0964**	**213.1598**	107.0835					I	1164.5314	582.7693	1147.5048	574.2560	1146.5208	573.7640	11
3	44.0495	**284.1969**	142.6021					A	**1051.4473**	526.2273	1034.4208	517.7140	**1033.4367**	517.2220	10
4	44.0495	355.2340	178.1206					A	**980.4102**	**490.7087**	963.3836	482.1955	962.3996	481.7035	9
5	102.0550	**484.2766**	242.6419			466.2660	233.6366	E	**909.3731**	**455.1902**	892.3465	446.6769	**891.3625**	**446.1849**	8
6	30.0338	541.2980	271.1527			523.2875	**262.1474**	G	**780.3305**	390.6689	763.3039	382.1556	**762.3199**	381.6636	7
7	102.0550	670.3406	335.6740			652.3301	326.6687	E	**723.3090**	362.1581	706.2825	353.6449	705.2985	353.1529	6
8	120.0478	817.3760	409.1917			799.3655	400.1864	M	**594.2664**	297.6369	577.2399	289.1236	576.2559	288.6316	5
9	87.0553	931.4190	466.2131	914.3924	457.6998	913.4084	457.2078	N	**447.2310**	224.1191	**430.2045**	215.6059	429.2205	215.1139	4
10	44.0495	1002.4561	501.7317	985.4295	493.2184	984.4455	492.7264	A	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	3
11	60.0444	1089.4881	545.2477	1072.4616	536.7344	1071.4775	536.2424	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
12	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ELSEQIQR**
Found in **P15311**, P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4

Match to Query 290: 1001.508814 from(501.761683,2+)

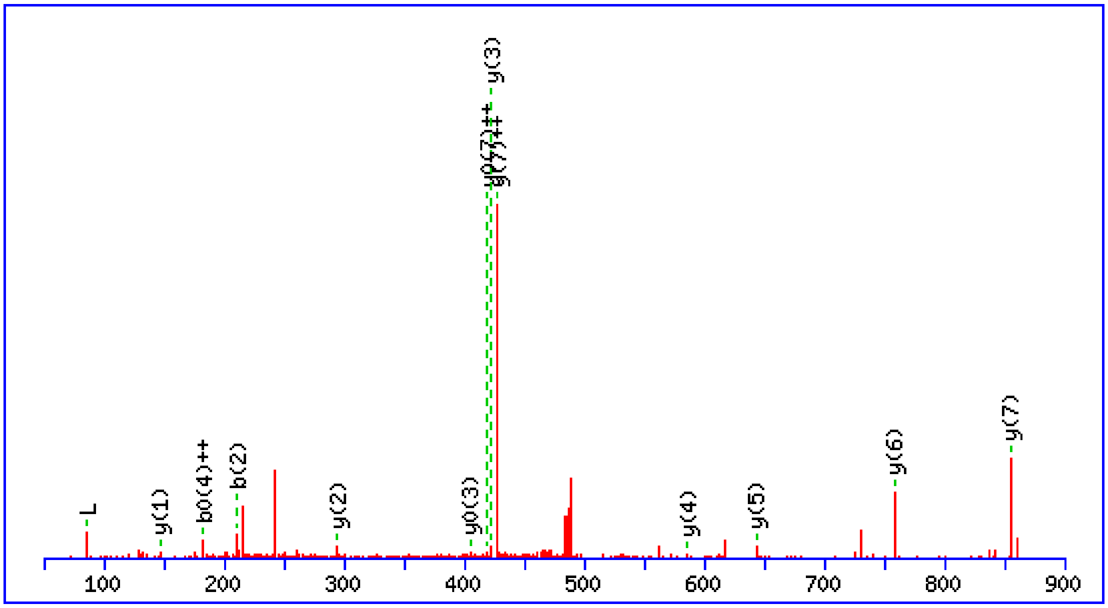


Monoisotopic mass of neutral peptide Mr(calc): 1001.5141
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.012
Matches (Bold Red): 10/76 fragment ions using 24 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286			112.0393	56.5233	E							8
2	86.0964	**243.1339**	122.0706			225.1234	113.0653	L	**873.4789**	437.2431	856.4523	428.7298	855.4683	428.2378	7
3	60.0444	330.1660	165.5866			312.1554	156.5813	S	**760.3948**	380.7010	743.3682	372.1878	742.3842	371.6958	6
4	102.0550	459.2086	230.1079			441.1980	221.1026	E	**673.3628**	337.1850	656.3362	328.6717	**655.3522**	328.1797	5
5	101.0709	587.2671	294.1372	570.2406	285.6239	569.2566	285.1319	Q	**544.3202**	272.6637	527.2936	264.1504			4
6	86.0964	700.3512	350.6792	683.3246	342.1660	682.3406	341.6740	I	**416.2616**	208.6344	399.2350	200.1212			3
7	101.0709	828.4098	414.7085	811.3832	406.1953	810.3992	405.7032	Q	**303.1775**	152.0924	286.1510	143.5791			2
8	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LPDGYEFK**
Found in **P09382**, P09382|LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2

Match to Query 286: 967.493274 from(484.753913,2+)

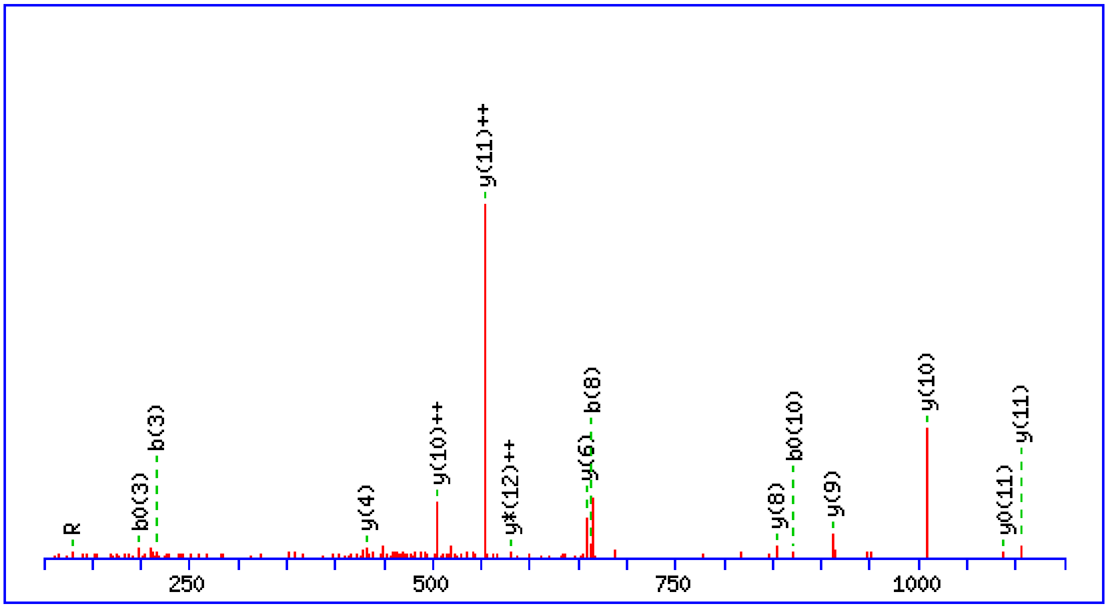


Monoisotopic mass of neutral peptide Mr(calc): 967.4651
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.0087
Matches (Bold Red): 13/70 fragment ions using 33 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			L							8
2	70.0651	**211.1441**	106.0757			P	**855.3883**	**428.1978**	838.3618	419.6845	837.3777	**419.1925**	7
3	88.0393	326.1710	163.5892	308.1605	154.5839	D	**758.3355**	379.6714	741.3090	371.1581	740.3250	370.6661	6
4	30.0338	383.1925	192.0999	365.1819	**183.0946**	G	**643.3086**	322.1579	626.2821	313.6447	625.2980	313.1527	5
5	136.0757	546.2558	273.6316	528.2453	264.6263	Y	**586.2871**	293.6472	569.2606	285.1339	568.2766	284.6419	4
6	102.0550	675.2984	338.1529	657.2879	329.1476	E	**423.2238**	212.1155	406.1973	203.6023	**405.2132**	203.1103	3
7	120.0808	822.3668	411.6871	804.3563	402.6818	F	**294.1812**	147.5942	277.1547	139.0810			2
8	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **GSAPPGPVPEGSIR**
Found in **P78417**, P78417|GSTO1_HUMAN Glutathione transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2

Match to Query 588: 1319.661692 from(660.838122,2+)

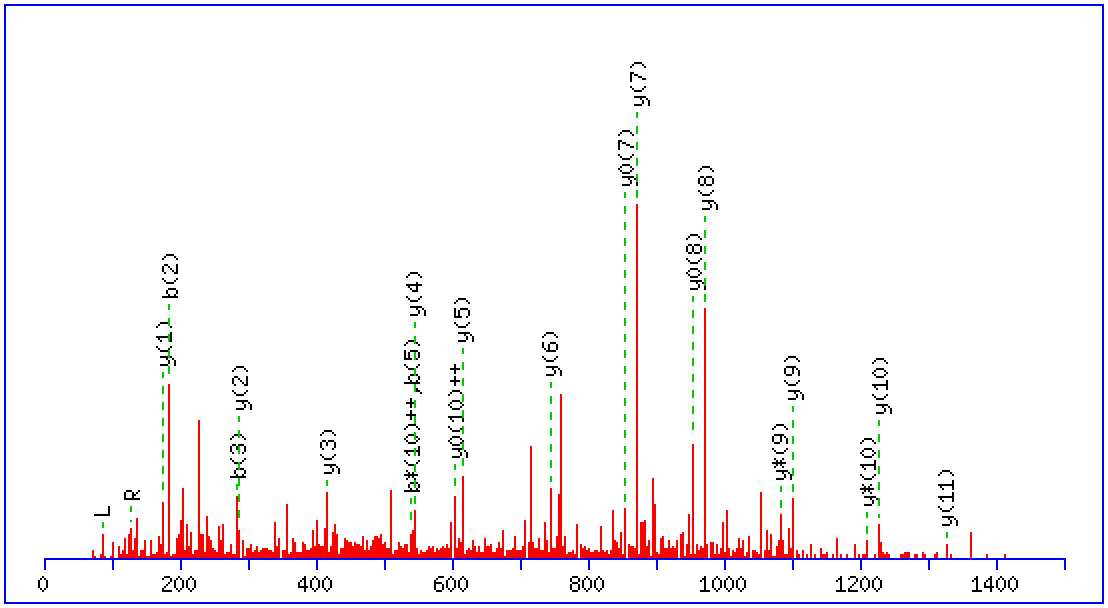


Monoisotopic mass of neutral peptide Mr(calc): 1319.6834
Fixed modifications: Carbamidomethyl (C)
Ions Score: 32 **Expect:** 0.049
Matches (Bold Red): 15/138 fragment ions using 34 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			G							14
2	60.0444	145.0608	73.0340	127.0502	64.0287	S	1263.6692	632.3382	1246.6426	623.8250	1245.6586	623.3329	13
3	44.0495	**216.0979**	108.5526	**198.0873**	99.5473	A	1176.6371	588.8222	1159.6106	**580.3089**	1158.6266	579.8169	12
4	70.0651	313.1506	157.0790	295.1401	148.0737	P	**1105.6000**	**553.3037**	1088.5735	544.7904	**1087.5895**	544.2984	11
5	70.0651	410.2034	205.6053	392.1928	196.6001	P	**1008.5473**	**504.7773**	991.5207	496.2640	990.5367	495.7720	10
6	30.0338	467.2249	234.1161	449.2143	225.1108	G	**911.4945**	456.2509	894.4680	447.7376	893.4839	447.2456	9
7	70.0651	564.2776	282.6425	546.2671	273.6372	P	**854.4730**	427.7402	837.4465	419.2269	836.4625	418.7349	8
8	72.0808	**663.3461**	332.1767	645.3355	323.1714	V	757.4203	379.2138	740.3937	370.7005	739.4097	370.2085	7
9	70.0651	760.3988	380.7030	742.3883	371.6978	P	**658.3519**	329.6796	641.3253	321.1663	640.3413	320.6743	6
10	102.0550	889.4414	445.2243	**871.4308**	436.2191	E	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
11	30.0338	946.4629	473.7351	928.4523	464.7298	G	**432.2565**	216.6319	415.2300	208.1186	414.2459	207.6266	4
12	60.0444	1033.4949	517.2511	1015.4843	508.2458	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	86.0964	1146.5790	573.7931	1128.5684	564.7878	I	288.2030	144.6051	271.1765	136.0919			2
14	**129.1135**					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LAVQQVEEAQQLR**
Found in **O00461**, O00461|GOLI4_HUMAN Golgi integral membrane protein 4 OS=Homo sapiens GN=GOLIM4 PE=1 SV=1

Match to Query 685: 1510.763410 from(756.388981,2+)

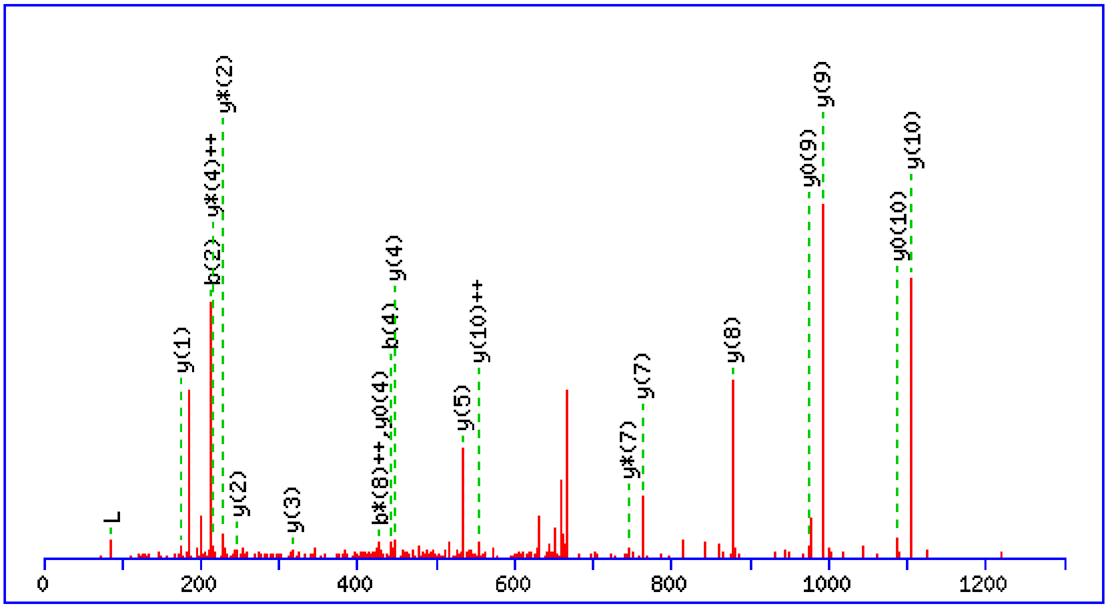


Monoisotopic mass of neutral peptide Mr(calc): 1510.8103
Fixed modifications: Carbamidomethyl (C)
Ions Score: 58 **Expect:** 0.00011
Matches (Bold Red): 23/129 fragment ions using 55 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**13**
2	44.0495	**185.1285**	93.0679					**A**	1398.7336	699.8704	1381.7070	691.3571	1380.7230	690.8651	**12**
3	72.0808	**284.1969**	142.6021					**V**	**1327.6965**	664.3519	1310.6699	655.8386	1309.6859	655.3466	**11**
4	101.0709	412.2554	206.6314	395.2289	198.1181			**Q**	**1228.6280**	614.8177	**1211.6015**	606.3044	1210.6175	**605.8124**	**10**
5	101.0709	**540.3140**	270.6607	523.2875	262.1474			**Q**	**1100.5695**	550.7884	**1083.5429**	542.2751	1082.5589	541.7831	**9**
6	72.0808	639.3824	320.1949	622.3559	311.6816			**V**	**972.5109**	486.7591	955.4843	478.2458	**954.5003**	477.7538	**8**
7	102.0550	768.4250	384.7162	751.3985	376.2029	750.4145	375.7109	**E**	**873.4425**	437.2249	856.4159	428.7116	**855.4319**	428.2196	**7**
8	102.0550	897.4676	449.2375	880.4411	440.7242	879.4571	440.2322	**E**	**744.3999**	372.7036	727.3733	364.1903	726.3893	363.6983	**6**
9	44.0495	968.5047	484.7560	951.4782	476.2427	950.4942	475.7507	**A**	**615.3573**	308.1823	598.3307	299.6690			**5**
10	101.0709	1096.5633	548.7853	1079.5368	**540.2720**	1078.5528	539.7800	**Q**	**544.3202**	272.6637	527.2936	264.1504			**4**
11	101.0709	1224.6219	612.8146	1207.5953	604.3013	1206.6113	603.8093	**Q**	**416.2616**	208.6344	399.2350	200.1212			**3**
12	**86.0964**	1337.7060	669.3566	1320.6794	660.8433	1319.6954	660.3513	**L**	**288.2030**	144.6051	271.1765	136.0919			**2**
13	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **VLLDDTQSEAAR**
Found in **Q14789**, Q14789|GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2

Match to Query 424: 1316.593316 from(659.303934,2+)

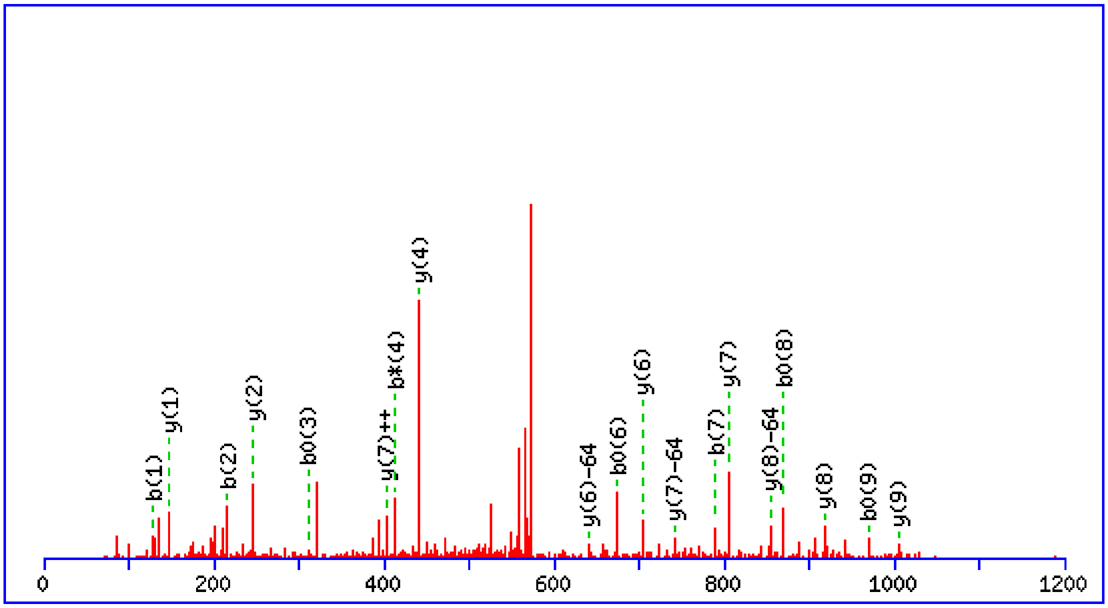


Monoisotopic mass of neutral peptide Mr(calc): 1316.6572
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.0033
Matches (Bold Red): 21/120 fragment ions using 38 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					**V**							**12**
2	**86.0964**	**213.1598**	107.0835					**L**	1218.5961	609.8017	1201.5695	601.2884	1200.5855	600.7964	**11**
3	**86.0964**	326.2438	163.6255					**L**	**1105.5120**	**553.2596**	1088.4855	544.7464	**1087.5014**	544.2544	**10**
4	88.0393	**441.2708**	221.1390			423.2602	212.1337	**D**	**992.4279**	496.7176	975.4014	488.2043	**974.4174**	487.7123	**9**
5	88.0393	556.2977	278.6525			538.2871	269.6472	**D**	**877.4010**	439.2041	860.3745	430.6909	859.3904	430.1989	**8**
6	74.0600	657.3454	329.1763			639.3348	320.1710	**T**	**762.3741**	381.6907	**745.3475**	373.1774	744.3635	372.6854	**7**
7	101.0709	785.4040	393.2056	768.3774	384.6923	767.3934	384.2003	**Q**	661.3264	331.1668	644.2998	322.6536	643.3158	322.1615	**6**
8	60.0444	872.4360	436.7216	855.4094	**428.2084**	854.4254	427.7164	**S**	**533.2678**	267.1375	516.2413	258.6243	515.2572	258.1323	**5**
9	102.0550	1001.4786	501.2429	984.4520	492.7297	983.4680	492.2376	**E**	**446.2358**	223.6215	429.2092	**215.1083**	**428.2252**	214.6162	**4**
10	44.0495	1072.5157	536.7615	1055.4891	528.2482	1054.5051	527.7562	**A**	**317.1932**	159.1002	300.1666	150.5870			**3**
11	44.0495	1143.5528	572.2800	1126.5263	563.7668	1125.5422	563.2748	**A**	**246.1561**	123.5817	**229.1295**	115.0684			**2**
12	129.1135							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **QSLTMDPVVK**
Found in **P34932**, P34932|HSP74_HUMAN Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4

Match to Query 327: 1132.546192 from(567.280372,2+)

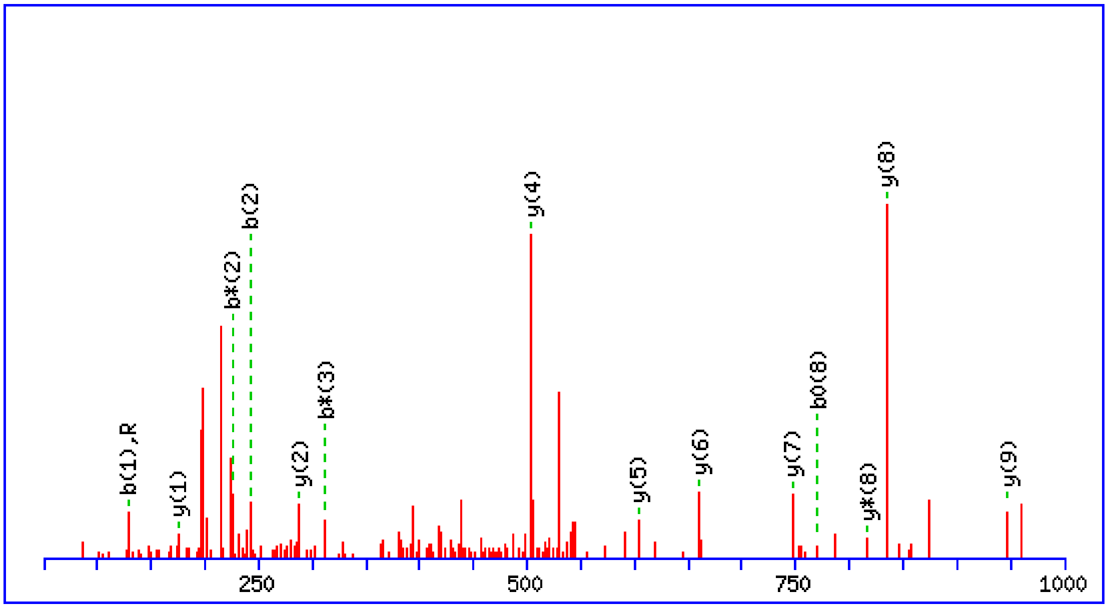


Monoisotopic mass of neutral peptide Mr(calc): 1132.5798
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 **Expect:** 0.0056
Matches (Bold Red): 19/163 fragment ions using 34 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	101.0709	**129.0659**	65.0366	112.0393	56.5233			**Q**							**10**
2	60.0444	**216.0979**	108.5526	199.0713	100.0393	198.0873	99.5473	**S**	**1005.5285**	503.2679	988.5020	494.7546	987.5179	494.2626	**9**
3	86.0964	329.1819	165.0946	312.1554	156.5813	**311.1714**	156.0893	**L**	**918.4965**	459.7519	901.4699	451.2386	900.4859	450.7466	**8**
4	74.0600	430.2296	215.6185	**413.2031**	207.1052	412.2191	206.6132	**T**	**805.4124**	**403.2098**	788.3859	394.6966	787.4019	394.2046	**7**
5	120.0478	577.2650	289.1362	560.2385	280.6229	559.2545	280.1309	**M**	**704.3647**	352.6860	687.3382	344.1727	686.3542	343.6807	**6**
6	88.0393	692.2920	346.6496	675.2654	338.1363	**674.2814**	337.6443	**D**	557.3293	279.1683	540.3028	270.6550	539.3188	270.1630	**5**
7	70.0651	**789.3447**	395.1760	772.3182	386.6627	771.3342	386.1707	**P**	**442.3024**	221.6548	425.2758	213.1416			**4**
8	72.0808	888.4131	444.7102	871.3866	436.1969	**870.4026**	435.7049	**V**	345.2496	173.1285	328.2231	164.6152			**3**
9	72.0808	987.4816	494.2444	970.4550	485.7311	**969.4710**	485.2391	**V**	**246.1812**	123.5942	229.1547	115.0810			**2**
10	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **QLSSGVSEIR**
Found in **P04792**, P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2

Match to Query 222: 1074.629174 from(538.321863,2+)

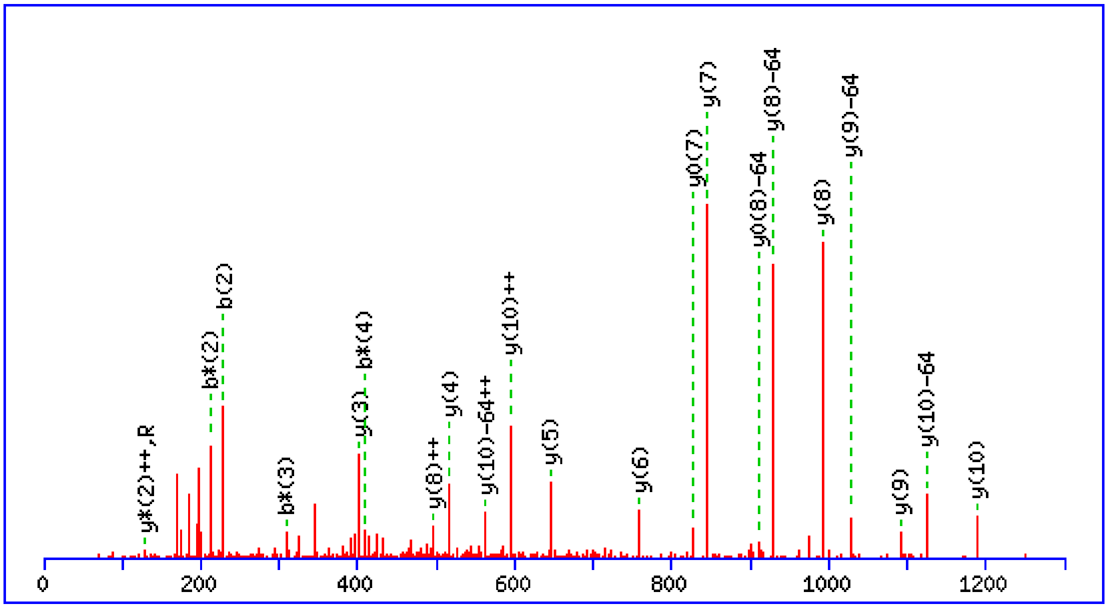


Monoisotopic mass of neutral peptide Mr(calc): 1074.5669
Fixed modifications: Carbamidomethyl (C)
Ions Score: 62 **Expect:** 5.5e-005
Matches (Bold Red): 15/110 fragment ions using 26 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	101.0709	**129.0659**	65.0366	112.0393	56.5233			**Q**							**10**
2	86.0964	**242.1499**	121.5786	**225.1234**	113.0653			**L**	**947.5156**	474.2615	930.4891	465.7482	929.5051	465.2562	**9**
3	60.0444	329.1819	165.0946	**312.1554**	156.5813	311.1714	156.0893	**S**	**834.4316**	417.7194	**817.4050**	409.2061	816.4210	408.7141	**8**
4	60.0444	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	**S**	**747.3995**	374.2034	730.3730	365.6901	729.3890	365.1981	**7**
5	30.0338	473.2354	237.1214	456.2089	228.6081	455.2249	228.1161	**G**	**660.3675**	330.6874	643.3410	322.1741	642.3570	321.6821	**6**
6	72.0808	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	**V**	**603.3461**	302.1767	586.3195	293.6634	585.3355	293.1714	**5**
7	60.0444	659.3359	330.1716	642.3093	321.6583	641.3253	321.1663	**S**	**504.2776**	252.6425	487.2511	244.1292	486.2671	243.6372	**4**
8	102.0550	788.3785	394.6929	771.3519	386.1796	**770.3679**	385.6876	**E**	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	**3**
9	86.0964	901.4625	451.2349	884.4360	442.7216	883.4520	442.2296	**I**	**288.2030**	144.6051	271.1765	136.0919			**2**
10	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **NNPVMSLQDQVR**
Found in **Q7LGA3**, Q7LGA3|HS2ST_HUMAN Heparan sulfate 2-O-sulfotransferase 1 OS=Homo sapiens GN=HS2ST1 PE=2 SV=1

Match to Query 369: 1415.659092 from(708.836822,2+)

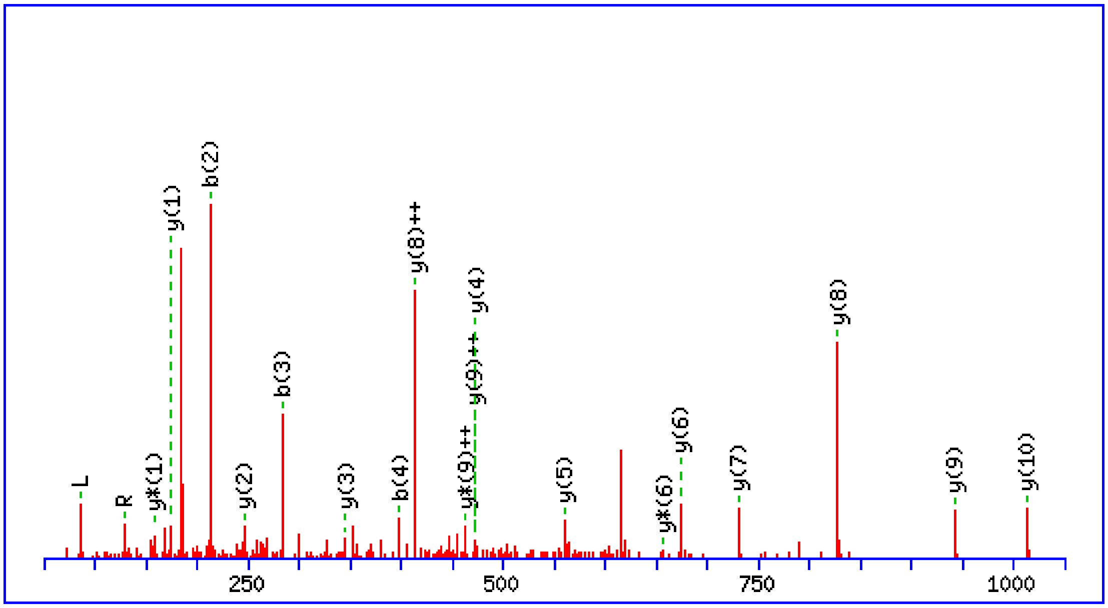


Monoisotopic mass of neutral peptide Mr(calc): 1415.6827
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 58 **Expect:** 0.0001
Matches (Bold Red): 22/193 fragment ions using 26 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	87.0553	115.0502	58.0287	98.0237	49.5155			N							12
2	87.0553	**229.0931**	115.0502	**212.0666**	106.5369			N	1238.6488	619.8280	1221.6222	611.3148	1220.6382	610.8227	11
3	70.0651	326.1459	163.5766	**309.1193**	155.0633			P	**1124.6059**	**562.8066**	1107.5793	554.2933	1106.5953	553.8013	10
4	72.0808	425.2143	213.1108	**408.1878**	204.5975			V	**1027.5531**	514.2802	1010.5265	505.7669	1009.5425	505.2749	9
5	56.0495	508.2514	254.6294	491.2249	246.1161			M	**928.4847**	464.7460	911.4581	456.2327	**910.4741**	455.7407	8
6	60.0444	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	S	**845.4476**	423.2274	828.4210	414.7141	**827.4370**	414.2221	7
7	86.0964	708.3675	354.6874	691.3410	346.1741	690.3570	345.6821	L	**758.4155**	379.7114	741.3890	371.1981	740.4050	370.7061	6
8	101.0709	836.4261	418.7167	819.3995	410.2034	818.4155	409.7114	Q	**645.3315**	323.1694	628.3049	314.6561	627.3209	314.1641	5
9	88.0393	951.4530	476.2302	934.4265	467.7169	933.4425	467.2249	D	**517.2729**	259.1401	500.2463	250.6268	499.2623	250.1348	4
10	101.0709	1079.5116	540.2594	1062.4851	531.7462	1061.5011	531.2542	Q	**402.2459**	201.6266	385.2194	193.1133			3
11	72.0808	1178.5800	589.7937	1161.5535	581.2804	1160.5695	580.7884	V	274.1874	137.5973	257.1608	**129.0840**			2
12	**129.1135**							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VLANPGNSQVAR**
Found in **Q14974**, Q14974|IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2

Match to Query 203: 1224.482298 from(613.248425,2+)

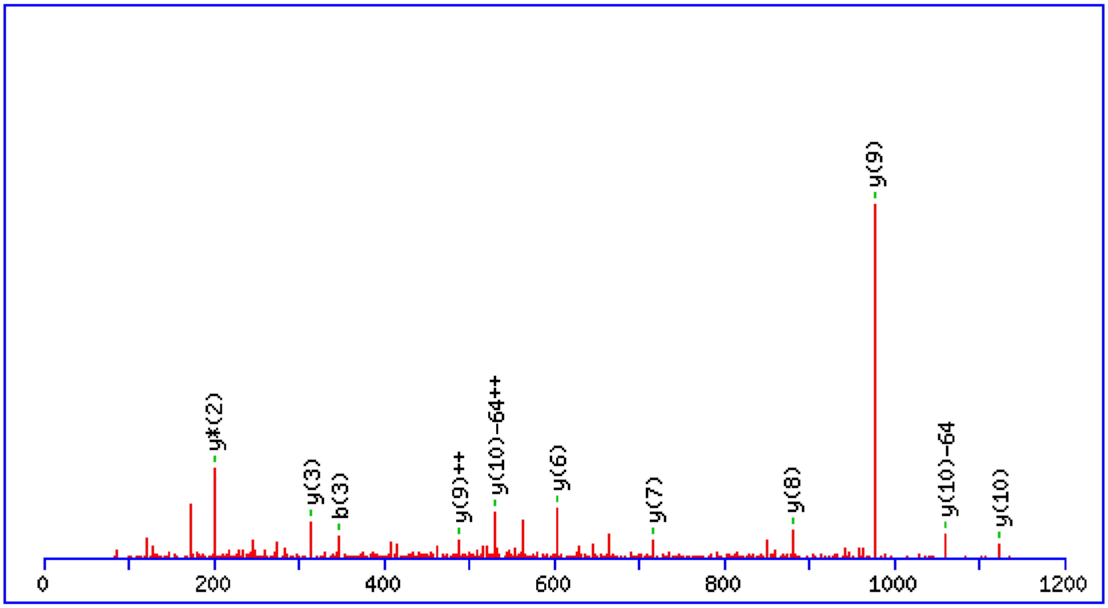


Monoisotopic mass of neutral peptide Mr(calc): 1224.6575
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 **Expect:** 5.5e-005
Matches (Bold Red): 20/116 fragment ions using 49 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					**V**							**12**
2	**86.0964**	**213.1598**	107.0835					**L**	1126.5963	563.8018	1109.5698	555.2885	1108.5858	554.7965	**11**
3	44.0495	**284.1969**	142.6021					**A**	**1013.5123**	507.2598	996.4857	498.7465	995.5017	498.2545	**10**
4	87.0553	**398.2398**	199.6235	381.2132	191.1103			**N**	**942.4752**	**471.7412**	925.4486	**463.2279**	924.4646	462.7359	**9**
5	70.0651	495.2926	248.1499	478.2660	239.6366			**P**	**828.4322**	**414.7198**	811.4057	406.2065	810.4217	405.7145	**8**
6	30.0338	552.3140	276.6606	535.2875	268.1474			**G**	**731.3795**	366.1934	714.3529	357.6801	713.3689	357.1881	**7**
7	87.0553	666.3570	333.6821	649.3304	325.1688			**N**	**674.3580**	337.6826	**657.3315**	329.1694	656.3474	328.6774	**6**
8	60.0444	753.3890	377.1981	736.3624	368.6849	735.3784	368.1928	**S**	**560.3151**	280.6612	543.2885	272.1479	542.3045	271.6559	**5**
9	101.0709	881.4476	441.2274	864.4210	432.7141	863.4370	432.2221	**Q**	**473.2831**	237.1452	456.2565	228.6319			**4**
10	72.0808	980.5160	490.7616	963.4894	482.2483	962.5054	481.7563	**V**	**345.2245**	173.1159	328.1979	164.6026			**3**
11	44.0495	1051.5531	526.2802	1034.5265	517.7669	1033.5425	517.2749	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
12	**129.1135**							**R**	**175.1190**	88.0631	**158.0924**	79.5498			**1**

MS/MS Fragmentation of **TVMPYISTTPAK**
Found in **P05556**, P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=1

Match to Query 586: 1323.632082 from(662.823317,2+)

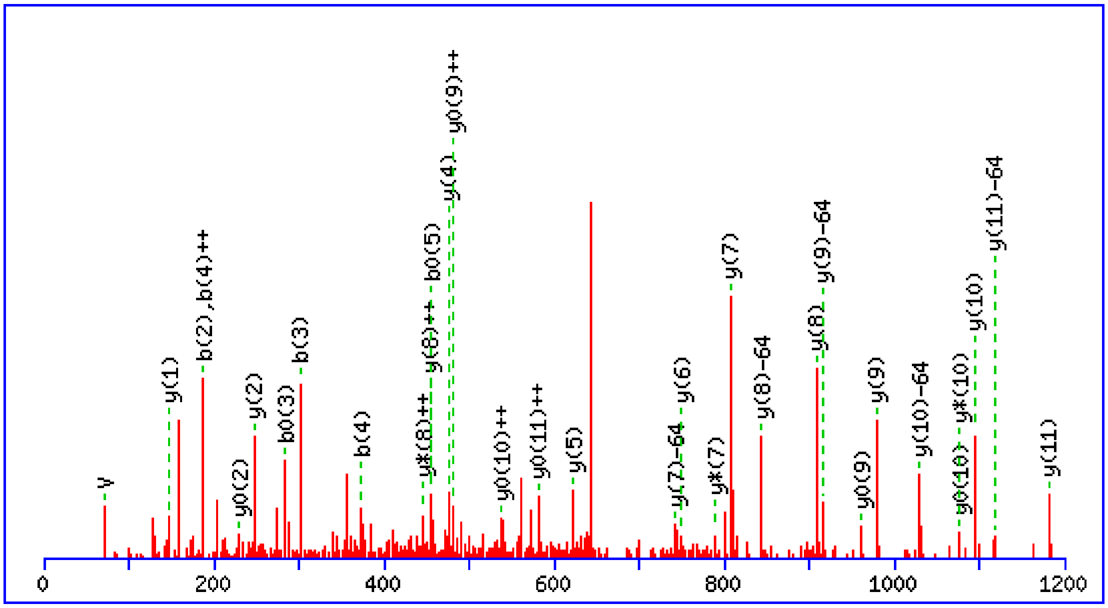


Monoisotopic mass of neutral peptide Mr(calc): 1323.6744
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 48 **Expect:** 0.0012
Matches (Bold Red): 12/165 fragment ions using 14 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							12
2	72.0808	**201.1234**	101.0653	183.1128	92.0600	V	1159.6358	580.3215	1142.6092	571.8082	1141.6252	571.3162	11
3	56.0495	284.1605	142.5839	266.1499	133.5786	M	**1060.5673**	**530.7873**	1043.5408	522.2740	1042.5568	521.7820	10
4	70.0651	381.2133	191.1103	363.2027	182.1050	P	**977.5302**	**489.2688**	960.5037	480.7555	959.5197	480.2635	9
5	136.0757	544.2766	272.6419	526.2660	263.6366	Y	**880.4775**	440.7424	863.4509	432.2291	862.4669	431.7371	8
6	86.0964	657.3606	329.1840	639.3501	320.1787	I	**717.4141**	359.2107	700.3876	350.6974	699.4036	350.2054	7
7	60.0444	744.3927	372.7000	726.3821	363.6947	S	**604.3301**	302.6687	587.3035	294.1554	586.3195	293.6634	6
8	74.0600	845.4404	423.2238	827.4298	414.2185	T	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	5
9	74.0600	946.4880	473.7477	928.4775	464.7424	T	416.2504	208.6288	399.2238	200.1155	398.2398	199.6235	4
10	70.0651	1043.5408	522.2740	1025.5302	513.2688	P	**315.2027**	158.1050	298.1761	149.5917			3
11	44.0495	1114.5779	557.7926	1096.5673	548.7873	A	218.1499	109.5786	**201.1234**	101.0653			2
12	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VSDATGQMNLTK**
Found in **P40121**, P40121|CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=1

Match to Query 312: 1279.748650 from(640.881601,2+)

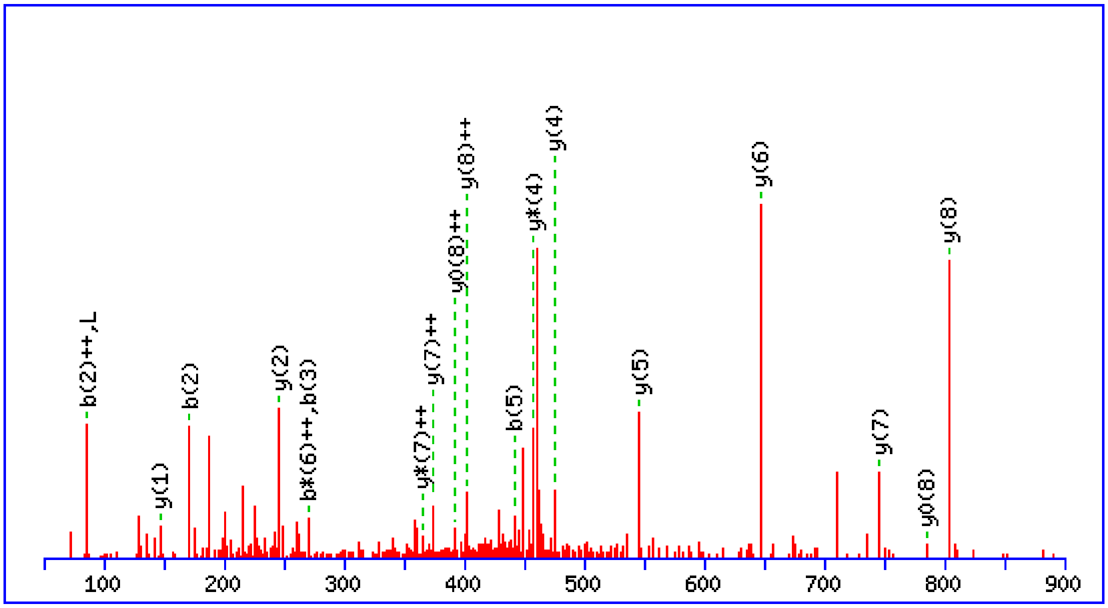


Monoisotopic mass of neutral peptide Mr(calc): 1279.6078
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 69 **Expect:** 8.8e-006
Matches (Bold Red): 32/195 fragment ions using 50 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**72.0808**	100.0757	50.5415					**V**							**12**
2	60.0444	**187.1077**	94.0575			169.0972	85.0522	**S**	**1181.5467**	591.2770	1164.5201	582.7637	1163.5361	**582.2717**	**11**
3	88.0393	**302.1347**	151.5710			**284.1241**	142.5657	**D**	**1094.5147**	547.7610	**1077.4881**	539.2477	**1076.5041**	**538.7557**	**10**
4	44.0495	**373.1718**	**187.0895**			355.1612	178.0842	**A**	**979.4877**	490.2475	962.4612	481.7342	**961.4771**	**481.2422**	**9**
5	74.0600	474.2195	237.6134			**456.2089**	228.6081	**T**	**908.4506**	**454.7289**	891.4240	**446.2157**	890.4400	445.7237	**8**
6	30.0338	531.2409	266.1241			513.2304	257.1188	**G**	**807.4029**	404.2051	**790.3764**	395.6918	789.3924	395.1998	**7**
7	101.0709	659.2995	330.1534	642.2729	321.6401	641.2889	321.1481	**Q**	**750.3815**	375.6944	733.3549	367.1811	732.3709	366.6891	**6**
8	120.0478	806.3349	403.6711	789.3084	395.1578	788.3243	394.6658	**M**	**622.3229**	311.6651	605.2963	303.1518	604.3123	302.6598	**5**
9	87.0553	920.3778	460.6926	903.3513	452.1793	902.3673	451.6873	**N**	**475.2875**	238.1474	458.2609	229.6341	457.2769	229.1421	**4**
10	86.0964	1033.4619	517.2346	1016.4353	508.7213	1015.4513	508.2293	**L**	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	**3**
11	74.0600	1134.5096	567.7584	1117.4830	559.2451	1116.4990	558.7531	**T**	**248.1605**	124.5839	231.1339	116.0706	**230.1499**	115.5786	**2**
12	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **LGVTANDVK**
Found in **P40925**, P40925|MDHC_HUMAN Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4

Match to Query 163: 915.506216 from(458.760384,2+)

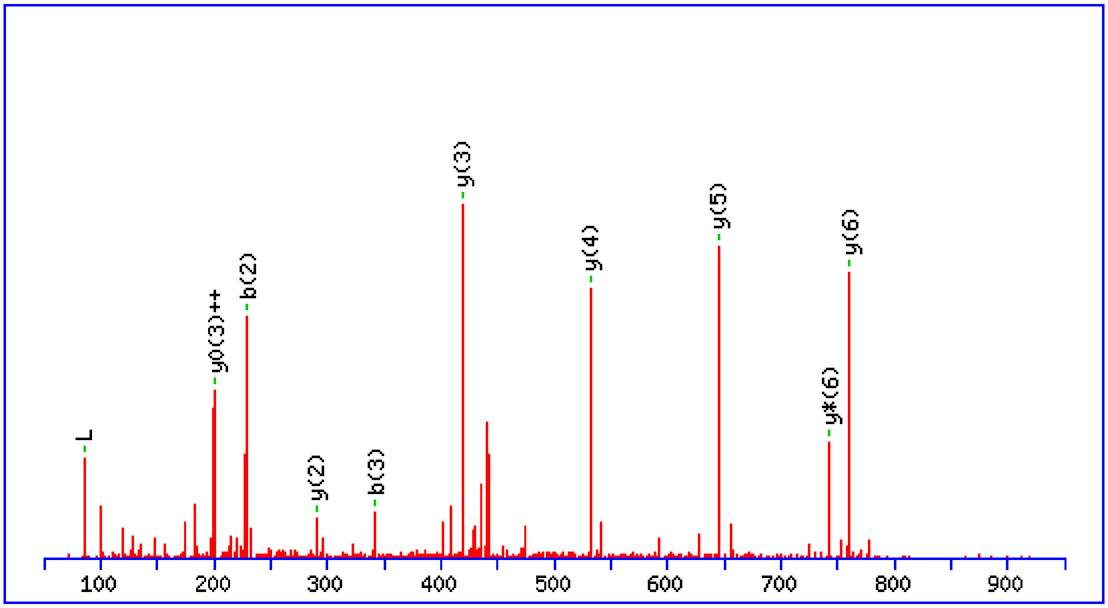


Monoisotopic mass of neutral peptide Mr(calc): 915.5025
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 **Expect:** 0.015
Matches (Bold Red): 19/85 fragment ions using 46 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							9
2	30.0338	**171.1128**	**86.0600**					G	**803.4258**	**402.2165**	786.3992	393.7032	**785.4152**	**393.2112**	8
3	72.0808	**270.1812**	135.5942					V	**746.4043**	**373.7058**	729.3777	**365.1925**	728.3937	364.7005	7
4	74.0600	371.2289	186.1181			353.2183	177.1128	T	**647.3359**	324.1716	630.3093	315.6583	629.3253	315.1663	6
5	44.0495	**442.2660**	221.6366			424.2554	212.6314	A	**546.2882**	273.6477	529.2617	265.1345	528.2776	264.6425	5
6	87.0553	556.3089	278.6581	539.2824	**270.1448**	538.2984	269.6528	N	**475.2511**	238.1292	**458.2245**	229.6159	457.2405	229.1239	4
7	88.0393	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
8	72.0808	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	V	**246.1812**	123.5942	229.1547	115.0810			2
9	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **LDLLEDR**
Found in **Q14697**, Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3

Match to Query 158: 872.429132 from(437.221842,2+)

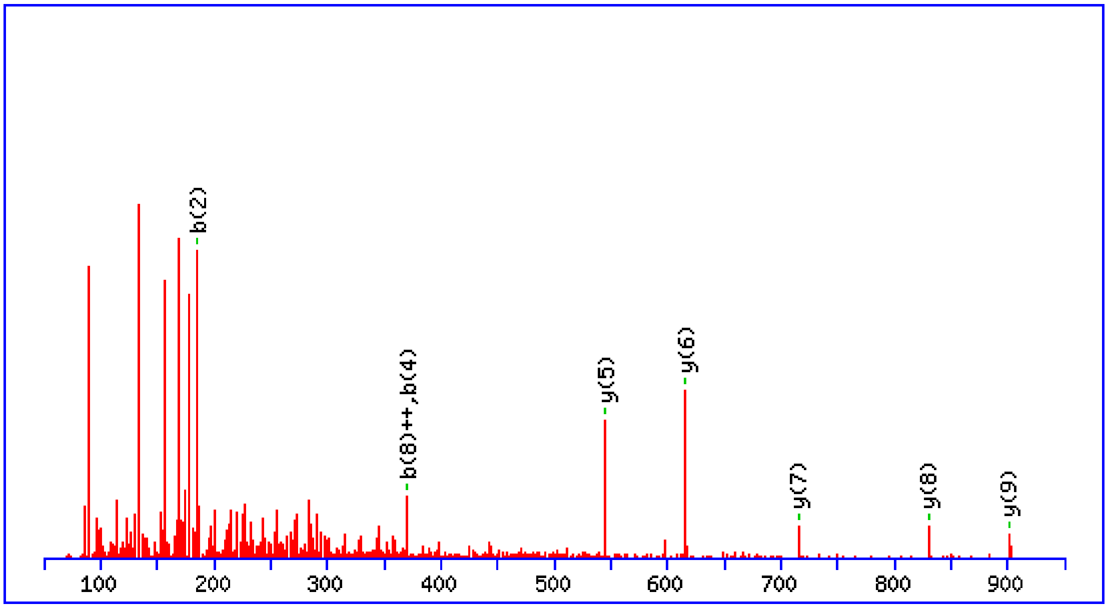


Monoisotopic mass of neutral peptide Mr(calc): 872.4603
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 **Expect:** 0.024
Matches (Bold Red): 12/63 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			L							7
2	88.0393	**229.1183**	115.0628	211.1077	106.0575	D	**760.3836**	380.6954	**743.3570**	372.1821	742.3730	371.6901	6
3	**86.0964**	**342.2023**	171.6048	324.1918	162.5995	L	**645.3566**	323.1819	628.3301	314.6687	627.3461	314.1767	5
4	**86.0964**	455.2864	228.1468	437.2758	219.1416	L	**532.2726**	266.6399	515.2460	258.1266	514.2620	257.6346	4
5	102.0550	584.3290	292.6681	566.3184	283.6629	E	**419.1885**	210.0979	402.1619	201.5846	401.1779	**201.0926**	3
6	88.0393	699.3559	350.1816	681.3454	341.1763	D	**290.1459**	145.5766	273.1193	137.0633	272.1353	136.5713	2
7	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ALADVATVLGR**
Found in **Q92542**, Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2

Match to Query 205: 1084.462440 from(543.238496,2+)

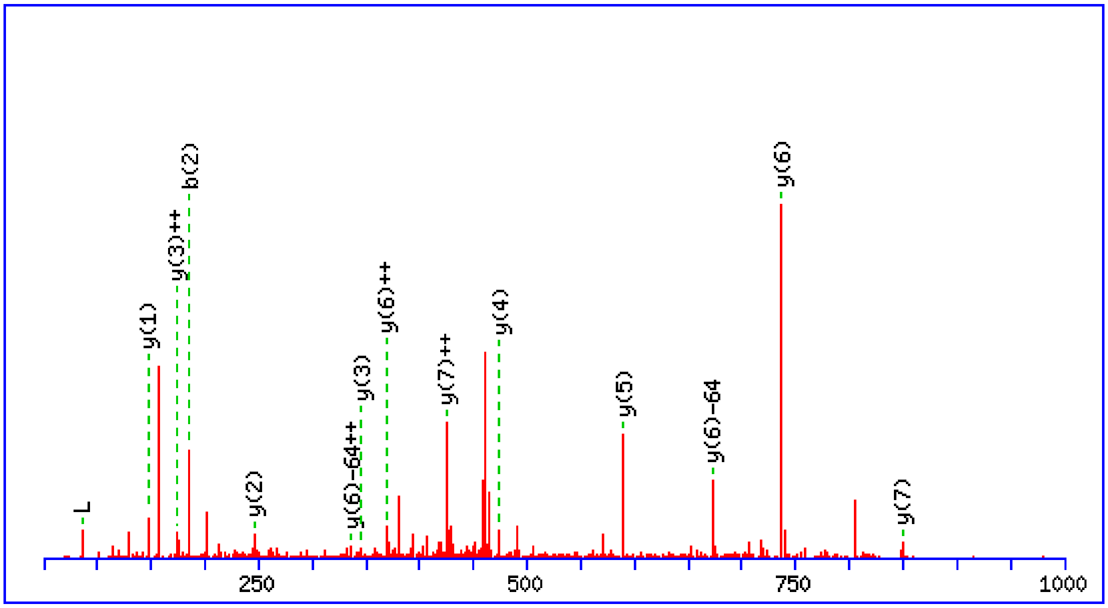


Monoisotopic mass of neutral peptide Mr(calc): 1084.6241
Fixed modifications: Carbamidomethyl (C)
Ions Score: 37 **Expect:** 0.017
Matches (Bold Red): 8/97 fragment ions using 10 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							11
2	86.0964	**185.1285**	93.0679			L	1014.5942	507.8007	997.5677	499.2875	996.5837	498.7955	10
3	44.0495	256.1656	128.5864			A	**901.5102**	451.2587	884.4836	442.7454	883.4996	442.2534	9
4	88.0393	**371.1925**	186.0999	353.1819	177.0946	D	**830.4730**	415.7402	813.4465	407.2269	812.4625	406.7349	8
5	72.0808	470.2609	235.6341	452.2504	226.6288	V	**715.4461**	358.2267	698.4196	349.7134	697.4355	349.2214	7
6	44.0495	541.2980	271.1527	523.2875	262.1474	A	**616.3777**	308.6925	599.3511	300.1792	598.3671	299.6872	6
7	74.0600	642.3457	321.6765	624.3352	312.6712	T	**545.3406**	273.1739	528.3140	264.6607	527.3300	264.1686	5
8	72.0808	741.4141	**371.2107**	723.4036	362.2054	V	444.2929	222.6501	427.2663	214.1368			4
9	86.0964	854.4982	427.7527	836.4876	418.7475	L	345.2245	173.1159	328.1979	164.6026			3
10	30.0338	911.5197	456.2635	893.5091	447.2582	G	232.1404	116.5738	215.1139	108.0606			2
11	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ALMDEVVK**
Found in **P00558**, P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3

Match to Query 140: 919.483968 from(460.749260,2+)

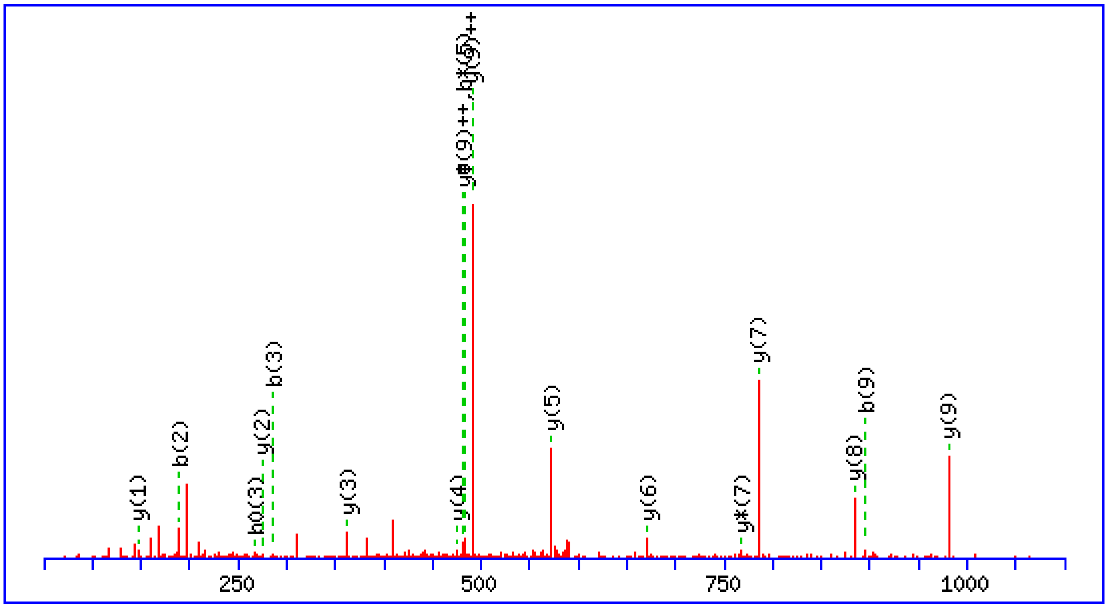


Monoisotopic mass of neutral peptide Mr(calc): 919.4685
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 38 **Expect:** 0.012
Matches (Bold Red): 14/97 fragment ions using 38 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							8
2	**86.0964**	**185.1285**	93.0679			L	**849.4386**	**425.2230**	832.4121	416.7097	831.4281	416.2177	7
3	120.0478	332.1639	166.5856			M	**736.3546**	**368.6809**	719.3280	360.1676	718.3440	359.6756	6
4	88.0393	447.1908	224.0990	429.1802	215.0938	D	**589.3192**	295.1632	572.2926	286.6499	571.3086	286.1579	5
5	102.0550	576.2334	288.6203	558.2228	279.6151	E	**474.2922**	237.6498	457.2657	229.1365	456.2817	228.6445	4
6	72.0808	675.3018	338.1545	657.2912	329.1493	V	**345.2496**	**173.1285**	328.2231	164.6152			3
7	72.0808	774.3702	387.6887	756.3597	378.6835	V	**246.1812**	123.5942	229.1547	115.0810			2
8	101.1073					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **STPVNVPISQK**
Found in **Q8WUM4**, Q8WUM4|PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1

Match to Query 527: 1168.607770 from(585.311161,2+)

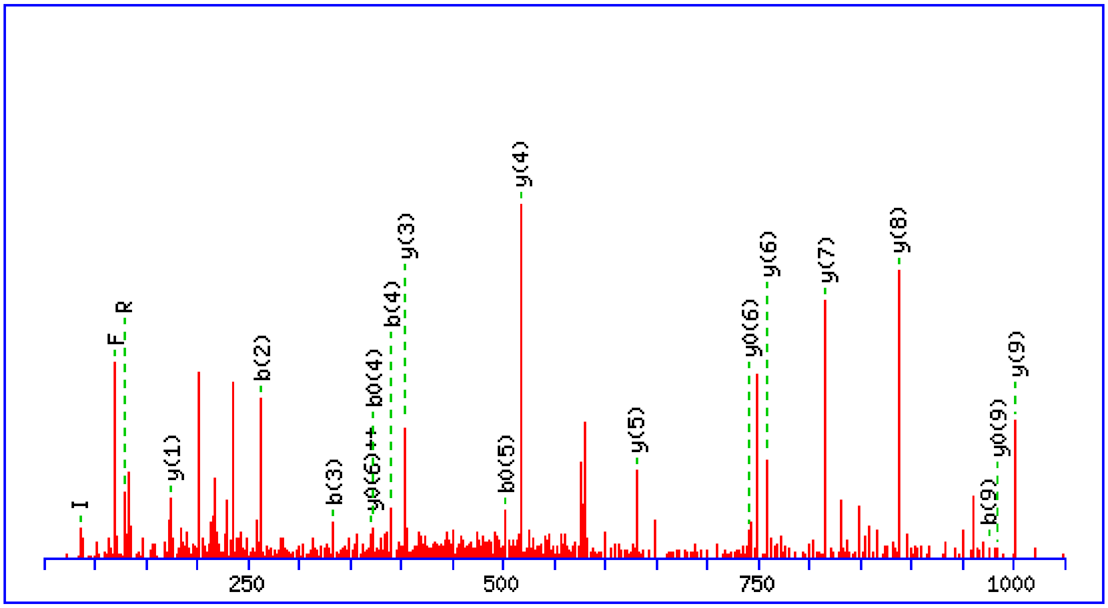


Monoisotopic mass of neutral peptide Mr(calc): 1168.6452
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.0084
Matches (Bold Red): 18/119 fragment ions using 61 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							11
2	74.0600	**189.0870**	95.0471			171.0764	86.0418	T	1082.6204	541.8139	1065.5939	533.3006	1064.6099	532.8086	10
3	70.0651	**286.1397**	143.5735			**268.1292**	134.5682	P	**981.5728**	**491.2900**	964.5462	**482.7767**	963.5622	**482.2847**	9
4	72.0808	385.2082	193.1077			367.1976	184.1024	V	**884.5200**	442.7636	867.4934	434.2504	866.5094	433.7584	8
5	87.0553	499.2511	250.1292	**482.2245**	241.6159	481.2405	241.1239	N	**785.4516**	393.2294	**768.4250**	384.7162	767.4410	384.2241	7
6	72.0808	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	V	**671.4087**	336.2080	654.3821	327.6947	653.3981	327.2027	6
7	70.0651	695.3723	348.1898	678.3457	339.6765	677.3617	339.1845	P	**572.3402**	286.6738	555.3137	278.1605	554.3297	277.6685	5
8	86.0964	808.4563	404.7318	791.4298	396.2185	790.4458	395.7265	I	**475.2875**	238.1474	458.2609	229.6341	457.2769	229.1421	4
9	60.0444	**895.4884**	448.2478	878.4618	439.7345	877.4778	439.2425	S	**362.2034**	181.6053	345.1769	173.0921	344.1928	172.6001	3
10	101.0709	1023.5469	512.2771	1006.5204	503.7638	1005.5364	503.2718	Q	**275.1714**	138.0893	258.1448	129.5761			2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **FDAGELITQR**
Found in **P35232**, P35232|PHB_HUMAN Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1

Match to Query 279: 1148.534592 from(575.274572,2+)

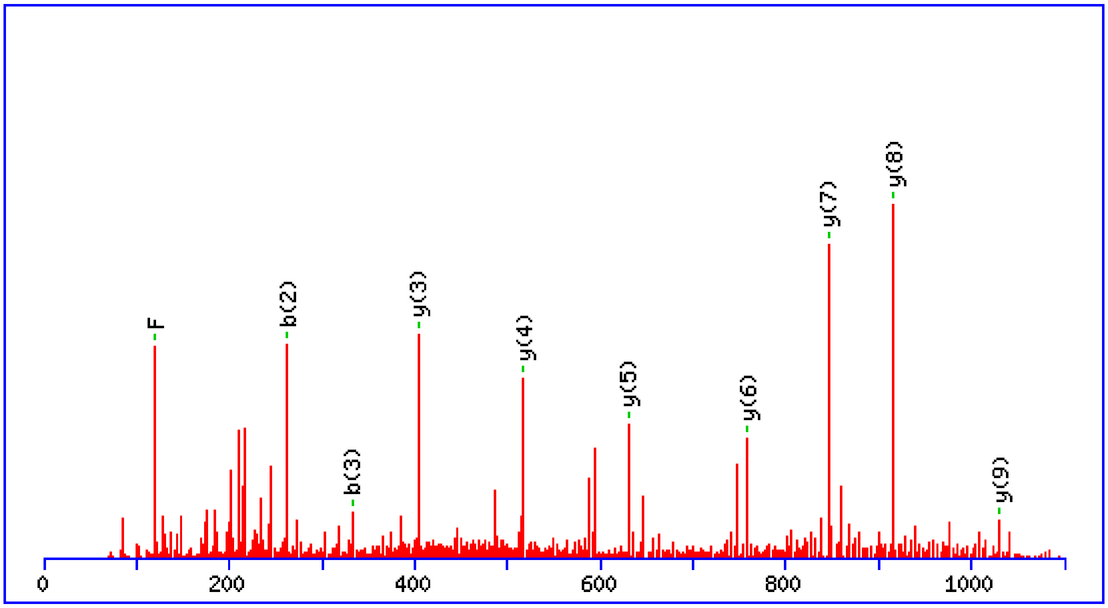


Monoisotopic mass of neutral peptide Mr(calc): 1148.5826
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.0094
Matches (Bold Red): 21/96 fragment ions using 54 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							10
2	88.0393	**263.1026**	132.0550			245.0921	123.0497	D	**1002.5215**	501.7644	985.4949	493.2511	**984.5109**	492.7591	9
3	44.0495	**334.1397**	167.5735			316.1292	158.5682	A	**887.4945**	444.2509	870.4680	435.7376	869.4839	435.2456	8
4	30.0338	**391.1612**	196.0842			**373.1506**	187.0790	G	**816.4574**	408.7323	799.4308	400.2191	798.4468	399.7271	7
5	102.0550	520.2038	260.6055			**502.1932**	251.6003	E	**759.4359**	380.2216	742.4094	371.7083	**741.4254**	**371.2163**	6
6	**86.0964**	633.2879	317.1476			615.2773	308.1423	L	**630.3933**	315.7003	613.3668	307.1870	612.3828	306.6950	5
7	**86.0964**	746.3719	373.6896			728.3614	364.6843	I	**517.3093**	259.1583	500.2827	250.6450	499.2987	250.1530	4
8	74.0600	847.4196	424.2134			829.4090	415.2082	T	**404.2252**	202.6162	387.1987	194.1030	386.2146	193.6110	3
9	101.0709	**975.4782**	488.2427	958.4516	479.7295	957.4676	479.2375	Q	303.1775	152.0924	286.1510	143.5791			2
10	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **FNASQLITQR**
Found in **Q99623**, Q99623|PHB2_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2

Match to Query 469: 1176.597604 from(589.306078,2+)

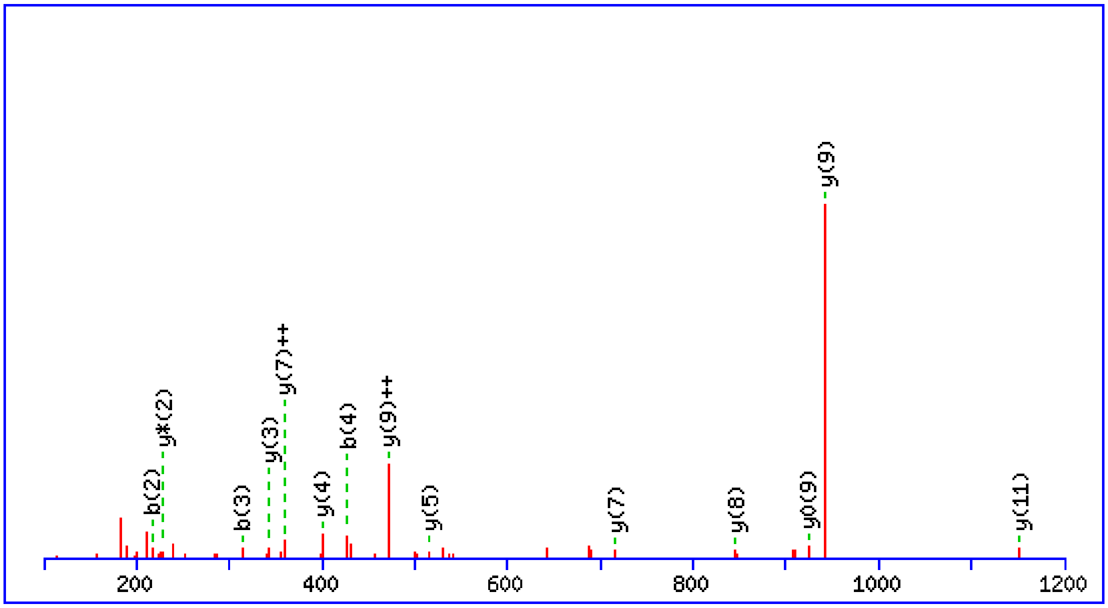


Monoisotopic mass of neutral peptide Mr(calc): 1176.6251
Fixed modifications: Carbamidomethyl (C)
Ions Score: 69 **Expect:** 1e-005
Matches (Bold Red): 10/106 fragment ions using 12 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					F							10
2	87.0553	**262.1186**	131.5629	245.0921	123.0497			N	**1030.5640**	515.7856	1013.5374	507.2724	1012.5534	506.7803	9
3	44.0495	**333.1557**	167.0815	316.1292	158.5682			A	**916.5211**	458.7642	899.4945	450.2509	898.5105	449.7589	8
4	60.0444	420.1878	210.5975	403.1612	202.0842	402.1772	201.5922	S	**845.4839**	423.2456	828.4574	414.7323	827.4734	414.2403	7
5	101.0709	548.2463	274.6268	531.2198	266.1135	530.2358	265.6215	Q	**758.4519**	379.7296	741.4254	371.2163	740.4414	370.7243	6
6	86.0964	661.3304	331.1688	644.3039	322.6556	643.3198	322.1636	L	**630.3933**	315.7003	613.3668	307.1870	612.3828	306.6950	5
7	86.0964	774.4145	387.7109	757.3879	379.1976	756.4039	378.7056	I	**517.3093**	259.1583	500.2827	250.6450	499.2987	250.1530	4
8	74.0600	875.4621	438.2347	858.4356	429.7214	857.4516	429.2294	T	**404.2252**	202.6162	387.1987	194.1030	386.2146	193.6110	3
9	101.0709	1003.5207	502.2640	986.4942	493.7507	985.5102	493.2587	Q	303.1775	152.0924	286.1510	143.5791			2
10	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **SEPIPESNDGPVK**
Found in **P30101**, P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4

Match to Query 389: 1367.737476 from(684.876014,2+)

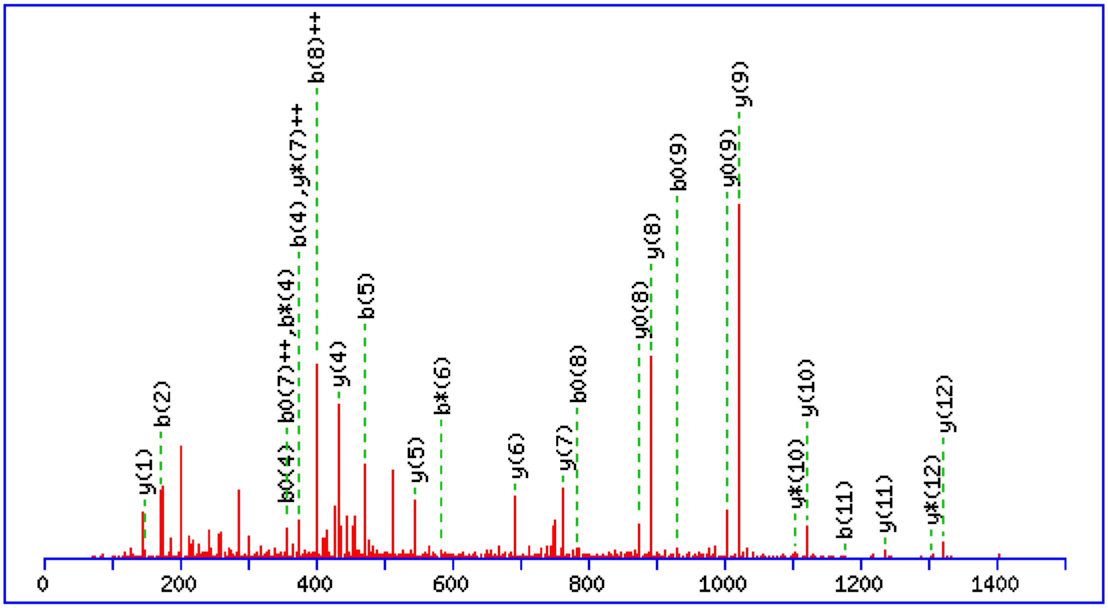


Monoisotopic mass of neutral peptide Mr(calc): 1367.6569
Fixed modifications: Carbamidomethyl (C)
Ions Score: 32 **Expect:** 0.043
Matches (Bold Red): 14/135 fragment ions using 36 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							13
2	102.0550	**217.0819**	109.0446			199.0713	100.0393	E	1281.6321	641.3197	1264.6056	632.8064	1263.6216	632.3144	12
3	70.0651	**314.1347**	157.5710			296.1241	148.5657	P	**1152.5895**	576.7984	1135.5630	568.2851	1134.5790	567.7931	11
4	86.0964	**427.2187**	214.1130			409.2082	205.1077	I	1055.5368	528.2720	1038.5102	519.7587	1037.5262	519.2667	10
5	70.0651	524.2715	262.6394			506.2609	253.6341	P	**942.4527**	**471.7300**	925.4262	463.2167	**924.4421**	462.7247	9
6	102.0550	653.3141	327.1607			635.3035	318.1554	E	**845.3999**	423.2036	828.3734	414.6903	827.3894	414.1983	8
7	60.0444	740.3461	370.6767			722.3355	361.6714	S	**716.3573**	**358.6823**	699.3308	350.1690	698.3468	349.6770	7
8	87.0553	854.3890	427.6982	837.3625	419.1849	836.3785	418.6929	N	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	6
9	88.0393	969.4160	485.2116	952.3894	476.6984	951.4054	476.2063	D	**515.2824**	258.1448	498.2558	249.6316	497.2718	249.1396	5
10	30.0338	1026.4374	513.7224	1009.4109	505.2091	1008.4269	504.7171	G	**400.2554**	200.6314	383.2289	192.1181			4
11	70.0651	1123.4902	562.2487	1106.4637	553.7355	1105.4796	553.2435	P	**343.2340**	172.1206	326.2074	163.6074			3
12	72.0808	1222.5586	611.7829	1205.5321	603.2697	1204.5481	602.7777	V	246.1812	123.5942	**229.1547**	115.0810			2
13	101.1073							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **TASNVEEAFINTAK**
Found in **P61019**, P61019|RAB2A_HUMAN Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1

Match to Query 669: 1493.745362 from(747.879957,2+)

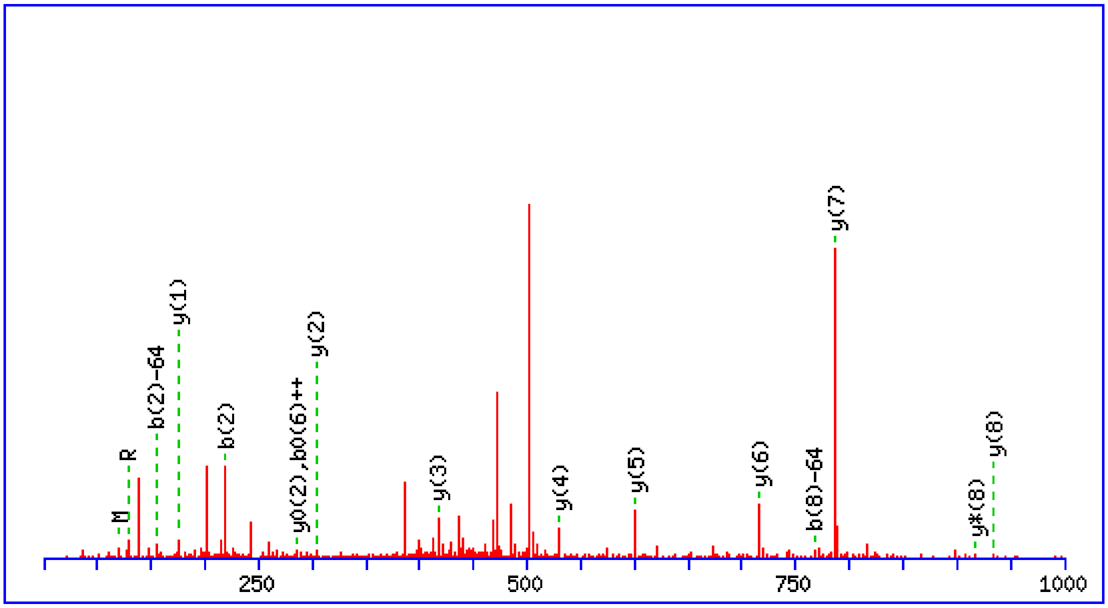


Monoisotopic mass of neutral peptide Mr(calc): 1493.7362
Fixed modifications: Carbamidomethyl (C)
Ions Score: 66 **Expect:** 1.7e-005
Matches (Bold Red): 26/160 fragment ions using 47 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	T							14
2	44.0495	**173.0921**	87.0497			155.0815	78.0444	A	1393.6958	697.3515	1376.6692	688.8383	1375.6852	688.3462	13
3	60.0444	260.1241	130.5657			242.1135	121.5604	S	**1322.6587**	661.8330	**1305.6321**	653.3197	1304.6481	652.8277	12
4	87.0553	**374.1670**	187.5871	**357.1405**	179.0739	**356.1565**	178.5819	N	**1235.6266**	618.3170	1218.6001	609.8037	1217.6161	609.3117	11
5	72.0808	**473.2354**	237.1214	456.2089	228.6081	455.2249	228.1161	V	**1121.5837**	561.2955	**1104.5572**	552.7822	1103.5732	552.2902	10
6	102.0550	602.2780	301.6427	**585.2515**	293.1294	584.2675	292.6374	E	**1022.5153**	511.7613	1005.4888	503.2480	**1004.5047**	502.7560	9
7	102.0550	731.3206	366.1640	714.2941	357.6507	713.3101	**357.1587**	E	**893.4727**	447.2400	876.4462	438.7267	**875.4621**	438.2347	8
8	44.0495	802.3577	**401.6825**	785.3312	393.1692	**784.3472**	392.6772	A	**764.4301**	382.7187	747.4036	**374.2054**	746.4196	373.7134	7
9	120.0808	949.4262	475.2167	932.3996	466.7034	**931.4156**	466.2114	F	**693.3930**	347.2001	676.3665	338.6869	675.3824	338.1949	6
10	86.0964	1062.5102	531.7587	1045.4837	523.2455	1044.4997	522.7535	I	**546.3246**	273.6659	529.2980	265.1527	528.3140	264.6606	5
11	87.0553	**1176.5531**	588.7802	1159.5266	580.2669	1158.5426	579.7749	N	**433.2405**	217.1239	416.2140	208.6106	415.2300	208.1186	4
12	74.0600	1277.6008	639.3040	1260.5743	630.7908	1259.5903	630.2988	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
13	44.0495	1348.6379	674.8226	1331.6114	666.3093	1330.6274	665.8173	A	218.1499	109.5786	201.1234	101.0653			2
14	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AMADALLER**
Found in **P34897**, P34897|GLYM_HUMAN Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3

Match to Query 376: 1004.464802 from(503.239677,2+)

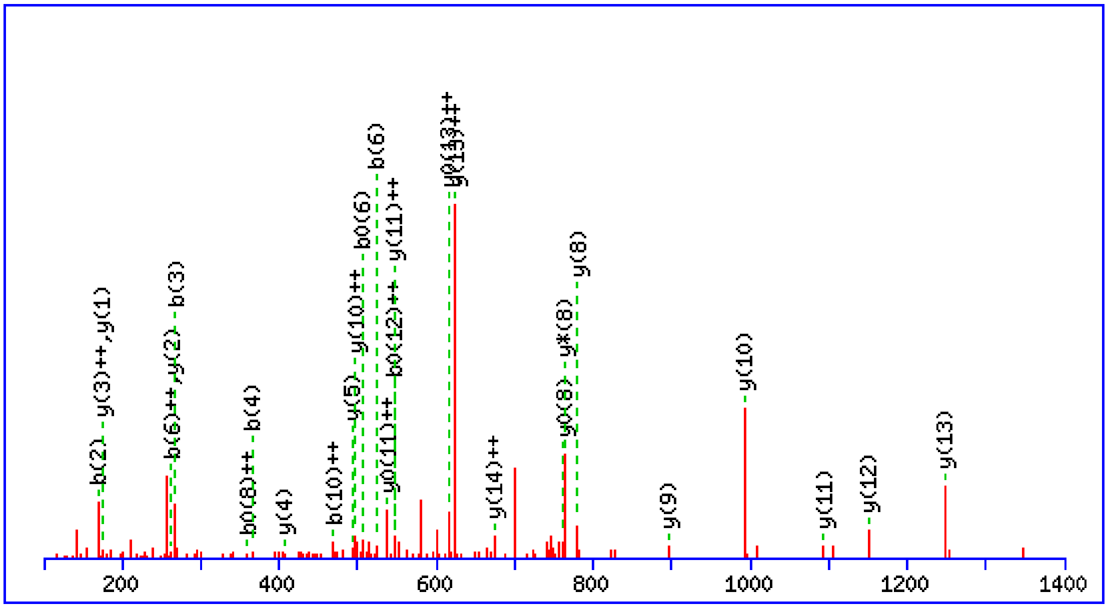


Monoisotopic mass of neutral peptide Mr(calc): 1004.4960
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 36 **Expect:** 0.023
Matches (Bold Red): 16/112 fragment ions using 41 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							9
2	**120.0478**	**219.0798**	110.0435			M	**934.4662**	467.7368	**917.4397**	459.2235	916.4557	458.7315	8
3	44.0495	290.1169	145.5621			A	**787.4308**	394.2191	770.4043	385.7058	769.4203	385.2138	7
4	88.0393	405.1439	203.0756	387.1333	194.0703	D	**716.3937**	358.7005	699.3672	350.1872	698.3832	349.6952	6
5	44.0495	476.1810	238.5941	458.1704	229.5888	A	**601.3668**	301.1870	584.3402	292.6738	583.3562	292.1817	5
6	86.0964	589.2650	295.1362	571.2545	**286.1309**	L	**530.3297**	265.6685	513.3031	257.1552	512.3191	256.6632	4
7	86.0964	702.3491	351.6782	684.3385	342.6729	L	**417.2456**	209.1264	400.2191	200.6132	399.2350	200.1212	3
8	102.0550	831.3917	416.1995	813.3811	407.1942	E	**304.1615**	152.5844	287.1350	144.0711	**286.1510**	143.5791	2
9	**129.1135**					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **APVPGTPDSLSSGSSR**
Found in **Q9UJZ1**, Q9UJZ1|STML2_HUMAN Stomatin-like protein 2 OS=Homo sapiens GN=STOML2 PE=1 SV=1

Match to Query 358: 1513.916032 from(757.965292,2+)

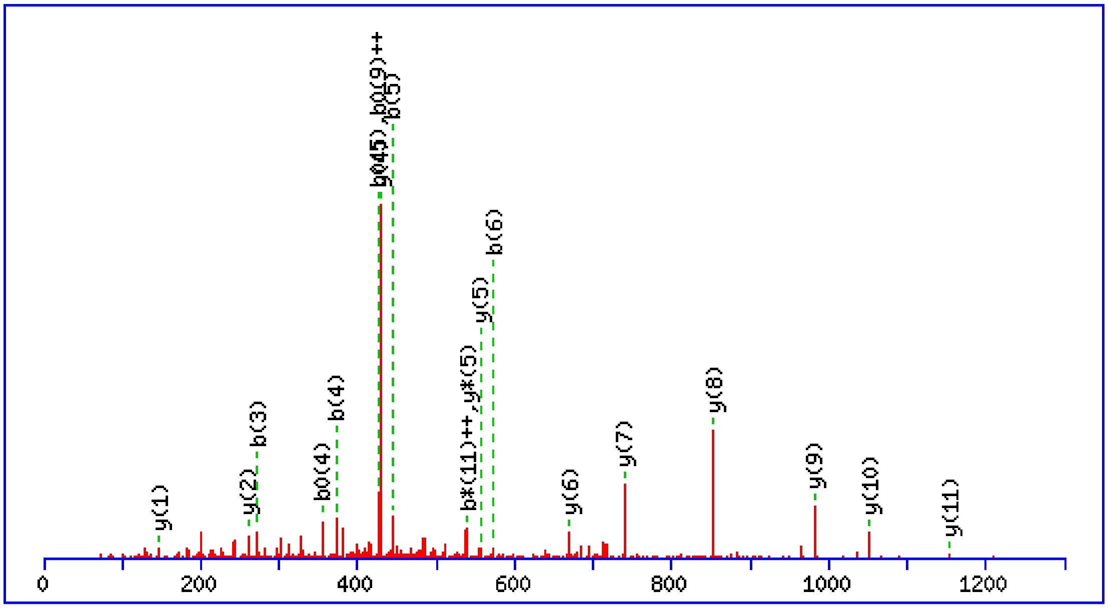


Monoisotopic mass of neutral peptide Mr(calc): 1513.7373
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 **Expect:** 0.0099
Matches (Bold Red): 28/154 fragment ions using 90 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258			A							16
2	70.0651	**169.0972**	85.0522			P	1443.7074	722.3573	1426.6809	713.8441	1425.6968	713.3521	15
3	72.0808	**268.1656**	134.5864			V	1346.6546	**673.8310**	1329.6281	665.3177	1328.6441	664.8257	14
4	70.0651	**365.2183**	183.1128			P	**1247.5862**	**624.2968**	1230.5597	615.7835	1229.5757	**615.2915**	13
5	30.0338	422.2398	211.6235			G	**1150.5335**	575.7704	1133.5069	567.2571	1132.5229	566.7651	12
6	74.0600	**523.2875**	**262.1474**	**505.2769**	253.1421	T	**1093.5120**	**547.2596**	1076.4855	538.7464	1075.5014	**538.2544**	11
7	70.0651	620.3402	310.6738	602.3297	301.6685	P	**992.4643**	**496.7358**	975.4378	488.2225	974.4538	487.7305	10
8	88.0393	735.3672	368.1872	717.3566	**359.1819**	D	**895.4116**	448.2094	878.3850	439.6961	877.4010	439.2041	9
9	60.0444	822.3992	411.7032	804.3886	402.6980	S	**780.3846**	390.6959	**763.3581**	382.1827	**762.3741**	381.6907	8
10	86.0964	935.4833	**468.2453**	917.4727	459.2400	L	693.3526	347.1799	676.3260	338.6667	675.3420	338.1747	7
11	60.0444	1022.5153	511.7613	1004.5047	502.7560	S	580.2685	290.6379	563.2420	282.1246	562.2580	281.6326	6
12	60.0444	1109.5473	555.2773	1091.5368	**546.2720**	S	**493.2365**	247.1219	476.2100	238.6086	475.2259	238.1166	5
13	30.0338	1166.5688	583.7880	1148.5582	574.7828	G	**406.2045**	203.6059	389.1779	195.0926	388.1939	194.6006	4
14	60.0444	1253.6008	627.3040	1235.5903	618.2988	S	349.1830	**175.0951**	332.1565	166.5819	331.1724	166.0899	3
15	60.0444	1340.6329	670.8201	1322.6223	661.8148	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
16	129.1135					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GDVTAQIALQPALK**
Found in **P04179**, P04179|SODM_HUMAN Superoxide dismutase [Mn], mitochondrial OS=Homo sapiens GN=SOD2 PE=1 SV=2

Match to Query 425: 1423.727704 from(712.871128,2+)

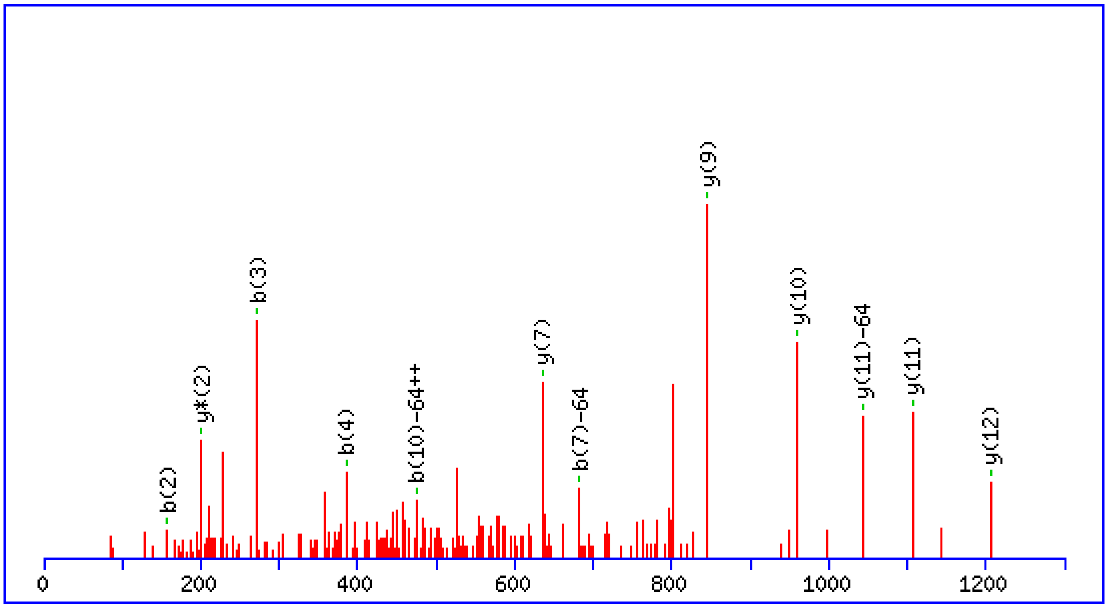


Monoisotopic mass of neutral peptide Mr(calc): 1423.8035
Fixed modifications: Carbamidomethyl (C)
Ions Score: 66 **Expect:** 1.6e-005
Matches (Bold Red): 19/138 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180					G							14
2	88.0393	173.0557	87.0315			155.0451	78.0262	D	1367.7893	684.3983	1350.7627	675.8850	1349.7787	675.3930	13
3	72.0808	**272.1241**	136.5657			254.1135	127.5604	V	1252.7624	626.8848	1235.7358	618.3715	1234.7518	617.8795	12
4	74.0600	**373.1718**	187.0895			**355.1612**	178.0842	T	**1153.6939**	577.3506	1136.6674	568.8373	1135.6834	568.3453	11
5	44.0495	**444.2089**	222.6081			**426.1983**	213.6028	A	**1052.6463**	526.8268	1035.6197	518.3135			10
6	101.0709	**572.2675**	286.6374	555.2409	278.1241	554.2569	277.6321	Q	**981.6091**	491.3082	964.5826	482.7949			9
7	86.0964	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	I	**853.5506**	427.2789	836.5240	418.7656			8
8	44.0495	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	A	**740.4665**	370.7369	723.4400	362.2236			7
9	86.0964	869.4727	435.2400	852.4462	426.7267	851.4621	**426.2347**	L	**669.4294**	335.2183	652.4028	326.7051			6
10	101.0709	997.5313	499.2693	980.5047	490.7560	979.5207	490.2640	Q	**556.3453**	278.6763	**539.3188**	270.1630			5
11	70.0651	1094.5841	547.7957	1077.5575	**539.2824**	1076.5735	538.7904	P	**428.2867**	214.6470	411.2602	206.1337			4
12	44.0495	1165.6212	583.3142	1148.5946	574.8009	1147.6106	574.3089	A	331.2340	166.1206	314.2074	157.6074			3
13	86.0964	1278.7052	639.8563	1261.6787	631.3430	1260.6947	630.8510	L	**260.1969**	130.6021	243.1703	122.0888			2
14	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **GVDIVMDPLGGSDTAK**
Found in **Q99536**, Q99536|VAT1_HUMAN Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2

Match to Query 622: 1589.687178 from(795.850865,2+)

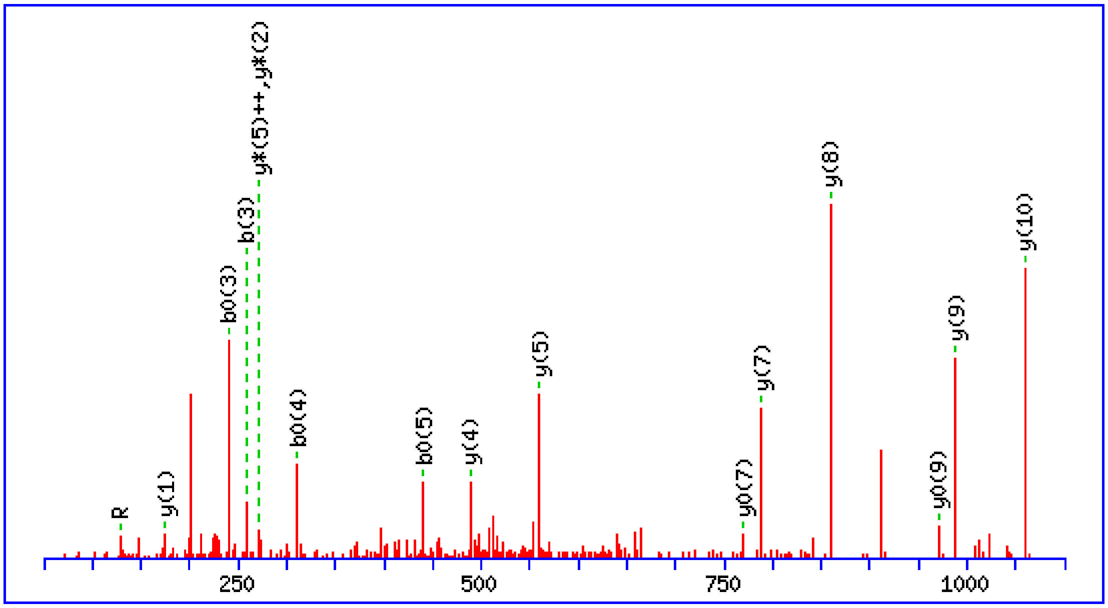


Monoisotopic mass of neutral peptide Mr(calc): 1589.7607
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 32 **Expect:** 0.042
Matches (Bold Red): 12/229 fragment ions using 20 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180			G							16
2	72.0808	**157.0972**	79.0522			V	1533.7465	767.3769	1516.7200	758.8636	1515.7359	758.3716	15
3	88.0393	**272.1241**	136.5657	254.1135	127.5604	D	1434.6781	717.8427	1417.6515	709.3294	1416.6675	708.8374	14
4	86.0964	**385.2082**	193.1077	367.1976	184.1024	I	1319.6511	660.3292	1302.6246	651.8159	1301.6406	651.3239	13
5	72.0808	484.2766	242.6419	466.2660	233.6366	V	**1206.5671**	603.7872	1189.5405	595.2739	1188.5565	594.7819	12
6	120.0478	631.3120	316.1596	613.3014	307.1543	M	**1107.4987**	554.2530	1090.4721	545.7397	1089.4881	545.2477	11
7	88.0393	746.3389	373.6731	728.3284	364.6678	D	**960.4633**	480.7353	943.4367	472.2220	942.4527	471.7300	10
8	70.0651	843.3917	422.1995	825.3811	413.1942	P	**845.4363**	423.2218	828.4098	414.7085	827.4258	414.2165	9
9	86.0964	956.4758	478.7415	938.4652	469.7362	L	748.3836	374.6954	731.3570	366.1821	730.3730	365.6901	8
10	30.0338	1013.4972	507.2522	995.4866	498.2470	G	**635.2995**	318.1534	618.2729	309.6401	617.2889	309.1481	7
11	30.0338	1070.5187	535.7630	1052.5081	526.7577	G	578.2780	289.6427	561.2515	281.1294	560.2675	280.6374	6
12	60.0444	1157.5507	579.2790	1139.5401	570.2737	S	521.2566	261.1319	504.2300	252.6186	503.2460	252.1266	5
13	88.0393	1272.5776	636.7925	1254.5671	627.7872	D	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4
14	74.0600	1373.6253	687.3163	1355.6148	678.3110	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
15	44.0495	1444.6624	722.8349	1426.6519	713.8296	A	218.1499	109.5786	**201.1234**	101.0653			2
16	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AADAEAEVASLNR**
Found in **P06753**, P06753|TPM3_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1

Match to Query 373: 1315.576542 from(658.795547,2+)

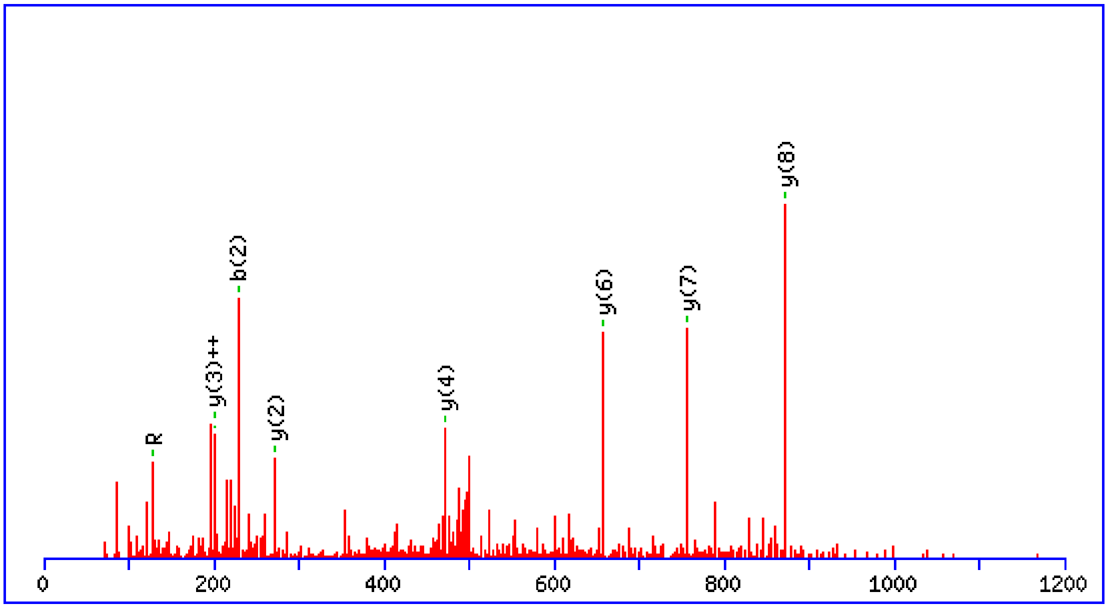


Monoisotopic mass of neutral peptide Mr(calc): 1315.6368
Fixed modifications: Carbamidomethyl (C)
Ions Score: 33 **Expect:** 0.037
Matches (Bold Red): 16/125 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							13
2	44.0495	143.0815	72.0444					A	1245.6070	623.3071	1228.5804	614.7938	1227.5964	614.3018	12
3	88.0393	**258.1084**	129.5579			**240.0979**	120.5526	D	1174.5699	587.7886	1157.5433	579.2753	1156.5593	578.7833	11
4	44.0495	329.1456	165.0764			**311.1350**	156.0711	A	**1059.5429**	530.2751	1042.5164	521.7618	1041.5323	521.2698	10
5	102.0550	458.1882	229.5977			**440.1776**	220.5924	E	**988.5058**	494.7565	971.4792	486.2433	**970.4952**	485.7513	9
6	44.0495	529.2253	265.1163			511.2147	256.1110	A	**859.4632**	430.2352	842.4367	421.7220	841.4526	421.2300	8
7	102.0550	658.2679	329.6376			640.2573	320.6323	E	**788.4261**	394.7167	771.3995	386.2034	**770.4155**	385.7114	7
8	72.0808	757.3363	379.1718			739.3257	370.1665	V	659.3835	330.1954	642.3569	321.6821	641.3729	321.1901	6
9	44.0495	828.3734	414.6903			810.3628	405.6850	A	**560.3151**	280.6612	543.2885	**272.1479**	542.3045	271.6559	5
10	60.0444	915.4054	458.2063			897.3949	449.2011	S	**489.2780**	245.1426	472.2514	236.6293	471.2674	236.1373	4
11	86.0964	1028.4895	514.7484			1010.4789	505.7431	L	402.2459	201.6266	385.2194	193.1133			3
12	87.0553	1142.5324	571.7698	1125.5059	563.2566	1124.5218	562.7646	N	289.1619	145.0846	**272.1353**	136.5713			2
13	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **IDVGEAEPR**
Found in **P54577**, P54577|SYYC_HUMAN Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4

Match to Query 292: 984.457102 from(493.235827,2+)

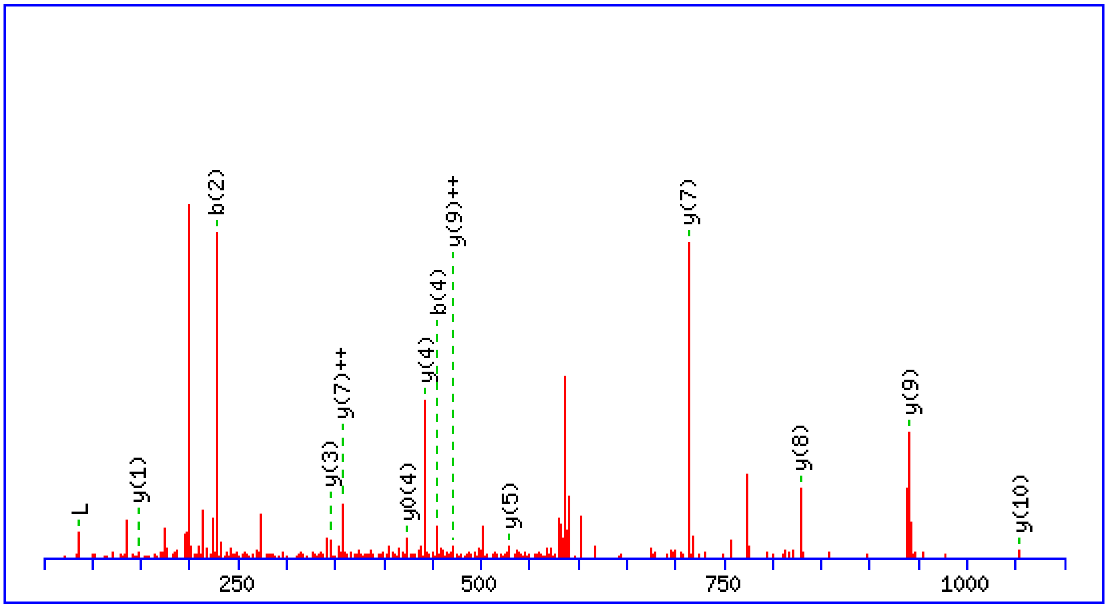


Monoisotopic mass of neutral peptide Mr(calc): 984.4876
Fixed modifications: Carbamidomethyl (C)
Ions Score: 35 **Expect:** 0.024
Matches (Bold Red): 8/83 fragment ions using 37 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	86.0964	114.0913	57.5493			I							9
2	88.0393	**229.1183**	115.0628	211.1077	106.0575	D	**872.4108**	436.7091	855.3843	428.1958	854.4003	427.7038	8
3	72.0808	328.1867	164.5970	310.1761	155.5917	V	**757.3839**	379.1956	740.3573	370.6823	739.3733	370.1903	7
4	30.0338	385.2082	193.1077	367.1976	184.1024	G	**658.3155**	329.6614	641.2889	321.1481	640.3049	320.6561	6
5	102.0550	514.2508	257.6290	496.2402	248.6237	E	601.2940	301.1506	584.2675	292.6374	583.2835	292.1454	5
6	44.0495	585.2879	293.1476	567.2773	284.1423	A	**472.2514**	236.6293	455.2249	228.1161	454.2409	227.6241	4
7	102.0550	714.3305	357.6689	696.3199	348.6636	E	401.2143	**201.1108**	384.1878	192.5975	383.2037	192.1055	3
8	70.0651	811.3832	406.1953	793.3727	397.1900	P	**272.1717**	136.5895	255.1452	128.0762			2
9	**129.1135**					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LLLDPSSPPTK**
Found in **Q6IAA8**, Q6IAA8|CK059_HUMAN UPF0404 protein C11orf59 OS=Homo sapiens GN=C11orf59 PE=1 SV=2

Match to Query 137: 1166.564074 from(584.289313,2+)

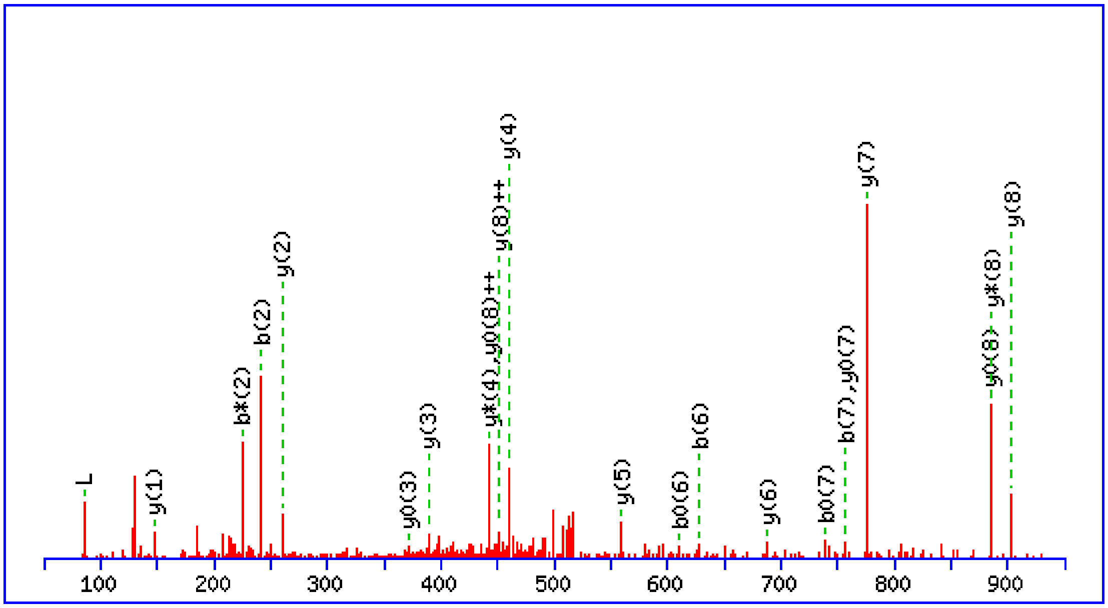


Monoisotopic mass of neutral peptide Mr(calc): 1166.6547
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 **Expect:** 0.0031
Matches (Bold Red): 16/103 fragment ions using 46 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			**L**							**11**
2	**86.0964**	**227.1754**	114.0913			**L**	**1054.5779**	527.7926	1037.5514	519.2793	1036.5673	518.7873	**10**
3	**86.0964**	340.2595	170.6334			**L**	**941.4938**	**471.2506**	924.4673	462.7373	923.4833	462.2453	**9**
4	88.0393	**455.2864**	228.1468	437.2758	219.1416	**D**	**828.4098**	414.7085	811.3832	406.1953	810.3992	405.7032	**8**
5	70.0651	552.3392	276.6732	534.3286	267.6679	**P**	**713.3828**	**357.1951**	696.3563	348.6818	695.3723	348.1898	**7**
6	60.0444	639.3712	320.1892	621.3606	311.1840	**S**	616.3301	308.6687	599.3035	300.1554	598.3195	299.6634	**6**
7	60.0444	726.4032	363.7053	708.3927	354.7000	**S**	**529.2980**	265.1527	512.2715	256.6394	511.2875	256.1474	**5**
8	70.0651	823.4560	412.2316	805.4454	403.2264	**P**	**442.2660**	221.6366	425.2395	213.1234	**424.2554**	212.6314	**4**
9	70.0651	920.5088	460.7580	902.4982	451.7527	**P**	**345.2132**	173.1103	328.1867	164.5970	327.2027	164.1050	**3**
10	74.0600	1021.5564	511.2819	1003.5459	502.2766	**T**	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**2**
11	101.1073					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **LQSEVAELK**
Found in **P53990**, P53990|K0174_HUMAN Uncharacterized protein KIAA0174 OS=Homo sapiens GN=KIAA0174 PE=1 SV=1

Match to Query 310: 1015.512622 from(508.763587,2+)

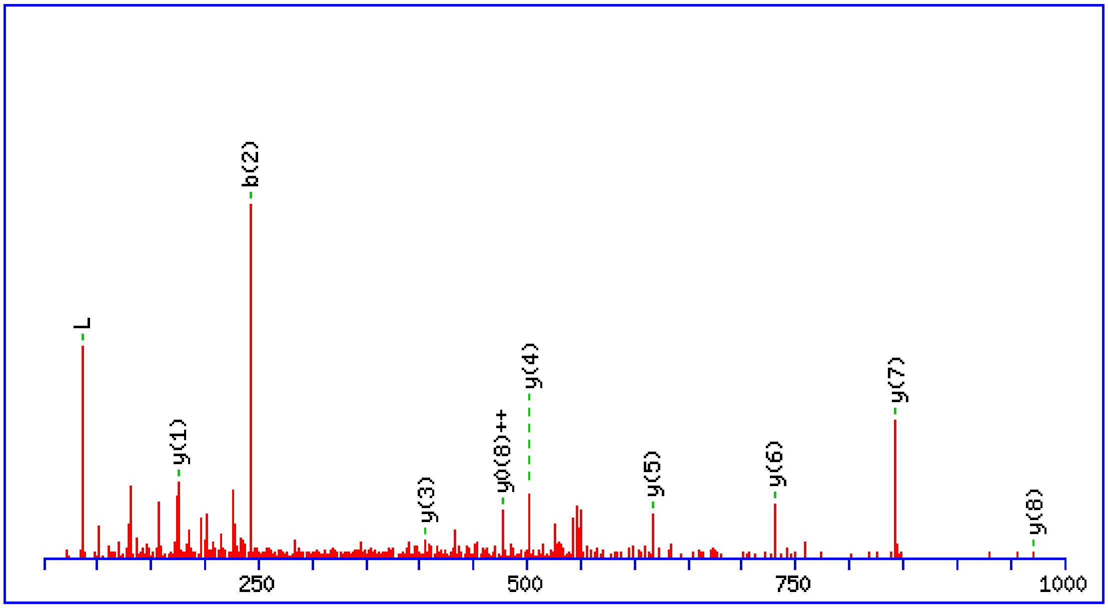


Monoisotopic mass of neutral peptide Mr(calc): 1015.5549
Fixed modifications: Carbamidomethyl (C)
Ions Score: 56 **Expect:** 0.00023
Matches (Bold Red): 23/95 fragment ions using 36 most intense peaks

#	Immon.	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							9
2	101.0709	**242.1499**	121.5786	**225.1234**	113.0653			Q	**903.4782**	**452.2427**	**886.4516**	443.7295	**885.4676**	**443.2374**	8
3	60.0444	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	S	**775.4196**	388.2134	758.3931	379.7002	**757.4090**	379.2082	7
4	102.0550	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	E	**688.3876**	344.6974	671.3610	336.1842	670.3770	335.6921	6
5	72.0808	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	V	**559.3450**	280.1761	542.3184	271.6629	541.3344	271.1709	5
6	44.0495	**628.3301**	314.6687	611.3035	306.1554	**610.3195**	305.6634	A	**460.2766**	230.6419	**443.2500**	222.1287	442.2660	221.6366	4
7	102.0550	**757.3727**	379.1900	740.3461	370.6767	**739.3621**	370.1847	E	**389.2395**	195.1234	372.2129	186.6101	**371.2289**	186.1181	3
8	**86.0964**	870.4567	435.7320	853.4302	427.2187	852.4462	426.7267	L	**260.1969**	130.6021	243.1703	122.0888			2
9	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IQLNNPTER**
Found in **Q8IYS2**, Q8IYS2|K2013_HUMAN Uncharacterized protein KIAA2013 OS=Homo sapiens GN=KIAA2013 PE=2 SV=1

Match to Query 180: 1083.398390 from(542.706471,2+)

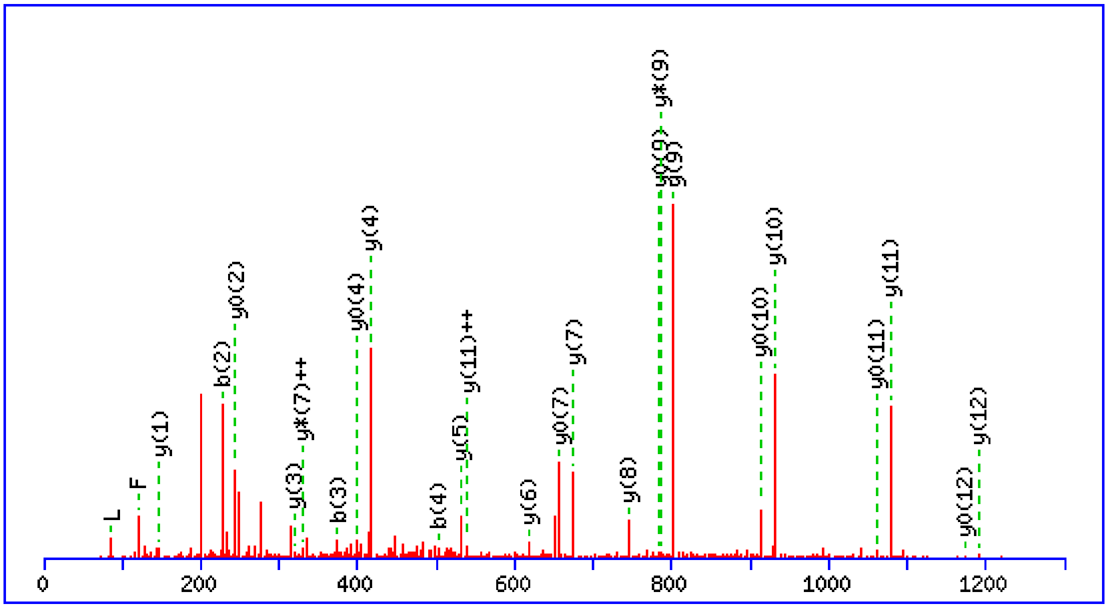


Monoisotopic mass of neutral peptide Mr(calc): 1083.5672
Fixed modifications: Carbamidomethyl (C)
Ions Score: 48 **Expect:** 0.0012
Matches (Bold Red): 11/89 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							9
2	101.0709	**242.1499**	121.5786	225.1234	113.0653			Q	**971.4905**	486.2489	954.4639	477.7356	953.4799	**477.2436**	8
3	**86.0964**	355.2340	178.1206	338.2074	169.6074			L	**843.4319**	422.2196	826.4054	413.7063	825.4213	413.2143	7
4	87.0553	469.2769	235.1421	452.2504	226.6288			N	**730.3478**	365.6776	713.3213	357.1643	712.3373	356.6723	6
5	87.0553	583.3198	292.1636	566.2933	283.6503			N	**616.3049**	308.6561	599.2784	300.1428	598.2944	299.6508	5
6	70.0651	680.3726	340.6899	663.3461	332.1767			P	**502.2620**	251.6346	485.2354	243.1214	484.2514	242.6293	4
7	74.0600	781.4203	391.2138	764.3937	382.7005	763.4097	382.2085	T	**405.2092**	203.1083	388.1827	194.5950	387.1987	194.1030	3
8	102.0550	910.4629	455.7351	893.4363	447.2218	892.4523	446.7298	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **LLFEGAGSNPGDK**
Found in **P61421**, P61421|VA0D1_HUMAN Vacuolar proton pump subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1

Match to Query 558: 1303.595526 from(652.805039,2+)

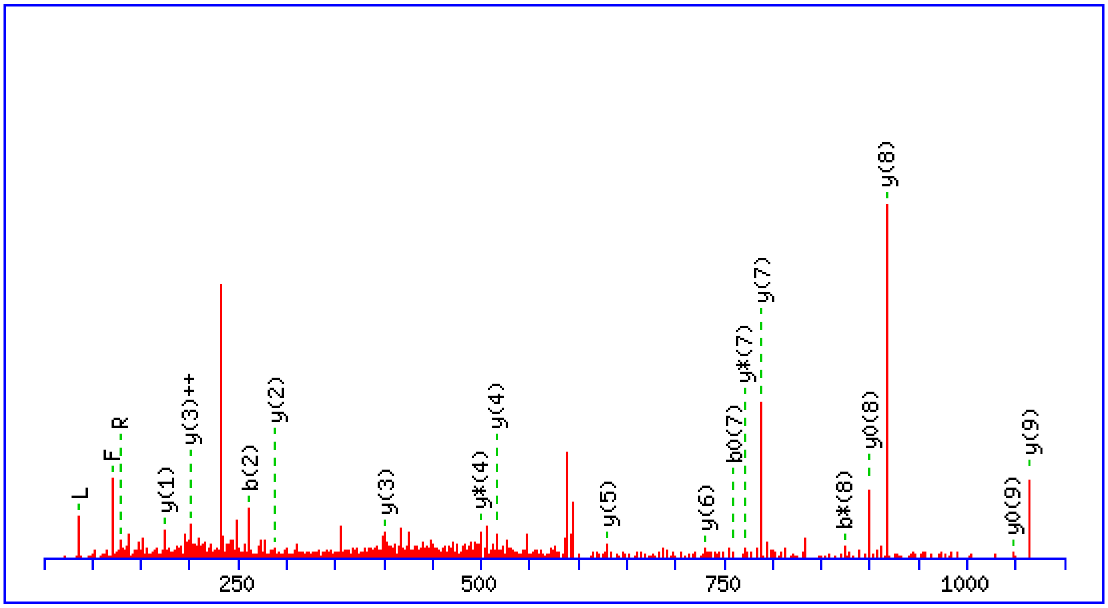


Monoisotopic mass of neutral peptide Mr(calc): 1303.6408
Fixed modifications: Carbamidomethyl (C)
Ions Score: 60 **Expect:** 7.9e-005
Matches (Bold Red): 27/133 fragment ions using 75 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					L							13
2	**86.0964**	**227.1754**	114.0913					L	**1191.5640**	596.2857	1174.5375	587.7724	**1173.5535**	587.2804	12
3	**120.0808**	**374.2438**	187.6255					F	**1078.4800**	**539.7436**	1061.4534	531.2304	**1060.4694**	530.7383	11
4	102.0550	**503.2864**	252.1468			485.2758	243.1416	E	**931.4116**	466.2094	914.3850	457.6961	**913.4010**	457.2041	10
5	30.0338	560.3079	280.6576			542.2973	271.6523	G	**802.3690**	401.6881	**785.3424**	393.1748	**784.3584**	392.6828	9
6	44.0495	631.3450	316.1761			613.3344	307.1709	A	**745.3475**	373.1774	728.3210	364.6641	727.3369	364.1721	8
7	30.0338	688.3665	344.6869			670.3559	335.6816	G	**674.3104**	337.6588	657.2838	**329.1456**	**656.2998**	328.6536	7
8	60.0444	775.3985	388.2029			757.3879	379.1976	S	**617.2889**	309.1481	600.2624	300.6348	599.2784	300.1428	6
9	87.0553	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	N	**530.2569**	265.6321	513.2304	257.1188	512.2463	256.6268	5
10	70.0651	986.4942	493.7507	969.4676	485.2374	968.4836	484.7454	P	**416.2140**	208.6106	399.1874	200.0974	**398.2034**	199.6053	4
11	30.0338	1043.5156	522.2615	1026.4891	513.7482	1025.5051	513.2562	G	**319.1612**	160.0842	302.1347	151.5710	301.1506	151.0790	3
12	88.0393	1158.5426	579.7749	1141.5160	571.2617	1140.5320	570.7696	D	262.1397	131.5735	245.1132	123.0602	**244.1292**	122.5682	2
13	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IFEGTNDILR**
Found in **P49748**, P49748|ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1

Match to Query 331: 1176.546026 from(589.280289,2+)

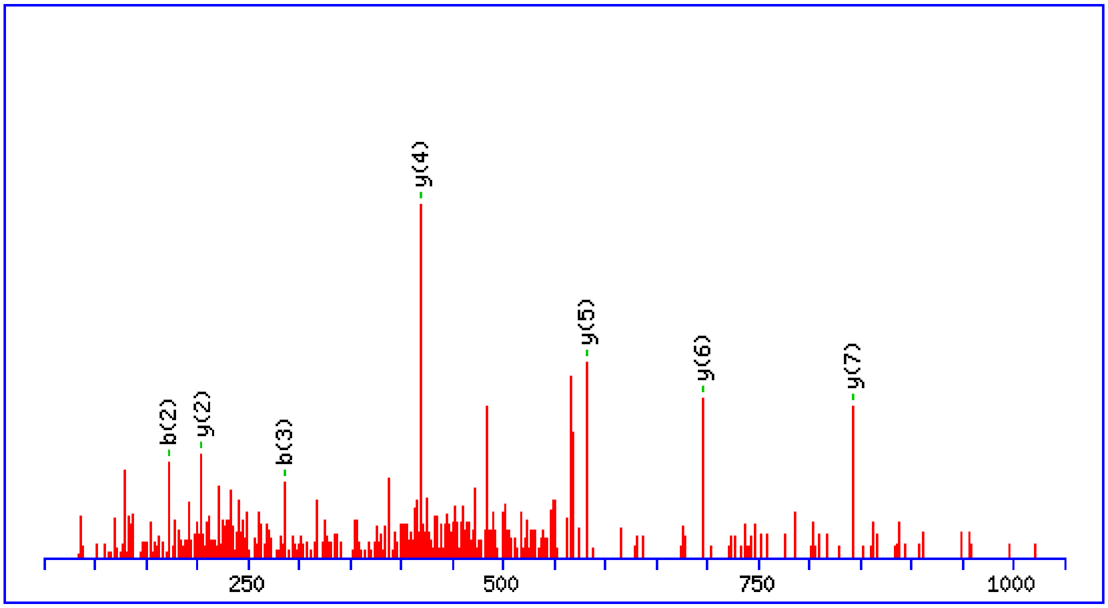


Monoisotopic mass of neutral peptide Mr(calc): 1176.6139
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 **Expect:** 0.019
Matches (Bold Red): 22/98 fragment ions using 61 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							10
2	**120.0808**	**261.1598**	131.0835					F	**1064.5371**	532.7722	1047.5106	524.2589	**1046.5265**	523.7669	9
3	102.0550	390.2023	195.6048			372.1918	186.5995	E	**917.4687**	459.2380	900.4421	450.7247	**899.4581**	450.2327	8
4	30.0338	447.2238	224.1155			429.2132	215.1103	G	**788.4261**	394.7167	**771.3995**	386.2034	770.4155	385.7114	7
5	74.0600	548.2715	274.6394			530.2609	265.6341	T	**731.4046**	366.2060	714.3781	357.6927	713.3941	357.2007	6
6	87.0553	662.3144	331.6608	645.2879	323.1476	644.3039	322.6556	N	**630.3569**	315.6821	613.3304	307.1688	612.3464	306.6768	5
7	88.0393	777.3414	389.1743	760.3148	380.6610	**759.3308**	380.1690	D	**516.3140**	258.6606	**499.2875**	250.1474	498.3035	249.6554	4
8	**86.0964**	890.4254	445.7163	**873.3989**	437.2031	872.4149	436.7111	I	**401.2871**	**201.1472**	384.2605	192.6339			3
9	**86.0964**	1003.5095	502.2584	986.4829	493.7451	985.4989	493.2531	L	**288.2030**	144.6051	271.1765	136.0919			2
10	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **GNNFLYTNGK**
Found in **O75083**, O75083|WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4

Match to Query 304: 1126.491692 from(564.253122,2+)

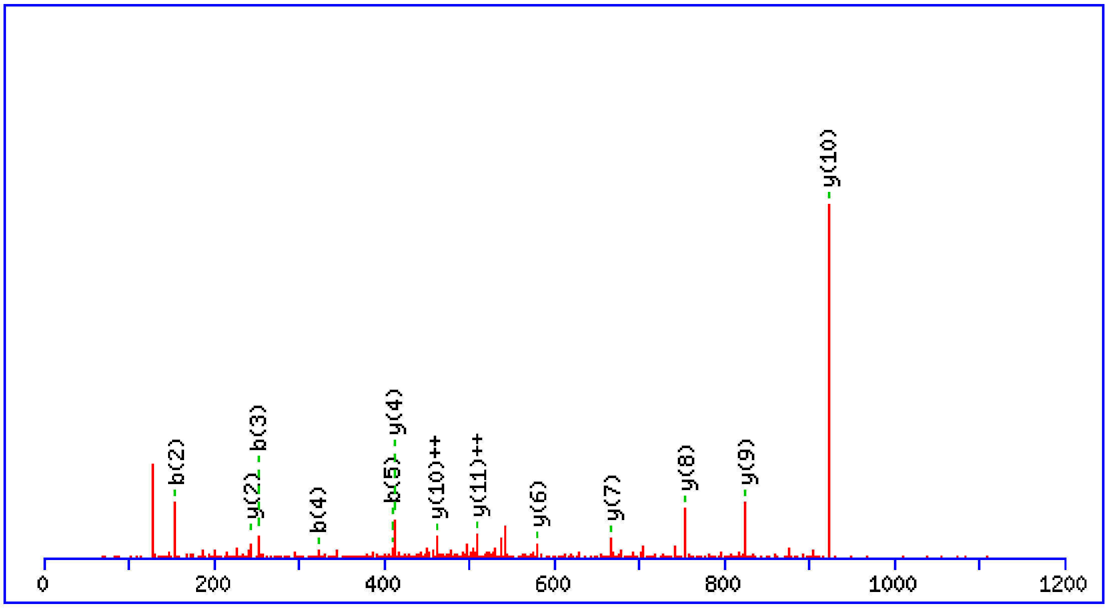


Monoisotopic mass of neutral peptide Mr(calc): 1126.5407
Fixed modifications: Carbamidomethyl (C)
Ions Score: 34 **Expect:** 0.027
Matches (Bold Red): 7/98 fragment ions using 14 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	30.0338	58.0287	29.5180					**G**							10
2	87.0553	**172.0717**	86.5395	155.0451	78.0262			**N**	1070.5265	535.7669	1053.5000	527.2536	1052.5160	526.7616	9
3	87.0553	**286.1146**	143.5609	269.0880	135.0477			**N**	956.4836	478.7454	939.4571	470.2322	938.4730	469.7402	8
4	120.0808	433.1830	217.0951	416.1565	208.5819			**F**	**842.4407**	421.7240	825.4141	413.2107	824.4301	412.7187	7
5	86.0964	546.2671	273.6372	529.2405	265.1239			**L**	**695.3723**	348.1898	678.3457	339.6765	677.3617	339.1845	6
6	136.0757	709.3304	355.1688	692.3039	346.6556			**Y**	**582.2882**	291.6477	565.2617	283.1345	564.2776	282.6425	5
7	74.0600	810.3781	405.6927	793.3515	397.1794	792.3675	396.6874	**T**	**419.2249**	210.1161	402.1983	201.6028	401.2143	201.1108	4
8	87.0553	924.4210	462.7141	907.3945	454.2009	906.4104	453.7089	**N**	318.1772	159.5922	301.1506	151.0790			3
9	30.0338	981.4425	491.2249	964.4159	482.7116	963.4319	482.2196	**G**	**204.1343**	102.5708	187.1077	94.0575			2
10	101.1073							**K**	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **GPPASSPAPAPK**
Found in **Q15942**, Q15942|ZYX_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1

Match to Query 436: 1075.530000 from(538.772276,2+)

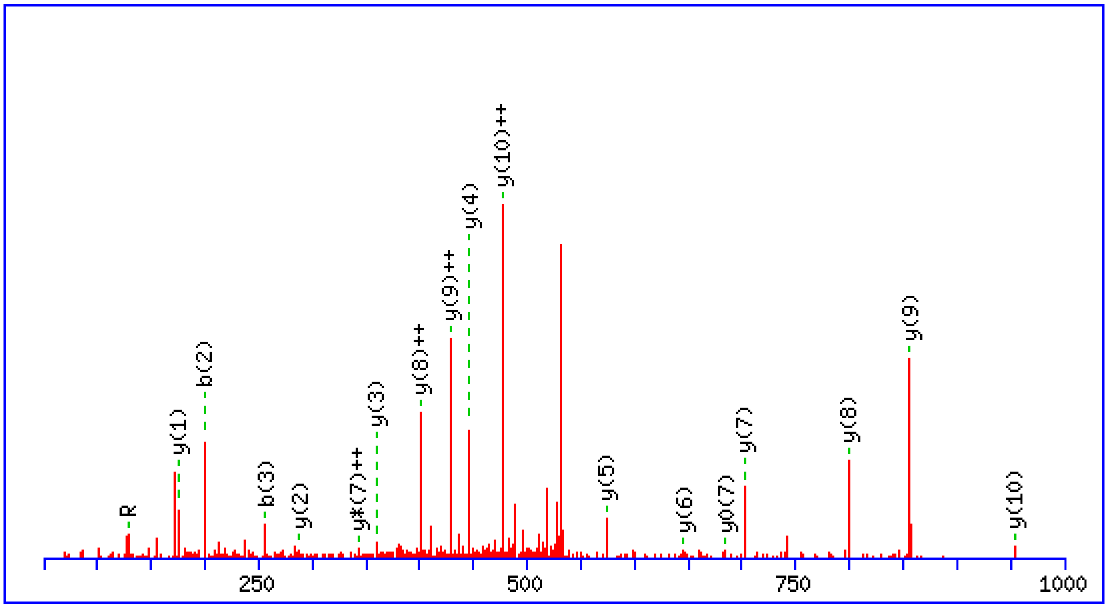


Monoisotopic mass of neutral peptide Mr(calc): 1075.5662
Fixed modifications: Carbamidomethyl (C)
Ions Score: 47 **Expect:** 0.0015
Matches (Bold Red): 13/102 fragment ions using 26 most intense peaks

#	**Immon.**	**b**	**b^{++}**	**b^{0}**	**b^{0++}**	**Seq.**	**y**	**y^{++}**	**y***	**y^{*++}**	**y^{0}**	**y^{0++}**	**#**
1	30.0338	58.0287	29.5180			**G**							**12**
2	70.0651	**155.0815**	78.0444			**P**	1019.5520	**510.2796**	1002.5255	501.7664	1001.5415	501.2744	**11**
3	70.0651	**252.1343**	126.5708			**P**	**922.4993**	**461.7533**	905.4727	453.2400	904.4887	452.7480	**10**
4	44.0495	**323.1714**	162.0893			**A**	**825.4465**	413.2269	808.4199	404.7136	807.4359	404.2216	**9**
5	60.0444	**410.2034**	205.6053	392.1928	196.6001	**S**	**754.4094**	377.7083	737.3828	369.1951	736.3988	368.7030	**8**
6	60.0444	497.2354	249.1214	479.2249	240.1161	**S**	**667.3774**	334.1923	650.3508	325.6790	649.3668	325.1870	**7**
7	70.0651	594.2882	297.6477	576.2776	288.6425	**P**	**580.3453**	290.6763	563.3188	282.1630			**6**
8	44.0495	665.3253	333.1663	647.3148	324.1610	**A**	483.2926	242.1499	466.2660	233.6366			**5**
9	70.0651	762.3781	381.6927	744.3675	372.6874	**P**	**412.2554**	206.6314	395.2289	198.1181			**4**
10	44.0495	833.4152	417.2112	815.4046	408.2060	**A**	315.2027	158.1050	298.1761	149.5917			**3**
11	70.0651	930.4680	465.7376	912.4574	456.7323	**P**	**244.1656**	122.5864	227.1390	114.0731			**2**
12	101.1073					**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **TPGPGAQSALR**
Found in **P62263**, P62263|RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3

Match to Query 108: 1053.428150 from(527.721351,2+)

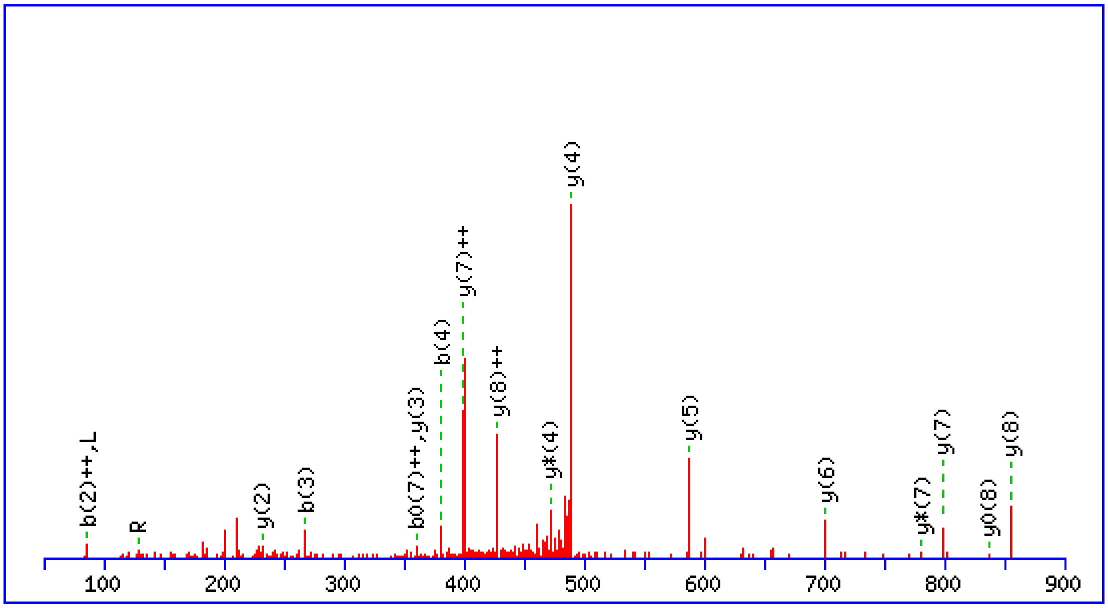


Monoisotopic mass of neutral peptide Mr(calc): 1053.5567
Fixed modifications: Carbamidomethyl (C)
Ions Score: 80 **Expect:** 5.9e-007
Matches (Bold Red): 18/113 fragment ions using 37 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	**T**							**11**
2	70.0651	**199.1077**	100.0575			181.0972	91.0522	**P**	**953.5163**	**477.2618**	936.4898	468.7485	935.5057	468.2565	**10**
3	30.0338	**256.1292**	128.5682			238.1186	119.5629	**G**	**856.4635**	**428.7354**	839.4370	420.2221	838.4530	419.7301	**9**
4	70.0651	353.1819	177.0946			335.1714	168.0893	**P**	**799.4421**	**400.2247**	782.4155	391.7114	781.4315	391.2194	**8**
5	30.0338	410.2034	205.6053			392.1928	196.6001	**G**	**702.3893**	351.6983	685.3628	**343.1850**	**684.3787**	342.6930	**7**
6	44.0495	481.2405	241.1239			463.2300	232.1186	**A**	**645.3679**	323.1876	628.3413	314.6743	627.3573	314.1823	**6**
7	101.0709	609.2991	305.1532	592.2726	296.6399	591.2885	296.1479	**Q**	**574.3307**	287.6690	557.3042	279.1557	556.3202	278.6637	**5**
8	60.0444	696.3311	348.6692	679.3046	340.1559	678.3206	339.6639	**S**	**446.2722**	223.6397	429.2456	215.1264	428.2616	214.6344	**4**
9	44.0495	767.3682	384.1878	750.3417	375.6745	749.3577	375.1825	**A**	**359.2401**	180.1237	342.2136	171.6104			**3**
10	86.0964	880.4523	440.7298	863.4258	432.2165	862.4417	431.7245	**L**	**288.2030**	144.6051	271.1765	136.0919			**2**
11	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LGPLVEQGR**
Found in **P02649**, P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

Match to Query 273: 967.468728 from(484.741640,2+)

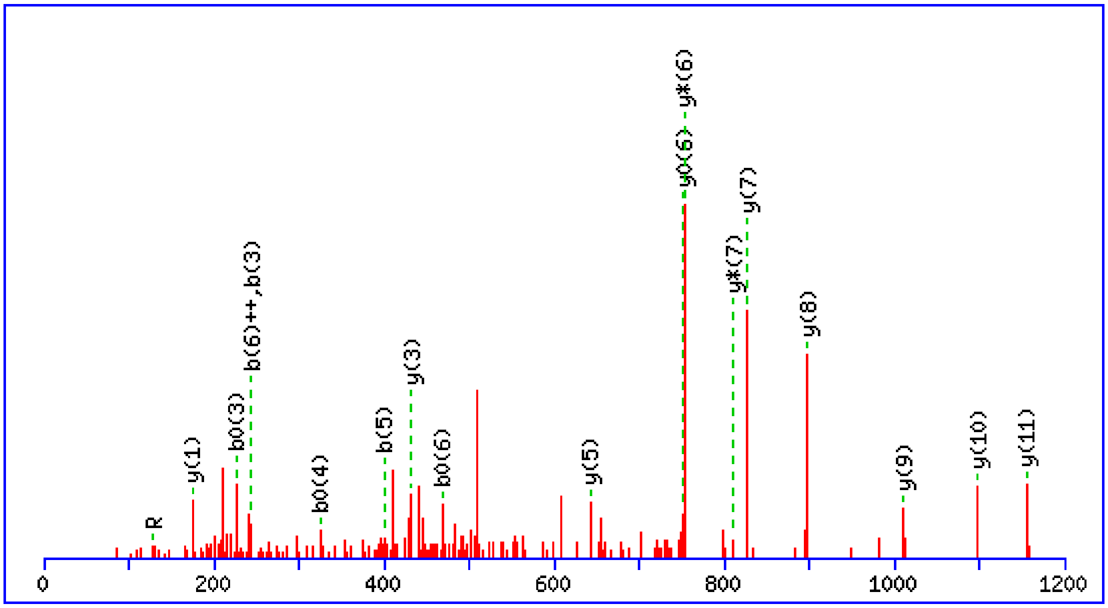


Monoisotopic mass of neutral peptide Mr(calc): 967.5451
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 **Expect:** 0.002
Matches (Bold Red): 19/77 fragment ions using 32 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					**L**							**9**
2	30.0338	171.1128	**86.0600**					**G**	**855.4683**	**428.2378**	838.4417	419.7245	**837.4577**	419.2325	**8**
3	70.0651	**268.1656**	134.5864					**P**	**798.4468**	**399.7271**	**781.4203**	391.2138	780.4363	390.7218	**7**
4	**86.0964**	**381.2496**	191.1285					**L**	**701.3941**	351.2007	684.3675	342.6874	683.3835	342.1954	**6**
5	72.0808	480.3180	240.6627					**V**	**588.3100**	294.6586	571.2835	286.1454	570.2994	285.6534	**5**
6	102.0550	609.3606	305.1840			591.3501	296.1787	**E**	**489.2416**	245.1244	**472.2150**	236.6112	471.2310	236.1191	**4**
7	101.0709	737.4192	369.2132	720.3927	360.7000	719.4087	**360.2080**	**Q**	**360.1990**	180.6031	343.1724	172.0899			**3**
8	30.0338	794.4407	397.7240	777.4141	389.2107	776.4301	388.7187	**G**	**232.1404**	116.5738	215.1139	108.0606			**2**
9	**129.1135**							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **AATVGSLAGQPLQER**
Found in **P02649**, P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

Match to Query 469: 1496.789604 from(749.402078,2+)

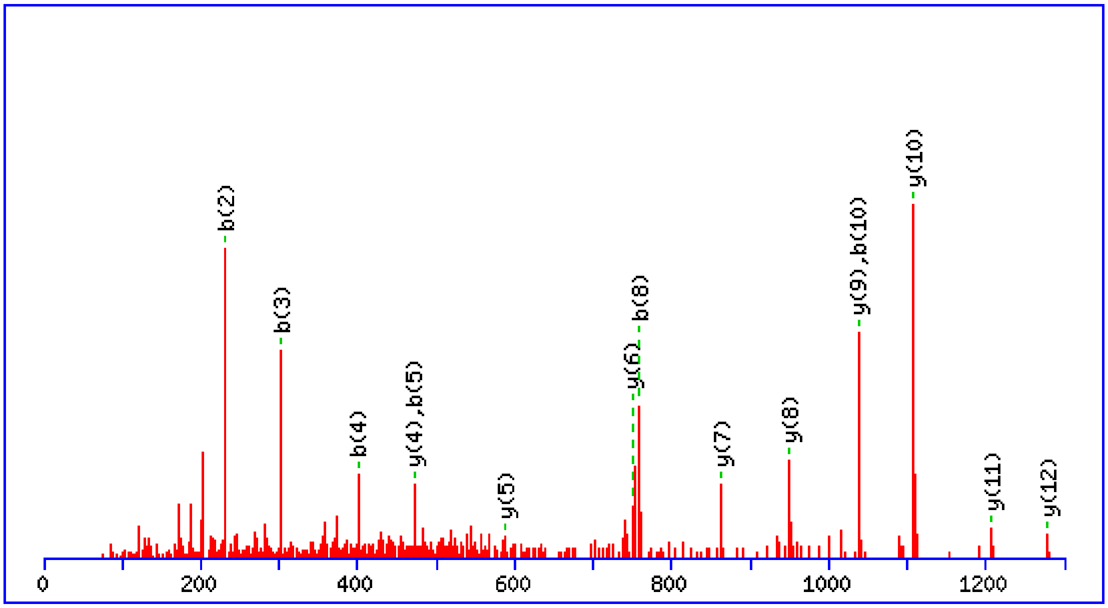


Monoisotopic mass of neutral peptide Mr(calc): 1496.7947
Fixed modifications: Carbamidomethyl (C)
Ions Score: 34 **Expect:** 0.025
Matches (Bold Red): 18/159 fragment ions using 39 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							15
2	44.0495	143.0815	72.0444					A	1426.7649	713.8861	1409.7383	705.3728	1408.7543	704.8808	14
3	74.0600	**244.1292**	122.5682			**226.1186**	113.5629	T	1355.7278	678.3675	1338.7012	669.8542	1337.7172	669.3622	13
4	72.0808	343.1976	172.1024			**325.1870**	163.0972	V	1254.6801	627.8437	1237.6535	619.3304	1236.6695	618.8384	12
5	30.0338	**400.2191**	200.6132			382.2085	191.6079	G	**1155.6117**	578.3095	1138.5851	569.7962	1137.6011	569.3042	11
6	60.0444	487.2511	**244.1292**			**469.2405**	235.1239	S	**1098.5902**	549.7987	1081.5637	541.2855	1080.5796	540.7935	10
7	86.0964	600.3352	300.6712			582.3246	291.6659	L	**1011.5582**	506.2827	994.5316	497.7694	993.5476	497.2774	9
8	44.0495	671.3723	336.1898			653.3617	327.1845	A	**898.4741**	449.7407	881.4476	441.2274	880.4635	440.7354	8
9	30.0338	728.3937	364.7005			710.3832	355.6952	G	**827.4370**	414.2221	**810.4104**	405.7089	809.4264	405.2169	7
10	101.0709	856.4523	428.7298	839.4258	420.2165	838.4417	419.7245	Q	770.4155	385.7114	**753.3890**	377.1981	**752.4050**	376.7061	6
11	70.0651	953.5051	477.2562	936.4785	468.7429	935.4945	468.2509	P	**642.3570**	321.6821	625.3304	313.1688	624.3464	312.6768	5
12	86.0964	1066.5891	533.7982	1049.5626	525.2849	1048.5786	524.7929	L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
13	101.0709	1194.6477	597.8275	1177.6212	589.3142	1176.6372	588.8222	Q	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	3
14	102.0550	1323.6903	662.3488	1306.6638	653.8355	1305.6797	653.3435	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
15	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TEAVASSLYDILAR**
Found in **P16278**, P16278|BGAL_HUMAN Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=1

Match to Query 371: 1507.852186 from(754.933369,2+)

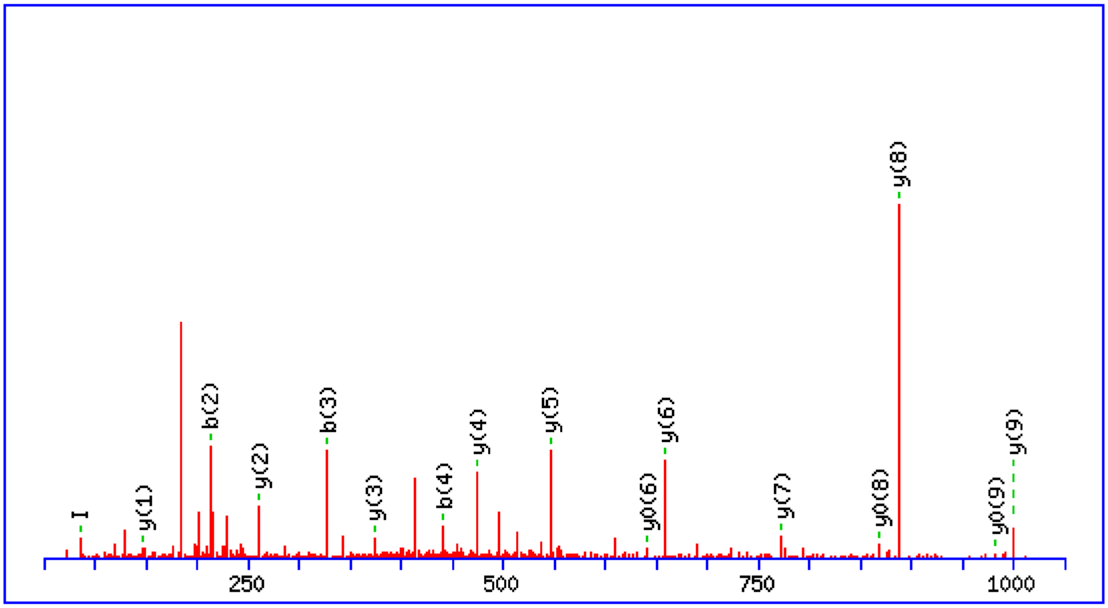


Monoisotopic mass of neutral peptide Mr(calc): 1507.7882
Fixed modifications: Carbamidomethyl (C)
Ions Score: 60 **Expect:** 6.7e-005
Matches (Bold Red): 15/136 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							14
2	102.0550	**231.0975**	116.0524	213.0870	107.0471	E	1407.7478	704.3775	1390.7213	695.8643	1389.7373	695.3723	13
3	44.0495	**302.1347**	151.5710	284.1241	142.5657	A	**1278.7052**	639.8563	1261.6787	631.3430	1260.6947	630.8510	12
4	72.0808	**401.2031**	201.1052	383.1925	192.0999	V	**1207.6681**	604.3377	1190.6416	595.8244	1189.6575	595.3324	11
5	44.0495	**472.2402**	236.6237	454.2296	227.6185	A	**1108.5997**	554.8035	1091.5732	546.2902	1090.5891	545.7982	10
6	60.0444	559.2722	280.1397	541.2617	271.1345	S	**1037.5626**	519.2849	1020.5360	510.7717	1019.5520	510.2796	9
7	60.0444	646.3042	323.6558	628.2937	314.6505	S	**950.5306**	475.7689	933.5040	467.2556	932.5200	466.7636	8
8	86.0964	**759.3883**	380.1978	741.3777	371.1925	L	**863.4985**	432.2529	846.4720	423.7396	845.4880	423.2476	7
9	136.0757	922.4516	461.7295	904.4411	452.7242	Y	**750.4145**	375.7109	733.3879	367.1976	732.4039	366.7056	6
10	88.0393	**1037.4786**	519.2429	1019.4680	510.2376	D	**587.3511**	294.1792	570.3246	285.6659	569.3406	285.1739	5
11	86.0964	1150.5626	575.7850	1132.5521	566.7797	I	**472.3242**	236.6657	455.2976	228.1525			4
12	86.0964	1263.6467	632.3270	1245.6361	623.3217	L	359.2401	180.1237	342.2136	171.6104			3
13	44.0495	1334.6838	667.8456	1316.6733	658.8403	A	246.1561	123.5817	229.1295	115.0684			2
14	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VLDIIATINK**
Found in **P07686**, P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3

Match to Query 387: 1098.663352 from(550.338952,2+)

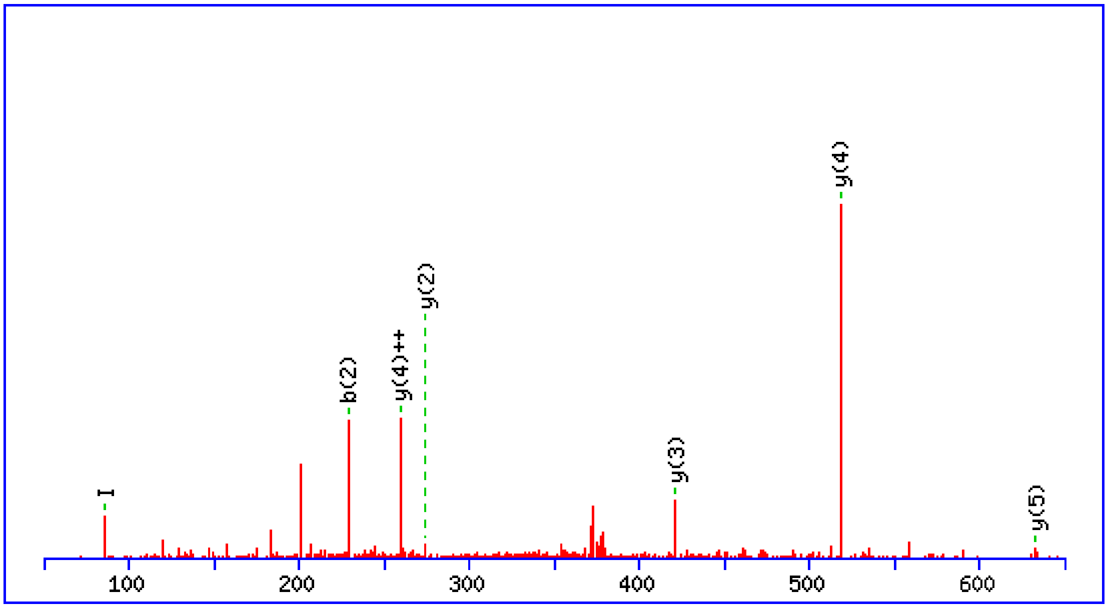


Monoisotopic mass of neutral peptide Mr(calc): 1098.6648
Fixed modifications: Carbamidomethyl (C)
Ions Score: 56 **Expect:** 0.00019
Matches (Bold Red): 19/92 fragment ions using 43 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0808	100.0757	50.5415					V							10
2	**86.0964**	**213.1598**	107.0835					L	**1000.6037**	500.8055	983.5772	492.2922	**982.5932**	491.8002	9
3	88.0393	**328.1867**	164.5970			310.1761	155.5917	D	**887.5197**	444.2635	870.4931	435.7502	**869.5091**	435.2582	8
4	**86.0964**	**441.2708**	221.1390			423.2602	212.1337	I	**772.4927**	386.7500	755.4662	378.2367	754.4822	377.7447	7
5	**86.0964**	554.3548	277.6811			536.3443	268.6758	I	**659.4087**	330.2080	642.3821	321.6947	**641.3981**	321.2027	6
6	44.0495	625.3919	313.1996			607.3814	304.1943	A	**546.3246**	273.6659	529.2980	265.1527	528.3140	264.6606	5
7	74.0600	726.4396	363.7234			708.4291	354.7182	T	**475.2875**	238.1474	458.2609	229.6341	457.2769	229.1421	4
8	**86.0964**	839.5237	420.2655			821.5131	411.2602	I	**374.2398**	187.6235	357.2132	179.1103			3
9	87.0553	953.5666	477.2869	936.5401	468.7737	935.5560	468.2817	N	**261.1557**	131.0815	244.1292	122.5682			2
10	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IDPFVR**
Found in **P39656**, P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2

Match to Query 86: 745.402394 from(373.708473,2+)

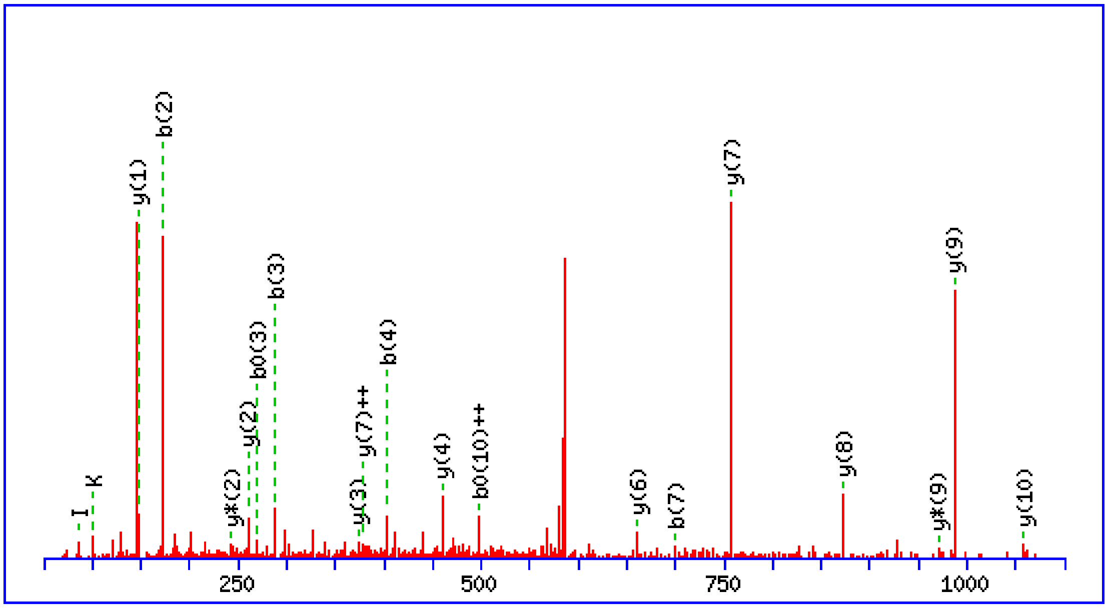


Monoisotopic mass of neutral peptide Mr(calc): 745.4123
Fixed modifications: Carbamidomethyl (C)
Ions Score: 41 **Expect:** 0.0079
Matches (Bold Red): 7/46 fragment ions using 15 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			I							6
2	88.0393	**229.1183**	115.0628	211.1077	106.0575	D	**633.3355**	317.1714	616.3089	308.6581	615.3249	308.1661	5
3	70.0651	326.1710	163.5892	308.1605	154.5839	P	**518.3085**	**259.6579**	501.2820	251.1446			4
4	120.0808	473.2395	237.1234	455.2289	228.1181	F	**421.2558**	211.1315	404.2292	202.6183			3
5	72.0808	572.3079	286.6576	554.2973	277.6523	V	**274.1874**	137.5973	257.1608	129.0840			2
6	129.1135					R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **TADDPSLSLIK**
Found in **P39656**, P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=2

Match to Query 308: 1158.708224 from(580.361388,2+)

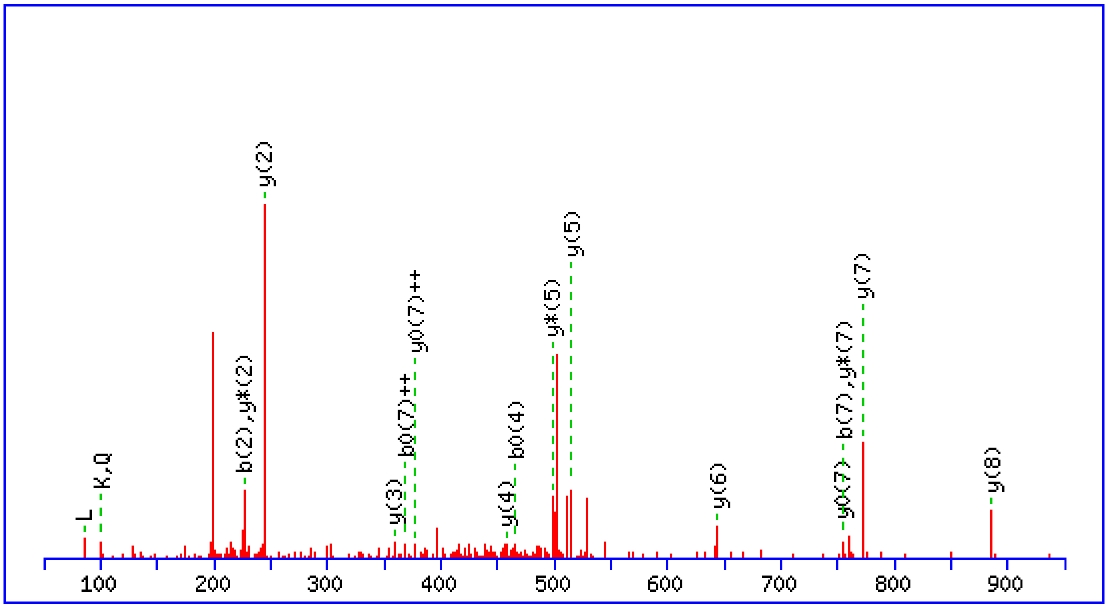


Monoisotopic mass of neutral peptide Mr(calc): 1158.6132
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 **Expect:** 0.004
Matches (Bold Red): 22/105 fragment ions using 60 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							11
2	44.0495	**173.0921**	87.0497	155.0815	78.0444	A	**1058.5728**	529.7900	1041.5463	521.2768	1040.5623	520.7848	10
3	88.0393	**288.1190**	144.5631	**270.1084**	135.5579	D	**987.5357**	494.2715	**970.5092**	485.7582	969.5251	485.2662	9
4	88.0393	**403.1460**	202.0766	385.1354	193.0713	D	**872.5088**	436.7580	855.4822	428.2447	854.4982	427.7527	8
5	70.0651	500.1987	250.6030	482.1882	241.5977	P	**757.4818**	**379.2445**	740.4553	370.7313	739.4713	370.2393	7
6	60.0444	587.2307	294.1190	569.2202	285.1137	S	**660.4291**	330.7182	643.4025	322.2049	642.4185	321.7129	6
7	**86.0964**	**700.3148**	350.6610	682.3042	341.6558	L	573.3970	287.2022	556.3705	278.6889	555.3865	278.1969	5
8	60.0444	787.3468	394.1771	769.3363	385.1718	S	**460.3130**	230.6601	443.2864	222.1468	442.3024	221.6548	4
9	**86.0964**	900.4309	450.7191	882.4203	441.7138	L	**373.2809**	187.1441	356.2544	178.6308			3
10	**86.0964**	1013.5150	507.2611	995.5044	**498.2558**	I	**260.1969**	130.6021	**243.1703**	122.0888			2
11	**101.1073**					K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ILQEGVDPK**
Found in **P40939**, P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2

Match to Query 53: 997.572054 from(499.793303,2+)

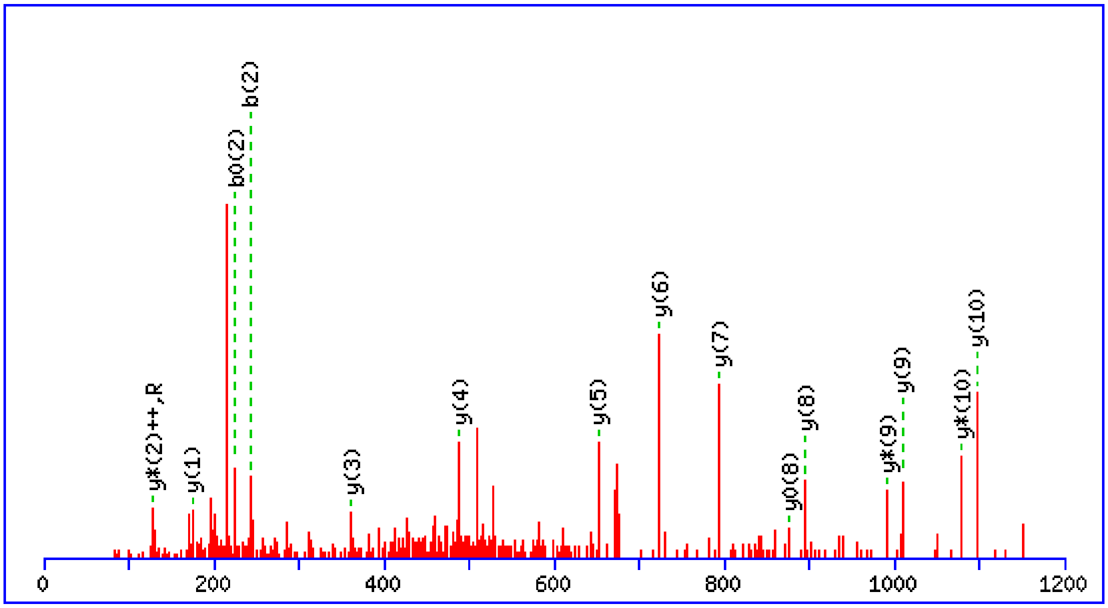


Monoisotopic mass of neutral peptide Mr(calc): 997.5444
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.00067
Matches (Bold Red): 20/91 fragment ions using 30 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							9
2	**86.0964**	**227.1754**	114.0913					L	**885.4676**	443.2375	868.4411	434.7242	867.4571	434.2322	8
3	**101.0709**	355.2340	178.1206	338.2074	169.6074			Q	**772.3836**	386.6954	**755.3570**	378.1821	**754.3730**	**377.6901**	7
4	102.0550	484.2766	242.6419	467.2500	234.1287	**466.2660**	233.6366	E	**644.3250**	322.6661	627.2984	314.1529	626.3144	313.6608	6
5	30.0338	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	G	**515.2824**	258.1448	**498.2558**	249.6316	497.2718	249.1396	5
6	72.0808	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	V	**458.2609**	229.6341	441.2344	221.1208	440.2504	220.6288	4
7	88.0393	**755.3934**	378.2003	738.3668	369.6871	737.3828	**369.1951**	D	**359.1925**	180.0999	342.1660	171.5866	341.1819	171.0946	3
8	70.0651	852.4462	426.7267	835.4196	418.2134	834.4356	417.7214	P	**244.1656**	122.5864	**227.1390**	114.0731			2
9	**101.1073**							K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **ELSNTAAYQSVR**
Found in **Q9HAT2**, Q9HAT2|SIAE_HUMAN Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=2 SV=1

Match to Query 440: 1337.716322 from(669.865437,2+)

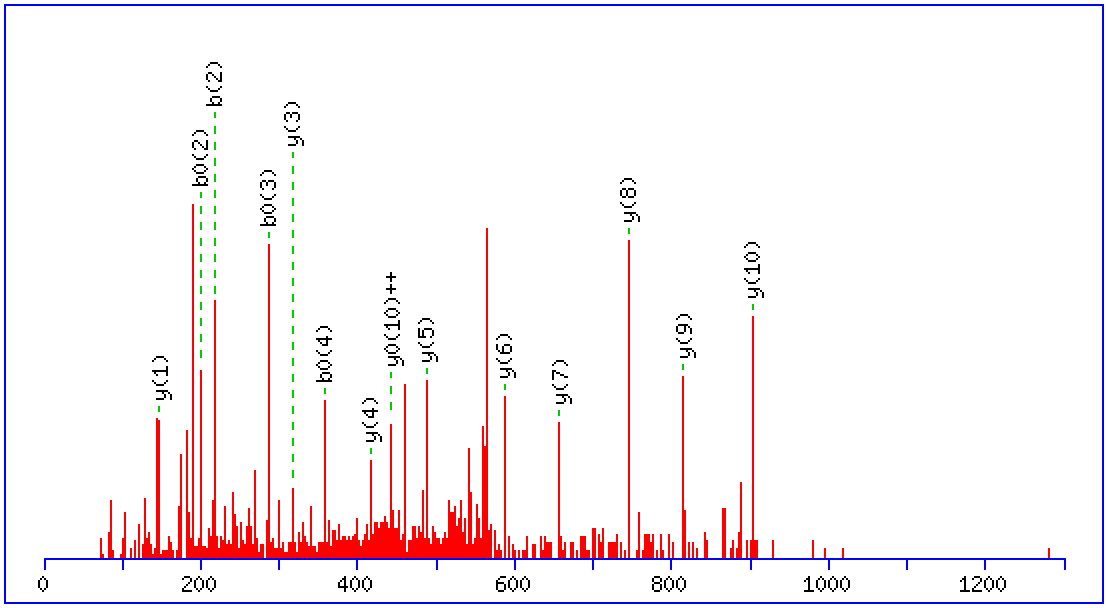


Monoisotopic mass of neutral peptide Mr(calc): 1337.6575
Fixed modifications: Carbamidomethyl (C)
Ions Score: 63 **Expect:** 3.8e-005
Matches (Bold Red): 16/134 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	102.0550	130.0499	65.5286			112.0393	56.5233	**E**							**12**
2	86.0964	**243.1339**	122.0706			**225.1234**	113.0653	**L**	1209.6222	605.3148	1192.5957	596.8015	1191.6117	596.3095	**11**
3	60.0444	330.1660	165.5866			312.1554	156.5813	**S**	**1096.5382**	548.7727	**1079.5116**	540.2594	1078.5276	539.7674	**10**
4	87.0553	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	**N**	**1009.5061**	505.2567	**992.4796**	496.7434	991.4956	496.2514	**9**
5	74.0600	545.2566	273.1319	528.2300	264.6186	527.2460	264.1266	**T**	**895.4632**	448.2352	878.4367	439.7220	**877.4526**	439.2300	**8**
6	44.0495	616.2937	308.6505	599.2671	300.1372	598.2831	299.6452	**A**	**794.4155**	397.7114	777.3890	389.1981	776.4050	388.7061	**7**
7	44.0495	687.3308	344.1690	670.3042	335.6558	669.3202	335.1638	**A**	**723.3784**	362.1928	706.3519	353.6796	705.3678	353.1876	**6**
8	136.0757	850.3941	425.7007	833.3676	417.1874	832.3836	416.6954	**Y**	**652.3413**	326.6743	635.3148	318.1610	634.3307	317.6690	**5**
9	101.0709	978.4527	489.7300	961.4262	481.2167	960.4421	480.7247	**Q**	**489.2780**	245.1426	472.2514	236.6293	471.2674	236.1373	**4**
10	60.0444	1065.4847	533.2460	1048.4582	524.7327	1047.4742	524.2407	**S**	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	**3**
11	72.0808	1164.5531	582.7802	1147.5266	574.2669	1146.5426	573.7749	**V**	274.1874	137.5973	257.1608	**129.0840**			**2**
12	**129.1135**							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **DTSASAVAVGLK**
Found in **P40939**, P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2

Match to Query 292: 1117.664762 from(559.839657,2+)

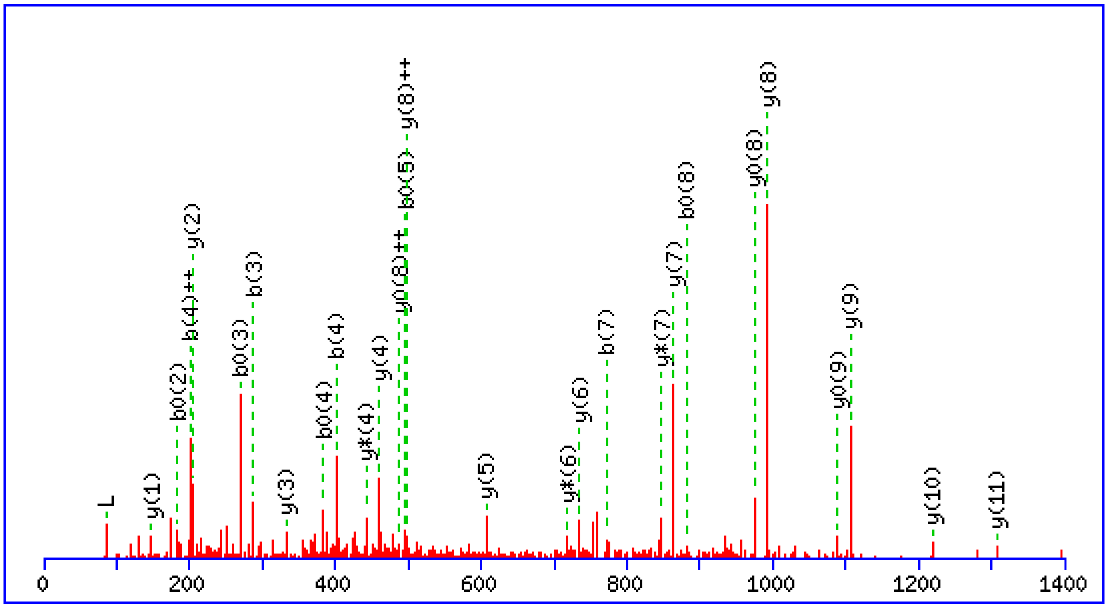


Monoisotopic mass of neutral peptide Mr(calc): 1117.5979
Fixed modifications: Carbamidomethyl (C)
Ions Score: 47 **Expect:** 0.0015
Matches (Bold Red): 14/108 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	116.0342	58.5207	98.0237	49.5155	**D**							**12**
2	74.0600	**217.0819**	109.0446	**199.0713**	100.0393	**T**	1003.5782	502.2928	986.5517	493.7795	985.5677	493.2875	**11**
3	60.0444	304.1139	152.5606	**286.1034**	143.5553	**S**	**902.5306**	451.7689	885.5040	443.2556	884.5200	**442.7636**	**10**
4	44.0495	375.1510	188.0792	**357.1405**	179.0739	**A**	**815.4985**	408.2529	798.4720	399.7396	797.4880	399.2476	**9**
5	60.0444	462.1831	231.5952	444.1725	222.5899	**S**	**744.4614**	372.7343	727.4349	364.2211	726.4509	363.7291	**8**
6	44.0495	533.2202	267.1137	515.2096	258.1084	**A**	**657.4294**	329.2183	640.4028	320.7051			**7**
7	72.0808	632.2886	316.6479	614.2780	307.6427	**V**	**586.3923**	293.6998	569.3657	285.1865			**6**
8	44.0495	703.3257	352.1665	685.3151	343.1612	**A**	**487.3239**	244.1656	470.2973	235.6523			**5**
9	72.0808	802.3941	401.7007	784.3836	392.6954	**V**	**416.2867**	208.6470	399.2602	200.1337			**4**
10	30.0338	859.4156	430.2114	841.4050	421.2061	**G**	**317.2183**	159.1128	300.1918	150.5995			**3**
11	86.0964	972.4997	486.7535	954.4891	477.7482	**L**	260.1969	130.6021	243.1703	122.0888			**2**
12	101.1073					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **ISSLLEEQFQQGK**
Found in **P62241**, P62241|RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2

Match to Query 602: 1505.792518 from(753.903535,2+)

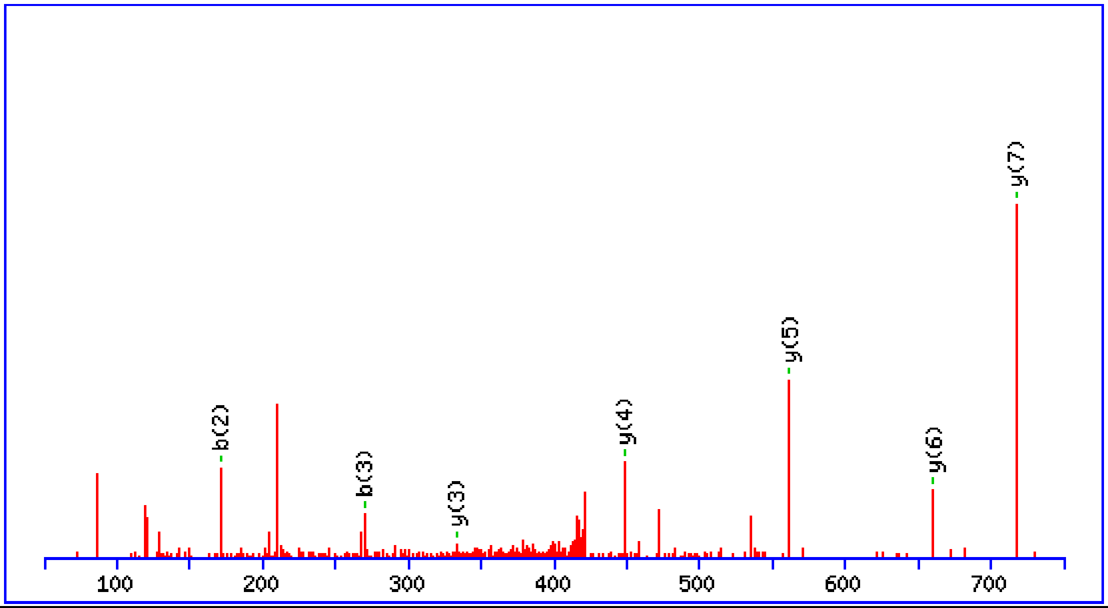


Monoisotopic mass of neutral peptide Mr(calc): 1505.7726
Fixed modifications: Carbamidomethyl (C)
Ions Score: 74 **Expect:** 3e-006
Matches (Bold Red): 31/129 fragment ions using 56 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**86.0964**	114.0913	57.5493					I							13
2	60.0444	**201.1234**	101.0653			**183.1128**	92.0600	S	1393.6958	697.3515	1376.6692	688.8383	1375.6852	688.3462	12
3	60.0444	**288.1554**	144.5813			**270.1448**	135.5761	S	**1306.6638**	653.8355	1289.6372	645.3222	1288.6532	644.8302	11
4	**86.0964**	**401.2395**	**201.1234**			**383.2289**	192.1181	L	**1219.6317**	610.3195	1202.6052	601.8062	1201.6212	601.3142	10
5	**86.0964**	514.3235	257.6654			**496.3130**	248.6601	L	**1106.5477**	553.7775	1089.5211	545.2642	**1088.5371**	544.7722	9
6	102.0550	643.3661	322.1867			625.3556	313.1814	E	**993.4636**	**497.2354**	976.4371	488.7222	**975.4530**	**488.2302**	8
7	102.0550	**772.4087**	386.7080			754.3981	377.7027	E	**864.4210**	432.7141	**847.3945**	424.2009	846.4104	423.7089	7
8	101.0709	900.4673	450.7373	883.4407	442.2240	**882.4567**	441.7320	Q	**735.3784**	368.1928	**718.3519**	359.6796			6
9	120.0808	1047.5357	524.2715	1030.5092	515.7582	1029.5251	515.2662	F	**607.3198**	304.1636	590.2933	295.6503			5
10	101.0709	1175.5943	588.3008	1158.5677	579.7875	1157.5837	579.2955	Q	**460.2514**	230.6293	**443.2249**	222.1161			4
11	101.0709	1303.6529	652.3301	1286.6263	643.8168	1285.6423	643.3248	Q	**332.1928**	166.6001	315.1663	158.0868			3
12	30.0338	1360.6743	680.8408	1343.6478	672.3275	1342.6638	671.8355	G	**204.1343**	102.5708	187.1077	94.0575			2
13	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **IGVLDEGK**
Found in **P46781**, P46781|RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3

Match to Query 156: 829.465812 from(415.740182,2+)

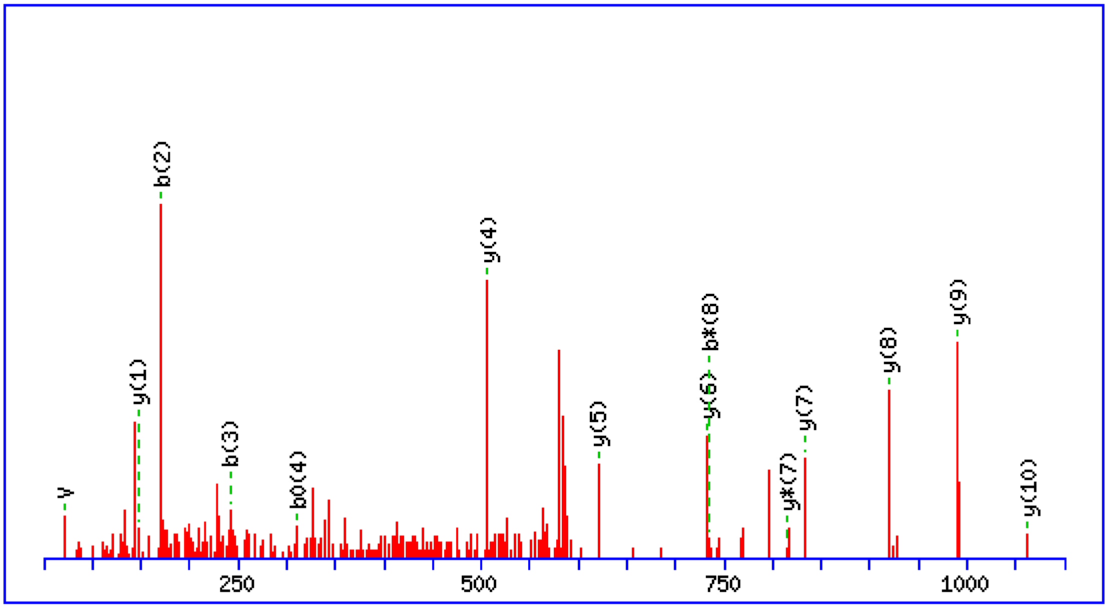


Monoisotopic mass of neutral peptide Mr(calc): 829.4545
Fixed modifications: Carbamidomethyl (C)
Ions Score: 47 **Expect:** 0.0019
Matches (Bold Red): 7/66 fragment ions using 19 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	86.0964	114.0913	57.5493			I							8
2	30.0338	**171.1128**	86.0600			G	**717.3777**	359.1925	700.3512	350.6792	699.3672	350.1872	7
3	72.0808	**270.1812**	135.5942			V	**660.3563**	330.6818	643.3297	322.1685	642.3457	321.6765	6
4	86.0964	383.2653	192.1363			L	**561.2879**	281.1476	544.2613	272.6343	543.2773	272.1423	5
5	88.0393	498.2922	249.6498	480.2817	240.6445	D	**448.2038**	224.6055	431.1773	216.0923	430.1932	215.6003	4
6	102.0550	627.3348	314.1710	609.3243	305.1658	E	**333.1769**	167.0921	316.1503	158.5788	315.1663	158.0868	3
7	30.0338	684.3563	342.6818	666.3457	333.6765	G	204.1343	102.5708	187.1077	94.0575			2
8	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **VAASVLNPYVK**
Found in **P48047**, P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1

Match to Query 148: 1159.580676 from(580.797614,2+)

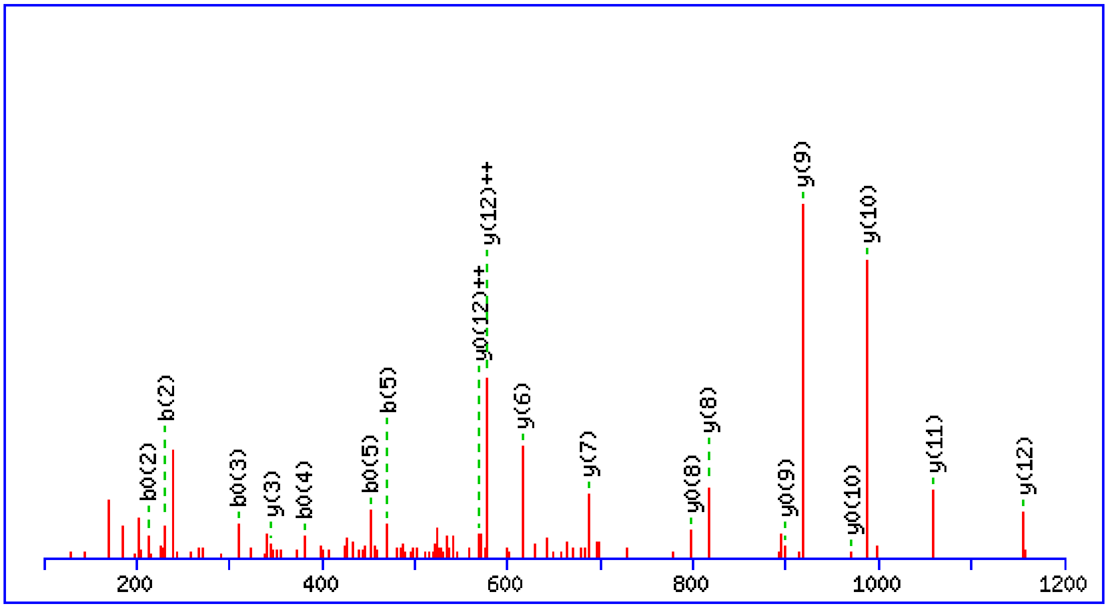


Monoisotopic mass of neutral peptide Mr(calc): 1159.6601
Fixed modifications: Carbamidomethyl (C)
Ions Score: 32 **Expect:** 0.046
Matches (Bold Red): 16/99 fragment ions using 49 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	**72.0808**	100.0757	50.5415					**V**							**11**
2	44.0495	**171.1128**	86.0600					**A**	**1061.5990**	531.3031	1044.5724	522.7898	1043.5884	522.2978	**10**
3	44.0495	**242.1499**	121.5786					**A**	**990.5619**	495.7846	973.5353	487.2713	972.5513	486.7793	**9**
4	60.0444	329.1819	165.0946			**311.1714**	156.0893	**S**	**919.5247**	460.2660	902.4982	451.7527	901.5142	451.2607	**8**
5	**72.0808**	428.2504	214.6288			410.2398	205.6235	**V**	**832.4927**	416.7500	**815.4662**	408.2367			**7**
6	86.0964	541.3344	271.1709			523.3239	262.1656	**L**	**733.4243**	367.2158	716.3978	358.7025			**6**
7	87.0553	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	**N**	**620.3402**	310.6738	603.3137	302.1605			**5**
8	70.0651	752.4301	376.7187	**735.4036**	368.2054	734.4195	367.7134	**P**	**506.2973**	253.6523	489.2708	245.1390			**4**
9	136.0757	915.4934	458.2504	898.4669	449.7371	897.4829	449.2451	**Y**	409.2445	205.1259	392.2180	196.6126			**3**
10	**72.0808**	1014.5619	507.7846	997.5353	499.2713	996.5513	498.7793	**V**	246.1812	123.5942	229.1547	115.0810			**2**
11	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **ETPAATEAPSSTPK**
Found in **P80723**, P80723|BASP_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2

Match to Query 578: 1385.629312 from(693.821932,2+)

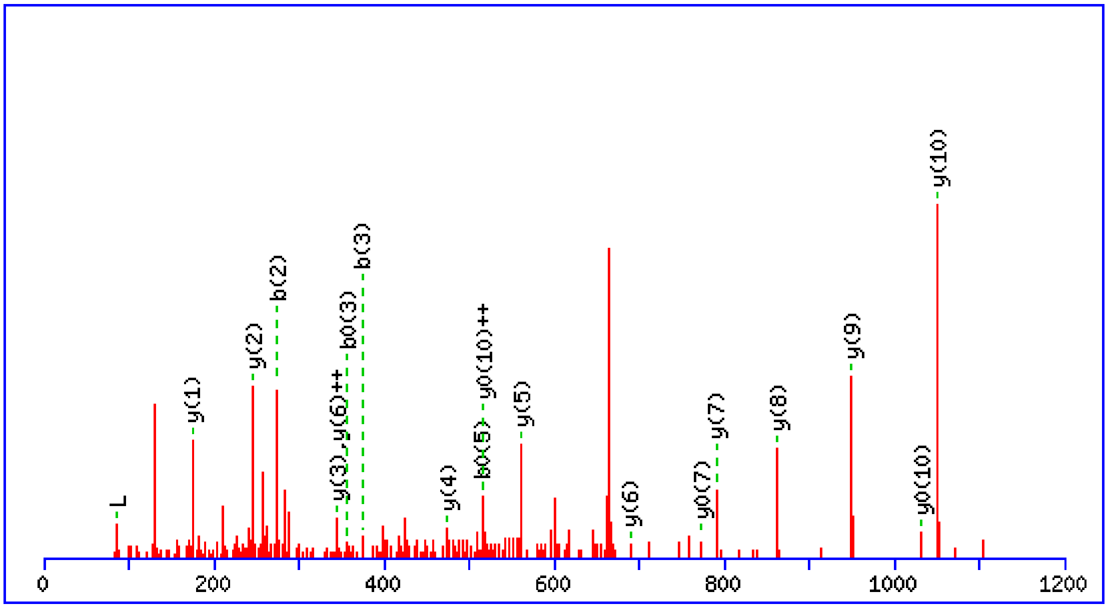


Monoisotopic mass of neutral peptide Mr(calc): 1385.6674
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.003
Matches (Bold Red): 19/140 fragment ions using 40 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286	112.0393	56.5233	**E**							**14**
2	74.0600	**231.0975**	116.0524	**213.0870**	107.0471	**T**	1257.6321	629.3197	1240.6056	620.8064	1239.6216	620.3144	**13**
3	70.0651	328.1503	164.5788	**310.1397**	155.5735	**P**	**1156.5844**	**578.7959**	1139.5579	570.2826	1138.5739	**569.7906**	**12**
4	44.0495	399.1874	200.0974	**381.1769**	191.0921	**A**	**1059.5317**	530.2695	1042.5051	521.7562	1041.5211	521.2642	**11**
5	44.0495	**470.2245**	235.6159	**452.2140**	226.6106	**A**	**988.4946**	494.7509	971.4680	486.2376	**970.4840**	485.7456	**10**
6	74.0600	571.2722	286.1397	553.2617	277.1345	**T**	**917.4575**	459.2324	900.4309	450.7191	**899.4469**	450.2271	**9**
7	102.0550	700.3148	350.6610	682.3042	341.6558	**E**	**816.4098**	408.7085	799.3832	400.1953	**798.3992**	399.7032	**8**
8	44.0495	771.3519	386.1796	753.3414	377.1743	**A**	**687.3672**	344.1872	670.3406	335.6740	669.3566	335.1819	**7**
9	70.0651	868.4047	434.7060	850.3941	425.7007	**P**	**616.3301**	308.6687	599.3035	300.1554	598.3195	299.6634	**6**
10	60.0444	955.4367	478.2220	937.4262	469.2167	**S**	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	**5**
11	60.0444	1042.4687	521.7380	1024.4582	512.7327	**S**	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	**4**
12	74.0600	1143.5164	572.2619	1125.5059	563.2566	**T**	**345.2132**	173.1103	328.1867	164.5970	327.2027	164.1050	**3**
13	70.0651	1240.5692	620.7882	1222.5586	611.7830	**P**	244.1656	122.5864	227.1390	114.0731			**2**
14	101.1073					**K**	147.1128	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **LCTSATESEVAR**
Found in **P31930**, P31930|QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3

Match to Query 370: 1322.685410 from(662.349981,2+)

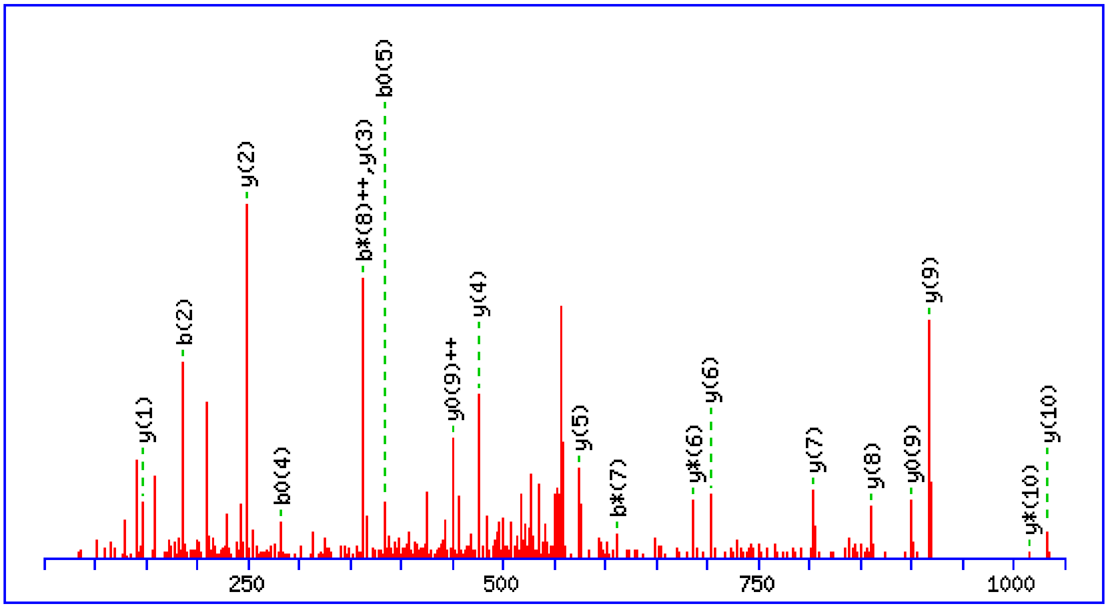


Monoisotopic mass of neutral peptide Mr(calc): 1322.6136
Fixed modifications: Carbamidomethyl (C)
Ions Score: 55 **Expect:** 0.00022
Matches (Bold Red): 19/112 fragment ions using 50 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			**L**							**12**
2	133.0430	**274.1220**	137.5646			**C**	1210.5368	605.7721	1193.5103	597.2588	1192.5263	596.7668	**11**
3	74.0600	**375.1697**	188.0885	**357.1591**	179.0832	**T**	**1050.5062**	525.7567	1033.4796	517.2435	**1032.4956**	**516.7515**	**10**
4	60.0444	462.2017	231.6045	444.1911	222.5992	**S**	**949.4585**	475.2329	932.4320	466.7196	931.4479	466.2276	**9**
5	44.0495	533.2388	267.1230	**515.2282**	258.1178	**A**	**862.4265**	431.7169	845.3999	423.2036	844.4159	422.7116	**8**
6	74.0600	634.2865	317.6469	616.2759	308.6416	**T**	**791.3894**	396.1983	774.3628	387.6850	**773.3788**	387.1930	**7**
7	102.0550	763.3291	382.1682	745.3185	373.1629	**E**	**690.3417**	**345.6745**	673.3151	337.1612	672.3311	336.6692	**6**
8	60.0444	850.3611	425.6842	832.3505	416.6789	**S**	**561.2991**	281.1532	544.2726	272.6399	543.2885	272.1479	**5**
9	102.0550	979.4037	490.2055	961.3931	481.2002	**E**	**474.2671**	237.6372	457.2405	229.1239	456.2565	228.6319	**4**
10	72.0808	1078.4721	539.7397	1060.4616	530.7344	**V**	**345.2245**	173.1159	328.1979	164.6026			**3**
11	44.0495	1149.5092	575.2583	1131.4987	566.2530	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
12	129.1135					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **ADGGTQVIDTK**
Found in **P09622**, P09622|DLDH_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=1

Match to Query 284: 1103.628828 from(552.821690,2+)

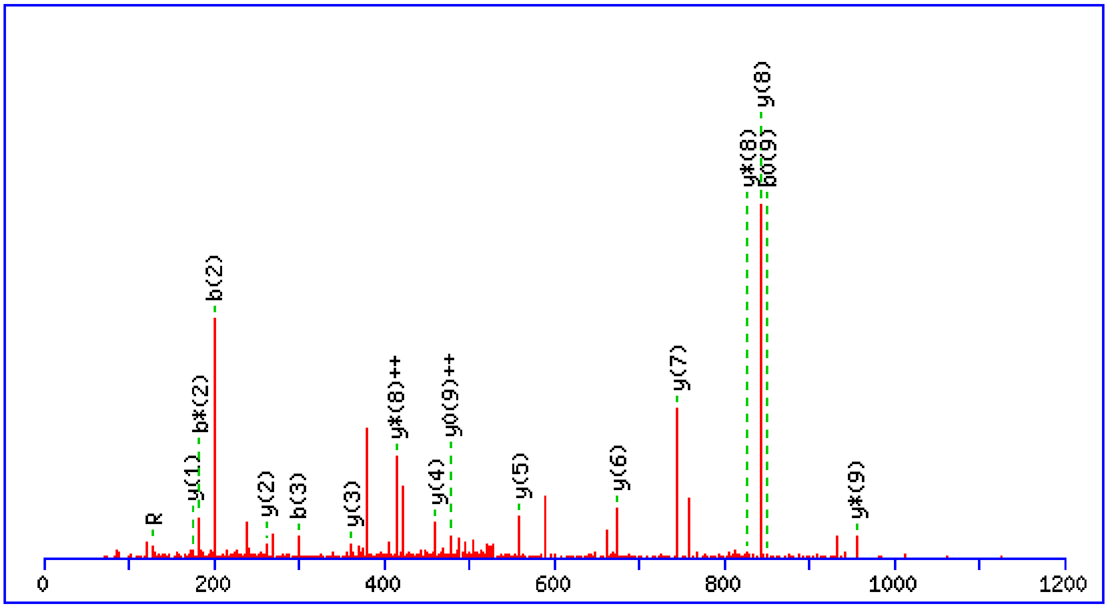


Monoisotopic mass of neutral peptide Mr(calc): 1103.5459
Fixed modifications: Carbamidomethyl (C)
Ions Score: 75 **Expect:** 2.5e-006
Matches (Bold Red): 19/117 fragment ions using 34 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							11
2	88.0393	**187.0713**	94.0393			169.0608	85.0340	D	**1033.5160**	517.2617	**1016.4895**	508.7484	1015.5055	508.2564	10
3	30.0338	244.0928	122.5500			226.0822	113.5448	G	**918.4891**	459.7482	901.4625	451.2349	**900.4785**	**450.7429**	9
4	30.0338	301.1143	151.0608			**283.1037**	142.0555	G	**861.4676**	431.2375	844.4411	422.7242	843.4571	422.2322	8
5	74.0600	402.1619	201.5846			**384.1514**	192.5793	T	**804.4462**	402.7267	787.4196	394.2134	786.4356	393.7214	7
6	101.0709	530.2205	265.6139	513.1940	257.1006	512.2100	256.6086	Q	**703.3985**	352.2029	**686.3719**	343.6896	685.3879	343.1976	6
7	72.0808	629.2889	315.1481	**612.2624**	306.6348	611.2784	306.1428	V	**575.3399**	288.1736	558.3134	279.6603	557.3293	279.1683	5
8	86.0964	742.3730	371.6901	725.3464	**363.1769**	724.3624	362.6849	I	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	4
9	88.0393	857.3999	429.2036	840.3734	420.6903	839.3894	420.1983	D	**363.1874**	182.0974	346.1609	173.5841	345.1769	173.0921	3
10	74.0600	958.4476	479.7274	941.4211	471.2142	940.4371	470.7222	T	**248.1605**	124.5839	231.1339	116.0706	230.1499	115.5786	2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **AQVADVVVSR**
Found in **P49327**, P49327|FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=2

Match to Query 353: 1042.580844 from(522.297698,2+)

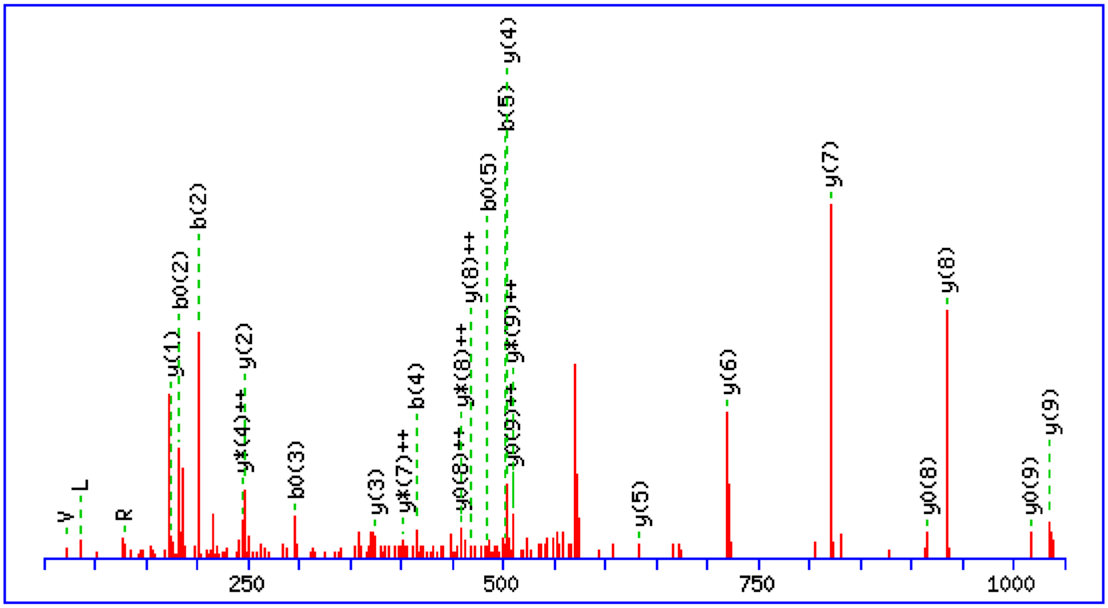


Monoisotopic mass of neutral peptide Mr(calc): 1042.5771
Fixed modifications: Carbamidomethyl (C)
Ions Score: 32 **Expect:** 0.047
Matches (Bold Red): 17/106 fragment ions using 50 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	44.0495	72.0444	36.5258					A							10
2	101.0709	**200.1030**	100.5551	**183.0764**	92.0418			Q	972.5473	486.7773	**955.5207**	478.2640	954.5367	**477.7720**	9
3	72.0808	**299.1714**	150.0893	282.1448	141.5761			V	**844.4887**	422.7480	**827.4621**	**414.2347**	826.4781	413.7427	8
4	44.0495	370.2085	185.6079	353.1819	177.0946			A	**745.4203**	373.2138	728.3937	364.7005	727.4097	364.2085	7
5	88.0393	485.2354	243.1214	468.2089	234.6081	467.2249	234.1161	D	**674.3832**	337.6952	657.3566	329.1819	656.3726	328.6899	6
6	72.0808	584.3039	292.6556	567.2773	284.1423	566.2933	283.6503	V	**559.3562**	280.1817	542.3297	271.6685	541.3457	271.1765	5
7	72.0808	683.3723	342.1898	666.3457	333.6765	665.3617	333.1845	V	**460.2878**	230.6475	443.2613	222.1343	442.2772	221.6423	4
8	72.0808	782.4407	391.7240	765.4141	383.2107	764.4301	382.7187	V	**361.2194**	181.1133	344.1928	172.6001	343.2088	172.1081	3
9	60.0444	869.4727	435.2400	852.4462	426.7267	**851.4621**	426.2347	S	**262.1510**	131.5791	245.1244	123.0659	244.1404	122.5738	2
10	**129.1135**							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **VTLTSEEEAR**
Found in **P00338**, P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2

Match to Query 252: 1133.591696 from(567.803124,2+)

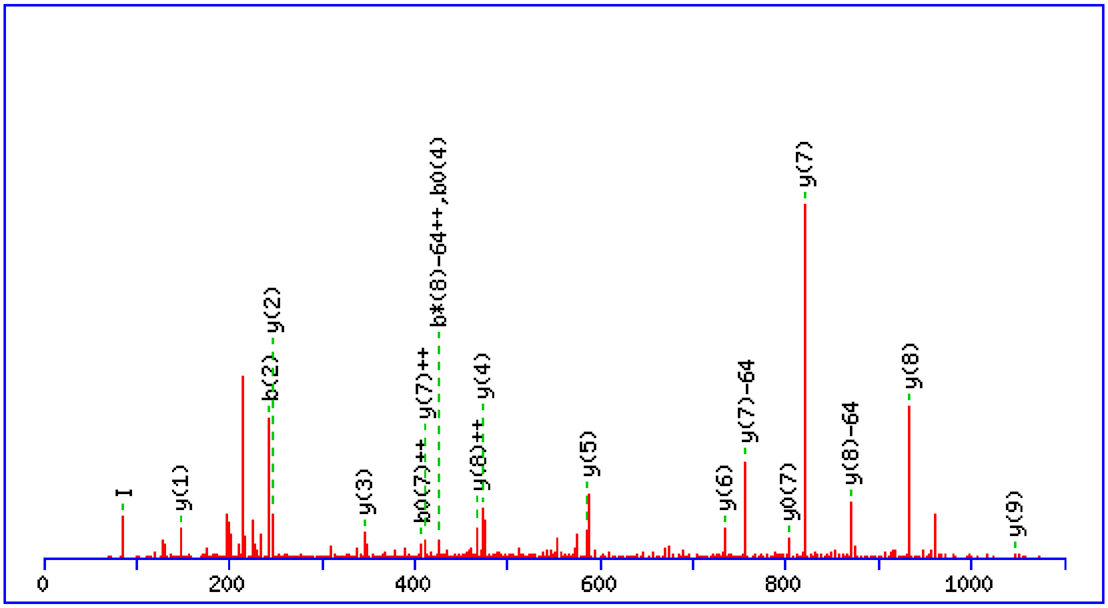


Monoisotopic mass of neutral peptide Mr(calc): 1133.5564
Fixed modifications: Carbamidomethyl (C)
Ions Score: 34 **Expect:** 0.029
Matches (Bold Red): 27/94 fragment ions using 91 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**72.0808**	100.0757	50.5415			V							10
2	74.0600	**201.1234**	101.0653	**183.1128**	92.0600	T	**1035.4953**	518.2513	1018.4687	**509.7380**	**1017.4847**	**509.2460**	9
3	**86.0964**	314.2074	157.6074	**296.1969**	148.6021	L	**934.4476**	**467.7274**	917.4211	**459.2142**	**916.4371**	**458.7222**	8
4	74.0600	**415.2551**	208.1312	397.2445	199.1259	T	**821.3636**	411.1854	804.3370	**402.6721**	803.3530	402.1801	7
5	60.0444	**502.2871**	251.6472	**484.2766**	242.6419	S	**720.3159**	360.6616	703.2893	352.1483	702.3053	351.6563	6
6	102.0550	631.3297	316.1685	613.3192	307.1632	E	**633.2838**	317.1456	616.2573	308.6323	615.2733	308.1403	5
7	102.0550	760.3723	380.6898	742.3618	371.6845	E	**504.2413**	252.6243	487.2147	**244.1110**	486.2307	243.6190	4
8	102.0550	889.4149	445.2111	871.4044	436.2058	E	**375.1987**	188.1030	358.1721	179.5897	357.1881	179.0977	3
9	44.0495	960.4520	480.7297	942.4415	471.7244	A	**246.1561**	123.5817	229.1295	115.0684			2
10	**129.1135**					R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **ELISMIQVVK**
Found in **P08575**, P08575|CD45_HUMAN Leukocyte common antigen OS=Homo sapiens GN=PTPRC PE=1 SV=2

Match to Query 450: 1174.650376 from(588.332464,2+)

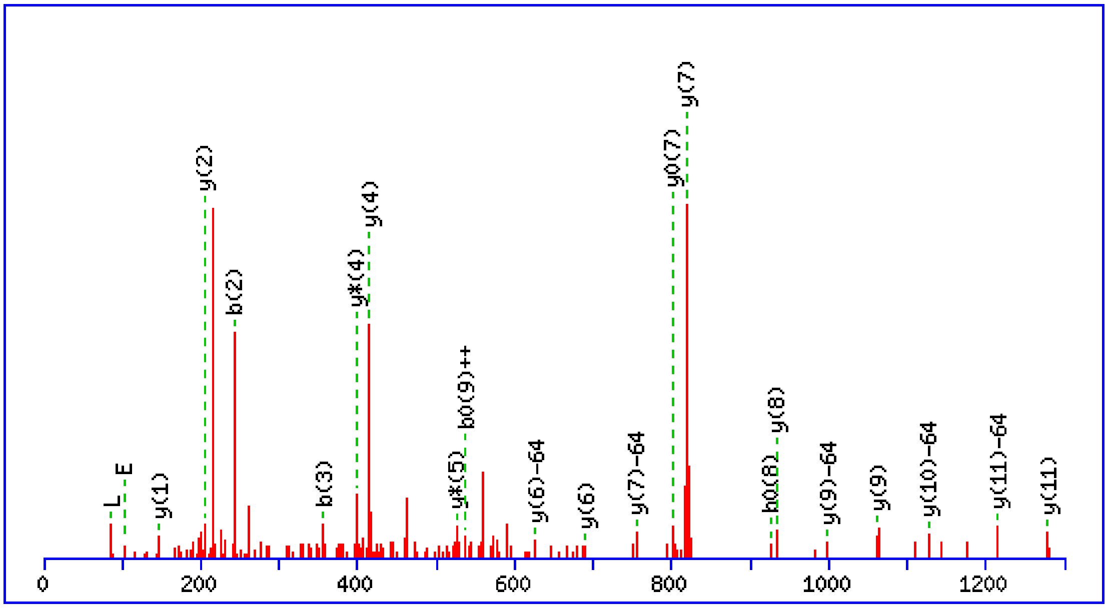


Monoisotopic mass of neutral peptide Mr(calc): 1174.6631
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 57 **Expect:** 0.00015
Matches (Bold Red): 21/143 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	130.0499	65.5286			112.0393	56.5233	**E**							**10**
2	**86.0964**	**243.1339**	122.0706			225.1234	113.0653	**L**	**1046.6278**	523.8176	1029.6013	515.3043	1028.6173	514.8123	**9**
3	**86.0964**	356.2180	178.6126			338.2074	169.6074	**I**	**933.5438**	**467.2755**	916.5172	458.7622	915.5332	458.2702	**8**
4	60.0444	443.2500	222.1287			**425.2395**	213.1234	**S**	**820.4597**	**410.7335**	803.4332	402.2202	**802.4491**	401.7282	**7**
5	120.0478	590.2854	295.6464			572.2749	286.6411	**M**	**733.4277**	367.2175	716.4011	358.7042			**6**
6	**86.0964**	703.3695	352.1884			685.3589	343.1831	**I**	**586.3923**	293.6998	569.3657	285.1865			**5**
7	101.0709	831.4281	416.2177	814.4015	407.7044	813.4175	**407.2124**	**Q**	**473.3082**	237.1577	456.2817	228.6445			**4**
8	72.0808	930.4965	465.7519	913.4699	457.2386	912.4859	456.7466	**V**	**345.2496**	173.1285	328.2231	164.6152			**3**
9	72.0808	1029.5649	515.2861	1012.5383	506.7728	1011.5543	506.2808	**V**	**246.1812**	123.5942	229.1547	115.0810			**2**
10	101.1073							**K**	**147.1128**	74.0600	130.0863	65.5468			**1**

MS/MS Fragmentation of **EILSEENEMQPNGK**
Found in **O60488**, O60488|ACSL4_HUMAN Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2

Match to Query 426: 1632.804198 from(817.409375,2+)

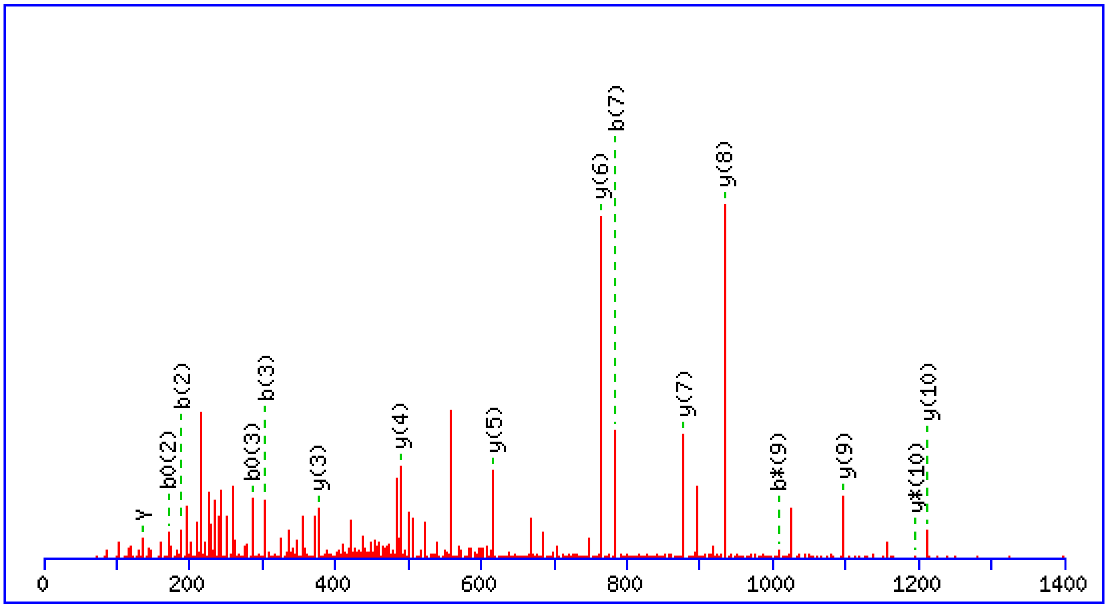


Monoisotopic mass of neutral peptide Mr(calc): 1632.7301
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M9 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.026
Matches (Bold Red): 26/223 fragment ions using 53 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**102.0550**	130.0499	65.5286			112.0393	56.5233	E							14
2	**86.0964**	**243.1339**	122.0706			225.1234	113.0653	I	1440.6965	720.8519	1423.6700	712.3386	1422.6860	711.8466	13
3	**86.0964**	**356.2180**	178.6126			338.2074	169.6074	L	1327.6125	664.3099	1310.5859	655.7966	1309.6019	655.3046	12
4	60.0444	443.2500	222.1287			425.2395	213.1234	S	**1214.5284**	607.7678	1197.5018	599.2546	1196.5178	598.7626	11
5	**102.0550**	572.2926	286.6499			554.2821	277.6447	E	**1127.4964**	564.2518	1110.4698	555.7385	1109.4858	555.2465	10
6	**102.0550**	701.3352	351.1712			683.3246	342.1660	E	**998.4538**	499.7305	981.4272	491.2172	980.4432	490.7252	9
7	87.0553	815.3781	408.1927	798.3516	399.6794	797.3676	399.1874	N	869.4112	435.2092	852.3846	426.6960	851.4006	426.2039	8
8	**102.0550**	944.4207	472.7140	927.3942	464.2007	**926.4102**	463.7087	E	**755.3682**	378.1878	738.3417	369.6745	737.3577	369.1825	7
9	56.0495	1027.4579	514.2326	1010.4313	505.7193	1009.4473	505.2273	M	**626.3257**	313.6665	609.2991	305.1532			6
10	101.0709	1155.5164	578.2619	1138.4899	569.7486	1137.5059	569.2566	Q	543.2885	272.1479	**526.2620**	263.6346			5
11	70.0651	1252.5692	626.7882	1235.5426	618.2750	1234.5586	617.7830	P	**415.2300**	208.1186	**398.2034**	199.6053			4
12	87.0553	1366.6121	683.8097	1349.5856	675.2964	1348.6016	674.8044	N	318.1772	159.5922	301.1506	151.0790			3
13	30.0338	1423.6336	712.3204	1406.6070	703.8072	1405.6230	703.3151	G	**204.1343**	102.5708	187.1077	94.0575			2
14	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **STDYGIFQINSR**
Found in **P61626**, P61626|LYSC_HUMAN Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1

Match to Query 563: 1399.674328 from(700.844440,2+)

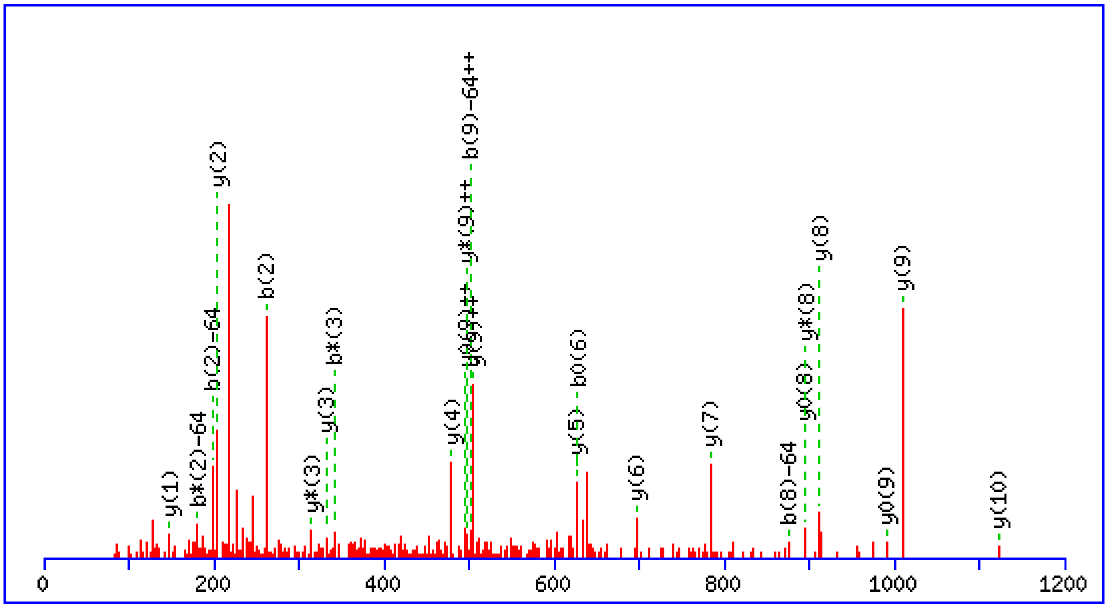


Monoisotopic mass of neutral peptide Mr(calc): 1399.6732
Fixed modifications: Carbamidomethyl (C)
Ions Score: 51 **Expect:** 0.00053
Matches (Bold Red): 16/128 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	60.0444	88.0393	44.5233			70.0287	35.5180	S							12
2	74.0600	**189.0870**	95.0471			**171.0764**	86.0418	T	1313.6484	657.3279	1296.6219	648.8146	1295.6379	648.3226	11
3	88.0393	**304.1139**	152.5606			**286.1034**	143.5553	D	**1212.6008**	606.8040	**1195.5742**	598.2907	1194.5902	597.7987	10
4	**136.0757**	467.1773	234.0923			449.1667	225.0870	Y	**1097.5738**	549.2905	1080.5473	540.7773	1079.5633	540.2853	9
5	30.0338	524.1987	262.6030			506.1882	253.5977	G	**934.5105**	467.7589	917.4839	459.2456	916.4999	458.7536	8
6	86.0964	637.2828	319.1450			619.2722	310.1397	I	**877.4890**	439.2482	860.4625	430.7349	859.4785	430.2429	7
7	120.0808	**784.3512**	392.6792			766.3406	383.6740	F	**764.4050**	382.7061	747.3784	374.1928	746.3944	373.7008	6
8	101.0709	912.4098	456.7085	895.3832	448.1953	894.3992	447.7032	Q	**617.3365**	309.1719	600.3100	300.6586	599.3260	300.1666	5
9	86.0964	1025.4938	513.2506	**1008.4673**	504.7373	1007.4833	504.2453	I	**489.2780**	245.1426	472.2514	236.6293	471.2674	236.1373	4
10	87.0553	1139.5368	570.2720	1122.5102	561.7587	1121.5262	561.2667	N	**376.1939**	188.6006	359.1674	180.0873	358.1833	179.5953	3
11	60.0444	1226.5688	613.7880	1209.5422	605.2748	1208.5582	604.7828	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12	129.1135							R	175.1190	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **MNPQSAFFQGK**
Found in **P22307**, P22307|NLTP_HUMAN Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2

Match to Query 161: 1269.497410 from(635.755981,2+)

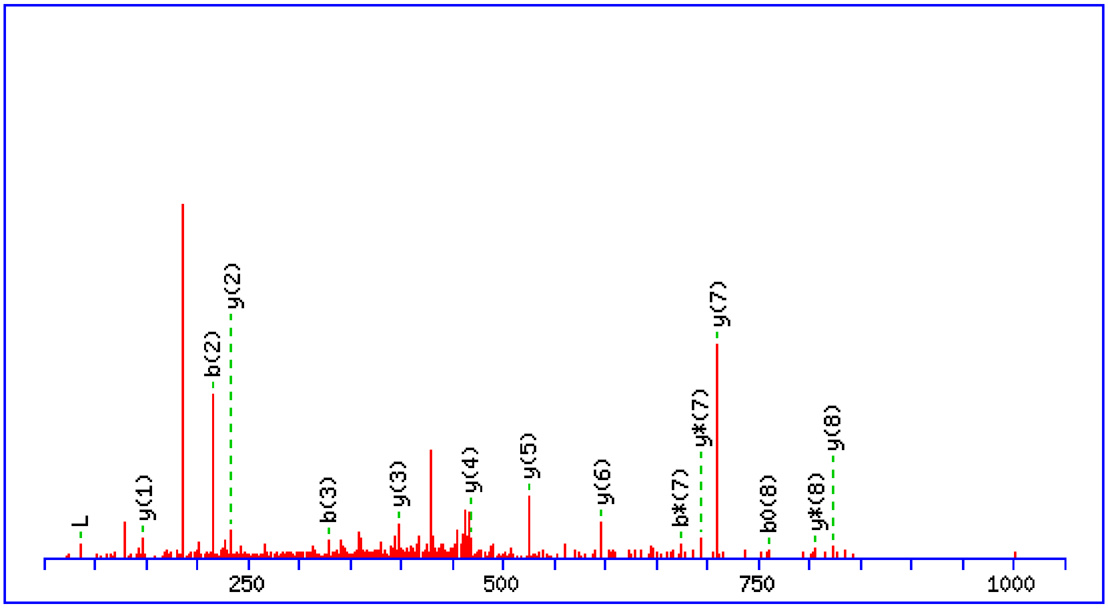


Monoisotopic mass of neutral peptide Mr(calc): 1269.5812
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 58 **Expect:** 0.00011
Matches (Bold Red): 24/160 fragment ions using 51 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	56.0495	84.0444	42.5258					M							11
2	87.0553	**198.0873**	99.5473	**181.0608**	91.0340			N	**1123.5531**	562.2802	1106.5265	553.7669	1105.5425	553.2749	10
3	70.0651	295.1401	148.0737	278.1135	139.5604			P	**1009.5102**	**505.2587**	992.4836	**496.7454**	**991.4996**	**496.2534**	9
4	101.0709	423.1987	212.1030	406.1721	203.5897			Q	**912.4574**	456.7323	**895.4308**	448.2191	**894.4468**	447.7271	8
5	60.0444	510.2307	255.6190	493.2041	247.1057	492.2201	246.6137	S	**784.3988**	392.7030	767.3723	384.1898	766.3883	383.6978	7
6	44.0495	581.2678	291.1375	564.2413	282.6243	563.2572	282.1323	A	**697.3668**	349.1870	680.3402	340.6738			6
7	120.0808	728.3362	364.6717	711.3097	356.1585	710.3257	355.6665	F	**626.3297**	313.6685	609.3031	305.1552			5
8	120.0808	**875.4046**	438.2060	858.3781	429.6927	857.3941	429.2007	F	**479.2613**	240.1343	462.2347	231.6210			4
9	101.0709	1003.4632	**502.2352**	986.4367	493.7220	985.4526	493.2300	Q	**332.1928**	166.6001	**315.1663**	158.0868			3
10	30.0338	1060.4847	530.7460	1043.4581	522.2327	1042.4741	521.7407	G	**204.1343**	102.5708	187.1077	94.0575			2
11	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **TLNAGAYSK**
Found in **P50897**, P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1

Match to Query 316: 923.460238 from(462.737395,2+)

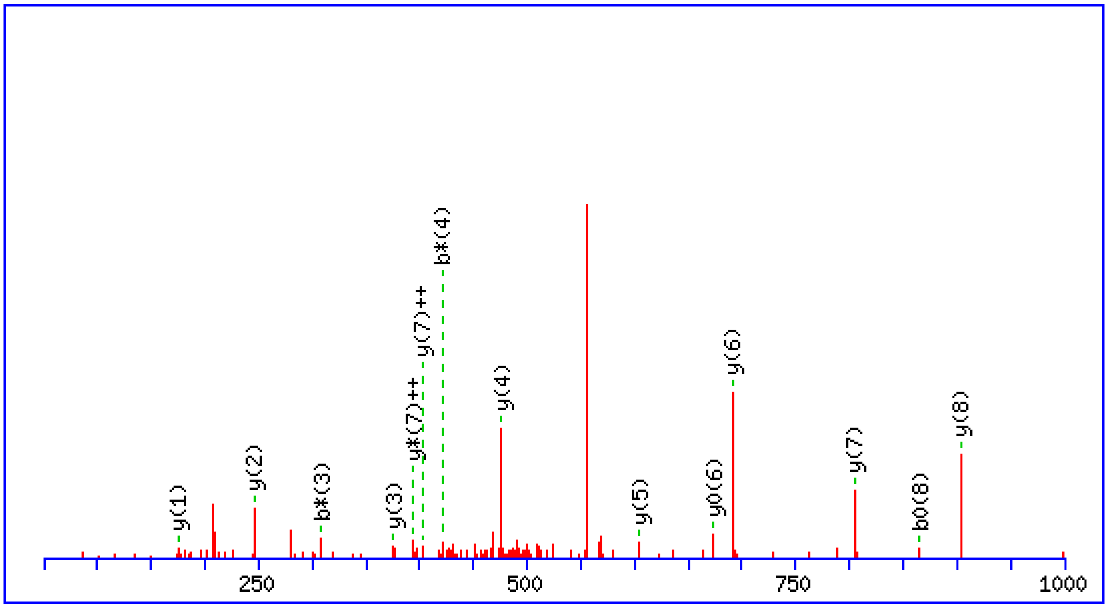


Monoisotopic mass of neutral peptide Mr(calc): 923.4712
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 **Expect:** 0.0061
Matches (Bold Red): 15/99 fragment ions using 35 most intense peaks

#	Immon.	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	74.0600	102.0550	51.5311			84.0444	42.5258	T							9
2	**86.0964**	**215.1390**	108.0731			197.1285	99.0679	L	**823.4308**	412.2191	**806.4043**	403.7058	805.4203	403.2138	8
3	87.0553	**329.1819**	165.0946	312.1554	156.5813	311.1714	156.0893	N	**710.3468**	355.6770	**693.3202**	347.1638	692.3362	346.6717	7
4	44.0495	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	A	**596.3039**	298.6556	579.2773	290.1423	578.2933	289.6503	6
5	30.0338	457.2405	229.1239	440.2140	220.6106	439.2300	220.1186	G	**525.2667**	263.1370	508.2402	254.6237	507.2562	254.1317	5
6	44.0495	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	A	**468.2453**	234.6263	451.2187	226.1130	450.2347	225.6210	4
7	136.0757	691.3410	346.1741	**674.3144**	337.6608	673.3304	337.1688	Y	**397.2082**	199.1077	380.1816	190.5944	379.1976	190.1024	3
8	60.0444	778.3730	389.6901	761.3464	381.1769	**760.3624**	380.6849	S	**234.1448**	117.5761	217.1183	109.0628	216.1343	108.5708	2
9	101.1073							K	**147.1128**	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **QPVLSQTEAR**
Found in **P28070**, P28070|PSB4_HUMAN Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4

Match to Query 251: 1127.518390 from(564.766471,2+)

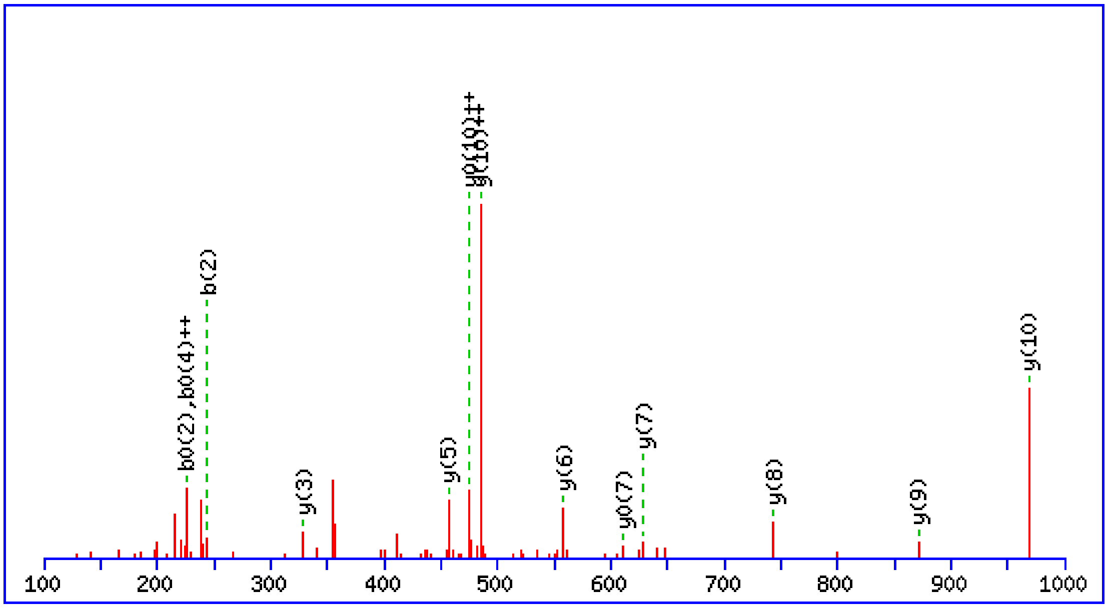


Monoisotopic mass of neutral peptide Mr(calc): 1127.5935
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 **Expect:** 6.2e-005
Matches (Bold Red): 14/106 fragment ions using 28 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	101.0709	129.0659	65.0366	112.0393	56.5233			Q							10
2	70.0651	226.1186	113.5629	209.0921	105.0497			P	1000.5422	500.7747	983.5156	492.2615	982.5316	491.7694	9
3	72.0808	325.1870	163.0972	**308.1605**	154.5839			V	**903.4894**	452.2483	886.4629	443.7351	885.4789	443.2431	8
4	86.0964	438.2711	219.6392	**421.2445**	211.1259			L	**804.4210**	**402.7141**	787.3945	**394.2009**	786.4104	393.7089	7
5	60.0444	525.3031	263.1552	508.2766	254.6419	507.2926	254.1499	S	**691.3369**	346.1721	674.3104	337.6588	**673.3264**	337.1668	6
6	101.0709	653.3617	327.1845	636.3352	318.6712	635.3511	318.1792	Q	**604.3049**	302.6561	587.2784	294.1428	586.2944	293.6508	5
7	74.0600	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	T	**476.2463**	238.6268	459.2198	230.1135	458.2358	229.6215	4
8	102.0550	883.4520	442.2296	866.4254	433.7164	**865.4414**	433.2243	E	**375.1987**	188.1030	358.1721	179.5897	357.1881	179.0977	3
9	44.0495	954.4891	477.7482	937.4625	469.2349	936.4785	468.7429	A	**246.1561**	123.5817	229.1295	115.0684			2
10	129.1135							R	**175.1190**	88.0631	158.0924	79.5498			1

MS/MS Fragmentation of **NEPQNATGAPGR**
Found in **P51148**, P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2

Match to Query 268: 1210.501952 from(606.258252,2+)

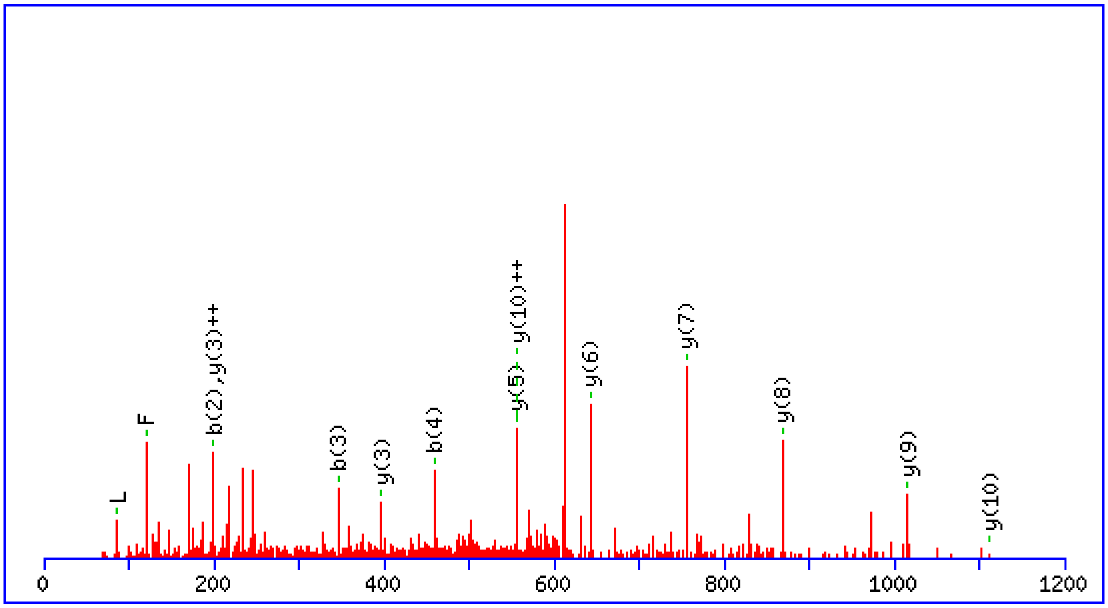


Monoisotopic mass of neutral peptide Mr(calc): 1210.5690
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.008
Matches (Bold Red): 13/132 fragment ions using 22 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	87.0553	115.0502	58.0287	98.0237	49.5155			**N**							**12**
2	102.0550	**244.0928**	122.5500	227.0662	114.0368	**226.0822**	113.5448	**E**	1097.5334	549.2703	1080.5069	540.7571	1079.5228	540.2651	**11**
3	70.0651	341.1456	171.0764	324.1190	162.5631	323.1350	162.0711	**P**	**968.4908**	**484.7490**	951.4643	476.2358	950.4803	**475.7438**	**10**
4	101.0709	469.2041	235.1057	452.1776	226.5924	451.1936	**226.1004**	**Q**	**871.4381**	436.2227	854.4115	427.7094	853.4275	427.2174	**9**
5	87.0553	583.2471	292.1272	566.2205	283.6139	565.2365	283.1219	**N**	**743.3795**	372.1934	726.3529	363.6801	725.3689	363.1881	**8**
6	44.0495	654.2842	327.6457	637.2576	319.1325	636.2736	318.6404	**A**	**629.3366**	315.1719	612.3100	306.6586	**611.3260**	306.1666	**7**
7	74.0600	755.3319	378.1696	738.3053	369.6563	737.3213	369.1643	**T**	**558.2994**	279.6534	541.2729	271.1401	540.2889	270.6481	**6**
8	30.0338	812.3533	406.6803	795.3268	398.1670	794.3428	397.6750	**G**	**457.2518**	229.1295	440.2252	220.6162			**5**
9	44.0495	883.3904	442.1989	866.3639	433.6856	865.3799	433.1936	**A**	400.2303	200.6188	383.2037	192.1055			**4**
10	70.0651	980.4432	490.7252	963.4167	482.2120	962.4326	481.7200	**P**	**329.1932**	165.1002	312.1666	156.5870			**3**
11	30.0338	1037.4647	519.2360	1020.4381	510.7227	1019.4541	510.2307	**G**	232.1404	116.5738	215.1139	108.0606			**2**
12	129.1135							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **TPFLLSGTSYK**
Found in **P55084**, P55084|ECHB_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3

Match to Query 330: 1212.721594 from(607.368073,2+)

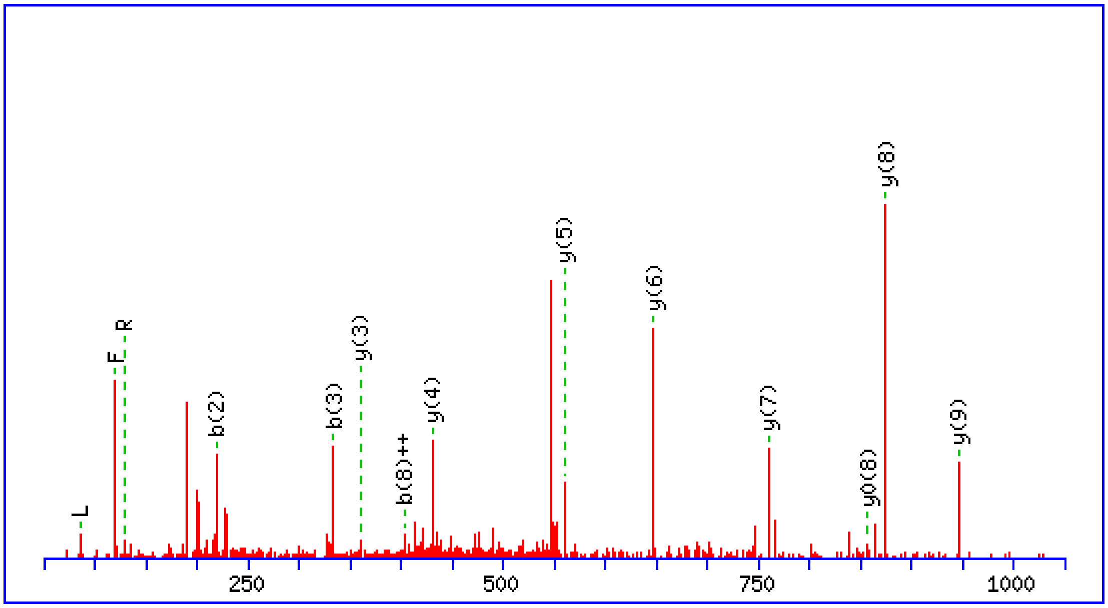


Monoisotopic mass of neutral peptide Mr(calc): 1212.6390
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00049
Matches (Bold Red): 15/107 fragment ions using 31 most intense peaks

#	Immon.	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	74.0600	102.0550	51.5311	84.0444	42.5258	T							11
2	70.0651	**199.1077**	100.0575	181.0972	91.0522	P	**1112.5986**	**556.8030**	1095.5721	548.2897	1094.5881	547.7977	10
3	**120.0808**	**346.1761**	173.5917	328.1656	164.5864	F	**1015.5459**	508.2766	998.5193	499.7633	997.5353	499.2713	9
4	**86.0964**	**459.2602**	230.1337	441.2496	221.1285	L	**868.4775**	434.7424	851.4509	426.2291	850.4669	425.7371	8
5	**86.0964**	572.3443	286.6758	554.3337	277.6705	L	**755.3934**	378.2003	738.3668	369.6871	737.3828	369.1951	7
6	60.0444	659.3763	330.1918	641.3657	321.1865	S	**642.3093**	321.6583	625.2828	313.1450	624.2988	312.6530	6
7	30.0338	716.3978	358.7025	698.3872	349.6972	G	**555.2773**	278.1423	538.2508	269.6290	537.2667	269.1370	5
8	74.0600	817.4454	409.2264	799.4349	400.2211	T	498.2558	249.6316	481.2293	241.1183	480.2453	240.6263	4
9	60.0444	904.4775	452.7424	886.4669	443.7371	S	**397.2082**	**199.1077**	380.1816	190.5944	379.1976	190.1024	3
10	136.0757	1067.5408	534.2740	1049.5302	525.2688	Y	310.1761	155.5917	293.1496	147.0784			2
11	101.1073					K	147.1128	74.0600	130.0863	65.5468			1

MS/MS Fragmentation of **FADLSEAANR**
Found in **P08670**, P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Match to Query 360: 1092.507450 from(547.261001,2+)

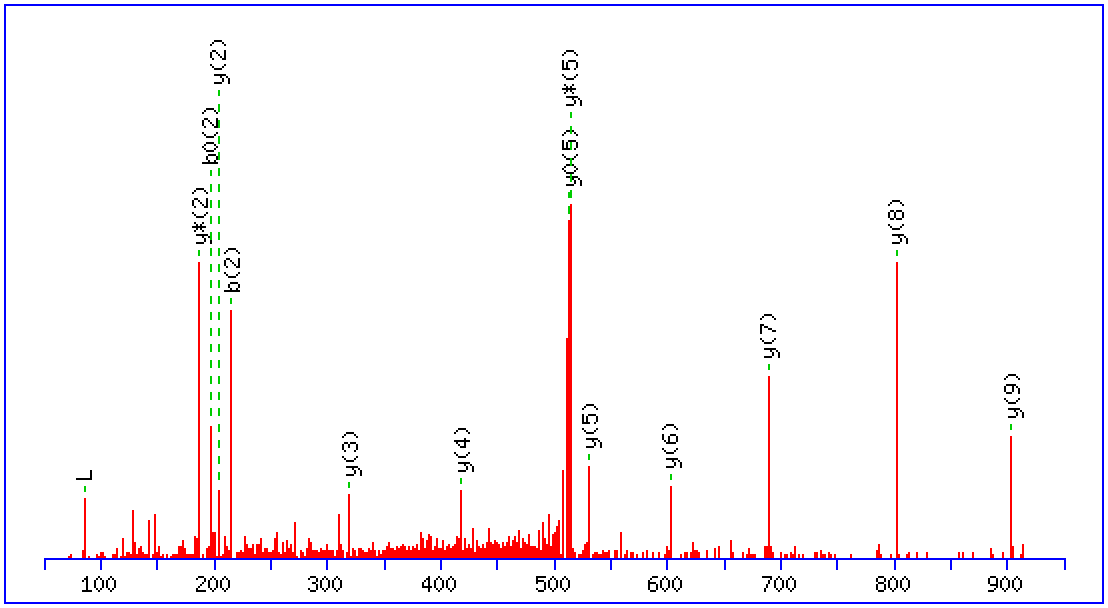


Monoisotopic mass of neutral peptide Mr(calc): 1092.5200
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 **Expect:** 0.0081
Matches (Bold Red): 14/90 fragment ions using 40 most intense peaks

#	Immon.	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**120.0808**	148.0757	74.5415					**F**							**10**
2	44.0495	**219.1128**	110.0600					**A**	**946.4588**	473.7331	929.4323	465.2198	928.4483	464.7278	**9**
3	88.0393	**334.1397**	167.5735			316.1292	158.5682	**D**	**875.4217**	438.2145	858.3952	429.7012	**857.4112**	429.2092	**8**
4	**86.0964**	447.2238	224.1155			429.2132	215.1103	**L**	**760.3948**	380.7010	743.3682	372.1878	742.3842	371.6958	**7**
5	60.0444	534.2558	267.6316			516.2453	258.6263	**S**	**647.3107**	324.1590	630.2842	315.6457	629.3002	315.1537	**6**
6	102.0550	663.2984	332.1529			645.2879	323.1476	**E**	**560.2787**	280.6430	543.2522	272.1297	542.2681	271.6377	**5**
7	44.0495	734.3355	367.6714			716.3250	358.6661	**A**	**431.2361**	216.1217	414.2096	207.6084			**4**
8	44.0495	805.3727	**403.1900**			787.3621	394.1847	**A**	**360.1990**	180.6031	343.1724	172.0899			**3**
9	87.0553	919.4156	460.2114	902.3890	451.6982	901.4050	451.2061	**N**	289.1619	145.0846	272.1353	136.5713			**2**
10	**129.1135**							**R**	175.1190	88.0631	158.0924	79.5498			**1**

MS/MS Fragmentation of **LTLSALVDGK**
Found in **P45880**, P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2

Match to Query 201: 1015.633952 from(508.824252,2+)



Monoisotopic mass of neutral peptide Mr(calc): 1015.5914
Fixed modifications: Carbamidomethyl (C)
Ions Score: 62 **Expect:** 5.3e-005
Matches (Bold Red): 16/94 fragment ions using 17 most intense peaks

#	Immon.	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**86.0964**	114.0913	57.5493			**L**							**10**
2	74.0600	**215.1390**	108.0731	**197.1285**	99.0679	**T**	**903.5146**	452.2609	886.4880	443.7477	885.5040	443.2556	**9**
3	**86.0964**	328.2231	164.6152	310.2125	155.6099	**L**	**802.4669**	401.7371	785.4403	393.2238	784.4563	392.7318	**8**
4	60.0444	415.2551	208.1312	397.2445	199.1259	**S**	**689.3828**	345.1951	672.3563	336.6818	671.3723	336.1898	**7**
5	44.0495	486.2922	243.6498	468.2817	234.6445	**A**	**602.3508**	301.6790	585.3243	293.1658	584.3402	292.6738	**6**
6	**86.0964**	599.3763	300.1918	581.3657	291.1865	**L**	**531.3137**	266.1605	**514.2871**	257.6472	**513.3031**	257.1552	**5**
7	72.0808	698.4447	349.7260	680.4341	340.7207	**V**	**418.2296**	209.6185	401.2031	201.1052	400.2191	200.6132	**4**
8	88.0393	813.4716	407.2395	795.4611	398.2342	**D**	**319.1612**	160.0842	302.1347	151.5710	301.1506	151.0790	**3**
9	30.0338	870.4931	435.7502	852.4825	426.7449	**G**	**204.1343**	102.5708	**187.1077**	94.0575			**2**
10	101.1073					**K**	147.1128	74.0600	130.0863	65.5468			**1**